Proceedings Vol.Ⅲ
ISSN 2672-0205

2026
社團法人 韓國畜産學會 國際學術發表會
2026 Annual International Conference of KSAST

“축산 70년의 비젼과 도약: 인간, 동물, 환경이 함께 걷는 지속가능한 축산 혁신”

Vision and Leap Forward of Livestock's 70 Years: Sustainable Innovation for Humans, Animals, and the Environment

제주국제컨벤션 센터 (ICC JEJU)
2026년 7월 8일(수)~10일(금)

- **주최/주관 :** (사)한국축산학회,(사)한국가금학회, 농림축산식품부,국립축산과학원, 축산관련단체 연합회
- **후원기관 :** 한국과학기술단체총연합회, 제주특별자치도
- **후원업체 :** 대한한돈협회, (사)전국한우협회, 한우자조금관리위원회, 서울우유협동조합, (주)우성사료, (주)이지홀딩스, (주)카길애그리퓨리나, BASF, 노보네시스 코리아, (주)모닝바이오, 우유자조금관리위원회, 제일사료 축산기술연구소, (주)팜스코, De Heus Korea, 농협경제지주, 낙농진흥회, 농축산용미생물산업육성지원센터, (주)다운, (주)선진, (주)솔로몬, 우리와(주), 유진바이오, 축산환경관리원, (주)파이지노믹스, (사)한국단미사료협회, (주)휘드베스트, 김유용 교수, 체리부로, (주)ACC, NH순한한우조합공동사업법인, 다산데이타, (주)마크로젠, (주)미래생명자원, 성우라이프사이언스, 에스엠티정보기술(주), (주)인프로, 정농바이오, (주)진바이오텍, 포스코리아, 한양사료주식회사, 한국반추미생물연구회, 달사랑 연구회, 고려비엔피, 나우피드, 대한사료(주), (주)대호, (주)도드람양돈서비스, (주)린도, 마리동물의학연구소, (주)솔톤바이오켐, 임실치즈&식품연구소, (주)티엔티리써치, 한국종축개량협회, 한국유가공협회, 전국낙농관련조합장협의회, 농심, 매일유업

(사) 한국축산학회
Korean Society of Animal Science and Technology

목 차

구두 발표

포스터 발표

학술대회 전체일정표

◆ **제주국제컨벤션 센터 (ICC JEJU)**

2026년 7월 8일 (수)

장소 시간	제주국제컨벤션 센터 (ICC JEJU)	
11:00~	등록 및 접수(3층 로비)	
12:00~	포스터 부착 (3층 로비) * 주의: 포스터 부착 시간 엄수 (7/8, 12:00~17:00)	
	탐라홀 A (5층)	
13:00~13:30	개회사 : 이상석(한국축산학회장) 환영사 : 민원기(한국가금학회회장) 축 사 : 권오남(한국과학기술단체총연합회회장) 축 사 : 이재식(농림축산식품부축산정책국장) 기념사 : 조용민(국립축산과학원장) 축 사 : 민경천(한우자조금관리위원회위원장) 축 사 : 이기홍(대한한돈협회장) 환영사 : 위성곤(제주특별자치도지사) 축 사 : 안병우(농협경제지주 축산경제 대표)	
13:30~14:00	학회시상 및 학술대상 시상	
14:00~14:50	Plenary Lecture 1 좌장: 김명후 교수	
	Prof. Andrea Rosati (EAAP)	Prospects and Development Plans of European Animal Science
14:50~15:40	Plenary lecture 2 좌장: 장영달 교수	
	김유용 교수 (서울대학교)	History of the KSAST and Future Development Directions of the Korean Livestock Industry
15:40~16:00	휴 식 (Coffee Break)	
16:00~16:30	JAST 편집위원 회의 (302호)	
16:00~17:00	한국가금학회 이사회 (304호)	
	기업 및 축산과학원 심포지엄&워크숍	
14:00~18:00	축산과학원 반려동물전주기고도화 기술개발 공동연구사업 성과공유 워크숍 (301호)	
15:00~18:00	가축 정밀영양사양 심포지엄: 축산분야 탄소중립을 위한 영양학적 접근 (한라홀 A, 3층)	
16:00~18:00	팜스코 기업 심포지엄: 한돈 산업의 현재와 미래 (303호)	
16:00~18:30	BASF 기업 심포지엄: Precision Enzyme Nutrition Unleashed (삼다홀 B, 3층)	
	탐라홀 B+C (5층)	
19:00~20:30	만찬	

2026년 7월 9일 (목)

<table>
<tr><th>장소
시간</th><th colspan="7">제주국제컨벤션 센터 (ICC JEJU)</th></tr>
<tr><td>08:00~</td><td colspan="7">등록 및 접수(3층 로비)</td></tr>
<tr><td></td><td colspan="7">한라홀 A+B (3층)</td></tr>
<tr><td rowspan="2">08:30~09:20</td><td colspan="7">Plenary Lecture 3
좌장: 서성원 교수</td></tr>
<tr><td colspan="4">이준헌 교수 (충남대학교)</td><td colspan="3">Animal Genetics, Past, Present and Future</td></tr>
<tr><td rowspan="2">09:30~12:00</td><td colspan="7">연구회 세션</td></tr>
<tr><td colspan="2">낙농연구회
(삼다홀 A)</td><td>동물마이크로
바이옴
연구회
(삼다홀 B)</td><td colspan="2">반려동물영양
연구회
(301호)</td><td>마연구회
(303호)</td><td>스마트축산
빅데이터
연구회
(401호)</td></tr>
<tr><td></td><td colspan="7">가금학회 특강 및 정기총회 (202호)</td></tr>
<tr><td>09:20~10:10</td><td colspan="7">한국가금학회 개회식 및 오당학술상 특강</td></tr>
<tr><td>10:10~11:10</td><td colspan="7">한국가금학회 가금질병 세미나</td></tr>
<tr><td>11:10~11:30</td><td colspan="7">한국가금학회 정기총회</td></tr>
<tr><td></td><td colspan="7">탐라홀 B+C (5층), 델리뷰 (4층)</td></tr>
<tr><td>11:30~12:30</td><td colspan="7">점심식사 & 정기총회</td></tr>
<tr><td></td><td colspan="7">한라홀 A+B (3층)</td></tr>
<tr><td rowspan="2">12:30~13:10</td><td colspan="7">Plenary Lecture 4
좌장: 김종남 교수</td></tr>
<tr><td colspan="4">Prof. Isaac Cann (University of Illinois Urbana-Champaign, USA)</td><td colspan="3">Plant Fiber Digestion, an Animal Scientist's Journey from the Cow Rumen to the Human Gut</td></tr>
<tr><td></td><td colspan="7">3층 로비</td></tr>
<tr><td>13:10~14:30</td><td colspan="7">포스터 발표 및 우수 포스터 심사</td></tr>
<tr><td rowspan="3">14:30~16:00</td><td colspan="7">학생 구두발표 I</td></tr>
<tr><td>단위영양 1
(삼다홀 A)</td><td>단위영양 2
(삼다홀 B)</td><td>단위영양 3
(301호)</td><td>반추영양 1
(303호)</td><td>동물생명공학1
(401호)</td><td>번식 및 생리
(402A호)</td><td>축산물
이용 및 가공
(402B호)</td></tr>
<tr><td>좌장:
박상우 교수</td><td>좌장:
이지환 교수</td><td>좌장:
성정열 교수</td><td>좌장:
오준표 교수</td><td>좌장:
황정호 교수</td><td>좌장:
박원형 교수</td><td>좌장:
서진규 교수</td></tr>
<tr><td>16:00~16:30</td><td colspan="7">휴 식 (Coffee Break)</td></tr>
<tr><td></td><td colspan="7">기업 심포지엄 및 축산과학원 워크숍</td></tr>
<tr><td>13:00~17:00</td><td colspan="7">KOICA (한국국제협력단) 축산분야 국제협력 심포지엄:
한국 축산의 국제사회 역할 전환: 수혜국에서 기여국으로 (400호)</td></tr>
</table>

장소 시간	제주국제컨벤션 센터 (ICC JEJU)					
13:10~15:10	축산과학원 가금연구센터 포럼 (202호)					
13:10~17:30	신농업기후변화대응체계구축사업 축산분야 워크숍 (201A호)					
14:00~16:00	카길 기업 심포지엄 (201B호)					
16:30~18:30	농촌진흥청 2026년 신규 공동연구개발사업 사업목표 달성을 위한 축산학회 연계 워크숍 (402B호)					
	가금학회 세션 1 (202호)					
15:10~16:20	한국가금학회 전문가 특강					
16:30~18:10	한국가금학회 차세대학술상 및 신진가금학자 특강					
16:30~18:15	**학생 구두발표 II**					
	단위영양 4 (삼다홀 A)	단위영양 5 (삼다홀 B)	유전, 육종 및 반추영양 기타 (301호)	반추영양 2 (303호)	동물생명공학 2 (401호)	환경 및 축산 기타 (402A호)
	좌장: 박상우 교수	좌장: 이지환 교수	좌장: 박종은 교수	좌장: 김원섭 교수	좌장: 황정호 교수	좌장: 이동준 교수
	오션뷰 (5층)					
18:30~20:00	기업과의 소연회					

2026년 7월 10일 (금)

장소 시간	제주국제컨벤션 센터 (ICC JEJU)	
08:00~	등록 및 접수(3층 로비)	
	한라홀 (3층)	
08:50~09:30	Plenary Lecture 5 좌장: 공창수 교수	
	김현범 교수 (단국대학교)	Understanding the Diversity and Roles of the Pig Gut Microbiome
09:40~11:40	**중견 & 신진과학자 세션**	
	영양사료 및 환경복지 (201호) 좌장: 장재철 교수	
	전중환 (강원대학교)	Philosophy of Animal Welfare and Application of Animal Behavior
	장영달 (University of Georgia)	The Role of Vitamin D in the Antioxidant Status of Pigs
	성정열 (부산대학교)	Amino Acid Nutrition in Pigs and Chickens
	유전/육종/생명공학 (202호) 좌장: 임규상 교수	
	김준모 (중앙대학교)	PRRSV Functional Genomics: Past Decade and Future Perspectives
	박원형 (충북대학교)	From Livestock Environmental Exposure to Cellular Dysfunction: Mechanistic Toxicology in Porcine Cells
	황정호 (건국대학교)	Current Research Trend in Xenotransplantation
	축산물 가공이용 및 축산환경 (203호) 좌장: 송수연 교수	
	정사무엘 (충남대학교)	Processing Strategies to Improve Animal Protein Digestibility for Age-Specific Customization
	김종규 (Michigan State University)	Heat Stress and Marbling Development in Beef Cattle
	이동준 (전남대학교)	From Waste to Resources: Multi-Pathway Approaches for Livestock Waste Resource Recovery and Greenhouse Gas Mitigation
	가금학회 세션 2 (삼다홀 A, 3층)	
9:50~12:00	한국가금학회 구두발표 및 시상식	

장소 시간	**제주국제컨벤션 센터 (ICC JEJU)**	
	한라홀 (3층)	
11:40~12:00	시상 및 폐회식 준비	
12:00~12:50	시상 및 폐회식	
	한국반추위미생물연구회 창립 30주년 기념 심포지엄 (삼다홀, 3층)	
14:00~14:20	등록(Registration)	
14:20~14:30	개회 / 회장 인사(Welcome Address by the President)	
14:30~15:20	Prof. Isaac Cann (University of Illinois Urbana-Champaign, USA)	Plant Cell Wall Degradation Strategies of Major Rumen Bacteria
15:30~16:20	Prof. Satoshi Koike (Hokkaido University, Japan)	From Early Feeding to Methane Control: Rumen Microbiota's Role in Ruminant Health and Productivity
16:20~17:10	Prof. Jakyeom Seo (Pusan National University, Korea)	Hanwoo (beef) Industry in South Korea: Challenges and Solutions
	한국반추위미생물연구회 창립 30주년 기념식 (삼다홀, 3층)	
17:30~17:50	개회사 / 축사 (Anniversary Ceremony)	
17:50~18:20	Prof. Myung-gi Baik (Former President, KSRFS)	한국반추위미생물연구회 창립 30주년: 성과와 과제 Celebrating 30 Years of KSRFS: Achievements and Challenges
18:20~20:00	Banquet	

	시간	07월 08일								시간	07월 09일							07월 09일							시간	07월 10일					
		ICC 5층		ICC 3층							ICC 5층	ICC 3층						ICC 4층				ICC 2층				ICC 3층			ICC 2층		
		탐라A	탐라BC	한라A	삼다B	301	302	303	304			로비	한라AB	삼다A	삼다B	301	303	401	402A	402B	400	202	201A	201B		한라AB	삼다A	삼다AB	201AB	202	203
8:30		-	-	-	-	-	-	-	-				PL3 이준헌	-	-	-	-	-	-	-	-	-	-	-		-	-	-	-	-	-
8:45																										PL5 김현범					
9:00	09시									09시															09시						
9:15													-									가금학회 특강 및 정기총회									
9:30														낙농 연구회	동물 마이크로 바이옴 연구회	반려동물 영양 연구회	마연구회	스마트 축산 빅데이터 연구회								-			중견&신진 과학자세션 (영양사료 및 환경복지)	중견&신진 과학자세션 (유전/ 육종/ 생명공학)	중견&신진 과학자세션 (축산물 가공이용 및 축산환경)
9:45																															
10:00	10시									10시															10시		가금학회 세션 2 구두발표 및 시상식				
10:15																															
10:30																															
10:45																															
11:00	11시									11시															11시						
11:15																															
11:30											점심 식사			-	-	-	-	-				-									
11:45																													-	-	-
12:00	12시									12시															12시	시상 및 폐회식	-				
12:15																															
12:30											-		PL4 Isaac Cann																		
12:45																										-					
13:00	13시	개회식								13시		포스터 세션	-								KOICA (한국국제 협력단) 축산분야 국제협력 심포지엄		신농업 기후변화 대응체계 구축사업 축산분야 워크숍		13시						
13:15																						축산 과학원 가금 연구센터 포럼									
13:30		시상식																													
13:45																															
14:00	14시	PL1 Andrea Rosati				축산 과학원 반려동물 전주기 고도화 기술 개발 공동연구 사업성과 공유 워크숍				14시														카길 기업 심포지엄	14시			등록/ 개회/ 회장 인사			
14:15																															
14:30												-		학생 구두발표 (단위영양 1)	학생 구두발표 (단위영양 2)	학생 구두발표 (단위영양 3)	학생 구두발표 (반추영양 1)	학생 구두발표 (동물생명 공학1)	학생 구두발표 (번식 및 생리)	학생 구두발표 (축산물 이용 및 가공)								한국반추 미생물 연구회 연사발표1			
14:45		PL2 김유용																													
15:00	15시			가축 정밀영양 사양 심포지엄						15시															15시						
15:15																						가금학회 세션 1						Break			
15:30																												한국반추 미생물 연구회 연사발표2			
15:45		Coffee Break	Coffee Break		Coffee Break		Coffee Break	Coffee Break	Coffee Break																						
16:00	16시	-	-		BASF 기업 심포지엄		JAST 편집위원 회의	팜스코 기업 심포지엄	가금학회 이사회	16시				Coffee Break				Coffee Break						-	16시						
16:15																												한국반추 미생물 연구회 연사발표3			
16:30							-							학생 구두발표 (단위영양 4)	학생 구두발표 (단위영양 5)	학생 구두발표 (유전, 육종 및 반추영양 기타)	학생 구두발표 (반추영양 2)	학생 구두발표 (동물생명 공학2)	학생 구두발표 (환경 및 축산기타)	농촌진흥청 2026년 신규 공동연구 개발사업 사업목표 달성을 위한 축산학회 연계 워크숍											
16:45																															
17:00	17시								-	17시											-				17시			Break			
17:15																															
17:30																							-					개회사/ 축사			
17:45																												한국반추 미생물 연구회 연사발표4			
18:00	18시			-						18시				-	-		-	-							18시						
18:15																-			-			-									
18:30					-															-								Banquet			
18:45																															
19:00	19시	-	만찬		-	-			-	19시	기업과의 소연														19시						

[The Korean Society of Animal Science and Technology (KSAST) 70th Anniversary Annual Conference]

Date: July 8 (Wed) - 10 (Fri), 2026
Place: Jeju International Convention Center (ICC JEJU)
Theme: Vision and Leap Forward of Livestock's 70 Years: Sustainable Innovation for Humans, Animals, and the Environment

Wednesday, July 8, 2026

Time	Program	
11:00~	Registration (3F Lobby)	
12:00~	Poster mounting (3F Lobby) Poster mounting time must be observed (Jul 8, 12:00~17:00)	
Tamna Hall A (5F)		
13:00~13:30	Opening Address: Sang-Suk Lee (President, Korean Society of Animal Science and Technology) Welcome Address: Won-Ki Min (President, Korean Poultry Science Association) Congratulatory Address: Oh-Nam Kwon (President, Korea Federation of Science and Technology Societies) Congratulatory Address: Jae-Sik Lee (Director General, Livestock Policy Bureau, Ministry of Agriculture, Food and Rural Affairs) Commemorative Address: Yong-Min Cho (Director General, National Institute of Animal Science) Congratulatory Address: Kyung-Cheon Min (Chairman, Hanwoo Board) Congratulatory Address: Ki-Hong Lee (President, Korea Pork Producers Association) Welcome Address: Seong-gon Wi (Jeju Provincial Government) Congratulatory Address: Byung-Woo Ahn (CEO, NongHyup Agribusiness Group)	
13:30~14:00	Society Awards & Academic Grand Prize Ceremony	
14:00~14:50	**Plenary Lecture 1** Chair: Prof. Myunghoo Kim	
	Prof. Andrea Rosati (The European Federation of Animal Science)	Prospects and Development Plans of European Animal Science
14:50~15:40	**Plenary Lecture 2** Chair: Prof. Young Dal Jang	
	Prof. Yoo Yong Kim (Seoul National University)	History of the KSAST and Future Development Directions of the Korean Livestock Industry
15:40~16:00	Coffee Break	
16:00~16:30	JAST Editorial Board Meeting (Room 302)	
16:00~17:00	Korean Poultry Science Association Board Meeting (Room 304)	
	Corporate & NIAS Symposia and Workshop	
14:00~18:00	NIAS Workshop: Outcomes of the Joint Research Project on Full-Life-Cycle Companion Animal Technology Development (Room 301)	
15:00~18:00	Symposium on Precision Nutrition Feeding of Livestock (Halla Hall A, 3F)	
16:00~18:00	Farmsco Corporate Symposium: The Present and Future of the Korean Pork Industry (Room 303)	
16:00~18:30	BASF Korea Corporate Symposium: Precision Enzyme Nutrition Unleashed (Samda Hall B, 3F)	
Tamna Hall B+C (5F)		
19:00~20:30	Dinner Banquet	

Thursday, July 9, 2026

Time	Program	
08:00~	Registration (3F Lobby)	
	Halla Hall A+B (3F)	
08:30~09:20	**Plenary Lecture 3** Chair: Prof. Seong-won Seo	
	Prof. Jun-heon Lee (Chungnam National University)	Animal Genetics: Past, Present and Future

Time	**Research Society Sessions**				
09:30~12:00	Dairy Science Research Society (Samda Hall A)	Animal Microbiome Research Society (Samda Hall B)	Companion Animal Nutrition Research Society (Room 301)	Equine Research Society (Room 303)	Smart Livestock Big Data Research Society (Room 401)

Time	Program	
	Korean Poultry Science Association — Special Lectures & General Assembly (Room 202)	
09:20~10:10	Opening Ceremony of the Korean Society of Poultry Science & Odang Academic Award Lecture	
10:10~11:10	Korean Society of Poultry Science - Poultry Disease Seminar	
11:10~11:30	Korean Poultry Science Association General Assembly	
	Tamna Hall B+C (5F), Deli View (4F)	
11:30~12:30	Lunch & General Assembly	
	Halla Hall A+B (3F)	
12:30~13:10	**Plenary Lecture 4** Chair: Prof. Jong Nam Kim	
	Prof. Isaac Cann (University of Illinois Urbana-Champaign, USA)	Plant Fiber Digestion, an Animal Scientist's Journey from the Cow Rumen to the Human Gut
	3F Lobby	
13:10~14:30	Poster Presentations & Outstanding Poster Judging	

Time	**Student Oral Presentations I**						
14:30~16:00	Monogastric Nutrition 1 (Samda Hall A)	Monogastric Nutrition 2 (Samda Hall B)	Monogastric Nutrition 3 (Room 301)	Ruminant Nutrition 1 (Room 303)	Animal Biotechnology 1 (Room 401)	Reproduction & Physiology (Room 402A)	Livestock Product Utilization & Processing (Room 402B)
	Chair: Prof. Sangwoo Park	Chair: Prof. Jihwan Lee	Chair: Prof. Jung Yeol Sung	Chair: Prof. Joonpyo Oh	Chair: Prof. Jeong Ho Hwang	Chair: Prof. Wonhyoung Park	Chair: Prof. Jin-Kyu Seo

Time	Program
16:00~16:30	Coffee Break

Corporate Symposia & NIAS Workshop

Time	Place	Program
13:00~17:00	Room 400	KOICA (Korea International Cooperation Agency) International Cooperation Symposium in Animal Science Transforming the Global Role of Korean Animal Industry: K-Livestock — From Recipient to Contributor
13:10~15:10	Room 202	National Institute of Animal Science, Poultry Research Center Forum
13:10~17:30	Room 201A	Livestock-Sector Workshop on the New Agro-Climate Change Response System
14:00~16:00	Room 201B	Cargill Corporate Symposium
16:30~18:30	Room 402B	KSAST-RDA Joint Workshop for Achieving the Goals of the 2026 New Collaborative Research and Development Program

Korean Poultry Science Association — Session 1 (Room 202)

Time	Program
15:10~16:20	Korean Poultry Science Association - Expert Special Lecture
16:30~18:10	Korean Poultry Science Association - Next-Generation Academic Award & Emerging Poultry Scientist Lecture

Student Oral Presentations II

Time	Program					
16:30~18:15	Student Oral Presentations II					
	Monogastric Nutrition 4 (Samda Hall A)	Monogastric Nutrition 5 (Samda Hall B)	Genetics, Breeding & Ruminant Nutrition (Misc.) (Room 301)	Ruminant Nutrition 2 (Room 303)	Animal Biotechnology 2 (Room 401)	Environment & Animal Science (Misc.) (Room 402A)
	Chair: Prof. Sangwoo Park	Chair: Prof. Jihwan Lee	Chair: Prof. Jong-Eun Park	Chair: Prof. Won Seob Kim	Chair: Prof. Jeong Ho Hwang	Chair: Prof. Dong-Jun Lee
	Ocean View (5F)					
18:30~20:00	Networking Reception with Industry Partners					

Friday, July 10, 2026

Time	Program	
08:00~	Registration (3F Lobby)	
	Halla Hall (3F)	
08:50~09:30	**Plenary Lecture 5** Chair: Prof. Changsu Kong	
	Prof. Hyeun Bum Kim (Dankook University)	Understanding the Diversity and Roles of the Pig Gut Microbiome
09:40~11:40	**Mid-Career & Early-Career Scientist Sessions**	
	Nutrition, Feed & Environmental Welfare (Room 201) Chair: Prof. Jaecheol Jang	
	Jung Hwan Jeon (Kangwon National University)	Philosophy of Animal Welfare and Application of Animal Behavior
	Young Dal Jang (University of Georgia)	The Role of Vitamin D in the Antioxidant Status of Pigs
	Jung Yeol Sung (Pusan National University)	Amino Acid Nutrition in Pigs and Chickens
	Genetics / Breeding / Biotechnology (Room 202) Chair: Prof. Kyu-Sang Lim	
	Jun-Mo Kim (Chung-Ang University)	PRRSV Functional Genomics: Past Decade and Future Perspectives
	Wonhyoung Park (Chungbuk National University)	From Livestock Environmental Exposure to Cellular Dysfunction: Mechanistic Toxicology in Porcine Cells
	Jeong Ho Hwang (Konkuk University)	Current Research Trends in Xenotransplantation
	Livestock Product Processing & Environment (Room 203) Chair: Prof. Sooyeon Song	
	Samooel Jung (Chungnam National University)	Processing Strategies to Improve Animal Protein Digestibility for Age-Specific Customization
	Jongkyoo Kim (Michigan State University)	Heat Stress and Marbling Development in Beef Cattle
	Dong-Jun Lee (Chonnam National University)	From Waste to Resources: Multi-Pathway Approaches for Livestock Waste Resource Recovery and Greenhouse Gas Mitigation
	Korean Poultry Science Association — Session 2 (Samda Hall A, 3F)	
09:50~12:00	Korean Poultry Science Association - Oral Presentations & Awards Ceremony	

	Halla Hall (3F)
11:40~12:00	Awards & Closing Ceremony Preparation
12:00~12:50	Awards & Closing Ceremony
	Technical Tour (Tourist Sites on Jeju Island)
13:00~	(For registered participants only)

- **Satellite Event: Korean Society of Rumen Function and Studies (KSRFS) 30th Anniversary Commemorative Symposium**

Time	Program	
	Samda Hall (3F)	
14:00~14:20	Registration	
14:20~14:30	Opening / Welcome Address by the President	
14:30~15:20	Prof. Isaac Cann (University of Illinois Urbana-Champaign, USA)	Plant Cell Wall Degradation Strategies of Major Rumen Bacteria
15:30~16:20	Prof. Satoshi Koike (Hokkaido University, Japan)	From Early Feeding to Methane Control: Rumen Microbiota's Role in Ruminant Health and Productivity
16:20~17:10	Prof. Jakyeom Seo (Pusan National University, Korea)	Hanwoo (beef) Industry in South Korea: Challenges and Solutions
	KSRFS 30th Anniversary Ceremony (Samda Hall, 3F)	
17:30~17:50	Opening Remarks / Congratulatory Address (Anniversary Ceremony)	
17:50~18:20	Prof. Myung-gi Baik (Former President, KSRFS)	Celebrating 30 Years of KSRFS: Achievements and Challenges
18:20~20:00	Banquet	

Poster Presentation

July 9 (Thursday), 13:10~14:30 (3F Lobby)

Section	Number	Poster No.
Monogastric Nutrition	80	PA26001 ~ PA26080
Ruminant Nutrition	78	PB26001 ~ PB26078
Animal Biotechnology	37	PC26001 ~ PC26037
Reproduction and Physiology	24	PD26001 ~ PD26024
Utilization and Processing of Livestock Products	19	PE26001 ~ PE26019
Genetic and Breeding	33	PF26001 ~ PF26033
Forage Science and Environment	28	PG26001 ~ PG26028

Oral Presentation Ⅰ

July 9 (Thursday), 14:30~16:00

Room	Section	Number	Poster No.
Samda Hall A	Monogastric Nutrition Ⅰ	6	OA26001 ~ OA26006
Samda Hall B	Monogastric Nutrition Ⅱ	6	OA26007 ~ OA26012
301	Monogastric Nutrition Ⅲ	6	OA26013 ~ OA26017, OD26001
303	Ruminant Nutrition Ⅰ	6	OB26001 ~ OB26006
401	Animal Biotechnology Ⅰ	6	OC26001 ~ OC26006
402A	Reproduction and Physiology	6	OD26002 ~ OD26007
402B	Utilization and Processing of Livestock Products	6	OE26001 ~ OE26006

Oral Presentation Ⅱ

July 9 (Thursday), 16:30~18:15

Room	Section	Number	Poster No.
Samda Hall A	Monogastric Nutrition Ⅳ	6	OA26018 ~ OA26023
Samda Hall B	Monogastric Nutrition Ⅴ	6	OA26024 ~ OA26029
301	Genetic, Breeding, and Other Ruminant Nutrition	6	OB26013 ~ OB26014 OD26008 OF26001 ~ OF26003
303	Ruminant Nutrition Ⅱ	6	OB26007 ~ OB26012
401	Animal Biotechnology Ⅱ	6	OC26007 ~ OC26012
402A	Environment and Other Animal Science Topics	7	OG26001 ~ OG26007

세부 일정 (7월 8일)

종합심포지엄

2026년 7월 8일(수) 11:00~20:30

- **주 제: 축산 70년의 비젼과 도약: 인간, 동물, 환경이 함께 걷는 지속가능한 축산 혁신**
  Vision and Leap Forward of Livestock's 70 Years: Sustainable Innovation for Humans, Animals, and the Environment

장소 시간	제주국제컨벤션 센터 (ICC JEJU)	
11:00~	등록 및 접수(3층 로비)	
12:00~	포스터 부착 (3층 로비) * 주의: 포스터 부착 시간 엄수 (7/8, 12:00~17:00)	
	탐라홀 A (5층)	
13:00~13:30	개회사 : 이상석(한국축산학회장) 환영사 : 민원기(한국가금학회회장) 축　사 : 권오남(한국과학기술단체총연합회회장) 축　사 : 이재식(농림축산식품부축산정책국장) 기념사 : 조용민(국립축산과학원장) 축　사 : 민경천(한우자조금관리위원회위원장) 축　사 : 이기홍(대한한돈협회장) 환영사 : 위성곤(제주특별자치도지사) 축　사 : 안병우(농협경제지주 축산경제 대표)	
13:30~14:00	학회시상 및 학술대상 시상	
14:00~14:50	Plenary Lecture 1 좌장: 김명후 교수	
	Prof. Andrea Rosati (EAAP)	Prospects and Development Plans of European Animal Science
14:50~15:40	Plenary lecture 2 좌장: 장영달 교수	
	김유용 교수 (서울대학교)	History of the KSAST and Future Development Directions of the Korean Livestock Industry
15:40~16:00	휴 식 (Coffee Break)	
16:00~16:30	JAST 편집위원 회의 (302호)	
16:00~17:00	한국가금학회 이사회 (304호)	
	기업 및 축산과학원 심포지엄&워크숍	
14:00~18:00	축산과학원 반려동물전주기고도화 기술개발 공동연구사업 성과공유 워크숍 (301호)	
15:00~18:00	가축 정밀영양사양 심포지엄: 축산분야 탄소중립을 위한 영양학적 접근 (한라홀 A, 3층)	
16:00~18:00	팜스코 기업 심포지엄: 한돈 산업의 현재와 미래 (303호)	
16:00~18:30	BASF 기업 심포지엄: Precision Enzyme Nutrition Unleashed (삼다홀 B, 3층)	
	탐라홀 B+C (5층)	
19:00~20:30	만찬	

반려동물전주기고도화 기술개발 공동연구사업 성과공유 워크숍 (301호)

2026년 7월 8일(수) 14:00~18:00

- **주 제 : 반려동물전주기고도화 기술개발 공동연구사업 성과공유 워크숍**

14:00~14:10	유동조 (국립축산과학원 생환부장)	인사 말씀
14:10~15:00	세션 I. 반려동물 기능성 사료개발 및 영양 연구	
14:10~14:20	박성권 (세종대학교)	국내산 축산물 활용 반려견 기능성 사료 및 안전성 증진기술 개발
14:20~14:30	이경우 (건국대학교)	신규 기능성 사료소재 개발 및 반려동물 맞춤형 건강개선 기능성 사료 개발
14:30~14:40	장현준 [(재)농축산용미생물 산업육성지원센터]	반려동물 사료소재별 주요 에너지원 체내 이용율 및 장내 미생물 군집 변화
14:40~14:50	송민호 (충남대학교)	반려동물 주요 품종별 · 연령별 영양소 이용성 평가 연구
14:50~15:00	조성호 [(사)농정연구센터]	반려동물 사료 기준 및 규격 제도 개선 연구
15:00~15:30	Coffee Break	
15:30~16:10	세션 II. 유전정보 · 세포자원을 활용한 반려동물 건강 연구	
15:30~15:40	이성림 (경상국립대학교)	반려동물 건강수명 연장을 위한 생물학적 나이 측정기술의 개발과 임상적 활용
15:40~15:50	김형석 [(주)페토바이오]	반려동물 건강검진 활성화를 위한 의료데이터 및 참조지표 활용방안
15:50~16:00	황태성 (경상국립대학교)	개 이첨판 폐쇄부전증의 진단 및 예후 평가를 위한 임상 · 유전체 통합 연구
16:00~16:10	이민국 (국립축산과학원)	반려견 줄기세포 유래인자의 국소염증 치료 기전 규명 및 활용 연구
16:10~16:30	세션 III. 반려동물 행동특성 연구	
16:10~16:20	양가영 (국립축산과학원)	반려동물 행동특성 평가 방법 및 시스템 개발
16:20~16:30	서동원 [(주)티엔티리써치]	반려견 공격행동 특성관련 유전인자 탐색
16:30~17:50	참석자	반려동물 중장기 연구전략 수립을 위한 종합토론
17:50~18:00	성필남 (동물복지과장)	마무리

2026년 가축 정밀영양사양 심포지엄 (한라홀 A, 3층)

2026년 7월 8일(수) 15:00~18:00

- **주 제 : 축산분야 탄소중립을 위한 영양학적 접근**

사회: 강환구 연구관 (국립축산과학원)
1부 좌장: 김지혁 교수 (공주대학교)
2부 좌장: 이홍구 교수 (건국대학교)

14:00~15:00	참가자 등록	
15:00~15:10	조용민 (국립축산과학원 원장)	참석자 소개 인사 말씀 기념 촬영
15:10~15:35	홍승탁 사무관 (농식품부)	축산분야 탄소중립을 위한 사료정책 방향
15:35~16:00	유재홍 박사 (제일사료)	산란계 질소저감을 위한 사료산업 동향 및 연구
16:00~16:10	휴식	
16:10~16:35	김법균 교수 (건국대학교)	돼지 유래 온실가스에 대한 영양학적 관점
16:35~17:00	이성신 연구사 (국립축산과학원)	반추가축 메탄저감제 개발 연구 현황
17:00~17:10	종합토론 준비	
17:10~18:00	가축정밀영양과장	종합 토론 및 폐회 *탄소중립을 위한 영양학적 접근 및 연구 혁신 방안

BASF 기업 심포지엄 (삼다홀 B, 3층)

2026년 7월 8일(수) 16:00~18:30

- **주 제 : Precision Enzyme Nutrition Unleashed**

사회 : Nicholas Yu (BASF Animal Nutrition Korea)

15:40~16:00	Registration & Reception Participant check-in, networking, and seat arrangement	
16:00~16:05	Nicholas Yu (BASF Animal Nutrition Korea)	Opening & Seminar Introduction
16:05~16:25	Dr. Hyung-Il Lee (Cargill MHS)	Practical application of Feed Enzymes
16:25~16:55	Prof. Jung-Min Heo (Chungnam National University)	Enzyme Matrix Values: Scientific Understanding, Challenges, and Future Perspectives
16:55~17:30	Dr. Ashley England (BASF Animal Nutrition)	Intelligent Enzyme Combinations: Converting Anti-Nutritional Factors into Value
17:30~18:05	Leon Hall (BASF Animal Nutrition)	Precision Enzyme Nutrition with NatuSynX Turning Enzyme Combinations into Profit
18:05~18:25	All Speakers	Q&A and Discussion
18:25~18:30	Nicholas Yu (BASF Animal Nutrition Korea)	Closing Remarks & Follow-up

세부 일정 (7월 9일)

종합심포지엄

2026년 7월 9일(목) 8:00~20:00

<table>
<tr><td>장소
시간</td><td colspan="7">제주국제컨벤션 센터 (ICC JEJU)</td></tr>
<tr><td>08:00~</td><td colspan="7">등록 및 접수(3층 로비)</td></tr>
<tr><td></td><td colspan="7">한라홀 A+B (3층)</td></tr>
<tr><td rowspan="2">08:30~09:20</td><td colspan="7">Plenary Lecture 3
좌장: 서성원 교수</td></tr>
<tr><td colspan="3">이준헌 교수 (충남대학교)</td><td colspan="4">Animal Genetics, Past, Present and Future</td></tr>
<tr><td rowspan="2">09:30~12:00</td><td colspan="7">연구회 세션</td></tr>
<tr><td colspan="2">낙농연구회
(삼다홀 A)</td><td>동물마이크로
바이옴
연구회
(삼다홀 B)</td><td colspan="2">반려동물영양
연구회
(301호)</td><td>마연구회
(303호)</td><td>스마트축산
빅데이터
연구회
(401호)</td></tr>
<tr><td></td><td colspan="7">가금학회 특강 및 정기총회 (202호)</td></tr>
<tr><td>09:20~10:10</td><td colspan="7">한국가금학회 개회식 및 오당학술상 특강</td></tr>
<tr><td>10:10~11:10</td><td colspan="7">한국가금학회 가금질병 세미나</td></tr>
<tr><td>11:10~11:30</td><td colspan="7">한국가금학회 정기총회</td></tr>
<tr><td></td><td colspan="7">탐라홀 B+C (5층), 델리뷰 (4층)</td></tr>
<tr><td>11:30~12:30</td><td colspan="7">점심식사 & 정기총회</td></tr>
<tr><td></td><td colspan="7">한라홀 A+B (3층)</td></tr>
<tr><td rowspan="2">12:30~13:10</td><td colspan="7">Plenary Lecture 4
좌장: 김종남 교수</td></tr>
<tr><td colspan="3">Prof. Isaac Cann (University of Illinois Urbana-Champaign, USA)</td><td colspan="4">Plant Fiber Digestion, an Animal Scientist's Journey from the Cow Rumen to the Human Gut</td></tr>
<tr><td></td><td colspan="7">3층 로비</td></tr>
<tr><td>13:10~14:30</td><td colspan="7">포스터 발표 및 우수 포스터 심사</td></tr>
<tr><td rowspan="3">14:30~16:00</td><td colspan="7">학생 구두발표 I</td></tr>
<tr><td>단위영양 1
(삼다홀 A)</td><td>단위영양 2
(삼다홀 B)</td><td>단위영양 3
(301호)</td><td>반추영양 1
(303호)</td><td>동물생명공학1
(401호)</td><td>번식 및 생리
(402A호)</td><td>축산물
이용 및 가공
(402B호)</td></tr>
<tr><td>좌장:
박상우 교수</td><td>좌장:
이지환 교수</td><td>좌장:
성정열 교수</td><td>좌장:
오준표 교수</td><td>좌장:
황정호 교수</td><td>좌장:
박원형 교수</td><td>좌장:
서진규 교수</td></tr>
<tr><td>16:00~16:30</td><td colspan="7">휴 식 (Coffee Break)</td></tr>
</table>

<table>
<tr><th>장소
시간</th><th colspan="6">제주국제컨벤션 센터 (ICC JEJU)</th></tr>
<tr><td></td><td colspan="6">기업 심포지엄 및 축산과학원 워크숍</td></tr>
<tr><td>13:00~17:00</td><td colspan="6">KOICA (한국국제협력단) 축산분야 국제협력 심포지엄:
한국 축산의 국제사회 역할 전환: 수혜국에서 기여국으로 (400호)</td></tr>
<tr><td>13:10~15:10</td><td colspan="6">축산과학원 가금연구센터 포럼 (202호)</td></tr>
<tr><td>13:10~17:30</td><td colspan="6">신농업기후변화대응체계구축사업 축산분야 워크숍 (201A호)</td></tr>
<tr><td>14:00~16:00</td><td colspan="6">카길 기업 심포지엄 (201B호)</td></tr>
<tr><td>16:30~18:30</td><td colspan="6">농촌진흥청 2026년 신규 공동연구개발사업 사업목표 달성을 위한 축산학회 연계 워크숍 (402B호)</td></tr>
<tr><td></td><td colspan="6">가금학회 세션 1 (202호)</td></tr>
<tr><td>15:10~16:20</td><td colspan="6">한국가금학회 전문가 특강</td></tr>
<tr><td>16:30~18:10</td><td colspan="6">한국가금학회 차세대학술상 및 신진가금학자 특강</td></tr>
<tr><td rowspan="3">16:30~18:15</td><td colspan="6">학생 구두발표 II</td></tr>
<tr><td>단위영양 4
(삼다홀 A)</td><td>단위영양 5
(삼다홀 B)</td><td>유전, 육종 및
반추영양 기타
(301호)</td><td>반추영양 2
(303호)</td><td>동물생명공학 2
(401호)</td><td>환경 및
축산 기타
(402A호)</td></tr>
<tr><td>좌장:
박상우 교수</td><td>좌장:
이지환 교수</td><td>좌장:
박종은 교수</td><td>좌장:
김원섭 교수</td><td>좌장:
황정호 교수</td><td>좌장:
이동준 교수</td></tr>
<tr><td></td><td colspan="6">오션뷰 (5층)</td></tr>
<tr><td>18:30~20:00</td><td colspan="6">기업과의 소연회</td></tr>
</table>

한국축산학회 산하 연구회 행사

2026년 7월 9일(목) 9:30~12:00

1. 낙농연구회 (삼다홀 A)

- **주제 : K-낙농의 현재와 과제**

좌장 : 강상기 부회장 (서울대학교 교수)

등록 / 개회식 진행 : 서자겸 상무이사 (부산대학교 교수)		
09:30~09:45	등록	
09:45~10:00	개회사 : 서성원 회장 (충남대학교 교수) 축사 : 김경규 회장 (낙농진흥회)	
초청강연		
10:00~10:30	오준표 교수 (서울대학교)	낙농 연구 최신 동향
10:30~11:00	한주석 팀장 (낙농진흥회)	전국단위 집유체계 구축을 통한 국내 낙농산업 구조개선 방안
11:00~11:30	정순태 총괄 ((주)제주우유)	제주 낙농 산업의 당면과제와 발전 방안
11:30~	폐회	

2. 동물마이크로바이옴연구회 (삼다홀 B)

- **주제 : 안전하고 지속가능한 동물생산을 위한 반추위 마이크로바이옴 혁신 전략**

Chairperson : Prof. Sejong Oh (Chonnam National University)

9:00~9:30	Registration	
연사 및 제목		
09:30~10:00	Prof. Jong Nam Kim (Dongseo University)	Modulation of Rumen Microbiome and Enteric Methane Reduction by SCOBY-based Probiotics: From *In Vitro* Fermentation to TMF Application
10:00~10:30	Prof. Myunghoo Kim (Seoul National University)	Technologies to Address Climate Change and Improve the Health of Ruminants by Utilizing the Microbiome and Metabolome
10:30~11:00	Prof. Min-Jin Kwak (Kookmin University)	Characterization of Core Microbiota and Methane-Related Functional Genes Associated with Methane Emissions and Growth Performance in Cattle
11:00~11:30	Prof. Younghoon Kim (Seoul National University)	Rumen-Derived Next Generation Probiotics for Sustainable Bioplastic Production and Microplastic Toxicity Mitigation

3. 반려동물영양연구회 (301호)

● **주 제 : 차세대 펫푸드 R&D 패러다임: 글로벌 트렌드부터 정책 및 연구 동향**

좌장 : 김기현 교수 (국립순천대학교)

10:00~10:15	등 록	
10:15~10:20	개 회 / 회장인사 / 안내말씀	
연 사 및 제 목		
10:20~10:40	소경민 농업연구관 (국립축산과학원)	펫푸드 글로벌 트렌드와 한국 R&D 정책, 산업의 나아갈 길
10:40~11:10	송광영 교수 (대구한의대학교)	단위축산동물과 반려동물의 질병 및 영양에 대한 비교 분석
11:10~11:40	박근현 책임연구원 ((주)우리와)	반려견의 식이역반응, 아토피 피부염 증상 완화를 위한 영양학적 관리
11:40~12:00	종합토론 및 폐회	

4. 마연구회 (303호)

● **주 제 : 국내 말(馬)산업 분야 연구 동향**

좌장 : 윤민중 교수 (경북대학교)

9:00~9:30	등 록	
9:30~9:40	개 회 / 회장인사 / 안내말씀	
연 사 및 제 목		
9:40~10:10	오정섭 석사과정생 (제주대학교)	말 장제 현장의 안전 · 복지 향상을 위한 한국형 하이브리드 모델 설계
10:10~10:40	최재영 박사 (난지축산연구센터)	난지축산연구센터 말 연구 현황
10:40~11:10	정용욱 박사과정생 (경북대학교)	Neurophysiological and Emotional Effects of Equine-Assisted Activities
11:10~11:30	종합토론 및 폐회	

5. 스마트축산빅데이터연구회 (401호)

- **주 제 : 축산데이터환류와 AI전환 전략**

좌장 : 김준모 교수 (중앙대학교)

10:00~10:10	등 록	
10:10~10:15	개 회 / 회장인사 / 안내말씀	
연 사 및 제 목		
10:15~10:35	Jame Koltes 교수 (Iowa State University)	Data Reuse in Agricultural Genomics Research
10:35~11:05	양희재 대표 ((주)코쿤)	탄자니아 낙농산업 저탄소화 역량강화를 위한 BIT기반 선진 축산 생태계 구축 전략
11:05~11:35	박종은 교수 (제주대학교)	기후변화 대응 동물 오믹스 빅데이터 활용 연구
11:35~11:55	채병호 박사 (전북대학교)	인공지능 기반 젖소 공태우 탐지 안전망
11:40~12:00	종합토론 및 폐회	

한국가금학회 개회식 및 오당학술상 특강 (202호)

2026년 7월 9일(목) 09:20~10:10

사회 : 이경우 교수 (건국대학교)

09:20~09:30	개회식	
09:30~10:10	오당학술상 특강	
	장형관 교수 (전북대학교)	Herpesvirus를 이용한 동물용 백신 개발 기술의 발전과 응용

한국가금학회 가금질병 세미나 (202호)

2026년 7월 9일(목) 10:10~11:10

좌장 : 허문 과장 (농림축산검역본부)

10:10~10:40	장일 연구사 (농림축산검역본부)	Dynamics of the Emerging Genogroup of Infectious Bursal Disease Virus Infection in Broiler Farms in South Korea
10:40~11:10	강성일 연구사 (농림축산검역본부)	해양미생물 기반 동물용 항생제 대체제의 활용 가능성

한국가금학회 정기총회 (202호)

2026년 7월 9일(목) 11:10~11:30

사회 : 이경우 교수 (건국대학교)

11:10 ~ 11:30	한국가금학회 정기총회

축산과학원 가금연구센터 포럼 (202호)

2026년 7월 9일(목) 13:10~15:10

좌장 : 김경운 센터장 (국립축산과학원 가금연구센터)

13:10~13:20	좌장 및 연사 소개	
13:20~13:40	추효준 박사 (국립축산과학원)	토종닭 순계 개량 및 품종 개발 현황
13:40~14:00	이준헌 교수 (충남대학교)	토종닭 유전체 연구 현황 및 최신 연구 동향
14:00~14:20	김영준 부장 (한국토종닭 협회)	국내 토종닭 산업 현황 및 발전 방향
14:20~14:40	신소연 사무관 (농림축산식품부)	토종닭 관련 정책 방향 및 제언
14:40~15:10	종합 토론	

한국가금학회 전문가 특강 (202호)

2026년 7월 9일(목) 15:10~16:20

좌장 : 홍영호 교수 (중앙대학교)

15:10~15:40	김종준 사무국장 (계란자조금관리위원회)	대한민국 미래자산 갈색 반도체 계란
15:40~16:00	김명섭 수의사 (HIPRA)	국내 IB 발생현황 및 유전자형 분류체계
16:00~16:20	최수원 수의사 (한국엘랑코동물약품)	유럽 식중독 살모넬라 관리 사례

한국가금학회 차세대학술상 및 신진가금학자 특강 (202호)

2026년 7월 9일(목) 16:30~18:10

좌장 : 강민 교수 (전북대학교)

한국가금학회 차세대학술상 특강

16:30~16:50	임천익 박사 (국립축산과학원)	하절기 유정란 열 자극을 통한 후성유전학 기반 고온내성 육계 생산 기술
16:50~17:10	유명환 소장 (한국친환경축산연구소)	Nutritional Strategies for Improving Alternative Feedstuffs in Poultry via Dietary Supplements: Potnetial Role of Physiological and Metabolic Pathways

한국가금학회 신진가금학자 특강

17:10~17:30	배해득 박사 (전북대학교)	국외 고병원성 조류인플루엔자(HPAI) 대응 동향 및 백신 개발 현황
17:30~17:50	송승언 박사 (카브)	파라믹소바이러스 벡터 기반 저병원성조류인플루엔자 생독배신의 개발 및 사독백신 병용 효능 평가
17:50~18:10	이아란 교수 (건국대학교 동물자원연구센터)	사슬 길이에 따른 폴리인산염 급여가 가금의 장 건강 및 장내 마이크로바이옴에 미치는 영향

KOICA (한국국제협력단) 축산분야 국제협력 심포지엄 (400호)

2026년 7월 9일(목) 13:00~17:00

- **주 제 : 한국 축산의 국제사회 역할 전환: K축산 – 수혜국에서 기여국으로 (글로벌 협력확산과 지속가능 축산)**

사회: 신동현 교수 (전북대학교)
1부 좌장: 황성구 교수 (한경국립대학교)
2부 좌장: 김수기 교수 (건국대학교)

13:00~13:10	이상석 한국축산학회 회장	개회 및 세션 소개
13:10~13:40	김경훈 교수 (서울대학교)	라오스 낙농교육 기반 구축과 축산 고등교육 협력
13:40~14:10	김수기 교수 (건국대학교)	베트남 국립농업대학교 축산고등교육 기반 강화 및 전문인력 양성
14:10~14:40	남인식 교수 (한경국립대학교)	몽골 생명과학대학교 산학 연계형 고등교육 역량강화 사업 구성과 성과
14:40~15:10	서강석 교수 (국립순천대학교)	아시아에서 아프리카까지 축산 개발 협력
15:10~15:30	네트워크 브레이킹	
15:30~16:00	이학교 교수 (전북대학교)	아시아 동물산업 특화 전문인력 양성사업 기반의 지속가능한 상생 발전 방안
16:00~16:30	황성구 교수 (한경국립대학교)	개발도상국 ODA 사업의 성공전략과 지속가능성 확보 방안
16:30~17:00	참석자 전체	종합토론
17:00~	폐회 및 기념촬영	

신농업기후변화대응체계구축사업 축산분야 워크숍 (201A호)

2026년 7월 9일(목) 13:10~17:30

● **주 제 : 신농업기후변화대응체계구축사업 축산분야 워크숍**

13:10~13:30	허정민 교수 (충남대학교)	고온환경에 따른 가금산물(계란, 계육)의 신선도 및 품질 저하 방지기술 개발
13:30~13:50	이경우 교수 (건국대학교)	닭의 동물복지 사육 시 고온기 생산성 저하 방지 기술 개발
13:50~14:10	하태환 교수 (충남대학교)	이상기상에 따른 가축의 고온스트레스 피해 경감기술 개발
14:10~14:40	Coffee Break	
14:40~15:00	장선식 연구관 (국립축산과학원)	고온스트레스 저감형 한우사양 프로그램 및 영양물질 첨가제 개발
15:00~15:20	박중훈 교수 (서울대학교)	기후변화 대응 고온기 한우 번식 효율 증진 기술 개발
15:20~15:40	장재철 교수 (경상국립대학교)	고온기 대비 돼지 번식 및 사료섭취량 저하 방지기술 개발
15:40~16:10	Coffee Break	
16:10~16:30	김진수 교수 (강원대학교)	고온기 번식능력 증진을 위한 모돈 영양소 이용효율 증진 첨가제 활용기술 개발
16:30~16:50	김명후 교수 (서울대학교)	고온기 젖소의 스트레스 개선 조건 구명 및 생산성 향상 기술 개발
16:50~17:10	김대현 교수 (전남대학교)	기후변화에 따른 하절기 젖소의 번식능력 향상 기술 개발
17:10~17:30	최용준 교수 (한경대학교)	기후변화에 따른 축종별 생산성 실태조사 및 영향·취약성 평가(2단계)

참고 : 과제 당 20분 발표 (15분 발표 후 5분 질의응답)

카길 기업 심포지엄 (201B호)

2026년 7월 9일(목) 14:00~16:00

- **주 제 : Dietary Strategy and Rearing Physiology as Drivers of Laying Persistency, Egg Production Curve Dynamics, and Sustainability in Modern Layer Systems**

사회: 임태정 (Cargill MHS Category manager)
통역: 신지은 (Cargill Poultry Category Manager)

14:00~15:40	Alexander De Leon (Cargill Global Technology Advisor – Poultry)	Dietary Strategy and Rearing Physiology as Drivers of Laying Persistency, Egg Production Curve Dynamics, and Sustainability in Modern Layer Systems
15:40~16:00	Q&A	

농촌진흥청 2026년 신규 공동연구개발사업 사업목표 달성을 위한 축산학회 연계 워크숍 (402B호)

2026년 7월 9일(목) 16:30~18:30

- **주 제 : ’26년 신규 공동연구사업 목표달성을 위한 연구추진 방향 공유 및 ’28년 신규 연구사업 기획을 위한 전문가 의견 수렴**

① 가축 생산비 절감 정밀사양 기술 고도화(’26～’30)	
16:30~16:40	등록, 내외빈 소개 및 사진 촬영
16:40~17:00	(가축생산비 절감) 사업 구성, 수행 및 성과관리 계획 설명
17:00~17:15	중간평가 대응 전략목표 및 성과지표(전략계획서) 안내
② 축산자원 활용 탄소중립 바이오 융합기술 개발(’26～’30)	
17:15~17:35	(축산자원활용탄소중립) 사업 구성, 수행 및 성과관리 계획 설명
17:35~17:50	중간평가 대응 전략목표 및 성과지표(전략계획서) 안내
17:50~18:30	2028년 신규 연구사업 기획을 위한 현장 의견수렴

포스터발표회

2026년 7월 9일(목) 13:10~14:30 (3층 로비)

분야	편수	포스터 NO.
단위영양	80	PA26001 ~ PA26080
반추영양	78	PB26001 ~ PB26078
동물생명공학	37	PC26001 ~ PC26037
번식 및 생리	24	PD26001 ~ PD26024
축산물 이용 및 가공	19	PE26001 ~ PE26019
유전 및 육종	33	PF26001 ~ PF26033
초지 및 환경	28	PG26001 ~ PG26028

구두발표회 I

2026년 7월 9일(목) 14:30~16:00

※ 발표자 1인당 10분 발표 / 5분 질의 및 응답

장소	분야	편수	구두발표 NO.
삼다홀 A	단위영양 1	6	OA26001 ~ OA26006
삼다홀 B	단위영양 2	6	OA26007 ~OA26012
301	단위영양 3	6	OA26013 ~ OA26017, OD26001
303	반추영양 1	6	OB26001 ~ OB26006
401	동물생명공학 1	6	OC26001 ~ OC26006
402A	번식 및 생리	6	OD26002 ~ OD26007
402B	축산물 이용 및 가공	6	OE26001 ~ OE26006

구두 발표회 II

2026년 7월 9일(목) 16:30~18:15

※발표자 1인당 10분 발표 / 5분 질의 및 응답

장소	분야	편수	구두발표 NO.
삼다홀 A	단위영양 4	6	OA26018 ~ OA26023
삼다홀 B	단위영양 5	6	OA26024 ~ OA26029
301	유전, 육종 및 반추영양 기타	6	OB26013 ~ OB26014 OD26008 OF26001 ~ OF26003
303	반추영양 2	6	OB26007 ~ OB26012
401	동물생명공학 2	6	OC26007 ~ OC26012
402A	환경 및 축산 기타	7	OG26001 ~ OG26007

세부 일정 (7월 10일)

종합심포지엄

2026년 7월 10일(금) 8:00~20:00

장소 시간	제주국제컨벤션 센터 (ICC JEJU)	
08:00~	등록 및 접수(3층 로비)	
	한라홀 (3층)	
08:50~09:30	**Plenary Lecture 5** 좌장: 공창수 교수	
	김현범 교수 (단국대학교)	Understanding the Diversity and Roles of the Pig Gut Microbiome
09:40~11:40	**중견 & 신진과학자 세션**	
	영양사료 및 환경복지 (201호) 좌장: 장재철 교수	
	전중환 (강원대학교)	Philosophy of Animal Welfare and Application of Animal Behavior
	장영달 (University of Georgia)	The Role of Vitamin D in the Antioxidant Status of Pigs
	성정열 (부산대학교)	Amino Acid Nutrition in Pigs and Chickens
	유전/육종/생명공학 (202호) 좌장: 임규상 교수	
	김준모 (중앙대학교)	PRRSV Functional Genomics: Past Decade and Future Perspectives
	박원형 (충북대학교)	From Livestock Environmental Exposure to Cellular Dysfunction: Mechanistic Toxicology in Porcine Cells
	황정호 (건국대학교)	Current Research Trend in Xenotransplantation
	축산물 가공이용 및 축산환경 (203호) 좌장: 송수연 교수	
	정사무엘 (충남대학교)	Processing Strategies to Improve Animal Protein Digestibility for Age-Specific Customization
	김종규 (Michigan State University)	Heat Stress and Marbling Development in Beef Cattle
	이동준 (전남대학교)	From Waste to Resources: Multi-Pathway Approaches for Livestock Waste Resource Recovery and Greenhouse Gas Mitigation

장소 시간	**제주국제컨벤션 센터 (ICC JEJU)**	
	가금학회 세션 2 (삼다홀 A, 3층)	
9:50~12:00	한국가금학회 구두발표 및 시상식	
	한라홀 (3층)	
11:40~12:00	시상 및 폐회식 준비	
12:00~12:50	시상 및 폐회식	
	한국반추위미생물연구회 창립 30주년 기념 심포지엄 (삼다홀, 3층)	
14:00~14:20	등록(Registration)	
14:20~14:30	개회 / 회장 인사(Welcome Address by the President)	
14:30~15:20	Prof. Isaac Cann (University of Illinois Urbana-Champaign, USA)	Plant Cell Wall Degradation Strategies of Major Rumen Bacteria
15:30~16:20	Prof. Satoshi Koike (Hokkaido University, Japan)	From Early Feeding to Methane Control: Rumen Microbiota's Role in Ruminant Health and Productivity
16:20~17:10	Prof. Jakyeom Seo (Pusan National University, Korea)	Hanwoo (beef) Industry in South Korea: Challenges and Solutions
	한국반추위미생물연구회 창립 30주년 기념식 (삼다홀, 3층)	
17:30~17:50	개회사 / 축사 (Anniversary Ceremony)	
17:50~18:20	Prof. Myung-gi Baik (Former President, KSRFS)	한국반추위미생물연구회 창립 30주년: 성과와 과제 Celebrating 30 Years of KSRFS: Achievements and Challenges
18:20~20:00	Banquet	

중견 & 신진 과학자 세션

2026년 7월 10일(금) 9:40~11:40

1. 영양사료 및 환경복지 (201A+B호)

좌장: 장재철 교수		
시간	**연사**	**제목**
09:40~10:20	전중환 (강원대학교)	Philosophy of Animal welfare and Application of Animal behavior
10:20~11:00	장영달 (University of Georgia)	The Role of Vitamin D in the Antioxidant Status of Pigs
11:00~11:40	성정열 (부산대학교)	Amino Acid Nutrition in Pigs and Chickens

2. 유전/육종/생명공학 (202A+B호)

좌장: 임규상 교수		
시간	**연사**	**제목**
09:40~10:20	김준모 (중앙대학교)	PRRSV Functional Genomics: Past Decade and Future Perspectives
10:20~11:00	박원형 (충북대학교)	From Livestock Environmental Exposure to Cellular Dysfunction: Mechanistic Toxicology in Porcine Cells
11:00~11:40	황정호 (건국대학교)	Current Research Trend in Xenotransplantation

3. 축산물 가공이용 및 축산환경 (203호)

좌장: 송수연 교수		
시간	**연사**	**제목**
09:40~10:20	정사무엘 (충남대학교)	Processing Strategies to Improve Animal Protein Digestibility for Age-Specific Customization
10:20~11:00	김종규 (Michigan State University)	Heat Stress and Marbling Development in Beef Cattle
11:00~11:40	이동준 (전남대학교)	From Waste to Resources: Multi-Pathway Approaches for Livestock Waste Resource Recovery and Greenhouse Gas Mitigation

발표논문시상식 및 폐회식

- 일 시 : 2026년 7월 10일(금) 12:00
- 장 소 : 한라홀 (3층)
- 시 상 : 이상석 한국축산학회장
- 대 상 : 전 회원 및 수상자

※ 구두발표 및 포스터 우수 발표자는 폐회식에서 시상 예정입니다.
발표자 전원 참석하여 주시길 부탁드립니다.
(대리수상을 불가하여 수상자가 불참 시, 차 순위자에게 시상합니다.)

한국반추위미생물연구회 창립 30주년 기념 심포지엄
(삼다홀, 3층)

2026년 7월 10일(금) 14:00~17:10

14:00~14:20	등록(Registration)	
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16:20~17:10	Prof. Jakyeom Seo (Pusan National University, Korea)	Hanwoo (beef) industry in South Korea: Challenges and Solutions

한국반추위미생물연구회 창립 30주년 기념식
(삼다홀, 3층)

2026년 7월 10일(금) 17:30~20:00

17:30~17:50	개회사 / 축사(Anniversary Ceremony)	
17:50~18:20	Prof. Myung-gi Baik (Former President, KSRFS)	한국반추위미생물연구회 창립 30주년: 성과와 과제 Celebrating 30 Years of KSRFS: Achievements and Challenges
18:20~20:00	Banquet	

구두 발표

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제1발표분야 : 단위영양

OA26001 Effects of different dietary fiber sources on reproductive performance, blood profiles and milk composition in gestating sows

S. H. Lee, M. S. Park, S. H. Park, B. C. Park, Y. Y. Kim

OA26002 Effects of dietary crude protein levels on growth performance, hematological parameters, and intestinal gene expression in weaning pigs

Hyunju Park, Hongjun Kim, Joeun Kim, Yejin Min, Yongdae Jeong, Chaibin Lim, Hyunjung Jung, Yohan Choi

OA26003 High-dose anandamide supplementation reduces treatment incidence in weaned pigs under elevated ambient temperature

Yujin Park, Yujin Jung, Jua Woo, Sarbani Biswas, Jinhyeon Yun

OA26004 Influence of dietary electrolyte balance reduction using calcium chloride at expense of limestone on growth performance and odorous compounds of growing pig

Inho Cho, Taemin Yoo, Ji Yeon Park, Changsu Kong

OA26005 The effect of a low-protein diet on growth performance and fecal odor compounds in finishing pigs

Geunyoung Park, Inho Cho, Bi Jang, Changsu Kong

OA26006 Effects of palm kernel by-product type and inclusion level on growth performance, pork quality, and carcass characteristics in growing-finishing pigs

M. S. Park, S. H. Park, B. C. Park, Y. Y. Kim

OA26007 Dietary bacteriophage on growth performance, fecal microbiome, diarrhea incidence, and nutrient digestibility in weaning pigs

S. H. Park, J. W. Kim, B. C. Park, Y. Y. Kim

OA26008 Weaning weight-related differences in growth performance, nutrient digestibility, blood profiles, and intestinal morphology in pigs

Hyuck Kim, Dongcheol Song, Kyeongho Jeon, Jinmo Yang, Hyohyeon Yu, Jinho Cho

OA26009 Solvens® supplementation improved immune and gut health in weaned piglets vaccinated with PRRSV

Dongcheol Song, Hyuck Kim, Kyeongho Jeon, Jinmo Yang, Hyohyeon Yu, Jinho Cho

OA26010 Partial replacement of molasses with monosodium glutamate-condensed molasses soluble improves growth performance while maintaining gut health in finishing pigs

…… Jeong Wook Jang, Eun Ju Ko, Vetriselvi Sampath, In Ho Kim

OA26011 Dietary Mycofix® plus 5.0, a toxin binder mitigates multi-mycotoxin induced impairments in growth performance, gut integrity, and reproductive indicators in finishing gilts

…… Kyejin Lee, Jeong Wook Jang, Vetriselvi Sampath, Jee Yeon Cho, Barbara Doupovec, Dian Schatzmayr, In Ho Kim

OA26012 Effects of supplementing zinc oxide and *Tenebrio molitor* larvae to nursery pig diets

…… Seong-Min Koo, Hae-Chan Shin, Jae-Hyeok Lee, Sang-Hyon Oh, Jae-Cheol Jang, Gyo Moon Chu

OA26013 A functional bioactive complex based on sustainable nutrition improves production performance, reduces harmful gas emissions, and mitigates lipopolysaccharide-induced immune stress in laying hens

…… Seungjin Yun, Se Yeon Jang, Weihan Zhao, In Ho Kim

OA26014 Effects of dietary starch and CP levels on growth performance, breast meat quality, gut health, and stress indicators in broiler chickens raised under heat stress

…… Ju Yeong Park, Geun Yong Park, Yeong Bin Kim, Ji Won Shin, Jin Ho Jeong, Sung Woo Kim, Jong Hyuk Kim

OA26015 Temporal dynamics and sex-specific differences in the gut microbiota of AA+ broilers

…… Sieun Kim, Biao Xuan, Eun Bae Kim

OA26016 Real-time individual broiler monitoring system using YOLOv12 with WIoU v3 and ByteTrack for automated feeding and drinking behavior analysis

…… Seojin Choi, Eun Bae Kim

OA26017 Effects of *in ovo* feeding of β-hydroxy-β-methylbutyrate on hatching performance, hatchability, and morphometric parameters in newly hatched Japanese quail chicks

…… Geun Yong Park, Yeong Bin Kim, Ju Yeong Park, Ji Won Shin, Jin Ho Jeong, Jong Hyuk Kim

OA26018 Effects of a coated functional feed additive on growth performance, nutrient digestibility, and meat quality in growing-finishing pigs

…… Jinmo Yang, Dongcheol Song, Kyeongho Jeon, Hyuck Kim, Hyohyeon Yu, Jinho Cho

OA26019 Precision livestock monitoring of lactating sows: YOLOv8-based behavioral analysis under varying feeding strategies

Ahsan Mehtab, Hong-Seok Mun, Eddiemar B. Lagua, Md Sharifuzzaman, Md Kamrul Hasan, Young-Hwa Kim, Jin-Gu Kang, Hae-Rang Park, Chul-Ju Yang

OA26020 Processing-dependent effects of black soldier fly larvae on nutrient digestibility, palatability, and fecal microbiota in cat

Kyeongho Jeon, Dongcheol Song, Hyuck Kim, Jinmo Yang, Hyohyeon Yu, Jinho Cho

OA26021 Evaluation of the nutritional value and feeding efficacy of Adzuki beans (*Vigna angularis*) as a pet food ingredient in dogs

Shahanaz Begum, Tae-Woong Baek, HyunWoo Song, Ki-Chang Nam, Sang-Suk Lee, Ki Hyun Kim

OA26022 Aflatoxin risk assessment of commercial dry dog food

Su-Hyeon Yang, A-Jin Lee, Min-Jeong Kim, Mi-seong Lee, Seung-Hee Baek, In-Sik Nam

OA26023 A novel procedure of the multi-sample simultaneous *in vitro* assay for protein digestibility of dog diets

Yujeong Hwang, Yoon Soo Song, Beob Gyun Kim

OA26024 Effect of dietary supplementation of magnesium oxide and magnesium sulfate on productive performance, egg quality, and eggshell ultrastructure in laying hens

Ryun Ha Kim, Dong Yong Kil

OA26025 Meta-analysis of interactive effects of dietary digestible total sulfur amino acids and crude protein on productive performance in early laying hens

Hyun Woo Kim, Dong Yong Kil

OA26026 Effects of multi-enzyme supplementation on growth, nutrient utilization, and intestinal health in broilers under nutrient-deficient diets

Nuwan Chamara Chathuranga, Myunghwan Yu, Shan Randima Nawarathne, Elijah Ogola Oketch, Haeeun Park, Sehyeok Oh, Ulvis Hewage Gavindu Madushan, Uwimbabazi Alphonsine, Nyiransabimana Agnes, Hans Lee, Jung Min Heo

OA26027 Effect of individual or combined supplementation of arginine and betaine in low-crude protein diets on growth performance, serum measurement, and liver health in broiler chickens raised under multiple stress conditions

Ji Hye Lee, Dong Yong Kil

OA26028 **Reduced energy diet reformulation enhances growth performance and feed efficiency via improved intestinal morphology in broiler chicken**

………… Ulvis Hewage Gavindu Madushan, Shan Randima Nawarathne, Nuwan Chamara Chathuranga, Elijah Ogola Oketch, Sehyeok Oh, Nyiransabimana Agnes, Uwimbabazi Alphonsine, Jung Min Heo

OA26029 **Modulatory effects of a novel functional oil feed additive on the intestinal microbiota of avian and mammalian models**

………… Sung Hyun Park, Eun Bae Kim

제2발표분야 : 반추영양

OB26001 Identifying critical temperature-humidity index thresholds for heat stress in growing Korean crossbred black goats

Yun-Seo Song, Ji-Yun Hwang, Xue-Cheng Jin, Jang-Hoon Jo, and Hong-Gu Lee

OB26002 Sporulation potential is associated with prophage carriage in bovine gut Bacillota

J. M. Kim, J. B. Moon, H. B. Kim, J. Seo

OB26003 Shotgun metagenomic and genome-resolved analysis of 3-nitrooxypropanol mediated methane mitigation in Hanwoo steers during the early fattening period

Ryukseok Kang, Rajaraman Bharanidharan, Kyoung-Hoon Kim, Tansol Park

OB26004 Comparison of growth performance, rumen fermentation characteristics, blood profiles, and carcass traits in finishing Hanwoo heifers divergent in genomic estimated breeding value for marbling score

Hyeonwook Shin, Dajeong Lim, Daekyeom Yoo, Joonbeom Moon, Jongmin Kim, Beomseok Kim, Seongjin Lee, Geuntae Kim, Jakyeom Seo

OB26005 Effects of total mixed ration with methane-mitigating microbes on growth performance, rumen fermentation, methane emissions, and rumen microbiota in Hanwoo steers

Khanza Syahira Dhia, Mozart Nuzul Aprilliza AM, Shahanaz Begum, Eun-Chan Lee, A-Rang Son, Michelle Miguel, Ye Pyae Naing, Keun-Sik Baik, Seon-Ho Kim, Sang-Suk Lee

OB26006 Effects of Methastop® supplementation on enteric methane emissions in Hanwoo cattle

Muhammad Raihan Qawwali, Andrian D. Ragandang, Hyunjin Cho, Hamin Kang, Chan-Soo Park, Seongwon Seo

OB26007 TMR의 발효 기간에 따른 반추위 소화율 및 메탄 발생량 평가

김지윤, 조현진, 장태경, 김원경, 서성원

OB26008 Effect of cashew nut meal replacement on enteric methane emissions in Holstein heifers

Si-Hyeon Lee, Jae-Sung Lee, Jang-Hoon Jo, Jun-Seo Kim, Chang-Sik Kim, Hong-Gu Lee

OB26009 A comparative study on the nutritional composition, *in vitro* rumen fermentation characteristics, and microbiome of diverse forages for goats

Sohyeon Kim, Gyeongjin Kim, Suyeo Baek, Eun Joong Kim

OB26010 **The effects of different vitamin mixtures on the productivity and physiological responses of Hanwoo heifers under heat stress conditions**

B. S. Kim, S. J. Lee, J. B. Moon, D. K. Yoo, J. M. Kim, H. W. Shin, G. T. Kim, J. K. Park, J. S. Ahn, J. H. Lee, D. J. S. Jeong, G. H. Son, J. K. Seo

OB26011 **Effects of L-citrulline supplementation on lactational performance and blood responses in lactating Holstein cows with A1 and A2 β-casein genotypes under heat stress condition**

Do-hye Heo, Min-Ah Park, Jae-Sung Lee, Hong-Gu Lee

OB26012 **인공지능(AI) 활용 스마트 축산을 위한 한우 사양 관리 온톨로지 개발**

박성원, 조현진, 이성훈, 박재화, 서성원

OB26013 **Characterizing rumen antimicrobial resistance gene composition across studies and its implications for microbiome–resistome integration**

Mylvie Alexis M. Batican, Joonpyo Oh, Tansol Park

OB26014 **Integrated processing of soybean meal as nutritional strategy to support performance in heat-stressed Holstein dairy cows**

Mozart Nuzul Aprilliza AM, Khanza Syahira Dhia, Tae-Woong Baek, Je-Ho Kang, A-Rang Son, Michelle Miguel, Ye Pyae Naing, Seon-Ho Kim, Sang-Suk Lee

제3발표분야 : 동물생명공학

OC26001 Propiconazole impairs mitochondrial OXPHOS through disruption of electron transport chain activity in porcine endometrial luminal epithelial cells

Jeongyeon Son, Wonhyoung Park

OC26002 Nest-building intensity in prepartum period is associated with distinct gut microbial profiles in loose-housed sows

Sarbani Biswas, Jinhyeon Yun

OC26003 Comparative analysis of SLA-DRB1 allelic diversity in Vietnamese and Jeju native pigs and their insights into antigen presentation potential

Nguyen Thu Uyen, Rida Arshad, Tayyaba Riaz, Yusu Park, Hilal Tayara, Jae-Young Heo, Ki-Duk Song

OC26004 Transcriptomic analysis of bovine peripheral blood mononuclear cells stimulated with antigens from bovine digital dermatitis associated treponemes

Edeneil Jerome Valete, Hector Espiritu, Kichan Lee, Sujeong Jin, Sulistiyoningtiyas Irmawanti, Ko Dain, Lee Yebin, Myunghwan Jung, Yongil Cho

OC26005 Effects of L-carnosine on oxidative stress and myogenic differentiation in bovine skeletal muscle-derived cells under heat stress

Jun-Hee Lee, Xue-Cheng Jin, Bo-Mi Kim, Jin-Soo Park, Hyeon-Jun Oh, Hong-Gu Lee

OC26006 Protein engineering of a novel recombined lytic enzymes against rumen methanogens in livestock

Hyeonjun Lee, Eun Bae Kim

OC26007 Comparative analysis of 2D and 3D culture systems using Hanwoo skeletal muscle-derived cells

Hyeon-Jun Oh, Xue-Cheng Jin, Jun-Hee Lee, Bo-Mi Kim, Hong-Gu Lee

OC26008 Sensor-based detection of alterations in social relationships in laying hens and dairy calves with diseases

Hyungwook Kang, Jinhyeon Yun

OC26009 Effects of TLR signaling on immune activation and metabolic regulation in chicken macrophages under distinct modes of *Salmonella* uptake

Keesun Yu, Young Jin Pyung, Da-Jeong Park, Ki-Duk Song, Hyuk-Joon Kwon, Yeong Ho Hong, Tina Sørensen Dalgaard, Younghoon Kim, Byung-Chul Park, Tae Sub Park, Cheol-Heui Yun

제4발표분야 : 번식 및 생리

OD26001 Effects of circadian rhythm-based vaccination timing on antigen-specific fecal IgA responses in broiler chickens

…… Seonju Lee, Eun Bae Kim

OD26002 Prolonged farrowing and impaired nursing behaviour are associated with gut microbial alterations in sows with large litters

…… Yujin Jung, Woohee Chung, Jua Woo, Juho Lee, Cheolju Park, Minseok Kim, Jinhyeon Yun

OD26003 Immortalization of Hanwoo reproductive cells for heat stress *in vitro* research

…… Ismail Shaleh, Sung Woo Kim, Tae Sub Park, Joonghoon Park

OD26004 Milk-derived extracellular vesicles enhance oocyte competence and embryo development during bovine *in vitro* maturation

…… Hyeong-Tae Jeon, Gyeong-Min Gim, Goo Jang, Junkoo Yi

OD26005 Ultrasonographic ovarian morphological characteristics according to the interval from calving to conception in postpartum primiparous Hanwoo cows

…… Yonghwan Kim, Sung-Sik Kang

OD26006 Integrating systematic labeling with machine learning for non-invasive reproductive stage detection in dairy cattle via feed intake patterns

…… Wookyung Lee, Dong-Hyeon Kim, Jae-Woo Song, Seung-Hyun Lee, Seongwon Seo, Wang-Hee Lee

OD26007 Effects of canine-assisted interventions on neurophysiological and psychological responses

…… Youngwook Jung, Gaeun Jeong, Yujin Song, Kayoung Yang, Kyongwon Yoo, Youngtae Heo, Minjung Yoon

OD26008 The effects of equine-assisted intervention on young adult women with depression

…… Gaeun Jeong, Suhyun Kim, Yujin Song, Youngwook Jung, Jae-Sung Lee, Hong-Gu Lee, Minjung Yoon

제5발표분야 : 축산물 이용 및 가공

OE26001 Effects of slaughter age on enteric methane emissions and production efficiency in Hanwoo steers

…… Shine Htet Aung, Sang-Suk Lee, Seon-Ho Kim, Nam Ki-Chang

OE26002 Predicting eating quality of pork shoulder butt using Vis/NIR hyperspectral imaging and machine learning models

…… Jeong Beom Ju, Hye-Jin Kim, Seokjun Lee, Dongheon Lee, Hyunsu Cho, Dae Seung Kim, Cheorun Jo

OE26003 Development of a non-destructive prediction model for crude fat and protein content in beef loin using hyperspectral imaging

…… Seul-Ki-Chan Jeong, Hayeon Jeon, Soeun Kim, Seokhee Han, Minkyung Woo, Samooel Jung

OE26004 Development of an oxygen-gradient-based 3D intestinal model platform for the discovery of next-generation livestock probiotics: validation of the intestinal barrier-enhancing effects of *Bifidobacterium adolescentis* OP820

…… Saeyoun Shin, Sejong Oh

OE26005 Protective effects of probiotic strains against gastric and intestinal inflammation and modeling of freeze-drying

…… Kiyeop Kim, Sejong Oh

OE26006 Impacts of whey protein isolate edible coating on digestibility and bioactivity of cheeses during *in vitro* digestion

…… Yupa Tin Soe, Gi-Ju Shin, An So Yeon, Mingi Jeong, Yeeun Bae, Ho-Kyung Ha

제6발표분야 : 유전 및 육종

OF26001 Multi-algorithmic translation of genomic estimated breeding value (GEBV) into fattening types of Hanwoo cattle

.... Jae-Woo Song, Dong-Hyeon Kim, Dajeong Lim, Dae-Hyun Lee, Seongwon Seo, Wang-Hee Lee

OF26002 Comparative unsupervised clustering of Hanwoo cattle based on genomic estimated breeding values for carcass traits

.... Dong-Hyeon Kim, Jae-Woo Song, Dajeong Lim, Dae-Hyun Lee, Seongwon Seo, Wang-Hee Lee

OF26003 Individual-level structural equation-based genome-wide association studies of direct and mediated genetic effects on carcass traits in Korean Jeju black cattle

.... Azizul MD Haque, Se-Pill Park, Jong-Joo Kim

제7발표분야 : 환경 및 축산 기타

OG26001 Social stability-related behavioural profiles linked to maternal performance and piglet outcomes, and reproductive feasibility of intermittent suckling in a communal farrowing system

…… Woohee Chung, Jinhyeon Yun

OG26002 Estimation of annual volatile solid excretion from pigs for the calculation of methane emission from manure in Korea

…… Donghyeon Lee, Beob Gyun Kim

OG26003 Multiclass acoustic monitoring in pigs: From model development to environmental respiratory stress detection

…… Md Sharifuzzaman, Hong-Seok Mun, Eddiemar B. Lagua, Md Kamrul Hasan, Jin-Gu Kang, Young-Hwa Kim, Ahsan Mehtab, Hae-Rang Park, Chul-Ju Yang

OG26004 Comparative effects of different noise stressors on growth performance and behavior in growing and finishing pigs

…… Jin-Gu Kang, Hong-Seok Mun, Eddiemar Lagua, Shariffuzzaman MD, Md Kamrul Hasan, Ahsan Mehtab, Young-Hwa Kim, Hae-Rang Park, Chul-Ju Yang

OG26005 Integrated computer vision and machine learning framework for multi-class anomaly detection in group-housed growing pigs

…… Eddiemar B. Lagua, Hong-Seok Mun, Md Sharifuzzaman, Md Kamrul Hasan, Ahsan Mehtab, Jin-Gu Kang, Hae-Rang Park, Young-Hwa Kim, Chul-Ju Yang

OG26006 Environmental enrichment and agonistic behavior in post-weaning pigs: A pilot study using artificial intelligence

…… Md Kamrul Hasan, Hong-Seok Mun, Keiven Mark B. Ampode, Eddiemar B. Lagua, Md Sharifuzzaman, Jin-Gu Kang, Young-Hwa Kim, Ahasan Mehtab, Hae-Rang Park, Chul-Ju Yang

OG26007 ICT 장비 도입에 따른 양돈 농가의 경제성 분석
Economic analysis of swine ICT equipment adoption on pig farm productivity

…… 이성호, 양철주

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OA26001

Effects of different dietary fiber sources on reproductive performance, blood profiles and milk composition in gestating sows

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This experiment was conducted to evaluate the effects of different dietary fiber sources on reproductive performance, blood profiles and milk composition in gestating sows. A total of 40 multiparous F1 sows (Yorkshire × Landrace) with an average body weight of 216.09 ± 0.59 kg were allotted to 4 dietary treatments with 10 replicates per treatment in a completely randomized design (CRD). The dietary treatments were as follows: 1) CON: basal diet, 2) BP: basal diet + 6% beet pulp, 3) WB: basal diet + 6% wheat bran, and 4) SH: basal diet + 6% soybean hull. In reproductive performance, litter weight gain tended to be higher in BP compared with CON ($p = 0.09$). In blood profiles, glucose concentration at day 105 of gestation was significantly higher in BP, followed by WB, CON, and SH ($p < 0.01$). Similarly, at day 21 of lactation, glucose concentration was significantly higher in BP and WB than in SH ($p < 0.01$). In piglets, total cholesterol concentration at 24 h postpartum was higher in BP than in CON and SH, while WB was higher than SH ($p = 0.02$). Colostrum fat concentration at 24 h postpartum was higher in BP than in the other treatments ($p = 0.04$). Consequently, beet pulp showed greater potential as a dietary fiber source for gestating sows compared with wheat bran and soybean hull.

Key words : gestating sows, lactating sows, beet pulp, wheat bran, soybean hull

OA26002

Effects of dietary crude protein levels on growth performance, hematological parameters, and intestinal gene expression in weaning pigs

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This study investigated the effects of dietary crude protein (CP) levels on the growth performance, hematological parameters, and intestinal gene expression of weaning pigs. A total of 120 weaning pigs (6.39 ± 0.093 kg) were assigned to 4 treatments with 6 replicates per treatment (5 pigs per pen). The treatments consisted of varying CP levels: 1) CP14: 14% CP, 2) CP16: 16% CP, 3) CP18: 18% CP, and 4) CP20: 20% CP. The results showed that although growth performance increased linearly with higher CP levels ($p < 0.01$), there were no significant differences in overall average daily gain and gain-to-feed ratio among the CP16, CP18, and CP20 groups ($p > 0.05$). Regarding fecal score, the CP16 group exhibited significantly lower scores compared to the CP20 group during PhaseI ($p < 0.05$), effectively mitigating post-weaning diarrhea. In PhaseII, hematological parameters such as hemoglobin and hematocrit in the CP16 group were not significantly different from those in the CP20 group ($p > 0.05$). Furthermore, the ileal mRNA expression of tight junction proteins (*MUC2, OCLN,* and *CLDN1*) in pigs fed 16% CP remained as high as those fed 20% CP ($p > 0.05$). In conclusion, reducing the dietary CP level to 16% serves as an optimal nutritional strategy to maintain growth performance while simultaneously improving gut health and reducing the incidence of diarrhea in weaning pigs.

Key words : crude protein levels, low-protein diet, tight junction proteins, fecal score, weaning pigs

OA26003

High-dose anandamide supplementation reduces treatment incidence in weaned pigs under elevated ambient temperature

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Post-weaning piglets are exposed to multiple stressors that can be exacerbated by elevated ambient temperatures, leading to impaired health status and increased therapeutic intervention. Anandamide (AEA) has been suggested to modulate stress-related physiological responses; however, its effects on health-related outcomes in weaned pigs under heat stress remain unclear. This study evaluated whether dietary AEA supplementation influences growth performance and treatment incidence (TI) in weaned pigs. A total of 600 weaned pigs were randomly assigned to four treatments: NC (2,000 ppm rice hulls), A1 (1,000 ppm AEA + 1,000 ppm rice hulls), A2 (2,000 ppm AEA), and CA (2,000 ppm citric acid). Supplements were top-dressed onto the basal diet for 7 days after weaning. Growth performance and mortality were evaluated on days 0, 7, and 21, while TI was recorded over 35 days post-weaning. Dietary treatments had no significant impact on growth performance, except for a lower ADG in the A1 group compared with the CA group between days 7 and 21 ($p < 0.05$). However, pigs in the A2 group exhibited lower TI than those in the NC and A1 groups by day 35 ($p < 0.05$), indicating reduced need for therapeutic intervention. In conclusion, AEA supplementation had limited effects on growth performance under high-temperature conditions. However, high dose of AEA was associated with reduced TI, suggesting a potential improvement in health-related outcomes and resilience to post-weaning stress.

Key words : anandamide, growth performance thermal stress, treatment rate, weaning piglets

OA26004

Influence of dietary electrolyte balance reduction using calcium chloride at expense of limestone on growth performance and odorous compounds of growing pig

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This study was conducted to investigate the effect of dietary electrolyte balance (dEB) on growth performance and concentration of volatile organic compounds and volatile fatty acids in fecal samples of growing pigs. A total of 90 crossbred barrows (34.1 ± 2.97 kg) were assigned to three dietary treatments with six replicates in a randomized complete block design. The dietary treatments consisted of three diets with dEB levels adjusted to 159, 80, or 1 mEq/kg, achieved by replacing limestone with anhydrous calcium chloride in the diets at 0%, 50%, or 100%, respectively. The pigs had free access to water and experimental diets and were reared in controlled environment. The experimental period lasted five weeks. Data were analyzed using the MIXED procedure of SAS, and linear and quadratic effects were evaluated using orthogonal polynomial contrasts. Statistical significance and tendency were defined at $p < 0.05$ and $0.05 \leq p < 0.10$, respectively. Average daily gain tended to decrease linearly as dEB decreased from 0 to 3 weeks ($p = 0.077$) and 0 to 5 weeks ($p = 0.059$). Average daily feed intake decreased linearly ($p = 0.002$) from 3 to 5 weeks and showed a quadratic response ($p = 0.029$) from 0 to 5 weeks as dEB decreased. Gain-to-feed ratio exhibited a quadratic response to decreasing dEB from 0 to 3 weeks ($p = 0.001$) and 0 to 5 weeks ($p < 0.001$). Decreasing dEB tended to reduce fecal p-cresol ($p = 0.086$) and skatole ($p = 0.073$) concentrations but did not affect volatile fatty acids concentrations in fecal samples. In conclusion, lower dEB may mitigate odor emission, but excess reduction of dEB can lead to a decline in growth performance.

Key words : calcium chloride, dietary electrolyte balance, growth performance, growing pigs, odorous compounds

OA26005

The effect of a low-protein diet on growth performance and fecal odor compounds in finishing pigs

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This study examined the effects of reducing dietary crude protein (CP) on growth performance and fecal odor-related compounds in finishing pigs. A total of 90 crossbred ([Yorkshire × Landrace] × Duroc) finishing pigs with an average body weight (BW) of 76.6 ± 2.43 kg were used. Pigs were allocated to three dietary treatments (10%, 12%, and 14% CP) in a randomized complete block design based on BW, with six replicates per treatment and five pigs per pen. All diets met or exceeded the recommended nutrient requirements except CP. On days 0, 21, and 35, BW and feed leftover were recorded, and fecal samples were collected on days 22 and 34 from the median-weight pig in each pen to determine volatile organic compounds and volatile fatty acids. Data were analyzed using the MIXED procedure of SAS, and linear and quadratic effects of dietary CP were evaluated by orthogonal polynomial contrasts. Lowering dietary CP resulted in linear decreases in BW and average daily gain during days 0–21 ($p < 0.05$), and gain-to-feed ratio tended to decrease ($p = 0.0751$). However, no differences in growth performance were observed during days 21–35 or over the entire period. Phenol and indole were not detected in fecal samples. On day 34, fecal p-cresol increased linearly with decreasing CP ($p < 0.05$), whereas skatole showed a tendency to increase ($p = 0.0610$). In fecal samples, isovaleric acid tended to increase ($p = 0.0883$), and n-valeric acid increased linearly ($p < 0.05$) as dietary CP decreased. Overall, reducing CP from 14% to 10% while meeting essential amino acid requirements did not affect growth performance over the entire experimental period, although some fecal odor-related compounds increased.

Key words : finishing pig, fecal odor compounds, growth performance, low protein

OA26006

Effects of palm kernel by-product type and inclusion level on growth performance, pork quality, and carcass characteristics in growing-finishing pigs

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This experiment was conducted to evaluate the effects of palm kernel by-product type and inclusion level on growth performance, pork quality, and carcass characteristics in growing-finishing pigs. A total of 126 growing pigs ([Yorkshire × Landrace] × Duroc), average 35.09 ± 0.47 kg body weight (BW), were allotted to 6 treatments by BW and sex in 3 replications with 7 pigs per pen in a randomized complete block (RCB) design. Dietary treatments included palm kernel expeller (PKE) or palm kernel meal (PKM) supplemented with 0.04% β-mannanase at inclusion levels of 4, 8, 12%. In growth performance, average daily gain (ADG) was higher in pigs fed PKM diets than in those fed PKE diets during the late growing-finishing phase and whole experimental period ($p = 0.05$; $p = 0.04$). Gain to feed ration (G:F) was increased as the inclusion level of palm kernel by-products increased during weeks 0 to 9 ($p = 0.02$). No significant differences were observed in pork quality traits ($p > 0.05$). However, backfat thickness increased with increasing inclusion levels of palm kernel by-products ($p = 0.02$), and carcass grade was significantly improved in pigs fed PKM diets compared with those fed PKE diets ($p = 0.03$). Consequently, PKM showed greater potential as a feed ingredient than PKE when supplemented with β-mannanase in growing-finishing pig diets.

Key words : growing-finishing pigs, palm kernel expeller, palm kernel meal, β-mannanase

OA26007

Dietary bacteriophage on growth performance, fecal microbiome, diarrhea incidence, and nutrient digestibility in weaning pigs

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This experiment was conducted to evaluate the effects of dietary bacteriophage supplementation on growth performance, nutrient digestibility, diarrhea incidence and fecal microbiome in weaning pigs. A total of 160 weaning pigs ([Yorkshire × Landrace] × Duroc), with an average initial body weight of 8.30 ± 0.14 kg, were allotted to 4 treatments in a randomized complete block (RCB) design. Dietary treatments included supplementation with 0, 0.05, 0.10, or 0.15% bacteriophage targeting *E. coli, Salmonella* spp., and *C. perfringens* for 5 weeks. The results showed that average daily gain (ADG) increased linearly during the late weaning and overall periods, leading to a tendency for increased body weight at week 5 (p = 0.03; 0.04; 0.10). Gain to feed ratio (G:F) tended to increase linearly during the early weaning period (p = 0.07). In addition, diarrhea incidence decreased linearly during the late weaning and overall periods with increasing levels of bacteriophage supplementation (p = 0.07; 0.04). Weighted UniFrac and LEfSe analyses indicated selective modulation of fecal microbial communities, including reduced abundance of Proteobacteria and increased abundance of beneficial genera such as *Bifidobacterium* and *Prevotella*. Consequently, supplementation with 0.15% bacteriophage improved growth performance and reduced post-weaning diarrhea through selective modulation of gut microbiota without disrupting microbial diversity.

Key words : bacteriophage, weaning pigs, growth performance, fecal microbiome

OA26008

Weaning weight-related differences in growth performance, nutrient digestibility, blood profiles, and intestinal morphology in pigs

Hyuck Kim, Dongcheol Song, Kyeongho Jeon, Jinmo Yang, Hyohyeon Yu, Jinho Cho

Chungbuk National University

This study was conducted to evaluate whether weaning weight (WW) at 28 d of age could serve as an indicator of postweaning robustness by comparing growth performance, nutrient digestibility, blood profiles, and intestinal morphology of pigs differing in body weight (BW). Among a total of 124 pigs, 74 pigs corresponding to the upper and lower 30% of the WW distribution were selected and assigned to heavy BW (HBW) and light BW (LBW) groups, respectively, and monitored until d 56 of age. In this study, the HBW group showed higher ($p < 0.05$) body weight, average daily gain, and apparent total tract digestibility of dry matter, crude protein, and gross energy than the LBW group. Differences in intestinal morphology were observed, HBW group exhibiting higher ($p < 0.05$) villus height (VH), villus width (VW) and villus height to crypt depth ratio (VH:CD). Blood profiles indicated elevated ($p < 0.05$) cortisol, tumor necrosis factor-α, interleukin-6, and interleukin-10 levels in LBW group, reflecting enhanced systemic stress and inflammatory activation. Correlation analysis further demonstrated positive associations between WW and growth performance and nutrient digestibility, VH, VW and VH:CD while showing negative correlations with inflammatory and stress markers. These results indicate that WW is closely linked to postweaning physiological responses and serve as a practical predictor of robustness, digestive capacity, and growth potential during the nursery phase.

Key words : weaning weight, robustness, nutrient digestibility, cytokines, intestinal morphology

OA26009

Solvens® supplementation improved immune and gut health in weaned piglets vaccinated with PRRSV

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Porcine reproductive and respiratory syndrome virus (PRRSV), which belongs to the family *Arteriviridae*, causes substantial economic losses in the pig industry worldwide. Solvens® is a feed additive based on *Bacillus* (*B. licheniformis* and *B. subtilis*). The objective of this study is to evaluate the efficacy of Solvens® on growth performance, gut health and the immune system in weaned piglets vaccinated with Porcine reproductive and respiratory syndrome virus (PRRSV). 96 crossbred weaning pigs are randomly allotted two treatments (12 replicates per treatment) based on body weight and the experiment conducted 28 days. The dietary treatments included VAC (basal diet + vaccinated with PRRSV) and VAC+PRO (VAC + 0.04% of solvens). VAC+PRO showed higher ADG and FCR during d 8–28, d 1–28, and BW at d 28 than VAC. Solvens® supplementation improved Diarrhea score during d 1–7 and d 1–28. Also, Solvens® supplementation improved ATTD of DM, CP, EE, and OM on d 7; DM and CP on d 14; and DM, CP, and GE on d 28. Solvens® supplementation improved AID of CP, GE, and OM on d 28. On d 7 and d 28, Solvens® supplementation improved IgG and serotonin TNF-α, IL-6, and cortisol. VAC+PRO showed higher villus height and lower crypt depth compared to VAC. Fecal acetate and propionate concentrations were significantly increased on d 28 in VAC+PRO. VAC+PRO showed lower *Ruminococcus* abundance on d 28 compared to VAC. These results consistently demonstrate that Solvens® supplementation improves overall health of piglets under PRRSV vaccination-induced immune stress.

Key words : weaned piglets, PRRSV, probiotics, immune, gut health

OA26010

Partial replacement of molasses with monosodium glutamate–condensed molasses soluble improves growth performance while maintaining gut health in finishing pigs

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A total of 210 crossbred pigs [(Landrace × Yorkshire) × Duroc] with an initial body weight (BW) of 53.92 ± 2.24 kg were used in this experiment. The pigs were randomly assigned to 1 of 3 dietary treatments in a completely randomized design, with 14 replicates of 3 females and 2 males / pen. The dietary treatments were CON: basal diet containing 4% Molasses; TRT1, basal diet with 2% molasses and 2 % Monosodium Glutamate–Condensed Molasses Soluble (MSG-CMS), while TRT3, basal diet with 4% MSG-CMS. The test diets were fed: Phase 1 (week 0–5) and Phase 2 (week 5–10). Data was analyzed using IBM SPSS version 16.0 via one-way ANOVA, difference among the treatments were identified using Tukey's test. $p < 0.05$ was set as significant. Across phase 1, 2, and the overall experimental period, the inclusion of 0.4% MSG-CMS in pigs diet exhibited higher ($p < 0.05$) average daily gain and average daily feed intake compared with the other treatment groups. However, no significant differences were observed in nutrient digestibility of dry matter, nitrogen, or energy, backfat thickness and lean meat percentage, nor meat quality and carcass characteristic among treatments. At week 10, pigs receiving 0.4% MSG-CMS exhibited a significantly higher ($p < 0.05$) blood insulin concentration compared to the other groups. The alpha diversity indices (observed features, Chao1, Shannon, Simpson, and Pielou's evenness) were not influenced by dietary treatments. Similarly, beta diversity analysis based on Bray–Curtis and unweighted UniFrac distances revealed no clear separation among treatment groups. At the phylum level, CON group showed the most abundant *Proteobacteria*, followed by *Bacteroidota*. At the genus level, *Prevotella* was more abundant in the CON group, followed by *Bacteroides*. In contrast, LEfSe consistently showed significant overgrowth of *Clostridium sensu stricto 1 Clostridium_sensu_stricto* in TRT2 group. In summary partial or complete replacement of molasses with MSG-CMS (up to 0.4%) improved growth performance (ADG and ADFI) in finishing pigs without negatively affecting feed efficiency, nutrient digestibility, carcass traits, meat quality, or gut microbial diversity. Overall, MSG-CMS can be considered a viable alternative to molasses in finishing pig diets, offering modest performance benefits without adverse physiological or microbiological effects.

Key words : nutrient digetsibilty, meat quality, condensed molasses, blood profile

OA26011

Dietary Mycofix® plus 5.0, a toxin binder mitigates multi-mycotoxin induced impairments in growth performance, gut integrity, and reproductive indicators in finishing gilts

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Multi-mycotoxin (MMT) contamination in swine diets poses a major threat to animal health and productivity, particularly female gilts are susceptible, often exhibiting impaired growth, nutrient utilization, and intestinal integrity. To address this challenge, n = 63 gilts [Landrace × Yorkshire) × Duroc; 70.84 ± 2.68 kg; 18 weeks old] were randomly allocated to three treatments in a completely randomized design for 7 weeks (7 replicates/treatment; 3 gilts/pen) to evaluate whether Mycofix® Plus 5.Z, a toxin deactivator can mitigate the adverse effects of multi-mycotoxin [Zearalenone (ZEN), Deoxynivalenol (DON) , Fumonisin (FUM)] on performance of finishing gilts. The diets were CON: basal diet; TRT1 (Challenge): a basal diet artificially contaminated with a MMT premix (770 g/ton) providing 250 ppb ZEN, 1,500 ppb DON, and 5,000 ppb FUM B1; and TRT2: TRT1 diet mixed with 2 kg/ton Mycofix® Plus 5.Z. All data were analyzed using the General Linear Model procedure of SAS (SAS 9.4, Institute Inc., Cary, NC, USA) using a one-way ANOVA. Differences among treatment means were determined using Tukey's multiple range test, and significance was declared at $p < 0.05$. Our results demonstrate that dietary Mycofix® Plus 5. Z significantly improved ($p < 0.05$) final body weight, average daily gain, and feed intake in gilts compared with the MMT group. Furthermore, mycotoxin challenge reduced ($p < 0.05$) dry matter and nitrogen digestibility; however, Mycofix® supplementation significantly restored nitrogen utilization. Intestinal morphology of MMT group showed significantly decreased ($p < 0.05$) villus height and VH:CD ratio and increased crypt depth. Similarly, the regulation of tight junction proteins (Claudin-4, Zonula Occludens-1, and Occludin) was significantly improved ($p < 0.05$) with Mycofix® Plus 5.Z. While alanine aminotransferase, gamma-glutamyl transferase, and malondialdehyde levels had tended to reduce in TRT2. At the phylum level, TRT1 exhibited dysbiosis (increased Bacillota. reduced Bacteroidota). Furthermore, at genus level, Mycofix® supplementation increased beneficial *Lactobacillus* and SCFA-producing bacteria while reducing harmful taxa. Based on this result, we suggest that adding 2 kg/ton a mycotoxin deactivator in gilts diet would be beneficial to counteract toxicity and maintain performance under contaminated feeding conditions.

Key words : zearalenone, deoxynivalenol, fumonisin, physiological responses, gut integrity

OA26012

Effects of supplementing zinc oxide and *Tenebrio molitor* larvae to nursery pig diets

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Weaning impairs intestinal homeostasis and growth in nursery pigs, and pharmacological ZnO has been widely used to alleviate these challenges. However, environmental concerns regarding ZnO have increased interest in sustainable alternatives such as Tenebrio molitor larvae (TML). Therefore, this study evaluated the effects of ZnO and TML on growth performance and intestinal health in nursery pigs under unhygienic conditions. A total of 128 pigs were assigned to four dietary treatments: basal diet (CON), basal diet + 2,000 ppm ZnO, basal diet with 5% TML, and basal diet containing both ZnO and TML. Partial replacement with TML improved body weight and average daily gain, while both ZnO and TML reduced feed intake and improved feed efficiency. Diarrhea scores were reduced by both additives, and TML decreased inflammatory markers and improved intestinal barrier integrity without negatively affecting intestinal morphology. These results suggest that TML may serve as a sustainable nutritional strategy to partially replace pharmacological ZnO in nursery pig diets.

Key words : nursery pigs, pharmacological zinc oxide, *Tenebrio molitor* larvae, under unhygienic condition, weaning stress

OA26013

A functional bioactive complex based on sustainable nutrition improves production performance, reduces harmful gas emissions, and mitigates lipopolysaccharide-induced immune stress in laying hens

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This study aimed to evaluate the effects of a sustainability-oriented functional bioactive compound (FBC, Probiotic and beta glucan) on production performance, egg quality, nutrient digestibility, excreta gas emissions, and immune responses under lipopolysaccharide (LPS)-induced stress in laying hens. For a period of 12-weeks n = 240 Hy-Line Brown laying hens (38 weeks of age) were randomly assigned to two dietary treatments: a basal diet (CON) or the basal diet supplemented with FBC (TRT, 0.1 % each), with 10 replicates per treatment and 12 hens per replicate. At the end of the feeding trial, an independent experiment was conducted to assess immune responses. N = 30 layers from each treatment were selected randomly and 15 birds were intraperitoneally injected with LPS (100 μg/kg) and the remaining 15 injected with an equivalent volume of saline. This experiment followed a 2 × 2 factorial design, with FBC supplementation and LPS challenge as the main factors. All experimental data were analyzed using SAS software (Version 9.4, using one-way ANOVA). Differences among treatment means were determined using Tukey's multiple range test, and significance was declared at $p < 0.05$. Birds fed FBC supplement showed increased body weight from week 6 and 12, and egg from weeks 7 to 12. Also, average egg weight increased during the late phase of the experiment (weeks 9–12). In terms of egg quality, FBC increased albumen height at week 6 and improved Haugh unit, eggshell strength, and eggshell thickness at week 12. However, FBC increased egg moisture loss on day 7 of storage at week 12. Nutrient digestibility analysis indicated that FBC enhanced the digestibility of nitrogen and Gross energy. Furthermore, FBC reduced ammonia and hydrogen sulfide emissions from excreta. Under LPS challenge, FBC reduced serum concentrations of pro-inflammatory cytokines, including interleukin-6 and tumor necrosis factor-α, with significant interactions observed between diet and LPS treatment suggesting that FBC partially alleviated LPS-induced inflammatory responses. In conclusion, dietary supplementation with FBC improved production performance and nutrient utilization reduced harmful gas emissions, and exerted anti-inflammatory and immunomodulatory effects under LPS-induced stress. We infer that FBC could serve as a functional feed additive for sustainable layer production.

Key words : immune modulation, lipopolysaccharide challenge, laying hens

OA26014

Effects of dietary starch and CP levels on growth performance, breast meat quality, gut health, and stress indicators in broiler chickens raised under heat stress

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This study was conducted to investigate the effects of dietary starch and crude protein (CP) levels on growth performance, breast meat quality, gut health, and stress indicators in broiler chickens raised under heat stress. A total of 192 21-day-old Ross 308 broiler chickens were randomly allotted to 4 treatments with 8 replicates in a 2 × 2 factorial arrangement with two starch levels (43.0% and 37.9%) and two CP levels (19.5% and 18.0%). All birds were exposed to cyclic heat stress (31.3 ± 0.7°C for 10 h/d and 23.5 ± 0.6°C for 14 h/d). Results indicated that dietary starch and CP levels had no significant interaction on growth performance, feather corticosterone, and ileal morphology. However, significant interactions ($p < 0.05$) between starch and CP levels were observed in ileal nutrient digestibility. A tendency toward an interaction ($p = 0.071$) was observed for breast meat yield. For main effects of starch levels, birds fed the high-starch diet had significantly greater ($p < 0.05$) water-holding capacity and TEER compared to those fed the low-starch diet. Regarding the main effects of CP levels, birds fed the lower CP diets showed increased ($p < 0.05$) CP digestibility and TBARS but decreased ($p < 0.05$) total antioxidant capacity, catalase activity, and TEER. In conclusion, dietary starch and CP levels do not affect growth performance under heat stress but interact to influence nutrient digestibility. Higher dietary starch improves breast meat quality and gut barrier function, whereas reduced dietary CP enhances protein digestibility while reducing antioxidant status and intestinal barrier function in broiler chickens exposed to heat stress.

Key words : broiler chicken, growth performance, gut health, heat stress, protein, starch

OA26015

Temporal dynamics and sex-specific differences in the gut microbiota of AA+ broilers

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The gut microbiota interacts with the host intestinal environment and plays a crucial role in the metabolism, immunity, and intestinal function of broiler chickens. In addition, sex is recognized as one of the major factors influencing the composition of gut microbial communities. This study was conducted to investigate the changes in gut microbiota across different growth stages and the sex-related differences in Arbor Acres Plus broilers. A total of 100 broiler chickens were raised for 20 days at the experimental farm of Yanbian University. Fecal samples and ileum contents (IC) were collected on 2, 10, 20 days. The collected samples were analyzed by amplifying the V3–V4 region of the 16S rRNA gene and sequencing using the Illumina MiSeq platform. The results showed that microbial diversity increased with the growth of broilers, and higher diversity was observed in ileum contents compared to fecal samples. At the genus level, the relative abundance of *Lactobacillus* was highest at day 20 (D20) in both fecal and ileum samples. In fecal samples, the abundance of *Lactobacillus* at D20 was significantly higher than at D2 and D10 ($p < 0.05$). *Faecalibacterium* also showed the highest abundance at D20, and its abundance in ileal content (IC) samples at D20 was significantly higher in females than in males ($p < 0.05$). These findings suggest that both growth stage and sex significantly shape the gut microbial composition in broilers, providing valuable insights for developing sex-specific and age-targeted strategies to optimize gut health and production performance. Supported by NRF/MSIT (RS-2024-00344849).

Key words : gur microbiota, broiler, 16S rRNA gene

OA26016

Real-time individual broiler monitoring system using YOLOv12 with WIoU v3 and ByteTrack for automated feeding and drinking behavior analysis

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Monitoring individual broiler behaviors is essential for early disease detection and flock management, yet manual observation remains impractical for continuous monitoring. This study aimed to develop a real-time system that detects and tracks individual broilers to automatically quantify feeding and drinking frequency. Video data were collected from a commercial broiler farm using overhead-mounted fixed cameras capturing 19 birds per frame, and YOLOv12m with ByteTrack was employed for detection and tracking, with ROIs defined around feeders and drinkers. Among the modifications tested, WIoU v3 loss achieved the highest detection accuracy (mAP@0.5 = 0.994), outperforming the baseline (0.988) and CBAM/SPD-Conv variants. Since the tracking pipeline relies on robust detection rather than sub-pixel localization, the WIoU v3 model was selected as the final detector. ByteTrack successfully maintained individual IDs despite frequent occlusions, and the ROI-based analysis automatically quantified per-bird feeding and drinking frequencies. Automated counts showed strong agreement with manual observations for both feeding (r = 0.906) and drinking (r = 0.970) visits, validating system accuracy. The proposed pipeline enables practical, non-invasive individual broiler monitoring applicable to precision livestock farming. Future work will correlate the measured behavioral patterns with growth performance and health indicators. Supported by NRF/MSIT (RS-2024-00344849).

Key words : broiler, precision livestock farming, YOLOv12, object tracking, behavior analysis

OA26017

Effects of *in ovo* feeding of *β*-hydroxy-*β*-methylbutyrate on hatching performance, hatchability, and morphometric parameters in newly hatched Japanese quail chicks

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This study evaluated the effects of *in ovo* feeding (IOF) of *β*-hydroxy-*β*-methylbutyrate (HMB) on hatching performance, hatchability, and morphometric parameters in newly hatched Japanese quail chicks. A total of 468 eggs from 16-week-old Japanese quail breeder flocks were randomly assigned to 3 treatments with 6 replicates of 26 eggs each. The treatments consisted of a non-injected control, a 1× PBS injection, and an HMB injection. On embryonic day 7, Japanese quail eggs in the injected groups received 50 μL of either 1× PBS or HMB solution into the air cell. The HMB solution contained 0.5% HMB dissolved in 1× PBS. All eggs were incubated at 37.5 ± 0.2°C and 60 ± 3% until embryonic day 14. Thereafter, the temperature was maintained at 37.5°C and relative humidity was increased to 70 ± 3% until hatching. After hatching, one 1-day-old chick per replicate with a body weight (BW) close to the average of each treatment group was selected to evaluate morphometric parameters. Results indicated that hatch of set was greater ($p < 0.05$) in the HMB group than in the PBS group. Chicks in the HMB group had greater ($p < 0.05$) BW and chick yield than those in the control and PBS groups. Furthermore, early embryonic mortality was lower ($p < 0.05$) in the HMB group than in the control and PBS groups. In conclusion, IOF of HMB may improve hatching performance and reduce early embryonic mortality in Japanese quail chicks.

Key words : embryonic day, hatching performance, *β*-hydroxy-*β*-methylbutyrate, *in ovo* feeding, Japanese quail

OA26018

Effects of a coated functional feed additive on growth performance, nutrient digestibility, and meat quality in growing-finishing pigs

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This study was conducted to evaluate the effects of dietary supplementation with a coated complex functional feed additive (coated essential oils, coated organic acids, vitamin E, and selenium) on growth performance, nutrient digestibility, blood profiles, and meat quality in growing-finishing pigs. A total of 90 three-way crossbred [(Landrace × Yorkshire) × Duroc] growing pigs (initial BW 59.39 ± 5.78 kg) were assigned to 3 treatments: CON (basal diet), T1 (CON + 0.02% additive), and T2 (CON + 0.05% additive), with 3 replicates of 10 pigs each for 9 weeks. T1 and T2 showed significantly improved average daily gain and feed conversion ratio throughout the experimental period ($p < 0.05$). At week 3, dry matter, crude protein, and gross energy digestibility were significantly higher in T1 and T2 than CON ($p < 0.05$). At week 9, eosinophil counts and MDA concentrations were significantly decreased, while blood selenium was significantly increased in additive-supplemented groups ($p < 0.05$). T1 and T2 exhibited significantly lower TBARS values at both week 0 and week 1 of storage compared with CON ($p < 0.05$). These results suggest that dietary supplementation with 0.02–0.05% of the coated complex additive improves growth performance, nutrient digestibility, and meat quality through oxidative stress reduction in growing-finishing pigs.

Key words : growing-finishing pigs, coated essential oils, organic acids, selenium, vitamin E, growth performance, meat quality

OA26019

Precision livestock monitoring of lactating sows: YOLOv8-based behavioral analysis under varying feeding strategies

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This study evaluated the effects of feeding frequency and thermal environment on lactating sow behavior using a YOLOv8l-based computer vision model. Eight behaviors were detected: feeding, not feeding, suckling, not suckling, lateral lying, sternal lying, standing, and sitting. The model showed high detection performance, with precision of 0.943, recall of 0.950, F1-score of 0.946, and mAP@50 of 0.965. Three groups were compared: feeding five times/day with air conditioning, hourly feeding with air conditioning, and hourly feeding without air conditioning. Hourly feeding with air conditioning increased suckling and feeding frequency and reduced feeding interval, indicating improved sow–piglet interaction. In contrast, hourly feeding without air conditioning increased lateral lying, suggesting thermoregulatory responses under warmer conditions. These results demonstrate that frequent feeding combined with thermal control can improve lactating sow behavioral patterns, while YOLOv8l provides a reliable tool for automated precision livestock monitoring.

Key words : feeding frequency, thermal environment, computer vision, YOLOv8, behavioral monitoring, posture analysis

OA26020

Processing-dependent effects of black soldier fly larvae on nutrient digestibility, palatability, and fecal microbiota in cat

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This study evaluated the effects of two drying methods (microwave drying and hot-air drying) for black soldier fly larvae (*Hermetia illucens*; HI) on nutrient digestibility, palatability, and fecal microbiota composition in cats. Three experimental diets were formulated: CON, basal diet; MW, basal diet with 3% poultry meal (PM) replaced by microwave-dried HI; HA, basal diet with 3% PM replaced by hot-air dried HI. *In vitro* digestibility (6 replicates/diet) showed significantly higher ($p < 0.05$) organic matter and crude protein (CP) digestibility in HA compared to MW and CON. Palatability assessed by two-bowl test (18 cats) showed no significant differences in any pairwise comparison. *In vivo* apparent total tract digestibility (12 cats, triplicated 3 × 3 Latin square) revealed significantly higher ($p < 0.05$) CP and ether extract digestibility in HA versus CON. Fecal microbiota analysis showed lower ($p < 0.05$) Chao1 index in MW at 10d, significant community separation by unweighted UniFrac, decreased ($p < 0.05$) *Prevotella* with HI inclusion, and reduced ($p < 0.05$) uncultured bacterial taxa in both HI groups. These results suggest that hot-air dried HI at 3% inclusion is a viable alternative protein source for cat diets, improving CP and EE digestibility without compromising palatability while inducing selective shifts in fecal microbiota.

Key words : black soldier fly larvae, cat, nutrient digestibility, palatability, drying method, fecal microbiota

OA26021

Evaluation of the nutritional value and feeding efficacy of Adzuki beans (*Vigna angularis*) as a pet food ingredient in dogs

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This study was conducted to evaluate the nutritional value of adzuki beans as a pet food ingredient, as well as their feeding safety and efficacy in dogs. Eight 7-year-old spayed female dogs were used as experimental subjects. The study was designed as a randomized 2 × 2 crossover design, comparing a control diet based on rice and chicken with a treatment diet containing 10% adzuki beans. All experimental diets met the recommended nutrient requirements established by the Association of American Feed Control Officials (AAFCO), and restricted feeding was implemented according to the metabolizable energy requirements of each individual. During the experimental period, body weight was maintained in the control group, whereas dogs in the treatment group showed an approximate 7.9% reduction in body weight at the end of the trial (10.19 kg) compared to baseline (11.08 kg) ($p < 0.01$). The apparent total tract digestibility of crude protein (98.7% vs. 87.1%) and total amino acids (93.80% vs. 88.58%) was lower in the treatment group compared to the control group ($p < 0.01$). Palatability and safety evaluations showed no significant differences between groups, and all hematological parameters (complete blood count and serum biochemistry) were within normal reference ranges. Following adzuki bean supplementation, microbial community composition (observed features and presence/absence-based beta diversity) was significantly altered, while overall diversity structure remained unchanged. Notably, in the treatment group, relative abundances of *Proteobacteria* (9.95% vs. 4.32%) and *Actinobacteriota* (5.31% vs. 1.54%) increased after supplementation compared to pre-supplementation, without major changes in dominant phyla composition.

Key words : Aduzki beans, dogs, ingredient, nutrition, gut microbiome

OA26022

Aflatoxin risk assessment of commercial dry dog food

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식품과 사료에는 다양한 유해 물질이 존재하며, 그중에서도 곰팡이 독소는 가장 광범위하게 오염되어 있고, 독성이 강한 물질로 알려져 있다. Aflatoxin(AF)은 강력한 독성과 발암성을 지닌 화합물로, 곡물 기반 사료 섭취를 통해 반려동물에게 노출될 수 있다. 특히 개는 AF에 민감하여 간독성과 면역억제를 유발할 수 있다. 따라서 반려동물 사료의 안전성 확보는 매우 중요하다. 본 연구는 한국에서 시판되는 건식 개 사료의 AF 오염 수준 및 위해를 평가하기 위해 수행되었다. 총 75개의 건식 개 사료 샘플을 수집하여 분쇄 및 균질화한 후 AF를 추출했다. 추출물은 면역친화성 컬럼(IAC)을 이용하여 정제하고 유도체화한 후 HPLC-FLD를 이용하여 정량 분석했다. 분석 방법은 검량곡선, 검출 한계(LOD), 정량 한계(LOQ), 회수율 및 반복성을 통해 검증했다. 체중 범주별 사료 섭취량을 적용하여 평균 및 극단적 노출 시나리오를 모두 고려한 노출 평가를 수행했다. 그 결과, 모든 샘플에서 AFB1이 검출되었으며, 체중이 적은 개일수록 노출 수준이 높았다. 특히 초소형 견에서 가장 높은 노출 수준과 암 발생 위험률(%) 증가가 나타났다. 또한 곡류를 포함한 식물성 원료 기반 사료에서 AF 오염이 상대적으로 높게 나타나는 경향이 관찰되었다. 이는 곡류 및 곡류 부산물이 곰팡이독소 오염에 취약한 특성에 기인한 것으로 판단된다. AFB1 함량은 법적 기준치를 초과하지 않았으나, 장기간 섭취 시 만성 질환 발생 위험이 있을 가능성이 MOE, ECR, EDI를 통해 확인했다. 장기간 동일 사료를 섭취하는 반려견의 특성을 고려할 때 이러한 노출은 더욱 중요하게 평가될 필요가 있음을 시사한다.

Key words : mycotoxin, aflatoxin, dog food, risk assessment, chronic toxicity, excess cancer risk

OA26023

A novel procedure of the multi-sample simultaneous *in vitro* assay for protein digestibility of dog diets

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The conventional *in vitro* method using flasks has a limitation that only one sample can be incubated per flask. However, the multi-sample simultaneous *in vitro* assay using the Daisy^{II} incubator, specifically designed to mimic protein digestion in dogs, has not yet been established. Therefore, the objective was to develop a novel *in vitro* procedure using the Daisy^{II} incubator for simultaneous assays of multiple dog diet samples. The *in vitro* ileal disappearance of crude protein (CP) determined using flasks ($IVID_{flask}$) in 18 commercial dog diets was obtained. To develop a novel *in vitro* ileal disappearance ($IVID_{Daisy}$) procedure using the Daisy^{II} incubator, 2 incubation periods (2 and 1 h in step 1 and 4 and 2 h in step 2) and 2 enzyme concentrations (pepsin 10 and 5 g/L in step 1 and pancreatin 100 and 50 g/L in step 2) were tested in a 2 × 2 factorial arrangement for 18 commercial dog diets. The $IVID_{Daisy}$ of CP in the 18 dog diets determined using the procedure with 5 g/L of pepsin supplementation and 2 h incubation for the stomach digestion and 50 g/L of pancreatin supplementation and 4 h incubation for the small intestine digestion was closest to the $IVID_{flask}$ of CP among the Daisy^{II} incubator procedures. In conclusion, a novel multi-sample simultaneous *in vitro* procedure was developed using the Daisy^{II} incubator by adjusting incubation periods and enzyme concentrations to determine protein digestibility of dog diets.

Key words : Daisy^{II} incubator, dogs, *in vitro*, protein digestibility

OA26024

Effect of dietary supplementation of magnesium oxide and magnesium sulfate on productive performance, egg quality, and eggshell ultrastructure in laying hens

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The current study aimed to investigate the effect of dietary supplementation with magnesium oxide (MgO; MO) and magnesium sulfate ($MgSO_4$; MS) on productive performance, egg quality, and eggshell ultrastructure in laying hens. A total of 180 Hy-Line Brown laying hens (37 weeks of age) were randomly allotted to 1 of 3 dietary treatments with 6 replicates consisting of 10 hens per replicate. The control (CON) diet was prepared to meet nutrient and energy requirement for laying hens. The CON diet contained 0.125% Mg. Two additional diets were prepared by supplementing 0.085% MgO or 0.512% MS, each providing an additional 0.05% Mg to the CON diet. Productive performance was determined for 12-week feeding trial. At the end of the experiment, egg quality was measured and eggshell ultrastructure was analyzed using a scanning electron microscope. Laying performance was not influenced by dietary treatments, except that the MS diet had greater ($p < 0.05$) feed intake than the MO diet. MO and MS diets had greater ($p < 0.05$) eggshell thickness than the CON diet, while the MS diet improved eggshell strength compared with the CON diet. For eggshell ultrastructure, both MO and MS diets increased ($p < 0.05$) overall thickness, effective layer thickness, and effective layer rate, but decreased ($p < 0.05$) mammillary layer rate compared with the CON diet. Between MO and MS diets, the MS diet showed greater ($p < 0.05$) overall thickness and effective layer thickness than the MO diet. Dietary supplementation of MO and MS at the level of 0.05% Mg in layer diets improves eggshell strength and ultrastructure. It appears that MS supplementation is more effective in improving eggshell ultrastructure than MO supplementation.

Key words : egg quality, eggshell ultrastructure, laying hen, magnesium oxide, magnesium sulfate

OA26025

Meta-analysis of interactive effects of dietary digestible total sulfur amino acids and crude protein on productive performance in early laying hens

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The current meta-analysis was conducted to determine the optimal relationship between digestible total sulfur amino acid (TSAA) and crude protein (CP) levels for improving productive performance in laying hens, with a specific focus on the early laying phase. A total of 28 studies published between 2010 and 2026 were selected according to PRISMA guidelines, and datasets belonging to early laying phase (less than 35 wk of age) were extracted for the analysis. To evaluate the interactive effects of digestible TSAA and CP in diets on laying performance (average daily feed intake, ADFI; egg production, EP; egg weight, EW; egg mass, EM; feed conversion ratio, FCR), a quadratic regression model based on the product term of dietary digestible TSAA and CP (TSAA×CP) was employed. The linear and quadratic terms of the TSAA×CP value were included as fixed effects, incorporating study as a random intercept. Models were selected to predict optimal values only when the intercept, linear coefficient, and quadratic coefficient were all significant ($p < 0.05$). Based on the selected models, optimal digestible TSAA levels were calculated by identifying the stationary point of the fitted quadratic equations across fixed dietary CP levels ranging from 12.0% to 20.0%. The quadratic regression models were significant ($p < 0.05$) for ADFI and FCR, with corresponding relative root mean square prediction error (RMSPE%) and concordance correlation coefficient (CCC) values of 9.8 and 0.14 for ADFI, and 16.1 and 0.24 for FCR, respectively. The model for FCR exhibited a greater CCC value compared with ADFI, indicating a stronger model agreement. This model also indicates that optimal digestible TSAA levels in the early laying phase to minimize FCR increased significantly by 0.01 to 0.05 percentage points for each 0.5 percentage point reduction in dietary CP levels. In conclusion, the present meta-analysis demonstrates that optimal digestible TSAA levels for early laying hens increase with decreasing CP levels in diets, providing a practical strategy for determining optimal TSAA levels under varying dietary CP levels to improve productive performance in early laying phase.

Key words : crude protein, laying hen, meta-analysis, productive performance, total sulfur amino acid

OA26026

Effects of multi-enzyme supplementation on growth, nutrient utilization, and intestinal health in broilers under nutrient-deficient diets

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This study evaluated the efficacy of multi-enzyme supplementation in mitigating the growth and physiological impairments caused by nutrient-deficient diets in broilers from 10 to 35 days of age. A total of 168 male Ross 308 broilers were assigned to three dietary treatments: a positive control (PC); a negative control (NC) with reduced metabolizable energy (–100 kcal/kg) and amino acids (–4.0%); and the NC diet supplemented with 500 g/ton of a multi-enzyme blend (NCME) containing xylanase, cellulase, β-glucanase, amylases, and proteases. Ileal segments and contents were collected for further analysis. Data were analysed using one-way ANOVA followed by Tukey's multiple range test. The nutrient-deficient NC diet significantly reduced body weight (BW) and average daily gain (ADG). However, multi-enzyme supplementation restored performance, with the NCME group (1,875.65 g) achieving a BW comparable to the PC group (1,960.03 g) by day 35. Average daily feed intake was not significant affected, whereas ADG was higher in NCME group (64.01 g/bird/day) than in the NC group and comparable to the PC group (67.27 g/bird/day) over the entire study period ($p = 0.002$). Multi-enzyme supplementation did not significantly influence most carcass traits (dressing, breast, fat pad percentages) of broilers at days 21 and 35, although it resulted in a significant increase in leg meat percentage compared to control groups at day 35. Multi-enzyme inclusion significantly improved the apparent ileal digestibility (AID) of dry matter, energy, and crude protein. Notably, on day 35, the NCME group exhibited significantly higher AID of crude protein (78.90%) compared to the NC group (73.04%). Morphological analysis showed that multi-enzyme supplementation significantly increased ileal villus height on day 21 (910.54 μm vs. 739.38 μmin NC) and day 35 (1045.41 μm vs. 920.87 μm in NC) ($p < 0.05$). In conclusion, multi-enzyme supplementation mitigated the adverse effects of nutrient-deficient diets by improving growth performance, nutrient digestibility, and intestinal morphology.

Key words : digestibility, intestinal morphology, multi-enzyme, reduced amino acids, reduced energy

OA26027

Effect of individual or combined supplementation of arginine and betaine in low-crude protein diets on growth performance, serum measurement, and liver health in broiler chickens raised under multiple stress conditions

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This study aimed to investigate the effect of individual or combined supplementation of arginine (ARG) and betaine (BET) in low-crude protein (LCP) diets on broiler performance, serum measurements, and liver health under multiple stress (MS) conditions. A total of 2,660 22-d-old Ross broiler chickens were randomly allotted to 5 dietary treatments with 7 replicates per treatment for a 14-d feeding trial. All birds were raised under MS conditions of heat stress (30.0 ± 0.43°C for 8 h/d and 25.1 ± 0.69°C for 16 h/d) and high stocking density (18 birds/m^2). Dietary treatments included control diet (CON), LCP diet by 3% CP reduction, and three LCP diets supplemented with 0.238% ARG, 0.20% BET, or their combination. Results indicated that the LCP diet did not affect performance, serum measurements, and liver health indicators compared with the CON diet. Compared with the LCP diet, however, BET supplementation improved body weight gain, but decreased feed conversion ratio ($p < 0.05$), while their improvements were numerically identified by ARG supplementation. No effect of ARG and BET combination on broiler performance was found. Individual and combined supplementation of ARG and BET reduced ($p < 0.05$) serum ALT levels without affecting serum AST and uric acid levels. While ARG or BET supplementation did not affect serum creatinine levels, their combination unexpectedly increased ($p < 0.05$) creatinine levels. Likewise, ARG or BET supplementation had no effects on liver health indicators, but their combination increased ($p < 0.05$) liver MDA levels with a numerical increase in hemorrhage score. In conclusion, LCP diets exert no negative impacts on broiler performance, serum measurements, and liver health. Individual ARG or BET supplementation in LCP diets improves broiler performance without synergistic effects of their combination. However, ARG and BET combination at the current supplemental levels may impair kidney and liver health.

Key words : arginine, betaine, broiler chicken, low crude protein diet, multiple stress condition

OA26028

Reduced energy diet reformulation enhances growth performance and feed efficiency via improved intestinal morphology in broiler chicken

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This study evaluated the effects of a reformulated wheat-corn based diet with partial replacement of corn with alternative ingredients, reduced metabolizable energy, and optimized amino acid balance across three feeding phases (pre-starter, starter, and grower) on growth performance, blood biochemical parameters, and intestinal morphology in broiler chickens. A total of 280 one day old Ross 308 male broilers were randomly assigned to four dietary treatments (Con: conventional diet throughout; T1: reformulated diet during pre-starter only; T2: reformulated diet during starter and grower phases; T3: reformulated diet throughout) in a completely randomized design (10 replicates per treatment, 7 birds per replicate) over 35 days. The control group received a conventional diet, whereas treatment groups were fed reformulated diets with reduced energy (approximately 50 kcal/kg) and balanced amino acid composition using crystalline amino acids. Growth performance was not affected during the pre-starter and starter phases ($p > 0.05$). However, final body weight at day 35 was significantly higher in T3 compared with the control (2,460.54 vs. 2,295.23 g; $p = 0.015$), and overall feed conversion ratio was significantly improved (1.28 vs. 1.33; $p = 0.015$). Intestinal morphology analysis showed a significant increase in villus height in T3 at day 21 ($p = 0.009$), whereas crypt depth was not affected ($p > 0.05$). Blood biochemical analysis at day 35 showed that triglyceride concentrations were significantly reduced in T3 compared with the control (221.25 vs. 153.55 mg/dL; $p = 0.041$), and total cholesterol was also significantly lower (132.67 vs. 113.17 mg/dL; $p = 0.005$), while glucose and liver enzyme activities remained unchanged. These findings indicate that the reformulated diet enhanced nutrient utilization and growth efficiency without adverse metabolic effects.

Key words : broiler chickens, diet reformulation, feed efficiency, intestinal morphology, lipid metabolism, reduced energy diet

OA26029

Modulatory effects of a novel functional oil feed additive on the intestinal microbiota of avian and mammalian models

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The intestinal microbiota composition is a critical determinant of health and physiological performance in livestock. This study investigated the modulatory influence of a newly developed functional oil-based feed additive on the gut microbiome of avian (chicken) and mammalian (mouse) models. Microbiome profiling via 16S rRNA gene sequencing revealed that oil supplementation significantly enhanced microbial richness and induced distinct structural reconfigurations in both models. In the chicken model, the additive effectively suppressed potential pathogens, including *Staphylococcus* ($p < 0.001$) and *Streptococcus* ($p < 0.05$), while promoting the proliferation of taxa associated with metabolic efficiency, such as *Cellulosilyticum* ($p < 0.001$), *Brevibacterium* ($p < 0.05$), and *Clostridium sensu stricto 1* ($p < 0.001$). In mice, the treatment exerted a prebiotic-like effect, characterized by a significant increase in the abundance of Lactobacillaceae ($p < 0.05$), *Bacteroides* ($p < 0.05$), and *Candidatus arthromitus* ($p < 0.05$), alongside a reduction in *Oscillibacter* ($p < 0.05$). Although body weight gain showed consistent numerical increases without reaching statistical significance, the observed microbial shifts suggest enhanced metabolic capacity and bolstered pathogen exclusion. These findings underscore the potential of this functional oil as a promising next-generation growth-promoting agent in diverse livestock species. Supported by NRF/MSIT (RS-2024-00344849).

Key words : functional oil, gut microbiome, 16S rRNA sequencing, growth promoter, pathogen suppression

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OB26001

Identifying critical temperature-humidity index thresholds for heat stress in growing Korean crossbred black goats

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This study aimed to characterize heat stress responses across temperature-humidity index (THI) levels in growing Korean crossbred black goats to establish breed-specific THI classifications. Following a 14-d thermoneutral adaptation period, 32 goats (≥ 20% Korean native black × Boer; 4 mo of age; initial BW 22.0 ± 2.9 kg) were assigned to one of eight 14-d heat stress groups (T70.0–T87.7; numbers indicate THI). Growth performance, physiological responses, and blood parameters were recorded throughout the experiment. Body weight did not differ among groups. During wk 1, ADG and water intake were greatest in T87.7 ($p < 0.05$). Respiration rate was higher in T79.8, T82.9, T84.1, and T87.7 than in T70.0, T71.7, T74.2, and T76.5 on d 3, 6, 9, and 12 ($p < 0.001$). Ocular mucosal temperature was higher in T79.8, T82.9, T84.1, and T87.7 than in T70.0 and T71.7 from d 3 to d 12 ($p < 0.001$), and ear base temperature was higher in T79.8, T82.9, T84.1, and T87.7 than in T71.7 from d 3 to d 12 ($p < 0.001$). Rectal temperature was higher in T87.7 than in T70.0, T71.7, and T74.2 at 1 w and 2 w ($p < 0.05$). TG was higher in T79.8 than in T71.7 and T76.5 at 1w ($p < 0.05$). In PBMCs, *HSP70* mRNA expression was lower in the higher THI groups (T74.2–T87.7) than in T70.0 on d 7, but was highest in T82.9 on d 14 ($p < 0.05$). *CAT* mRNA expression was lower in T82.9 than in T70.0, T74.2, T76.5, and T79.8 on d 7, and *SOD1* expression was lower in T79.8 and T84.1 than in T70.0 on d 7 ($p < 0.05$). These findings indicate that a THI of approximately 79.8 represents a critical threshold above which physiological and cellular responses to heat stress are markedly altered in growing Korean crossbred black goats, providing a physiological basis for the development of breed-specific THI classifications.

Key words : Korean crossbred black goat, heat stress, critical THI, HSP70, peripheral blood mononuclear cells

OB26002

Sporulation potential is associated with prophage carriage in bovine gut Bacillota

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Endospore formation is a major life-history trait in Bacillota and can promote persistence and transmission in gut-associated microbial communities. Because prophages are inherited with bacterial hosts during lysogeny, prophage persistence may be influenced by host traits that enhance long-term survival and dispersal. Although phage–sporulation relationships have been reported in model spore-forming bacteria and phage-centered gut studies, whether prophage carriage is broadly associated with host sporulation potential across complex gut microbial communities remains unclear. Here, we analyzed high-quality rumen Bacillota metagenome-assembled genomes to test whether provirus carriage is associated with host sporulation potential. Sporulation potential was quantified using spo0A (master regulator for sporulation) and 112 sporulation-related genes spanning major developmental stages. Spo0A+genomes encoded more complete sporulation repertoires than Spo0A− genomes and showed higher provirus prevalence. Provirus prevalence also increased across sporulation gene completeness quartiles and was observed across major Bacillota lineages. These findings suggest that prophage carriage is associated with sporulation-capable host genomic backgrounds in bovine gut Bacillota, providing community-scale evidence linking bacterial dormancy potential and temperate phage retention.

Key words : spore-forming bacteria, Bacillota, provirus

OB26003

Shotgun metagenomic and genome-resolved analysis of 3-nitrooxypropanol mediated methane mitigation in Hanwoo steers during the early fattening period

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3-Nitrooxypropanol (3-NOP) is a well-known methane inhibitor that targets methyl-coenzyme M reductase. In this study, 12 Hanwoo steers in the early fattening period were assigned to a randomized 3×3 Latin square design with three dietary treatments: control (CON), 100 ppm 3-NOP, and 150 ppm 3-NOP. Shotgun metagenomic sequencing was subsequently performed to investigate the taxonomic composition and functional profiles of the rumen microbiome. In addition, metagenome-assembled genomes (MAGs) were reconstructed to characterize genome-resolved microbial responses to 3-NOP. Statistical analyses of metagenomic features were conducted using MaAsLin3, with significance defined as a Q-value < 0.05. With a dose-dependent methane reduction, the archaeal genera *Methanobrevibacter* and *Methanosphaera* showed linear decreases following 3-NOP supplementation. The treatment also significantly affected several bacterial genera, including *Acinetobacter*, *Bacteroides*, *Parabacteroides*, and *Segatella*, as well as the fungal species *Neocallimastix californiae* and the protozoal family Isotrichidae. Functional profiling revealed decreased cofactor biosynthesis modules, including NAD biosynthesis and thiamine/TPP biosynthesis, whereas the acetyl-CoA pathway was increased. Among 1,310 reconstructed MAGs, 128 were significantly differed in response to 3-NOP. Pangenome analysis of these 3-NOP-responsive MAGs identified 7,672 gene clusters, including 2,087 clusters specific to increased MAGs and 1,394 specific to decreased MAGs. These results indicate that 3-NOP supplementation differs the rumen microbiome not only through taxonomic and functional shifts but also through distinct genome-resolved changes.

Key words : methane mitigation, 3-nitrooxypropanol, metagenome assembled genome, shotgun metagenome

OB26004

Comparison of growth performance, rumen fermentation characteristics, blood profiles, and carcass traits in finishing Hanwoo heifers divergent in genomic estimated breeding value for marbling score

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This study compared growth performance, rumen fermentation characteristics, blood profiles, and carcass traits in finishing Hanwoo heifers with divergent genomic estimated breeding values (GEBV) for marbling score. Eighteen Hanwoo heifers were classified into high (HGMS, n = 9) and low (LGMS, n = 9) marbling score GEBV groups. GEBV for carcass weight and eye muscle area were similar between groups, allowing the comparison to focus on marbling potential. Growth performance, dry matter intake (DMI), rumen fermentation parameters, serum biochemical profiles, hematological parameters, and carcass traits were evaluated. Repeated measures data were analyzed using a mixed model with treatment, week, and their interaction as fixed effects, and animal within treatment as a random effect. Initial body weight did not differ between groups, whereas average daily gain was greater in HGMS than in LGMS (0.64 vs. 0.52 kg/d, $p = 0.0456$). Total and concentrate DMI tended to be higher in HGMS ($p < 0.10$). In the HGMS group, total volatile fatty acid concentration was lower ($p < 0.05$), whereas ruminal pH tended to be higher ($p < 0.10$). Blood parameters and carcass traits did not differ between groups, except for lower creatinine in HGMS ($p < 0.05$). These results suggest that GEBV for marbling score may be associated with growth performance and metabolic status, although carcass traits were not clearly differentiated under the present finishing conditions.

Key words : genomic estimated breeding value, Hanwoo heifers, growth performance, rumen fermentation characteristics, carcass traits

OB26005

Effects of total mixed ration with methane-mitigating microbes on growth performance, rumen fermentation, methane emissions, and rumen microbiota in Hanwoo steers

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This study aimed to evaluate the effects of a total mixed ration (TMR) with methane-mitigating microbial strains (MMM) on growth performance, rumen fermentation characteristics, methane (CH_4) emissions, and rumen microbiota in Hanwoo steers. Eight steers (277 ± 22 kg) were used in a 2-period crossover design and assigned to one of two experimental groups: (1) CON (control; commercial TMR) or (2) TMR + MMM (TMR with methane-mitigating microbes). Rumen fermentation parameters (pH, ammonia-nitrogen, and volatile fatty acids) were analyzed. Total weight gain, average daily gain, dry matter intake (DMI), and feed efficiency were calculated. Enteric CH_4 emissions were measured using the GreenFeed system and expressed as daily production (g/d), yield (g/kg DMI), and intensity (g/kg $BW^{0.75}$). The 16S rRNA amplicon sequencing was employed to characterize the rumen microbial composition. Feeding of TMR with methane-mitigating microbes (MMM) did not influence growth performance and rumen fermentation parameters of Hanwoo steers ($p > 0.05$). Steers fed TMR + MMM showed numerically reduced CH_4 production (5.0%), yield (2.7%), and intensity (5.1%) compared with the CON group ($p > 0.05$). Taxonomic analysis revealed that Bacteroidota and Bacillota were the most dominant phyla. The TMR + MMM group exhibited a lower relative abundance of Bacteroidota and a higher Bacillota compared to the CON group. Relative abundance of *Methanobrevibacter* was lower in TMR + MMM compared to the CON group (97.5% vs. 99.1%). These findings suggest that feeding TMR with methane-mitigating microbes did not negatively affect growth performance or rumen fermentation in Hanwoo steers, while showing potential to reduce methane emissions. Further studies are warranted to enhance the methane-mitagation efficacy of this TMR diet.

Key words : Hanwoo, methane, methane-mitigating microbes, rumen, TMR

OB26006

Effects of Methastop® supplementation on enteric methane emissions in Hanwoo cattle

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This study aimed to evaluate the potential of Methastop® as a feed additive for reducing methane emissions in Hanwoo cattle. Four Hanwoo steers (687 ± 71.4 kg BW; 33 months of age) and five Hanwoo heifers (565 ± 68.9 kg BW; 32 months of age) were assigned to a 3 × 3 Latin square design. Each experimental period lasted 21 d, consisting of a 14-d adaptation, a 2-d sampling, and a 5-d washout phase. Animals were allocated to one of three dietary treatments: 1) no additive (CON) as the negative control, 2) Bovaer® (NOP) as the positive control, and 3) Methastop® (MES). Each additive was supplemented at 0.2% of the offered concentrate mix. Diets were offered twice daily (0800 and 1800 h); the concentrate mix was offered at a fixed rate of 0.5% of BW per feeding, whereas forage was offered *ad libitum*. Individual concentrate intake was determined daily by the difference between the amount offered and the orts, whereas individual forage intake was automatically recorded daily using a forage intake monitoring system. Methane emissions were measured using the laser methane detector technique. Dry matter intake (DMI) and methane emissions did not differ among treatments ($p > 0.05$). However, methane yield (MY; ppm/kg of DMI) differed among treatments during respiration ($p < 0.05$) and tended to differ during eructation ($p = 0.1$). Compared with CON, NOP reduced MY by 23% during respiration and by 21% during eructation, while MES reduced MY by 24% and 15%, respectively. In conclusion, supplementation with Methastop® has the potential to mitigate methane yield in Hanwoo cattle without adverse effects on feed intake.

Key words: methane yield, laser methane detector, Methastop®, Bovaer®, Hanwoo

OB26007

TMR의 발효 기간에 따른 반추위 소화율 및 메탄 발생량 평가

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본 연구는 TMR의 발효 기간이 *in vitro* 반추위 소화율, 가스 및 메탄 발생량에 미치는 영향을 평가하고자 수행되었다. 공시 시료로 상업용 한우 비육기 TMR을 사용하였으며, TMR의 발효 기간에 따라 0일(D0), 7일(D7), 14일(D14) 처리구로 구분하였다. D7 및 D14 처리구는 1L 플라스크에 250g의 시료를 충진하여 상온(20°C) 조건에서 각 기간 동안 밀폐 발효하였다. 발효 후 각 처리구의 TMR은 동결건조한 후 분쇄하였다. 분쇄한 각 처리구별 시료는 *in vitro* 반추위 배양 시스템을 이용하여 반추위 발효 및 소화율을 평가하였다. 총 가스와 메탄 발생량은 배양 2, 4, 6, 24시간 후에 측정하였다. 진정 건물 소화율(TDMD)은 배양 6시간 및 24시간 후에, 중성세제섬유소 소화율(NDFD)은 배양 24시간 배양 후에 분석하였다. 총 가스 발생량은 2, 4, 6시간에 처리구 간 유의적인 차이가 없었으나($p > 0.05$), 24시간에는 D0에 비해 D14의 가스 발생량이 7.4% 낮았다($p = 0.023$). 메탄 발생량은 배양 시간에 상관없이 발효 기간에 따른 유의적인 차이가 없었다($p > 0.05$). 24시간 TDMD는 발효 기간이 증가함에 따라 증가하는 경향을 보였다($p = 0.062$). 24시간 NDFD는 D14가 D0과 D7에 비해 각각 17.3%, 22.8% 높았다($p = 0.006$). 결론적으로, TMR의 발효 기간의 증가는 반추위 가스 발생량은 줄이나 섬유소 소화율은 증가시켰고, 반추위 메탄 발생량에는 영향을 미치지 않았다.

Key words : TMR, *In vitro*, 반추위 소화율, 메탄, 가스 발생량

OB26008

Effect of cashew nut meal replacement on enteric methane emissions in Holstein heifers

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Methane emissions from ruminants, produced during rumen fermentation, are a major source of greenhouse gases and represent a loss of dietary energy. This study evaluated the effects of cashew nut meal (CNM) supplementation on methane emissions in Holstein heifers. Nine Holstein heifers (average age: 10.3 months) were assigned to a 3 × 3 Latin square design with three dietary treatments: control (CON), 10% CNM replacement (Trt-1), and 15% CNM replacement (Trt-2). Methane concentrations were measured twice daily (08:00 and 16:00) for 3 days using a Microportable Greenhouse Gas Analyzer (GLA131-GGA; ABB Inc., Quebec, Canada), and daily methane emissions were estimated using a previously validated regression equation based on body weight, DMI, and TDN. Compared with CON, Trt-1 reduced CH_4 emissions, CH_4 yield, and CH_4 intensity by 7.9%, 7.9%, and 8.2%, respectively, whereas Trt-2 reduced these parameters by 21.8%, 20.5%, and 22.4%, respectively ($p < 0.01$). Trt-2 exhibited greater methane mitigation effects than Trt-1 across all measured parameters. Although DMI was reduced by approximately 2.2% in Trt-2 compared with CON ($p < 0.01$), CNM supplementation did not adversely affect ADG, FCR or hematological parameters, suggesting that methane reduction was not solely attributable to reduced feed intake. These findings indicate that 15% CNM replacement may serve as a promising functional feed ingredient for enteric methane mitigation in ruminants.

Key words : Holstein heifer, cashew nut meal, enteric methane mitigation, microportable GHG analyzer (MGGA)

OB26009

A comparative study on the nutritional composition, *in vitro* rumen fermentation characteristics, and microbiome of diverse forages for goats

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This study was conducted to evaluate the nutritional composition, including amino acid and fatty acid profiles, and *in vitro* rumen fermentation (24 h, 48 h) and microbiome after 48 h fermentation of forages commonly used in domestic goat farms in Korea. Thirty-one forage samples were collected from local goat farms, which included 17 types of forages. Chemical composition varied among forages, especially between crude protein (CP) and fiber fractions — crude fiber (CF), neutral detergent fiber (NDF), acid detergent fiber (ADF) — had a negative correlation (CF, NDF: $p < 0.01$; ADF: $p < 0.05$). Also, the overall CP content of forages is lower than that reported by NRC (2007). An *in vitro* rumen fermentation study was conducted in two separate experiments using different forage groups ($n = 16$); timothy hay was included as a standard forage in each experiment. Rumen fluid used in this study was obtained from three goats slaughtered at a local abattoir per experiment, resulting in donor-driven variability of rumen fluid activity between experiments 1 and 2. Accordingly, gas production and dry matter digestibility (DMD) of the standard forage were different between the two experiments. Corn silage and oat hay samples, even among the same forage type, showed differences in rumen fermentation traits; CP and DMD were significantly different. These findings provide a comprehensive understanding of forages utilized in goats, contributing to the establishment of standardized nutritional guidelines and improved feed efficiency in the domestic goat industry.

Key words : forage, goats, nutritional composition, *in vitro* rumen fermentation, rumen fluid

OB26010

The effects of different vitamin mixtures on the productivity and physiological responses of Hanwoo heifers under heat stress conditions

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Rapid temperature increases associated with climate change reduce livestock productivity by inducing endocrine and metabolic imbalances and decreasing feed intake, highlighting the need for nutritional strategies to improve animal resilience. Therefore, this study evaluated the effects of complex functional feed additives on growth performance, rumen fermentation, blood metabolic profiles, and heat stress biomarkers in Hanwoo heifers under summer heat stress conditions. Fifteen Hanwoo heifers were assigned to a 3 × 3 Latin square design over 11 weeks. The treatments were as follows: i) control, no additive; ii) Mix A, containing vitamin B_6 and choline chloride; and iii) Mix B, containing niacin and vitamin E. The average temperature–humidity index during the experimental period was 78.5, indicating severe heat stress. Mix A significantly increased forage dry matter intake compared with the control and tended to maintain higher blood hemoglobin concentrations, suggesting a potential role in supporting feed intake and hematological stability under heat stress. Mix B tended to improve average daily gain and feed efficiency and significantly decreased serum cortisol concentration compared with the control, indicating reduced endocrine stress. Rumen fermentation characteristics were largely unaffected by treatment, except for a lower isobutyrate proportion in Mix B. In blood biochemical profiles, Mix B significantly decreased serum total protein concentration and tended to decrease albumin concentration, whereas Mix A tended to increase alanine aminotransferase activity. Serum HSP70 and HSP90 concentrations were not affected by treatment. In conclusion, under summer heat stress conditions, the choline- and vitamin B6-based additive improved forage intake and may support hematological stability, whereas the niacin- and vitamin E-based additive reduced cortisol concentration and showed potential to improve growth performance and feed efficiency. These findings suggest that complex functional feed additives may provide distinct physiological and metabolic benefits depending on their active components in heat-stressed Hanwoo heifers.

Key words : Hanwoo heifers, heat stress, feed additives, productivity, metabolic parameter

OB26011

Effects of L-citrulline supplementation on lactational performance and blood responses in lactating Holstein cows with A1 and A2 β-casein genotypes under heat stress condition

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This study aimed to evaluate the effects of L-citrulline supplementation on lactational performance and metabolic responses of early- to mid-lactation Holstein cows under heat stress conditions. A total of 40 lactating Holstein cows were assigned to either a control group or an L-citrulline-supplemented group. The cows averaged 71.3 ± 33.8 d in milk, 32.4 ± 9.6 kg/d milk yield, and 2.8 ± 1.8 parity at the beginning of the experiment. Following a 7-day adaptation period, cows received the experimental treatment for 4 weeks. L-citrulline was supplemented at 0.5% of dry matter intake as a top-dressing. Milk yield, milk composition, dry matter intake, and blood parameters were analyzed. L-citrulline supplementation did not affect milk yield, milk composition, or dry matter intake. However, L-citrulline supplementation increased blood urea nitrogen ($p < 0.01$) and albumin ($p < 0.01$) levels, with tendencies toward increased creatinine ($p = 0.09$). In addition, A2 cows showed higher milk protein ($p < 0.05$) and hemoglobin ($p < 0.05$) levels than A1 cows under heat stress, suggesting that the A2 β-casein genotype may be associated with greater heat stress resistance. No significant interaction between L-citrulline supplementation and β-casein genotype was observed, indicating that L-citrulline responses were not genotype-dependent. In conclusion, L-citrulline supplementation modulated nitrogen metabolism without improving lactational performance under heat stress conditions. In contrast, A2 cows exhibited potentially greater physiological adaptability to heat stress than A1 cows.

Key words : L-citrulline, dairy cows, A1/A2 genotype, lactational performance, heat stress

OB26012

인공지능(AI) 활용 스마트 축산을 위한 한우 사양 관리 온톨로지 개발

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인공지능(AI) 시대의 한우 사양에서는 한우의 영양, 사료 및 사양 관리에 관한 방대하고 복잡한 정보 및 지식을 AI가 이해할 수 있는 형태로 구조화하고 체계화한 모델, 즉 온톨로지(ontology)의 구축이 필수적이다. 본 연구는 생성형 AI가 농장 관리자의 질의에 응답하고, 사료 급여 전략의 평가 및 수정에 근거 기반 도구로 활용할 수 있는 한우 사양 관리 온톨로지 개발을 목적으로 수행되었다. 한우의 사육 및 고급육 생산 과정에서 영양, 사료 및 사양 관리를 관심 대상(도메인)으로 정의하였다. Ontology Development 101과 Methontology를 결합한 방법론을 채택하고, Protégé ver. 5.6.7을 개발 플랫폼으로 활용하여 웹 온톨로지 언어(OWL) 기반 온톨로지를 구축하였다. 다양한 문헌을 활용하여 지식을 분석한 후, 대규모 언어 모델인 Google Gemini 2.5를 활용하여 역량 질문(Competency Questions, CQs)을 생성하였고, 생성된 질문과 응답 과정에서 도출된 용어를 바탕으로 핵심 개념(클래스)을 추출하였다. 상향식 접근법과 하향식 접근법을 병행하여 추가의 클래스와 클래스 계층 구조를 정의하고, 클래스 간 관계를 나타내는 속성(property)을 부여하였다. 또한 클래스의 주석과 속성의 제한 조건을 설정하였다. 개발된 온톨로지는 문헌 검토와 CQs 재평가를 통해 누락된 클래스, 속성 및 제한 조건을 보완하는 과정을 거쳤으며, 구조적 지표를 활용하여 충실도를 평가하였다. 또한 Protégé에 내장된 HermiT 및 Pellet 추론기를 이용하여 논리적 일관성을 검증하였다. 결론적으로 본 연구에서 개발한 한우 사양 관리 온톨로지는 충실도 기준을 만족하였으며, 구조적 일관성과 논리적 정합성을 갖춘 것으로 나타났다.

Key words : 사양, 영양, 온톨로지, 인공지능(AI), Protégé, 한우

OB26013

Characterizing rumen antimicrobial resistance gene composition across studies and its implications for microbiome-resistome integration

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Antimicrobial resistance (AMR) poses an increasing challenge to sustainable livestock production and One Health by connecting human, livestock, and environmental health. The beef cattle rumen microbiome represents a complex microbial ecosystem that may act as a reservoir of antimicrobial resistance genes (ARGs), yet cross-study characterization of rumen resistome patterns across production contexts remains limited. This study performed a cross-study meta-resistome analysis of publicly available shotgun metagenomic datasets to characterize the beef cattle rumen resistome and assess resistome variation across production settings. A systematic literature search identified 10 eligible studies comprising 225 rumen fluid metagenomes. Sequencing data underwent quality control and ARG annotation using a standardized bioinformatics workflow, generating normalized ARG and AMR class abundance profiles. Diversity analyses, ordination, PERMANOVA, and mixed-effects modeling were applied. Tetracycline-associated ARGs dominated the rumen resistome, with tet(Q), tet(W), tet(O/W), and tet(44) consistently detected across samples. Core ARGs included determinants associated with tetracycline, multidrug, macrolide-lincosamide-streptogramin, bacitracin, vancomycin, and polymyxin resistance classes. Study identity explained most resistome variation ($R^2 = 0.73$; $p = 0.001$), whereas diet, age, and country showed limited independent effects after accounting for study structure, highlighting substantial cross-study heterogeneity and metadata confounding. These findings reveal conserved resistome signatures and support harmonized metagenomic surveillance as a foundation for sustainable and resilient livestock systems.

Key words: beef cattleumen microbiome, resistome, antimicrobial resistance genes, metagenomics, sustainable livestock

OB26014

Integrated processing of soybean meal as nutritional strategy to support performance in heat-stressed Holstein dairy cows

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This study evaluated fermented soybean meal (FSBM), produced through sequential acid pre-treatment, lactic acid bacterial inoculation, and thermal processing, as a nutritional strategy for dairy cows under heat stress. *In vitro* rumen fermentation demonstrated that this integrated processing approach significantly increased the crude protein (CP) content of FSBM ($p < 0.001$). Compared with conventional soybean meal, FSBM significantly reduced total gas production and methane emissions ($p < 0.001$). No differences in volatile fatty acid (VFA) concentrations were observed at 12 h ($p > 0.05$). However, after 24 h of incubation, FSBM significantly altered fermentation characteristics, resulting in higher concentrations of total VFA ($p < 0.001$), acetate ($p < 0.001$), propionate ($p < 0.001$), and butyrate ($p < 0.01$), along with increased ammonia nitrogen (NH_3-N) levels ($p < 0.001$), while the acetate-to-propionate ratio remained unchanged ($p > 0.05$). In the *in vivo* study, supplementation with 0.1% FSBM did not affect dry matter intake or milk yield ($p > 0.05$). However, it significantly reduced milk somatic cell count ($p < 0.01$) and improved feed efficiency across lactation stages ($p < 0.01$). Overall, these findings suggest that properly processed FSBM can enhance rumen fermentation while supporting udder health and improving feed efficiency in lactating dairy cows under heat stress.

Key words : fermented soybean meal, by-pass protein, rumen, dairy cows, heat stress

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OC26001

Propiconazole impairs mitochondrial OXPHOS through disruption of electron transport chain activity in porcine endometrial luminal epithelial cells

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Propiconazole (PCZ) is a widely used triazole fungicide detected in environmental matrices and biological tissues and is also an endocrine disruptor with potential to impair mitochondrial function. We hypothesized that PCZ may influence implantation-related cells, a process strongly dependent on mitochondrial activity. To test this, porcine endometrial luminal epithelial (pLE) cells were analyzed to evaluate endometrial receptivity. PCZ reduced mitochondrial enzyme activity and content as demonstrated by live-cell imaging. Seahorse assays revealed decreased ATP production, oxygen consumption rate, and respiratory capacity, indicating impaired oxidative phosphorylation. Co-treatment with pyrroloquinoline quinone (PQQ) partially restored cell viability in a dose-dependent manner, as assessed by MTT assay. PCZ increased proton leak and reduced *VDAC1* expression, suggesting altered membrane permeability. qRT-PCR showed suppression of complex I-related genes, whereas transcripts associated with complex IV and ATP synthase were elevated. Genes involved in mtDNA replication, transcriptional stability, and antioxidant defense were upregulated, indicating compensatory biogenesis and oxidative stress responses. These findings demonstrate that PCZ disrupts mitochondrial respiration in pLE cells primarily through complex I inhibition. The induction of complex IV genes, mtDNA maintenance factors, and antioxidant pathways reflects a compensatory response. Overall, these results provide insights into the reproductive toxicity of PCZ.

Key words : Propiconazole, mitochondrial dysfunction, endometrial receptivity

OC26002

Nest-building intensity in prepartum period is associated with distinct gut microbial profiles in loose-housed sows

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Prepartum nest-building is an instinctive maternal behavior driven by endocrine changes. Given the bidirectional gut–brain axis, variations in this behavior may reflect distinct gut microbial compositions. Therefore, this study evaluated whether prepartum nest-building intensity is associated with gut microbiota profiles in loose-housed sows. Thirty-nine crossbred sows were categorized into two groups according to their nest-building duration in the 24 h preceding parturition: shorter nest-building (SN, n = 19, 144.04 ± 64.21 min) and longer nest-building (LN, n = 20, 310.99 ± 54.88 min). Faecal samples were collected on day 1 after farrowing. Beta diversity differed consistently ($p < 0.05$) between SN and LN groups. Taxonomic analysis at the genus level revealed *Lactobacillus* was more abundant in the LN groups, while *Romboutsia* and *Terrisporobacter* were reduced. At the species level, the LN group exhibited higher abundances of *Lactobacillus amylovorus* and *L. ruminis* and lower abundances of *Clostridium butyricum*. LEfSe analysis identified *Peptococcus*, *Treponema*, *Oribacterium*, *Megasphaera*, *Catenisphaera*, and *Lactobacillus* as key microbial biomarkers for the LN group ($p < 0.05$), while *Romboutsia* and *Turicibacter* were more abundant in the SN group ($p < 0.01$). Functional prediction analysis revealed enrichment of pathways related to core metabolism and biosynthesis processes in the LN group, whereas transport and signal transduction pathways were enriched in the SN group ($p < 0.05$). In conclusion, these findings suggest that variation in prepartum nest-building behavior is associated with early postpartum divergence in gut microbiota structure and predicted function in loose-housed sows.

Key words: farrowing environment, functional pathways, gut-microbial alteration, maternal behavior, nest-building categories

OC26003

Comparative analysis of SLA-DRB1 allelic diversity in Vietnamese and Jeju native pigs and their insights into antigen presentation potential

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The SLA-DRB1 gene encodes the beta chain of SLA-DR molecules, which play a vital role in recognizing and responding to pathogens by presenting antigens. Identification of DRB1 alleles in pig populations is an important consideration when developing a multi-epitope vaccine. This study aimed to investigate the SLA-DRB1 allele diversity in several Vietnamese native pig populations and compare it with that of the Jeju Korean native pig population. The Sequence-based typing (SBT), a high-resolution genotyping method combining Sanger sequencing and PCR-based sequence-specific primers (SSPs), was adapted for genotyping exon 2 of the SLA-DRB1 gene. In addition, the translated DRB1 amino acid sequences were combined with immunoinformatics to evaluate the potential of DR molecules to present pathogen peptides from circulating Foot and Mouth (FMD) immunological serotypes. As a result, a high number of novel DRB1 variants were discovered. Several peptide epitopes from FMDV VP1 serotype O were found to have strong and relatively stable binding potential to DR molecules. This work provides valuable insights into the SLA-DRB1 genetic diversity and suggests utilizing it in bioinformatics to rapidly assess their ability to resist specific pathogens, such as FMD virus.

This research was supported by the Regional Innovation System & Education (RISE) program through the Jeonbuk RISE Center, funded by the Ministry of Education (MOE) and the Jeonbuk State, Republic of Korea.(2025-RISE-13-JBU).

Key words : SLA-DRB1, foot and mouth disease, immunoinformatics, Korean native pig, Vietnamese native pigs

OC26004

Transcriptomic analysis of bovine peripheral blood mononuclear cells stimulated with antigens from bovine digital dermatitis associated treponemes

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Bovine digital dermatitis (BDD) is an infectious disease in cattle associated with multiple *Treponema* species yet information on the immune responses of circulating immune cells to these pathogens are limited. This study utilized RNA sequencing to characterize transcriptomic changes in bovine peripheral blood mononuclear cells (PBMCs) following stimulation with combined antigens derived from three BDD-associated *Treponema* species. A total of 3,898 differentially expressed genes were identified, including 2,013 upregulated and 1,885 downregulated genes (BH-FDR adjusted $p < 0.05$). Notable upregulated genes included *IFNγ, CXCL10, IL17F, IL1B, IL6, MMP9*, and *MMP14* suggesting activation of Th1 and Th17 associated inflammatory responses and extracellular matrix remodeling. In contrast, genes associated with antimicrobial activity, complement regulation, and immune modulation, such as *LYZ, KLF4, CCL23, CFD,* and *A2M,* were markedly downregulated, suggesting suppression of innate immune response and regulatory mechanisms potentially favoring a pro-inflammatory state in PBMCs. KEGG pathway analysis revealed enrichment of notable pathways like mitogen activated protein kinase signaling and tumor necrosis factor pathway which are associated in pro-inflammatory signaling and ECM processes. The enrichment of the NOD-like receptor pathway indicates that *Treponema* spp. antigens may influence inflammasome-associated and non-canonical inflammatory programs. Collectively, these findings suggest that PBMCs exhibit a pro-inflammatory transcriptional response following stimulation with *Treponema* spp. antigens, providing new insights into host–pathogen interactions in BDD.

Key words : bovine digital dermatitis; *Treponema* spp.; peripheral blood mononuclear cells; RNA sequencing; differentially expressed genes

OC26005

Effects of L-carnosine on oxidative stress and myogenic differentiation in bovine skeletal muscle-derived cells under heat stress

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This study investigated the effects of L-carnosine on oxidative stress responses and myogenic differentiation in bovine skeletal muscle-derived cells (BSMCs) under heat stress conditions. BSMCs were isolated from the *longissimus thoracis* muscle of slaughtered Korean native cattle, cultured for 2 days of growth, and then induced to differentiate for 6 days under either normothermic or heat-stress conditions. Cells were treated with L-carnosine at concentrations of 0, 0.01, 0.1, 1, and 10 mM during differentiation. In the heat stress experiment, cells were exposed to 41°C from days 2 to 4 of differentiation with the same L-carnosine treatments, followed by recovery at 37°C until day 6. Cell viability, malondialdehyde (MDA) levels, myogenic and stress-related gene expression, and myotube morphology (fusion index and myotube width) were evaluated. Under normal conditions, 10 mM L-carnosine significantly increased cell proliferation, while 1 mM L-carnosine increased MyoG and Myf6 expression and enhanced myotube width, suggesting promotion of myotube maturation. Heat stress significantly decreased cell viability and impaired myogenic differentiation compared with the 37°C control group. However, 1 and 10 mM L-carnosine significantly restored cell viability, fusion index, and myotube width under heat stress conditions. In addition, 1 mM L-carnosine significantly decreased MDA levels compared with the 0 mM heat-stressed group. Heat stress decreased Myf5 and Myf6 expression compared with the 37°C control group, whereas 1 and 10 mM L-carnosine increased MyoD, MyoG, and Myf6 expression compared with the 0 mM heat-stressed group ($p < 0.05$). L-carnosine treatment also increased HSP70, GPX1, SOD2, and NRF2 expression compared with the 0 mM heat-stressed group ($p < 0.01$). During the recovery period after heat stress, 1 and 10 mM L-carnosine increased myotube width compared with the 0 mM heat-stressed group ($p < 0.01$), suggesting enhanced myotube maturation during recovery. In conclusion, L-carnosine improved cell viability and myogenic differentiation and reduced oxidative damage in BSMCs under heat stress conditions. These findings suggest that L-carnosine may be a potential functional nutrient for supporting skeletal muscle development in cattle under heat stress.

Key words : bovine skeletal muscle-derived cells, heat stress, L-carnosine, myogenic differentiation, oxidative stress

OC26006

Protein engineering of a novel recombined lytic enzymes against rumen methanogens in livestock

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Agricultural activities account for one-third of anthropogenic methane, with 70% of these emissions generated by rumen methanogens such as *Methanobrevibacter ruminantium* and *Methanobrevibacter smithii*. Various strategies, including endolysin therapy, have been investigated to inhibit methanogen growth. In this study, we evaluated MetRE, a novel lytic enzyme constructed by combining binding and catalytic domains from two distinct endolysins. The structure of the recombined enzyme was predicted via AlphaFold3, and domain conservation was analyzed against natural counterparts using TM-align. Furthermore, both the wild-type and the novel recombined enzymes were expressed in a *Lactiplantibacillus plantarum*. Structural alignment of MetRE yielded a TM-score of 0.9800 with the natural binding domain and 0.9954 with the catalytic domain. Western blot analysis confirmed the successful expression of both wild-type and recombined enzymes in *L. plantarum*. Consequently, the recombined enzyme maintains the 3D structure of its natural counterparts with high precision while exhibiting stable expression. These findings suggest that the newly designed lytic enzyme can be produced in practice as a promising tool for inhibiting rumen methanogens, supported by its high structural precision and stable microbial expression. Supported by NRF/MSIT (RS-2024-00344849).

Key words: ruminant, rumen, methanogen, protein engineering, endolysin

OC26007

Comparative analysis of 2D and 3D culture systems using Hanwoo skeletal muscle-derived cells

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This study aimed to establish a three-dimensional (3D) culture using bovine skeletal muscle-derived cells (BSMCs) from Hanwoo cattle and to compare it with a conventional two-dimensional (2D) culture. BSMCs were isolated from the longissimus thoracis muscle of Hanwoo cattle, and 3D constructs were bio-printed into scaffold using a gelatin methacryloyl(GelMA)-based bioink. Cell viability and proliferation were evaluated, and mRNA expression of myogenic regulatory factors and myosin heavy chain (*MYH*) isoforms were analyzed by RT-qPCR. Myotube formation and alignment were evaluated by immunocytochemistry (ICC) based on MYH-positive area, myotube length, and directionality. Cell viability remained above 90% throughout the culture period in the 3D. Proliferation in 2D increased up to day 5 and decreased at day 7, whereas proliferation in 3D was maintained after day 5 ($p < 0.05$). During differentiation, *MyoG* and *Myf6* expression increased in both systems, and at day 8, 3D showed higher expression of *MyoG, Myf6, MYH1*, and *MYH2* than 2D ($p < 0.05$). ICC showed that myotubes were longer in 2D than in 3D at day 4 ($p = 0.0002$), but longer in 3D at days 6 and 8 ($p = 0.0019$ and $p < 0.0001$). MYH-positive area was higher in 3D than in 2D at days 6 and 8 ($p = 0.0343$ and $p = 0.0013$). Directionality analysis showed less organized myotube alignment in 2D but directional alignment in 3D. In conclusion, the 3D culture promoted sustained proliferation, enhanced late-stage myotube formation, and improved directional alignment compared with the 2D culture.

Key words : 2D culture, 3D culture, bovine skeletal muscle-derived cells (BSMCs), myogenic differentiation, Hanwoo cattle

OC26008

Sensor-based detection of alterations in social relationships in laying hens and dairy calves with diseases

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These studies focused on the changes in social interaction between animals (dairy calves and laying hens) in relation to sickness signs. Two studies were conducted to compare social interaction data obtained from human observations with data collected using wearable sensors.

In the hen study, 20 previously unvaccinated hens (Hy-Line Brown, 25-35 weeks old) were used in 5 replicated experiments (4 hens/replicate). Hens were placed in groups of 4 to 180 m^2 room. On day 1, TrackLab sensor (Tracksys Ltd.) was mounted on each hen's back to detect changes in social interaction (m/day) from day 1–12. On day 3, saline (control) was administered to all birds by nasal and ocular drops. On day 6, birds were given ILT (Infectious Laryngotracheitis) vaccine using the same method. In the calf study, 69 dairy calves (Holstein, 3–25 days old) were born at the farm. Calves were distributed into 3 Pens (22-25 calves per pen) according to their birth date. At 3–7 days of age, each calf was fitted with a GoChip sensor (GoChip Pet tech.) to detect social distance for 16 days. Behavioural changes were analysed from 3 days before to 3 days after the onset of clinical signs (day 0). All data was analysed in RStudio using linear mixed models.

In the hen study, there was a significant difference between days in the mean proximity frequency from TrackLab sensors (p = 0.003). In the calf study, the estimated social distance detected by GoChip devices also showed a significant day effect (p = 0.001). There were no significant differences between days in social data via human observations.

These findings suggest that wearable sensor technologies may provide a more sensitive tool for detecting disease-associated changes in social behaviours than human observations.

Key words : social behaviour, animal disease, disease detection, wearable sensor, social distance

OC26009

Effects of TLR signaling on immune activation and metabolic regulation in chicken macrophages under distinct modes of *Salmonella* uptake

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Salmonella survives and replicates within macrophages by evading host immune defenses and adapting to the intracellular environment. Although Toll-like receptor (TLR) signaling is implicated in host defense against *Salmonella*, its role in avian macrophages remains unclear. Here, we investigated how TLRs regulate bacterial handling, immune activation, and metabolic adaptation in gene edited chicken macrophages under phagocytosis and opsonophagocytosis conditions. Among them, TLR4$^{-/-}$ macrophages showed the most distinct phenotype. Under phagocytosis conditions, TLR4$^{-/-}$ macrophages exhibited reduced bacterial uptake, attenuated activation associated responses, impaired bacterial clearance, and transcriptional reprogramming away from immune related pathways toward cell cycle associated programs. In contrast, under opsonophagocytosis conditions, TLR4$^{-/-}$ macrophages showed enhanced bacterial clearance together with enrichment of innate immune pathways. Metabolic analyses further revealed that TLR4 deficiency promoted enhanced glycolytic dependence under both uptake conditions, while metabolomic changes differed according to the mode of uptake. Histidine metabolism was enriched in WT macrophages under phagocytosis, whereas tyrosine metabolism and tryptophan metabolism were preferentially associated with WT and TLR4$^{-/-}$ macrophages, respectively, under opsonophagocytosis. Integration of transcriptomic and metabolomic pathway analyses revealed that directional coupling according to the mode of uptake. These findings show that the effects of TLR4 on macrophage immune and metabolic responses to *Salmonella* in chickens depend on the mode of bacterial uptake.

Key words : avian immunology, macrophages, Toll-like receptor, *Salmonella*, cell metabolism

OC26010

Comparative genomic analysis of *Akkermansia muciniphila* and *Akkermansia massiliensis* and their potential impact on growth performance in livestock

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Akkermansia muciniphila is an intestinal symbiont recognized as a biomarker for host health and weight regulation. While it has recently been identified in cattle and swine, functional research on its related species in livestock remains insufficient. This study conducted a comparative genomic analysis between *A. muciniphila* and *A. massiliensis* to verify the identification of weight-loss-related genes and their potential impact on animal growth. and their distribution in Korean and Chinese broilers by sequencing. Genomic data from 24 complete genomes (12 per species) were analyzed via RAST Subsystem, revealing that the two species share 156 out of 191 functional subsystems (about 81%). P9-like weight-loss gene was identified in *A. massiliensis*, with blastn (100% coverage, 91.4% identity) and blastp (99% coverage, 98.24% identity) confirming high homology. Microbiota analysis of the ileum showed a high prevalence *A. muciniphila* in both groups, 75% of Korean (67/89) and 100% of Chinese (41/41) broilers. In contrast, *A. massiliensis* was absent in Korean samples and only rarely detected in 4.9% of Chinese samples (2/41). These findings indicate that *A. massiliensis* possesses subsystems similar to those of *A. muciniphila*, which can modulate energy metabolism and nutrient utilization. Thus, microbiome strategies like targeted vaccines to regulate specific *Akkermansia* species, offer a promising approach to enhancing livestock productivity by promoting weight gain. Supported by NRF/MSIT (RS-2024-00344849).

Key words: gut microbiome, comparative genomics, *Akkermansia muciniphila, Akkermansia massiliensis*, livestock productivity

OC26011

Computational investigation of PD-L1 dimer interfaces in human and canine systems for cross-species analysis of small-molecule inhibitors

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Small-molecule inhibitors targeting the PD-1/PD-L1 immune checkpoint have emerged as promising alternatives to antibodies for cancer therapy, offering improved tissue penetration and oral bioavailability. Studies show that compounds such as BMS-202 stabilize PD-L1 dimerization, forming a protein–protein interface that blocks PD-1 binding. However, cross-species variation in PD-L1 highlights the need to evaluate inhibitor binding in canine systems. In this study, computational approaches were used to investigate species-specific structural differences. Sequence alignment was performed, followed by canine structure prediction and dimer construction based on human crystal templates. The dimer interface was refined by protein–protein docking, yielding a modified binding-pocket architecture in the canine complex. Comparative docking of PD-L1 inhibitors revealed ligand-dependent binding, including retained or lost binding, variations in affinity, and differences in binding modes relative to the human structure. These results indicate that, although the canine pocket shares features with the human interface, subtle but functionally significant structural differences influence ligand recognition and binding efficiency. These findings provide structural insights for designing species-specific inhibitors and a foundation for developing targeted cancer therapeutics in canine systems.

This research was supported by the Regional Innovation System & Education (RISE) program through the Jeonbuk RISE Center, funded by the Ministry of Education (MOE) and the Jeonbuk State, Republic of Korea (2025-RISE-13-JBU).

Key words: cancer immunotherapy, computational modeling, PD-L1, small-molecule inhibitors, cross-species analysis

OC26012

Predicting solute-solvent interactions via paired molecular graph attention networks

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Solute-solvent interactions are a fundamental determinant of thermodynamic properties in chemical and biological systems, governing solvation free energies, partition coefficients, and aqueous solubility across diverse molecular environments. In this study, we developed and evaluated SolvGAT, a dual-graph attention network architecture that jointly encodes solute and solvent molecular graphs and learns pairwise interaction representations through a cross-graph attention pooling mechanism. The model was trained and validated on solute-solvent pairs sourced from the BigSolDB 2.0 and MixtureSolDB databases encompassing aqueous, organic, and mixed-solvent systems, using ten-fold cross-validation data partitioning strategy. Under a random split, SolvGAT achieved an R^2 of 0.91 ± 0.01 and RMSE of 0.14 ± 0.02 logS.

Key words : drug discovery, ADMET, aqueous solubility, molecular SMILES, feature extraction

번식 및 생리

OD26001

Effects of circadian rhythm-based vaccination timing on antigen-specific fecal IgA responses in broiler chickens

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Recent studies highlight the role of circadian rhythms in modulating immune function; however, vaccination strategies incorporating circadian rhythms remain limited in the poultry industry. Avian immune responses exhibit circadian variation driven by melatonin and metabolic activity. Therefore, understanding antibody dynamics associated with circadian rhythms is essential for optimizing vaccine efficacy. This study evaluated how vaccination timing in relation to circadian rhythms modulates immunogenicity in chickens. Chickens were divided into morning (10:30) and afternoon (18:00) vaccination groups, and each group received the same dose of antigen via oral administration twice at 2-week intervals (four total administrations). Fecal samples were collected one week after the final immunization, and antigen-specific IgA titers were measured using sandwich ELISA. The results showed that, despite identical antigen dosage and administration frequency, significant differences in fecal antigen-specific IgA titers were observed depending on the time of vaccination. Notably, the morning group exhibited significantly higher antibody titers than the afternoon group (Paired *t*-test, $p < 0.001$). These findings demonstrate that circadian rhythm–based vaccination timing significantly influences fecal IgA responses and suggest that such strategies provide a practical approach to enhance vaccine immunogenicity within the livestock industry. Supported by NRF/MSIT (RS-2024-00344849).

Key words : circadian rhythm, vaccination, antigen-specific IgA, oral administration

OD26002

Prolonged farrowing and impaired nursing behaviour are associated with gut microbial alterations in sows with large litters

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Increased litter size in modern pig production has been associated with prolonged farrowing and impaired maternal behaviour. Given the role of the gut microbiota in regulating neuroendocrine and behavioural processes, this study investigated whether maternal dysfunction associated with large litter size is related to alterations in gut microbial composition. A total of 22 primiparous sows (Landrace × Large White) were classified into normal litter (NL, litter size 11.5 ± 1.0, range 7-14, n = 8) and large litter (LL, litter size 15.6 ± 0.3, range 15-18, n = 14) groups. Maternal traits, including colostral prolactin levels and nursing behaviour, were evaluated. Faecal microbiota was analysed using full-length 16S rRNA sequencing on the PacBio platform. Taxa more abundant in the NL group, particularly *Lactobacillus* spp. (e.g., *L. reuteri* and *L. gasseri*), were positively correlated with colostral prolactin levels ($r = 0.47$, $p < 0.05$) and nursing frequency ($r = 0.48$, $p < 0.05$). In contrast, taxa more abundant in the LL group, including *Roseburia* and *Campylobacter*-related taxa, were positively correlated with farrowing duration ($r = 0.43–0.46$, $p < 0.05$). In addition, *Campylobacter coli* showed a tendency for a negative correlation with nursing duration ($r = −0.40$, $p = 0.06$). These results indicate that prolonged farrowing and impaired nursing behaviour in large litter sows are associated with distinct gut microbial profiles. The correlation results further suggest a potential role of microbiota-neuroendocrine interaction in hyperprolific sows.

Key words : farrowing duration, gut microbiota, hyperprolific sow, maternal behaviour, maternal hormone

OD26003

Immortalization of Hanwoo reproductive cells for heat stress *in vitro* research

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Substantial increase in global temperature induces heat stress (HS) in livestock animals particularly dysregulating cattle reproductive capacity leading to economic loss. Development of *in vitro* models in cattle reproduction is a critical process to unveil molecular basis of HS destructive effects and to elaborate treatments for mitigation. Therefore, this research proposes to immortalize reproductive cells isolated from Hanwoo, native Korean cattle that are susceptible to HS, and to examine HS-associated response using molecular markers and omics techniques. This research successfully establishes three immortalized Hanwoo cells i.e. cumulus cells (CC), oviduct epithelial cells (OEC), and endometrium epithelial cells (EEC) by integrating SV40T Ag into genome using *piggy bac* transfection system confirmed by PCR. Specific biomarkers showed high positivity score (> 98%), particularly on CC and OEC cell populations. In general, HS treatment at 41.5°C for 4 h triggered intracellular reactive oxygen species (ROS) accumulation in all three cell lines. Nevertheless, delayed response of oxidative stress genes (*SOD1, CAT, GPX1*) were observed with significant upregulation (2–3x foldchange, $p < 0.05$) peaking at 24 h HS treatment. Besides, rapid increase of HSP70 protein chaperone (~10x foldchange, $p < 0.05$) was detected under the 4 h HS peaking at 12 h HS treatments, while ER-stress marker BiP/GRP78 protein showed various upregulation time points among different cells. Prolonged response of the stress markers was also presented during recovery period. Additionally, transcriptomics and proteomics profile showed that HS treatment altered more than 550 and 250 differentially expressed genes (DEG) and proteins (DEP), respectively. Based on this gene list, enrichment analysis on gene ontology and pathway database presented upregulated process related to protein folding, heat shock proteins (HSPs) and response to ROS, representing direct protective mechanisms to HS. Other highlighted altered functions include extracellular matrix remodeling, immune response, and nutrients metabolism which might suggest cellular dysregulation or adaptation. Further study is required to confirm these effects. In conclusion, immortalized Hanwoo reproductive cells and molecular data in this study are valuable for further investigation of HS effect in cattle reproduction and developing preventive strategies.

Key words: *Bos taurus,* Hanwoo, cumulus, oviduct epithelial cells, endometrium epithelial cells, heat stress, livestock reproduction

OD26004

Milk-derived extracellular vesicles enhance oocyte competence and embryo development during bovine *in vitro* maturation

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Extracellular vesicles (EVs) are bioactive mediators increasingly applied to reproductive culture systems; however, the effect of milk-derived EVs on bovine oocyte maturation remains unclear. This study evaluated whether milk-derived EV supplementation during bovine *in vitro* maturation (IVM) improves oocyte competence. Cumulus–oocyte complexes were matured with milk-derived EVs at 1×10^7, 1×10^8, or 1×10^9 particles/mL, and oocyte maturation, embryo development, oxidative status, apoptosis/autophagy-related responses, and gene expression were assessed. EV-associated fluorescence signals were observed within cumulus–oocyte complexes after co-incubation with labeled milk-derived EVs. Milk-derived EV supplementation increased first polar body extrusion and cleavage rates, whereas blastocyst formation and hatching were most consistently improved in the 1×10^8 particles/mL group. This group also showed increased oocyte competence- and antioxidant defense-related gene expression, reduced H_2O_2 and NO levels, increased GSH levels, and decreased caspase-3 activity. In conclusion, milk-derived EV supplementation during bovine IVM improved oocyte maturation, at least in part, by reducing ROS-associated oxidative stress in oocytes.

Key words : milk-derived extracellular vesicles, bovine oocytes, *in vitro* maturation, oxidative stress, embryo development

OD26005

Ultrasonographic ovarian morphological characteristics according to the interval from calving to conception in postpartum primiparous Hanwoo cows

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Ovarian morphological parameters may serve as indicators of fertility in cattle. This study investigated whether ovarian morphological parameters at postpartum estrus are related to the interval from calving to conception in primiparous Hanwoo cows. Ultrasonography was performed on 16 primiparous cows at estrus and at 7 and 14 days after estrus to measure the diameter of ovary, follicle, and corpus luteum (CL), and intraovarian follicle and CL ratios. Artificial insemination was performed at each estrus, and conception was diagnosed at 30 days. Cows were classified as normal or abnormal estrus (Normal estrus: estrus interval ≥ 18 days, presence of CL at 14 days after estrus). Cows were also categorized into early (≤ 45 days, n = 8) and delayed conception groups (> 45 days, n = 8). Normal estrus showed greater ovarian diameter, CL diameter, and CL ratio at 7 days than abnormal estrus ($p < 0.05$). The early group had larger follicle diameter than the delayed group ($p < 0.05$). In the delayed group, CL diameter (1st vs. 2nd vs. 3rd estrus = 12.8 ± 2.7^{a} vs. 18.2 ± 1.4^{b} vs. 17.3 ± 1.5^{b} mm, $p < 0.05$) and CL ratio (1st vs. 2nd vs. 3rd estrus = 57.6 ± 5.5^{a} vs. 72.6 ± 3.5^{b} vs. $65.2 \pm 7.0\%^{ab}$, $p < 0.05$) at 14 days during the first postpartum estrus were lower than in subsequent cycles ($p < 0.05$). These results suggest that follicle diameter and CL development during the first postpartum estrus may be related to the interval from calving to conception.

Key words : Hanwoo cows, ovarian morphology, primiparous, ultrasonography

OD26006

Integrating systematic labeling with machine learning for non-invasive reproductive stage detection in dairy cattle via feed intake patterns

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Reproduction is arguably the most foundational biological process in livestock production systems, as it directly governs the efficiency, profitability, and long-term sustainability of any operation. However, traditional methods for monitoring livestock reproductive cycles are often limited by high costs, labor intensity, and animal stress. While automated feeding systems provide continuous data, the link between raw feed intake and physiological reproductive status is not yet fully utilized. Leveraging the fundamental relationship between feeding behavior and reproductive cycles, this study investigates the feasibility of predicting specific reproductive stages exclusively through feed intake patterns. By integrating a systematic labeling strategy with machine learning, we defined six distinct gestational phases and developed a Random Forest (RF) model. The model classification accuracy averaged 0.916, and the F1-score was 0.905. Utilizing time-series feed intake features from dairy cows, this model effectively classifies reproductive stages based solely on feeding dynamics. The results demonstrated that feed intake patterns harbor inherent biological signals directly related to reproductive physiology. This research offers a significant technical contribution by establishing a non-invasive, cost-effective biomarker for reproductive monitoring. The proposed framework serves as a practical decision-support tool, facilitating precision reproduction management within the smart farming ecosystem.

Key words : precision reproduction, feed intake pattern, random forest, non-invasive monitoring, dairy cattle

OD26007

Effects of canine-assisted interventions on neurophysiological and psychological responses

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Canine-assisted interventions (CAIs) have emerged as a promising complementary approach for improving mental health. Nevertheless, studies integrating both physiological and psychological measures to evaluate CAI effects remain limited. This study aimed to evaluate the neurophysiological and psychological effects of CAIs in humans under experimentally induced stress and to assess physiological responses in dogs. Sixteen healthy adults (8 males and 8 females) and three dogs (one male and two females) participated in a randomized crossover design. The Trier Social Stress Task (TSST) was administered prior to each condition to induce stress. Four conditions were tested: meditation, cognitive stress task, static activity, and dynamic activity. Meditation and the cognitive stress task served as control conditions. Static activity involved interaction with dogs, such as petting and talking to them. Dynamic activity consisted of higher-intensity, play-based interactions, such as agility and disc dog. In humans, salivary cortisol, electroencephalography (EEG), heart rate variability (HRV), and emotional states were measured at multiple time points before and after each activity. In dogs, salivary cortisol was measured repeatedly during each condition. Data were analyzed using linear mixed-effects models. Following static activity, concentrations of cortisol at the post-activity were lower than those observed after the cognitive stress task. In EEG, high-beta power decreased after the static activity. In HRV, SDNN and RMSSD increased following static activity. Following dynamic activity, high-beta power decreased in EEG, and the LF/HF ratio decreased in HRV. Physiological responses often varied by sex. Both static and dynamic activities improved emotional states. In dogs, concentrations of cortisol decreased after dynamic activity. Overall, these findings support beneficial physiological effects of CAIs in both humans and dogs, with additional psychological benefits observed in humans. These results highlight the importance of integrating multimodal measures when evaluating CAI outcomes.

This research was supported by the National Institute of Agricultural Sciences, Rural Development Administration, Republic of Korea (RS-2023-00232319).

Key words: canine-assisted intervention, human-animal interaction, stress response, cortisol, electroencephalography, heart rate variability, emotional state

OD26008

The effects of equine-assisted intervention on young adult women with depression

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Equine-assisted intervention (EAI) has gained attention as an alternative approach for improving emotional regulation and reducing stress in individuals with depression. This study investigated the neurophysiological and autonomic effects of EAI in young adult women according to depression status. Twenty female college students were classified into a depression group (n = 10) and a non-depression group (n = 10) based on Korean Beck Depression Inventory scores. The intervention consisted of 15 min of pre-counseling followed by 50 min of natural horsemanship-based ground activities. Electroencephalography (EEG) and electrocardiography (ECG) were recorded for 3 min before and after the program using QEEG-64FX. Relative power was assessed for the alpha (8–12 Hz), low-beta (13–19 Hz) and high-beta (20–30 Hz) frequency bands. All data were analyzed using PROC MIXED. EEG analysis showed a significant increase in alpha power after the intervention ($p < 0.05$), whereas low and high beta power showed no significant changes in either group. These findings suggest that EAI may promote relaxation and neural stabilization without inducing excessive cortical arousal. RR intervals extracted from ECG data were analyzed using Kubios software to calculate heart rate variability (HRV) indices. The PNS index significantly increased after EAI in both groups ($p < 0.05$), whereas the SNS index remained unchanged. RMSSD increased only in the depression group ($p < 0.05$), while SDNN and LF/HF ratio showed no significant changes. HRV results suggest that EAI may enhance parasympathetic regulation, particularly in young adult women with depressive symptoms, without inducing excessive physiological arousal. In summary, EAI may contribute to relaxation, neural stabilization, and autonomic stabilization in both depression and non-depression groups.

This work was supported by the National Research Foundation of Korea (NRF) grand funded by the Korea government (MSIT) (No. RS-2023-00217567).

Key words : equine-assisted intervention, depression, electroencephalography, heart rate variability, autonomic regulation

축산물 이용 및 가공

OE26001

Effects of slaughter age on enteric methane emissions and production efficiency in Hanwoo steers

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Beef cattle production is a major source of methane (CH_4) emissions due to enteric fermentation, contributing substantially to greenhouse gas outputs and reducing production efficiency. This study evaluated the effects of slaughter age on enteric methane emissions, production efficiency, and carcass characteristics in Hanwoo steers. Animals were slaughtered at 26, 28, and 30 months, and growth performance, feed intake, methane emissions, and emission intensity were compared. Slaughter age did not significantly affect final body weight, carcass weight, or dry matter intake; however, meat yield and lower loin weight were higher at 28 and 30 months. Average daily methane emissions were similar across treatments, indicating no effect of age on daily emission rates. However, total methane emissions and emission intensity per live weight, carcass weight, and meat yield increased significantly with slaughter age. These results indicate that extended feeding periods increase cumulative emissions without proportional efficiency gains. Although meat yield improved at 28 months, extending to 30 months provided limited additional benefits while increasing environmental impact. Therefore, slaughtering at 28 months appears to balance productivity and environmental efficiency under this study. Overall, optimizing slaughter age is an effective strategy to improve sustainability in Hanwoo beef production systems.

Key words : Hanwoo, methane emissions, slaughter age, efficiency, sustainability

OE26002

Predicting eating quality of pork shoulder butt using Vis/NIR hyperspectral imaging and machine learning models

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Predicting eating quality of pork is challenging due to its complex characteristics. Therefore, this study aimed to developed a framework for predicting pork eating quality clusters (EQC) by integrating sensory evaluation and electronic tongue data with visible/near-infrared hyperspectral imaging (Vis/NIR HSI). Pork shoulder butt samples (n = 189) were collected from four pig farms, and pork EQC were defined using k-means clustering (k = 2 and 3) based on saltiness and umami taste intensities obtained from both sensory and electronic tongue analyses. HSI data from muscle, fat, and entire meat were acquired using a two-stage partial least squares-discriminant analysis approach. Among these regions, MUSCLE spectra showed the highest classification performance. Feature selection and data augmentation were systematically evaluated using support vector machine (SVM), logistic regression (LR), and light gradient boosting machine models. In the binary classification, the combination of uninformative variable elimination and combined transformation yielded the best performance, with LR achieving a test F1-score of 0.806. In the three-class classification, SVM showed superior and more stable performance, achieving a test F1-score of 0.696. These results demonstrate that Vis/NIR HSI-based framework provides a non-destructive and practical approach for predicting and classifying pork eating quality in the meat industry.

Key words : pork shoulder butt, eating quality, hyperspectral imaging, machine learning

OE26003

Development of a non-destructive prediction model for crude fat and protein content in beef loin using hyperspectral imaging

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This study was conducted to non-destructively predict the crude fat and crude protein content (%) of beef loin using hyperspectral imaging (HSI) in the spectral range of 350–1,002 nm. A total of 120 beef loin samples were utilized for the analysis, which were partitioned into a calibration set and a prediction set at a ratio of 7:3 (n = 84 and 36, respectively). To improve prediction performance, various preprocessing methods, including standard normal variate (SNV), multiplicative scatter correction (MSC), and the first derivative, were compared. Furthermore, three variable selection methods, including Variable Importance in Projection (VIP), Random Frog, and Competitive Adaptive Reweighted Sampling (CARS), were applied to enhance model efficiency. The results demonstrated that the models using 21 and 25 optimal wavelengths selected by CARS for crude fat and crude protein, respectively, achieved the best performance. For crude fat, the prediction performance was $R^2_P = 0.72$, RMSEP = 3.172, and RPD = 1.90. For crude protein, the model achieved an R^2_P of 0.71, an RMSEP of 0.785, and an RPD of 1.86. Also, chemical distribution maps of these chemical components were visualized using the partial least squares regression (PLSR) models using optimal wavelengths. These findings indicate that HSI technology is a promising tool for the rapid and real-time monitoring of crude fat and protein in the meat industry

Key words: hyperspectral imaging, beef loin, crude fat, crude protein, PLSR

OE26004

Development of an oxygen-gradient-based 3D intestinal model platform for the discovery of next-generation livestock probiotics: validation of the intestinal barrier-enhancing effects of *Bifidobacterium adolescentis* OP820

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Early weaning in piglets induces intestinal barrier disruption and gut microbial imbalance, which are closely associated with diarrhea and reduced productivity. This study established an oxygen-gradient-based 3D villi co-culture system mimicking the intestinal microenvironment and evaluated the epithelial adhesion and barrier-enhancing effects of *Bifidobacterium adolescentis* OP820 selected from diverse environmental samples. The established system was designed to simultaneously reproduce hypoxic luminal conditions and oxygenated basal conditions. OP820 exhibited stable viability and strong adhesion ability within the system, particularly showing selective localization in the mucin-rich glycocalyx region. In addition, reduced adhesion under MUC13 and MUC17 knockdown conditions suggested that epithelial adhesion of OP820 was regulated in a transmembrane mucin-dependent manner. Furthermore, OP820 treatment restored the expression of TJP1, OCLN, and CLDN1 reduced under inflammatory conditions, thereby alleviating intestinal barrier dysfunction. These findings suggest that OP820 is a promising probiotic candidate adaptable to the intestinal mucosal environment and that the oxygen-gradient-based 3D co-culture system may serve as a useful platform for evaluating livestock probiotics.

Key words : livestock probiotics, gut commensal bacteria, *Bifidobacterium adolescentis* OP820, 3D villi co-culture system

OE26005

Protective effects of probiotic strains against gastric and intestinal inflammation and modeling of freeze-drying

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Lactobacillus johnsonii JNU3402 has attracted increasing attention as a functional probiotic strain due to its beneficial effects on gut health and anti-inflammatory activity. However, industrial applications of probiotics require improved stability during freeze-drying processes and scientific validation of their protective effects against gastrointestinal inflammation. Therefore, this study evaluated the freeze-drying characteristics of JNU3402 and its protective effects against gastritis and intestinal inflammation. Various cryoprotectant formulations based on trehalose, whey powder, and monosodium glutamate (MSG) were optimized using a modified simplex lattice model to improve the viability of JNU3402 during freeze-drying. The protective effects of JNU3402 were evaluated in inflammation-induced cell and animal models through histological and inflammatory analyses. Whole-genome analysis confirmed the presence of thioredoxin-related genes in JNU3402. Furthermore, probiotic treatment reduced reactive oxygen species (ROS) production and suppressed inflammatory cytokine expression, including TNF-α and IL-6, suggesting that the anti-inflammatory effects of JNU3402 may be associated with thioredoxin-related antioxidative mechanisms. Overall, this study provides fundamental insights into the industrial applicability and gastrointestinal protective potential of JNU3402 as a functional probiotic material.

Key words : *Lactobacillus johnsonii* JNU3402, freeze-drying, gastritis, intestinal inflammation

OE26006

Impacts of whey protein isolate edible coating on digestibility and bioactivity of cheeses during *in vitro* digestion

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This study investigated the effect of whey protein isolate (WPI) edible coating on the *in vitro* digestibility, bioactive properties, and metabolomic profiles of soft, semi-soft, and hard cheeses during simulated salivary, gastric, and intestinal digestion. WPI-coated cheeses exhibited significantly ($p < 0.05$) higher digestibility during selected digestion stages, particularly during intestinal digestion, compared with uncoated cheeses. Angiotensin-converting enzyme (ACE) inhibitory activity and antioxidant capacities, assessed by 2,2-diphenyl-1-picrythydrazyl (DPPH) and 2,2`-azinobis-(-3ethylbenzothiazoline-6-sulfonic acid) ($ABTS^+$) radical scavenging, were also significantly ($p < 0.05$) enhanced in coated samples depending on cheese type and digestion phase. The improved bioactivities were associated with increased release of bioactive peptides and amino acid metabolites during gastrointestinal digestion. NMR-based metabolomic analysis revealed distinct stage-specific metabolic patterns, with coated cheeses showing elevated levles of glutamine, glutamate, proline, carnosine, glycine, and arginine. Variable Importance in Projection analysis identified these metabolites as key contributors to digestion-stage discrimination and functional activities. Overall, WPI edible coatings significantly improved the nutritional functionality, antioxidant potential, and antihypertensive properties of cheeses, highlighting their potential application in the development of functional dairy products.

Key words : whey protein isolate (WPI), edible coating, cheese, *in vitro* digestion, digestibility, antioxidant activity

유전 및 육종

OF26001

Multi-algorithmic translation of genomic estimated breeding value (GEBV) into fattening types of Hanwoo cattle

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Hanwoo (Korean native cattle) production systems have increasingly adopted extended fattening periods and high-energy feeding programs to enhance carcass quality; however, these practices have concurrently driven up management costs and imposed substantial economic burdens on producers. Consequently, there is a growing demand for individualized feeding strategies that align nutritional management with the genetic potential of each animal. Although genomic estimated breeding values (GEBVs) enable early and accurate assessment of genetic merit, their practical application in on-farm feeding management remains largely limited. In this study, we present a framework that transforms GEBV data into biologically meaningful genetic growth categories to facilitate individual-specific precision feeding. Approximately 18,000 Hanwoo cattle with both GEBV and carcass trait records were used to derive four composite genetic types reflecting distinct growth patterns. To enable early-stage application, statistical and machine learning approaches were employed to predict these genetic types using only GEBV information during the initial fattening period. Among the tested models, CatBoost achieved the best overall predictive performance, with R^2 values ranging from 0.58 for the least accurately predicted genetic type to 0.65 for the most accurately predicted type. Collectively, these findings demonstrate that translating genomic information into discrete genetic classifications can meaningfully support data-driven decision-making in Hanwoo production systems. However, the full predictive utility of such classifications is contingent upon the integration of additional covariates—including environmental conditions, herd management practices, and nutritional history—to enable more comprehensive and accurate phenotypic assessments. Nonetheless, this study establishes a foundational framework for advancing both economic viability and production sustainability in Hanwoo operations through the systematic implementation of precision feeding strategies.

Key words : genetic type, genomic estimated breeding value (GEBV), machine learning, smart livestock

OF26002

Comparative unsupervised clustering of Hanwoo cattle based on genomic estimated breeding values for carcass traits

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As a primary indicator for genetic progress and early-stage individual selection, GEBV (Genomic Estimated Breeding Value) offers significant potential for pre-emptively determining optimal feeding strategies. "However, its applicability as a criterion for clustering has not been sufficiently verified, particularly by using artificial intelligence; this study sought to classify GEBV-based clusters by using unsupervised AI-based clustering algorithms. GEBV data for four carcass traits—backfat thickness, carcass weight, eye muscle area, and marbling score—from 18,079 Hanwoo cattle were standardized and four different clustering algorithms were applied. To address limitations posed by the heteroscedasticity and unimodal distribution of the data, four clustering techniques with complementary mathematical foundations—K-means++ (distance-based), Gaussian Mixture Modeling (probability-based), HDBSCAN (density-based), and Spectral Clustering (graph-similarity-based)—were applied. The optimal number of clusters (K) was determined with reference to the results of the Gap statistic and NbClust, and cluster validity was assessed using the Silhouette Score and Davies-Bouldin Index. NbClust identified K = 2, 3, and 4 as the most supported cluster numbers (7, 6, and 5 votes, respectively) across 26 indices, with Davies-Bouldin Index values decreasing marginally from 1.437 at K = 2 to 1.349 at K = 4. This study presents a methodological framework for GEBV-based clustering in Hanwoo breeding programs with application of AI algorithms, and by comparing results across four distinct clustering algorithms, it is expected to provide practical guidelines for selecting clustering methods suitable for high-dimensional GEBV data.

Key words: clustering algorithm, genomic selection, Hanwoo, carcass traits, statistics

OF26003

Individual-level structural equation-based genome-wide association studies of direct and mediated genetic effects on carcass traits in Korean Jeju black cattle

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Carcass weight (CWT), eye muscle area (EMA), backfat thickness (BF), and marbling score (MS) are major economic traits in beef cattle. However, the genetic relationships among these traits and the biological pathways through which genomic variants influence them are still not fully understood. Conventional genome-wide association studies (GWAS) generally analyze each trait separately and therefore cannot distinguish direct genetic effects from mediated or opposing structural effects. In this study, we applied individual-level structural equation model GWAS (SEM-GWAS) to 1,826 genotyped Jeju Black Cattle (JBC) to investigate the structural genetic relationships underlying carcass trait variation. Among four competing SEM structures, a biologically informed model (Model D: CWT → EMA, BF; EMA + BF → MS) showed the best fit to the data (CFI = 0.977, RMSEA = 0.137, ΔBIC = −5,196 compared with the one-factor baseline model). Analysis of 150K autosomal SNPs detects 12 suggestive loci at the Bonferroni-adjusted threshold ($p < 1.60 \times 10^{-6}$; corrected based on 31,266 independent SNPs) and 197 additional loci at a secondary exploratory threshold ($p < 5 \times 10^{-5}$). Most loci showed direct trait-specific effects (91.5%), whereas 5.0% displayed both direct and mediated effects, and 2.5% showed antagonistic effects across structural pathways. Mediation analysis indicated that the CWT → EMA → MS pathway explained 19.5% of the total genetic effect on MS, while the CWT → BF → MS pathway explained an additional 5.3%, resulting in 24.8% of the total effect being indirectly mediated. Notably, SEM-GWAS identified 204 of 209 suggestive SNPs (97.1%) that were not detected by conventional single-trait GWAS, highlighting its substantially greater interpretive capacity. Candidate gene annotation highlighted *KIAA0586*, *ZNF385B*, *FSTL5*, *LPIN1*, *DROSHA*, and *UQCRFS1* as promising genes associated with adipogenesis, lipid metabolism, muscle energy metabolism, and marbling development. These findings define the structural genomic architecture of carcass traits in JBC and show that SEM-GWAS can uncover biologically meaningful pleiotropic effects that remain hidden in conventional univariate analyses with practical relevance for genomic selection and conservation breeding programs.

Key words : carcass traits, mediation analysis, direct effects, antagonistic pleiotropy

환경 및 축산 기타

OG26001

Social stability-related behavioural profiles linked to maternal performance and piglet outcomes, and reproductive feasibility of intermittent suckling in a communal farrowing system

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Sows are highly social animals, but modern farrowing systems typically restrict social interactions between sows and piglets, which may increase stress, impair maternal behaviour, and limit early social development in piglets. Communal farrowing systems have therefore been proposed as an alternative housing strategy that may improve behavioural adaptation and welfare, but their practical implementation may depend on stable post-regrouping group formation and reproductive performance. This study aims to investigate whether stable social relationships formed in communal housing are associated with maternal performance and piglet outcomes, while also evaluating the reproductive feasibility of intermittent suckling during prolonged lactation. In this prospective observational study, a total of 20 multiparous sows (Landrace × Large White) will be assigned to two communal pens across two batches. Framework 1 includes (1) quantification of prepartum social behaviours (e.g., nosing, allogrooming, aggression, avoidance) with group stability indicators (e.g., lesion scores, spatial integration), (2) classification of socio-positive behavioural patterns using principal components derived from social behaviours and group stability indicators, and (3) evaluation of whether these behavioural patterns are associated with maternal behaviour, farrowing process, and piglet performance. Framework 2 includes (1) application of intermittent suckling from 28 days after farrowing for 7 days with late weaning at 9 weeks, and (2) assessment of oestrus rate, follicular growth, and conception. This study may provide practical behavioural indicators for supporting social adaptation and stable farrowing and lactation processes, while evidence on the reproductive feasibility without separation between sows and piglets may support productivity and welfare in communal housing systems.

Key words : communal group housing, farrowing and lactation process, maternal behaviour, social behaviour, social cohesion

OG26002

Estimation of annual volatile solid excretion from pigs for the calculation of methane emission from manure in Korea

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The Intergovernmental Panel on Climate Change (IPCC) reported volatile solid (VS) excretion of pigs to estimate the annual methane emissions from pig manure. The National Greenhouse Gas Inventory Report of Korea (2024) used the Western European values suggested by the IPCC. Therefore, the objective of this study was to estimate annual VS excretion from market pigs in Korea. The Gompertz model with days of age was used to calculate body weight (BW). Daily gross energy (GE) intake was calculated using a polynomial model. Daily total GE output was calculated as the sum of fecal and urinary GE output. Daily VS excretion was estimated using the following equation suggested by the IPCC (2006): daily VS excretion (kg/day) = [daily GE intake (MJ/day) × {1 – energy digestibility (%) ÷ 100} + daily GE intake (MJ/day) × urinary energy excretion rate (% of GE intake) ÷ 100] × [{1 – ash (% in feed dry matter) ÷ 100} ÷ 18.45 (MJ/kg dry matter)] = daily GE output (MJ/day) × {organic matter content (% in feed dry matter) ÷ 100} ÷ 18.45 (MJ/kg dry matter). The average daily fecal GE output, urinary GE output, and daily total GE output were 2.84, 0.70, and 3.54 MJ/day, respectively. The average daily VS excretion from market pigs was 0.18 kg/day which less than 0.30 kg/day suggested by the IPCC (2006). Therefore, methane emissions from pig manure in Korea using VS excretion suggested by the IPCC were overestimated.

Key words : energy output, intergovernmental panel on climate change, methane, swine, volatile solid

OG26003

Multiclass acoustic monitoring in pigs: From model development to environmental respiratory stress detection

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This study developed and deployed a multiclass AI acoustic framework for pig respiratory and welfare monitoring. Audio was annotated into five classes: coughing, sneezing, aggressive vocalizations, normal vocalizations, and silence. The dataset included 8,094 clips evaluated as 1.0 s segments with a stratified 70/10/20 split. Among multiclass pipelines, Audio Spectrogram Transformer (AST) achieved highest validation macro-F1 (0.953), test accuracy (0.949), and test macro-F1 (0.947), outperforming XGBoost, Mel-CNN, and MFCC-CNN. In 48 h continuous-audio validation, AST ranked highest for deployment suitability (mean primary rank 1.667; composite score 0.897). The selected AST was applied in a 28-day room-level study of 52 growing pigs in standard-ventilation and ventilation-restricted rooms, showing agreement with 24 h manual annotations (Pearson r = 0.976–0.998). The ventilation-restricted room showed higher coughing, aggressive and normal vocalizations, lower silence, poorer growth, and degraded air quality. Coughing clustered at 19:00–22:00, peaked at 20:00 (2.84 standardized detections), and co-varied positively with NH_3, temperature, and CO_2. These findings support AST-based acoustic monitoring as a non-invasive room-level tool for respiratory-stress surveillance, while replicated multi-room validation remains necessary.

Key words : precision livestock farming, environmental stress, bioacoustic monitoring, pig respiratory health, cough detection

OG26004

Comparative effects of different noise stressors on growth performance and behavior in growing and finishing pigs

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Anthropogenic noise around pig farms, including construction, industrial/environmental, and traffic noise, may impair pig productivity and welfare. This study evaluated the effects of different noise stressors on growth performance and behavior in growing and finishing pigs under practical farm conditions. In growing pigs, noise exposure showed a negative tendency in productivity, with final body weight, average daily gain, and average daily feed intake reduced by 3.35%, 15.84%, and 5.35%, respectively, while feed conversion ratio increased by 6.50%. Drinking water intake increased by 19.52%, and behavioral analysis showed altered activity patterns, including higher standing and drinking frequencies. In finishing pigs, the effects were smaller, with final body weight, average daily gain, and average daily feed intake reduced by 1.28%, 5.17%, and 3.14%, respectively, while feed conversion ratio increased by 2.19%. Behavioral responses were also less pronounced than in growing pigs. These findings indicate that noise stress effects differ by growth stage, with growing pigs more sensitive than finishing pigs. Environmental noise should therefore be considered an important management factor in swine production systems.

Key words : noise stress, growing pigs, finishing pigs, growth performance, behavior

OG26005

Integrated computer vision and machine learning framework for multi-class anomaly detection in group-housed growing pigs

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This study proposed a multi-class anomaly detection framework for group-housed pigs by integrating computer vision and machine learning. Nine classification algorithms were trained to identify five pig conditions—normal, heat stress, poor ventilation, infection, and recovery—using 10 combinations of feeding, drinking, and posture variables. Distinct behavioral patterns were observed across stress conditions. Among the tested models, Linear Discriminant Analysis (LDA) using all feeding and drinking variables achieved strong performance, with precision, recall, F1-score, and accuracy of 96.2%, 96.0%, 96.0%, and 96.0%, respectively, and an AUC of 98.7%. However, Random Forest and XGBoost trained on feeding and drinking variables achieved perfect classification. These results indicate that feeding and drinking behaviors alone are sufficient for robust anomaly detection when paired with suitable classifiers. Although posture variables did not consistently improve accuracy, they enhanced the interpretability of behavioral responses. Overall, the findings demonstrate that stressor-specific anomaly detection based on behavioral data is feasible and offers a practical, scalable approach for early stress detection, improved health and welfare monitoring, and more efficient precision livestock management.

Key words : smart farm, health monitoring, object detection, automatic system, artificial intelligence

OG26006

Environmental enrichment and agonistic behavior in post-weaning pigs:
A pilot study using artificial intelligence

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Weaning is a major stressor for pigs, often increasing agonistic behaviors such as aggression, ear biting, and tail biting, which can impair growth and welfare. This study evaluated the combined effect of rubber sticks and Italian ryegrass hay as environmental enrichment (EE) on growth performance, agonistic behavior, ear and tail biting lesion development, fecal consistency, and blood biochemical parameters. A total of 64 pigs (8 pigs × 4 pens × 2 groups) at 7 weeks of age were assigned to control (without EE) and treatment (with EE) groups for four weeks. Pens were the experimental unit for growth, fecal scores, lesion scoring, and behavioral outcomes. Growth and fecal consistency were measured weekly, while ear and tail lesions were scored at the end. Agonistic behavior was quantified using overhead RGB cameras and a YOLOv8-based AI system with high accuracy, mAP50 = 0.953, validated against manual observations, with behavioral outputs aggregated at the pen level from a single representative pen per group. Combined EE reduced lesion severity, lowered free fatty acids, improved fecal consistency, and decreased agonistic behavior, without affecting growth. AI-based monitoring offers a promising tool for quantifying social stress, although further studies with greater pen-level replication are warranted.

Key words : environmental enrichment, agonistic behavior, pig, AI monitoring, welfare

OG26007

ICT 장비 도입에 따른 양돈 농가의 경제성 분석
Economic analysis of swine ICT equipment adoption on pig farm productivity

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본 연구는 ICT 장비(8종)를 도입한 96개 양돈 농가를 대상으로 장비 도입이 농가 생산성, 노동 효율, 경제성에 미치는 효과를 실증적으로 분석하였다. 도입 전·후 지표를 대응시킨 Wilcoxon 부호순위 검정(비모수)과 Cohen's d 효과 크기를 활용하여 통계적 유의성을 확보하였으며, 장비·규모·도입개수·활용연수로 세분화 분석과 함께 증분 순이익 기반의 경제성 분석을 수행하였다. 분석결과, LSY[Litters per Sow per Year] (+4.15%, $p = 0.001$), PSY [Pig per Sow per Year] (+6.00%, $p < 0.001$), MSY[Marketted-pigs per Sow per Year] (+6.97%, $p = 0.002$), 1등급 출현율(+7.40%, $p < 0.001$), 출하 두당 사료량(−4.49%, $p = 0.023$), 1인당 관리두수(+24.68%, $p < 0.001$)에서 통계적으로 유의한 개선이 확인되었다. FCR[Feed Conversion Ratio] ($p = 0.613$)과 분만율($p = 0.168$)은 유의성에 미치지 못하였다. 장비별로는 포유모돈자동급이기(N = 72, PSY +5.74%, $p < 0.001$), 환경관리기(N=65, PSY +6.56%, $p < 0.001$), 임신돈군사급이기(N = 33, PSY +7.10%, $p < 0.001$)의 효과가 높게 나타났다. 2종의 장비 도입 농가에서 성과가 크게 도출되었으며, 도입 1년 후 유의한 시차 효과가 확인되었다. 농장의 경제효과 총액은 평균 상시모돈수 385두 기준 연간 약 1억 4,553만 원으로 산출되었으며, 수입 증가(출하증가 4,008만 원 + 등급개선 146만 원)가 28.5%, 비용 감소(사료비 절감 8,838만 원 + 노동비 절감 1,560만 원)가 71.5%를 차지하였다. 본 연구는 국내 양돈 ICT 경제성 실증 연구로서 양돈 ICT장비 도입을 위한 의사결정에 활용성 될 것으로 기대한다.

Key words : 양돈, ICT, 스마트팜, 경제성분석

포스터 발표

제1발표분야 : 단위영양

PA26001 Effects of various dietary fiber sources on growth performance, hematological parameters, and fecal score in weaning pigs

……… Hongjun Kim, Hyunju Park, Hyunjung Jung, Joeun Kim, Yejin Min, Yongdae Jeong, Chaibin Lim, Yohan Choi

PA26002 Eggshell quality in brown laying hens: formation, challenges, and nutritional strategies

……… Jin Ho Jeong, Yeong Bin Kim, Ju Yeong Park, Geun Yong Park, Ji Won Shin, Jong Hyuk Kim

PA26003 Interactive effects of *in ovo* β-hydroxy-β-methylbutyrate and different embryonic day on hatching performance and intestinal morphology in Japanese quail

……… Ji Won Shin, Geun Yong Park, Yeong Bin Kim, Ju Yeong Park, Jin Ho Jeong, Jong Hyuk Kim

PA26004 Differential heat stress responses in chicken breast and leg muscle satellite cells: implications for oxidative stress and apoptosis

……… Jongryun Kim, Leecheon Kim, Darae Kang, Kwanseob Shim

PA26005 Analysis of key determinants and correlations of productivity in laying hens during the mid-laying period

……… Leecheon Kim, Jongryun Kim, Kwanseob Shim, Darae Kang

PA26006 A comprehensive analysis of breed-associated predispositions in canine metabolic disorders

……… Yeongjae Chae, Jinok Kwak, Juyoun Kang, Yejin Choi, Haram Kim, Suyoung Lee, Sheena Kim, Hyeun Bum Kim

PA26007 산란계 복지 및 생산지표에 대한 환경 풍부화물 제공 효과와 영향 요인

……… 문예진, 김찬호, 이우도, 김수미, 방한태, 양가영

PA26008 Impact of dietary crude protein and fiber levels during the early weaning on growth performance, blood profiles, and fecal score in weaning pigs

……… Yohan Choi, Hyunju Park, Hongjun Kim, Joeun Kim, Yejin Min, Yongdae Jeong, Chaibin Lim, Hyunjung Jung

PA26009 Comparative effects of different dietary fiber sources on ileal and colonic health: Insights into gut integrity and microbial interactions in weaning pigs

……… Hyunju Park, Hongjun Kim, Hyunjung Jung, Joeun Kim, Yejin Min, Yongdae Jeong, Chaibin Lim, Yohan Choi

PA26010 Effects of dietary calcium and phosphorus supply levels based on total versus standardized ileal digestible specifications on growth performance of broiler chickens

……… C. W. Lee, J. S. Yoo, C. Kong

PA26011 Evaluation of antioxidant activity of ergothioneine using a co-culture microfluidic chip with canine skeletal muscle and liver cells

Seyeon Chang, Won Yong Jung, Han Tae Bang, Kyoung-Min So, Min Young Lee, Sang-Yeob Lee, Woo-Do Lee, Hyun-Woo Cho, Ju Lan Chun

PA26012 *In vitro* digestibility of cat diets varying in carbohydrate source

Seyeon Chang, Won Yong Jung, Han Tae Bang, Kyoung-Min So, Min Young Lee, Sang-Yeob Lee, Woo-Do Lee, Hyun-Woo Cho, Hyunjun Jang, Sung Ho Lee, Ju Lan Chun

PA26013 Arginine supplementation enhances intestinal barrier integrity via jejunal microbiota modulation in broiler chickens raised under multiple stress conditions

Yeong Bin Kim, Chiwoong Lim, Ju Yeong Park, Geun Yong Park, Ji Won Shin, Jun-Mo Kim, Jong Hyuk Kim

PA26014 Nutritional composition and antioxidant properties of young alfalfa as a functional feed additive for dogs

Won Yong Jung, Seyeon Chang, Han Tae Bang, Kyoung-Min So, Min Young Lee, Sang-Yeob Lee, Woo-Do Lee, Hyun-Woo Cho, Ki Won Lee, Ju Lan Chun

PA26015 Effects of dietary supplementation with *Gloiopeltis tenax* on gut microbiota composition and functional profiles in dogs

Won Yong Jung, Seyeon Chang, Han Tae Bang, Kyoung-Min So, Min Young Lee, Sang-Yeob Lee, Woo-Do Lee, Hyun-Woo Cho, Il Ki Hwang, Ju Lan Chun

PA26016 Contribution of compromised feed intake and feed efficiency to growth reduction in nursery pigs challenged with F18$^+$ *E. coli*

Yejune Kim, Jung Yeol Sung

PA26017 Comparison of nutritional characteristics of protein hydrolysates derived from different sources and evaluation of *in vitro* ileal digestibility in dog diets

Da-Hyun Choi, Sang-Yoon Kim, In-Ki Kang, Ji-Su Nam, Gui-Seck Bae, Chang-Hyun Kim

PA26018 Effects of breed-specific feeding programs on growth performance of Hy-Line Brown and Lohmann Brown-Lite pullets

Hye Suk Kim, In Ho Kim

PA26019 상업농장 현장 비교를 통한 이유자돈 사료내 감미제 급여의 생산성 개선 가능성 평가

서재석, 박현수, 유영범, 손동신, 윤성조, 조현웅

PA26020 Effects of dietary amino acids and chromium picolinate supplementation on growth performance and meat characteristics in Woori Heukdon pigs

Yejin Min, Hyunju Park, Yohan Choi, Joeun Kim, Yongdae Jeong, Hongjun Kim, Chaibin Lim, Hyunjung Jung

PA26021 Behavioural and affective responses of heat-stressed weaned pigs supplemented with anandamide or citric acid

Seungwoo Jung, Yujin Jung, Jua Woo, Hyungwook Kang, Jinhyeon Yun

PA26022 Dietary coated omega-3 supplementation modifies egg fatty acid profile without impairing performance or egg quality in late-phase Hy-Line Brown laying hens

Sun Gu Yu, Eun Seo Gwon, Hatem M. Eltahan, In Ho Kim

PA26023 Dietary glycozyme supplementation enhances reproductive performance in sows and pre-weaning growth in piglets

Eun ju Ko, Kye jin Lee, Ji Hye Lee, In Ho Kim

PA26024 Variation in social interaction following regrouping is associated with neuromodulation-related gut microbial functions in growing pigs

Woohee Chung, Junsik Kim, Cheolju Park, Minseok Kim, Jinhyeon Yun

PA26025 Dietary microbial bioactive complex improves feed efficiency by modulating gut microbial fermentation in weaned piglets

Mi Ae Park, Soyeon Park, Hee Seop Yu, Da Jung Lim, Seoyun Son, Yong Hee Yoon, Dae-Hyuk Kim, Yangseon Kim

PA26026 Growth performance and fecal characteristics of growing-finishing pigs fed a DDGS – palm kernel meal-based diet in mash or crumble form

Joo Hee Kim, Sun Gu Yu, Hatem M. Eltahan, In Ho Kim

PA26027 Evaluation of ileal amino acid digestibility in bakery and biscuit by-products fed to growing pigs

Yongdae Jeong, Chaibin Lim, Hongjun Kim, Hyunju Park, Yohan Choi, Yejin Min, Joeun Kim, Hyunjung Jung

PA26028 Effect of *Agastache rugosa* Kuntze (Korean mint) extract supplementation on growth performance, nutrient digestibility, blood profile in beagles

Eun Seo Gwon, Joo Hee Kim, In Ho Kim

PA26029 Optimization of phase-feeding programs to improve pork belly thickness in growing – finishing pigs

Se Yeon Jang, Seung Jin Yun, Ji Hye Lee, In Ho Kim

PA26030 Establishment of a meta-regression approach for predicting performance model in pigs

Jun Young Mun, Priscilla Neves Silvestre, Jae Min Yang, Jin Soo Kim

PA26031 **Evaluation of nutrient and amino acid digestibility by age group in small-breed dogs: maltese and poodles**

Min Young Lee, Kyoung-Min So, Sang-Yeob Lee, Hyun-Woo Cho, Ju Lan Chun, Hayeon Wi, Seyeon Chang, Won Yong Jung

PA26032 **Evaluation of the nutritional composition of food additive by-products as potential alternative feed resources for broilers**

Jin Young Jeong, Minji Kim, Hyun Sang Kim, Su Hyun An, Han-Ha Chai, Hyun-Jeong Lee

PA26033 **Energy availability and nitrogen utilization of cheese by-products in growing pigs**

Chaibin Lim, Hyunjung Jung, Joeun Kim, Yejin Min, Yohan Choi, Hongjun Kim, Hyunju Park, Yongdae Jeong

PA26034 **Capsaicin, Piperine, Sinigrin이 Salmonella thompson의 SPI-1 유전자 발현 및 마우스 장 상피세포 침투에 미치는 억제 효과**

Mi-seong Lee, Chang-Geun Lim, Min Jeong Kim, Su Hyeon Yang, Seung-Hee Baek, In-Sik Nam

PA26035 **Plasma metabolic responses to reduced dietary crude protein and graded lysine supplementation in finishing pigs**

Seong Hun Shim, Son Ji Seon, Hwan Ku Kang

PA26036 **Effects of replacing animal protein with *Bacillus*-fermented soybean meal-based functional protein on gut microbiota of weaned pigs**

Hyunjin Kyoung, Kyeong Il Park, Jinmu Ahn, Yonggu Kang, Hansol Hwang, Eunbin Kim, Hyewon Jo, Yoon Tack Jang, Minho Song

PA26037 **Evaluation of *Bacillus*-fermented soybean meal based functional protein substitute for animal-derived protein on growth performance and intestinal morphology of weaned pigs**

Kyeong Il Park, Hyunjin Kyoung, Jinmu Ahn, Yonggu Kang, Hansol Hwang, Hyewon Jo, Eunbin Kim, Yoon Tack Jang, Minho Song

PA26038 **Evaluation of *Bacillus*-fermented soybean meal as a functional protein substitute for animal-derived sources on diarrhea frequency, blood profiles, and immune responses**

Yonggu Kang, Kyeong Il Park, Hyunjin Kyoung, Jinmu Ahn, Hansol Hwang, Hyewon Jo, Eunbin Kim, Yoon Tack Jang, Minho Song

PA26039 **Effects of fermented soybean meal-based functional protein on growth performance, nutrient digestibility, and intestinal morphology of weaned pigs**

Jinmu Ahn, Hyunjin Kyoung, Kyeong Il Park, Yonggu Kang, Hansol Hwang, Hyewon Jo, Eunbin Kim, Yoon Tack Jang, Minho Song

PA26040 Effects of fermented soybean meal-based functional protein on immune responses and diarrhea incidence of weaned pigs

…… Hansol Hwang, Hyunjin Kyoung, Kyeong Il Park, Jinmu Ahn, Yonggu Kang, Hyewon Jo, Eunbin Kim, Yoon Tack Jang, Minho Song

PA26041 Effects of dietary bacteriophage supplementation on growth performance, jejunal morphology, and cecal bacterial population in broiler chickens raised under multiple stress conditions

…… Ye Jin Jeong, Ryun Ha Kim, Hyun Woo Kim, Ji Hye Lee, Dong Yong Kil

PA26042 Meta-analysis of the effect of reducing crude protein levels in diets on growth performance in broiler chickens during growing and finishing phases

…… Ji Hye Lee, Ryun Ha Kim, Ye Jin Jeong, Dong Yong Kil

PA26043 Monitoring and detection characteristics of 327 pesticide residues in animal feed distributed in South Korea

…… Subin Gwon, Yeon-Joo Jeong, Sung-Youn Kim, Eun Hee Chang, Ji Hye Lee, Hyo-young Kim, Kangmin Seo, Han-Sub Chang

PA26044 Monitoring and occurrence of pesticide residues in complete pet food distributed in the Korean market: a three-year study (2023-2025)

…… Yeon-Joo Jeong, Subin Gwon, Sung-Youn Kim, Eun Hee Chang, Ji Hye Lee, Hyo-young Kim, Kangmin Seo, Han-Sub Chang

PA26045 Development of an LC-MS/MS-based simultaneous analytical method for vitamins A and D in pet feeds

…… Seong-Won Kim, Ji Hye Lee, Sung-Youn Kim, Hyo-young Kim, Kangmin Seo, Han-Sub Chang

PA26046 Effects of combined synbiotic and benzoic acid supplementation on short-chain fatty acid profiles and fecal microbiota in swine

…… Eun Jeong Ko, Sun Bong Choi, Young Bin Park, Sung Ho Lee, Hyun Jun Jang

PA26047 Monitoring and characterization of multi-component pesticide residue patterns in single-ingredient feed

…… Kangmin Seo, Subin Gwon, Yeon-Joo Jeong, Sung-Youn Kim, Eun Hee Chang, Ji Hye Lee, Hyo-young Kim, Han-Sub Chang

PA26048 Effects of crude protein reduction and a moderate increase in metabolizable energy on growth performance, digestibility, and blood metabolites in pigs

…… Sangsik Lee, Junyoung Mun, Jinsu Baik, Jinsoo Kim

PA26049 Effects of feed processing and different energy and protein level in lactating sows under hot ambient

Jae Min Yang, Habeeb Tajudeen, Jun Young Mun, Nguyen Minh Thu, Jin Soo Kim

PA26050 Host-derived *Limosilactobacillus reuteri* supplementation improves piglet growth and gut integrity in heat-stressed sows

Jin Su Baik, Priscilla Neves Silvestre, Sang Sik Lee, Nguyen Minh Thu, Jin Soo Kim

PA26051 Strategic nutritional restriction followed by refeeding induces compensatory growth, improves jejunal morphology, and modulates the gut microbiome in weaning pigs

George Kalaivanan Michelle Aquilera Costa, Minchul Jeon, Sungbo Cho

PA26052 Dietary supplementation with *Limosilactobacillus reuteri* enhances lactational performance and mitigates heat stress induced physiological disturbances in sows

Nguyen Minh Thu, Habeeb Tajudeen, Jin Su Baik, Abdolreza Hosseindoust, Jin Soo Kim

PA26053 Classification and market analysis of commercial prescription diets in Korea according to PARNUTs particular nutritional purposes

Hyun-Woo Cho, Min Young Lee, Sang-Yeob Lee, Ju Lan Chun, Hayeon Wi, Kyoung-Min So

PA26054 Cytotoxic effects of deoxynivalenol and fumonisin B1 in porcine ileum-derived organoids

Su Hyun An, Minji Kim, Hyun Sang Kim, Jiseon Son, Han-Ha Chai, Hyun-Jeong Lee, Jin Young Jeong

PA26055 Fatty acid composition and anti-inflammatory activity of black soldier fly (*Hermetia illucens*) larval oil

Seung-Won Yi, So-Young Lee, Haesung Lee, Ra-Yeong Choi, Ji Hae Lee, Joon Ha Lee, Minchul Seo, Heui-Sam Lee, You-Young Jo

PA26056 Effects of *Lactobacillus amylovorus* supplementation dosage on lactation performance and physiological responses in heat stressed sows

Priscilla Neves Silvestre, Sang Sik Lee, Jae Min Yang, Abdolreza Hosseindoust, Jin Soo Kim

PA26057 Correlation analysis of bioactive compounds with antioxidant and anti-inflammatory properties in black soldier fly (*Hermetia illucens*) larval oil

Seung-Won Yi, So-Young Lee, Haesung Lee, Ra-Yeong Choi, Ji Hae Lee, Joon Ha Lee, Minchul Seo, Heui-Sam Lee, You-Young Jo

제2발표분야 : 반추영양

PB26001 **Effects of different dietary crude protein and energy levels on growth performance of post-weaning Hanwoo calves: sex-based differences**
…… Ji Yun Shin

PB26002 **반추위 보호 카르니틴 급여 수준이 거세 한우 도체 성적 및 비육기간에 미치는 영향**
…… 이기환, 이경근, 이대동, 이상민, 김경진, 김은중

PB26003 **Effect of feeding hot-air dried alfalfa hay on the productivity of growing Holstein heifers**
…… Dong-Hyeon Kim, Dong-Hyun Lim, Seong-Min Park, Ji-Hoo Park, Jeong-hee Yun, Jun-Sik Eom, Young-Lae Kim, Tae-Jeong Choi

PB26004 **Circadian-aware and individualized activity modeling improves early estrus prediction in dairy cows**
…… Seong-min Park, Tae-jung Choi, Dong-hyun Lim, Dong-hyun Kim, Ji-hwan Lee, Kyoung-lim Yoo

PB26005 **유전체 육종가 수준이 거세 한우의 성장과 도체 성적 및 육질 특성에 미치는 영향**
…… 백명기, 정진우, 서주형

PB26006 **경산우 고에너지 급여에 따른 비육기간별 생산성 및 수익성 평가**
…… 박명선, 장선식, 문성진, 엄경환, 김재성, 백열창

PB26007 **Impact of palm oil supplementation on growth performance, rumen fermentation, and methane emissions in Hanwoo steers**
…… Ahmad Hassan, Ye Pyae Naing, Michelle Miguel, A-Rang Son, Bo-Moon Choi, Se-Min Song, Seon-Ho Kim, Sang-Suk Lee

PB26008 **Evaluation of kaolinite-based feed additive and fumarate supplementation on *in vitro* rumen fermentation and methane production**
…… Adomako Daniel Boateng, Khanza Syahira Dhia, Dae-Ho Shin, A-Rang Son, Michelle Miguel, Ye Pyae Naing, Seon-Ho Kim, Sang-Suk Lee, Kwang-Wook Park

PB26009 **Effects of sodium sulfite on methane mitigation in goats**
…… Gyeonjin Kim, Sohyeon Kim, Eun Joong Kim

PB26010 **Effects of thiamine diphosphate (ThDP) supplementation on methane emissions and milk productivity in lactating Holstein cows**
…… J. K. Park, D. H. Lim, T. J. Choi, S. M. Park, D. H. Kim, J. H. Lee, S. B. Han, S. B. Kim

PB26011 Synergistic influence of exogenous fibrolytic enzymes and probiotics on *in vitro* rumen fiber digestion in Korean native black goats

…… Ha Guyn Sung, Seon Ho Kim

PB26012 제주흑우 수소(비거세우)의 생후 초기 성장특성 연구

…… 원미영, 신상민, 김언태, 이승은, Shokrollahi Borhan

PB26013 The effects of mixture of thiamine pyrophosphate and plant oils on the *in vitro* methane production and rumen fermentation characteristics

…… Seong Shin Lee, Huyn Sang Kim, Seong Uk Jo, and Maro Lee

PB26014 Development of an automatic feeder-specific calf milk replacer through analysis of its physical and chemical properties

…… In-ki Kang, Sang-yoon Kim, Da-hyun Choi, Ji-su Nam, Gwi-seok Bae, Chang-hyun Kim

PB26015 Effects of dietary L-citrulline supplementation on adipogenic and arginine metabolism–related gene expression in finishing Hanwoo steers

…… Xue-Cheng Jin, Hyeon-Jun Oh, Dae-Hee Jang, Yun-Seo Song, Do-Hye Heo, Min-Ah Park, Hong-Gu Lee

PB26016 Growth performance, nutrient intake, and digestibility in female goats fed low versus high levels of different type of alfalfa

…… Eun-Do Lee, Byamungu Mayange Tomple, Hyo Jin Kim, Sung June Byun, Kwan-Woo Kim

PB26017 Effects of feeding level on nutrient intake, digestibility and nitrogen balance in hybrid goats offered a locally produced alfalfa

…… Byamungu Mayange Tomple, Eun-Do Lee, Hyo Jin Kim, Sung June Byun, Kwan-Woo Kim

PB26018 Early growth performance, feed intake, and phenotypic traits of uncastrated Jeju black bulls

…… Shokrollahi Borhan, 신상민, 김언태, 이승은, 함준상, 원미영

PB26019 Development of a body condition score prediction algorithm for dairy cows using 3D point cloud data based on a pointpillar model

…… D. H. Lim, S. B. Han, T. J. Choi, S. M. Park, D. H. Kim, S. W. Kim, J. H. Lee, G. L. Ryu, J. K. Park

PB26020 Rumen protozoal and fungal community composition in Hanwoo steers with divergent residual feed intake phenotypes

…… C. J. Park, E. S. Kim, M. Kim

PB26021 **Site-specific microbiome features reveal functional specialization of fecal and vaginal microbiomes in Holstein dairy cows**

…… Seongjae Park, Eun Tae Kim, Dong-Hyeon Kim, Dong-Hyun Lim, Tai-Young Hur, Sang-Bum Kim, Gi-Won Park, Tansol Park

PB26022 **Low versus high forage levels of alfalfa: effects on growth performance and morphological characteristics of male Korean Crossbred Goats**

…… Hyo Jin Kim, Eun-Do Lee, Byamungu Mayange Tomple, Sung June Byun, Kwan-Woo Kim

PB26023 **성장단계별 육용 염소의 혈중 대사물질 및 생리적 지표 변화 분석**

…… 김재진, 김영래, 이소희, 최준, 정운혁, 최지우, 안준상, 손기활, 박병기, 김민지

PB26024 **Effects of nutrient levels in concentrate feed on rumen fermentation characteristics, growth performance, plasma metabolites, and carcass characteristics in Hanwoo steers**

…… Ouk Jae Lee, So Hee Lee, Young Lae Kim, Jun Cui, Yun He Zheng, Ji Woo Choi, Jae Jin Kim, Yun Ho Ji, Hye Bin Lee, Yun Chae Sung, Jeong Ho Jang, Jae Yong Song, Jong Suh Shin, Min Ji Kim, Byung Ki Park

PB26025 **Effects of nano-formulated vitamin supplementation on milk production characteristics in lactating Holstein cows**

…… Yun He Zheng, So Hee Lee, Young Lae Kim, Jun Cui, Ji Woo Choi, Jae Jin Kim, Yun Ho Ji, Ouk Jae Lee, Hye Bin Lee, Yun Chae Sung, Jeong Ho Jang, Jong Suh Shin, Min Ji Kim, Byung Ki Park

PB26026 **Effects of genetic potential and dietary soybean meal-to-lupin ratio on growth performance, plasma metabolites, and carcass characteristics in Hanwoo steers**

…… Jun Cui, So Hee Lee, Young Lae Kim, Yun He Zheng, Ji Woo Choi, Jae Jin Kim, Yun Ho Ji, Ouk Jae Lee, Hye Bin Lee, Jae Yong Song, Joong Kook Park, Jun Sang Ahn, Suk Jun Yun, Gi Hwal Son, Jong Suh Shin, Min Ji Kim, Byung Ki Park

PB26027 **Effects of genetic potential on growth performance, plasma metabolites, and carcass characteristics in Hanwoo steers under a 28-month production system**

…… Yun Ho Ji, Nam O Kim, So Hee Lee, Young Lae Kim, Jun Cui, Yun He Zheng, Ji Woo Choi, Jae Jin Kim, Ouk Jae Lee, Hye Bin Lee, Yun Chae Sung, Jeong Ho Jang, Jae Yong Song, Jong Suh Shin, Min Ji Kim, Byung Ki Park

PB26028 **Effects of genetic potential on growth performance, plasma metabolites, and carcass characteristics in Hanwoo Steers under a 26-month short-term fattening system**

…… Hye Bin Lee, EuyKyung Lee, So Hee Lee, Young Lae Kim, Jun Cui, Ji Woo Choi, Yun He Zheng, Yun Ho Ji, Ouk Jae Lee, Jeong Ho Jang, Yun Chae Sung, Jae Yong Song, Jong Suh Shin, Min Ji Kim, Byung Ki Park

PB26029 **Effects of dietary soybean protein by-product meal supplementation levels on rumen fermentation characteristics, growth performance, and carcass characteristics in Hanwoo steers**

……… Ji Woo Choi, So Hee Lee, Young Lae Kim, Jun Cui, Yun He Zheng, Jae Jin Kim, Yun Ho Ji, Ouk Jae Lee, Hye Bin Lee, Yun Chae Sung, Jeong Ho Jang, Jong Suh Shin, Min Ji Kim, Byung Ki Park

PB26030 **Effects of thiamine diphosphate and soybean oil supplementation on rumen fermentation and methane production in Hanwoo steers**

……… Jun Sik Eom, Hyun Sang Kim, Seong Uk Jo, Ma Ro Lee, Seong Shin Lee

PB26031 **Effects of genomic estimated breeding values and sucrose supplementation on growth performance, rumen fermentation, blood profiles, and meat quality traits in Hanwoo steers**

……… Jaesung Lee, Juhyung Seo, Jinwoo Jeong, Myunggi Baik, Myunghoo Kim

PB26032 **Distinct effects of oleic and palmitic acid on intramyocellular lipid accumulation in bovine myotubes under heat stress**

……… Donghun Kang, Erika P. Eckhardt, Jongkyoo Kim

PB26033 **Effects of glycerol monolaurate supplementation on growth performance, blood metabolites, and disease incidence in Hanwoo and Holstein calves**

……… Gi Hwal Son, Woo Hyung Lee, Jun Sang Ahn, Suk Jun Yun, Jae Yong Song, Jeong Heon Lee, Da Jin Sol Jung, Hong Rip Min, So Young Choi, Joong Kook Park

PB26034 **Effects of different injection levels of vitamins A, D$_3$, and E on blood metabolites and growth- and adipogenesis-related gene expression in Hanwoo calves**

……… Kyung-Hwan Um, Shil Jin, Sung Jin Moon, Myungsun Park, Youl-Chang Baek, Sun Sik Jang

PB26035 **Effects of vitamins A, D$_3$, and E injection at birth on growth and expression of genes related to adipogenesis and angiogenesis across different feeding stages in Hanwoo steers**

……… Kyung-Hwan Um, Shil Jin, Sung Jin Moon, Myungsun Park, Youl-Chang Baek, Sun Sik Jang

PB26036 **한우 미경산우의 성성숙 개시 시기 및 생리적 변화 평가**

……… 조현진, 정신용, 강계원, 전서영, 이민경, 강하민, 서성원

PB26037 **Effects of alfalfa produced in Korea at different inclusion levels in TMR on rumen fermentation and methane production *in vitro***

……… Sungjin Moon, Sunsik Jang, Myungsun Park, Kyunghwan Um, Jeongsung Jung, Youlchang Baek

PB26038 Comparison of DNA, PMA-treated DNA, and RNA-based rumen microbial profiles in Hanwoo steers fed low-protein diets

Woo Hyung Lee, Gi Hwal Son, Suk Jun Yun, Jae Yong Song, Jeong Heon Lee, Jun Sang Ahn, Da Jin Sol Jung, Joong Kook Park, Hongrip Min, Soyoung Choi, Tan Sol Park

PB26039 Imported alfalfa at two feeding levels: impacts on nutrient utilization and body conformation in female and male crossbred goats

Kwan-Woo Kim, Eun-Do Lee, Hyo Jin Kim, Sung June Byun, Byamungu Mayange Tomple

PB26040 Effect of TMR feeding compared to conventional feeding during the performance testing period of growing Hanwoo bull

Jeong Il Won, Shil Jin, Sung-Sik Kang, Ji Min Kang, Hanwool Do, Yonghwan Kim, Jun kyu Son

PB26041 Evaluation of carcass and meat quality traits under methane-mitigation feeding strategies

KyoungBo Ko, SeoYoung Ryu, YounChul Ryu

PB26042 Effects of hot water-extracted plant materials on *in vitro* ruminal fermentation and methane production

Maro Lee, Hyun Sang Kim, Seong shin Lee, Seong UK Jo, Byul Kim, Jun Sik Eom

PB26043 Impact of heat stress on metabolic changes and the effects of heat-treated fermented soybean meal supplementation on lactation performance in Holstein cows under heat stress environmental condition

SungYong Joo, Jaesung Lee, Seonho Kim, Myunghoo Kim

PB26044 Effects of creatinolfosfate supplementation level on *in vitro* rumen fermentation characteristics and methane production

Seong Uk Jo, Jun Sik Eom, Maro Lee, Hyun Sang Kim, Hwan Ku Kang, Seong Shin Lee

PB26045 Effects of synbiotics-based FTMR on rumen fermentation and host metabolism in ruminants

Tae-Yong Kim, Ga-Yeon Seo, Jong-Nam Kim, Myung-Hoo Kim

PB26046 Effects of *Bjerkandera adusta* on *in vitro* rumen fermentation and methane production

E. S. Kim, C. J. Park, C. S. Lee, M. Kim

PB26047 The effects of additional pressure processing of lupin flake on protein degradation characteristics

G. T. Kim, S. J. Lee, J. B. Moon, D. K. Yoo, J. M. Kim, H. W. Shin, B. S. Kim, G. Y. Sok, J. Y. Song, G. H. Son. J. K. Seo

PB26048 **Analysis of genomic estimated breeding value (GEBV) application based on growth traits in Hanwoo steers**

Bohye Park, Sukjun Yun, Jaeyong Song, Junsang Ahn, Joongkook Park, Kiyong Chung

PB26049 **Integrative metagenomic characterization of the bovine colostrum virome and candidate bacteria–virus interactions**

Yeonsue Gwon, Eun Tae Kim, Dong-Hyeon Kim, Dong-Hyun Lim, Tai-Young Hur, Sang-Bum Kim, Gi-Won Park, RyukSeok Kang, Tansol Park

PB26050 **Effects of enzyme, probiotic supplementation and fermentation period on the fermentation characteristics and quality of total mixed ration under summer temperature conditions**

Suyeo Baek, Gyeongjin Kim, Sohyeon Kim, Gihwal Son, Jaeyong Song, Eun Joong Kim

PB26051 **Effects of carcass weight genomic estimated breeding values (GEBV) on productivity and carbon reduction in Hanwoo steers**

Bohye Park, Yousam Kim, Myunghum Park, Kiyong Chung

PB26052 **Storage stability of glucose and ketone in blood samples from Korean native cattle**

Eunju Kim, Min Sung Kim, Youl Chang Baek, Myung Sun Park, Sung Jin Moon, Kyung Hwan Um, Jun-Kyu Son

PB26053 **Effects of a microcurrent-generating mineral mixture on ruminal nitrogen utilization and microbial composition *in vitro***

Yu-Been Cho, Jun-Seo Kim, Jun-Hee Lee, Hong-Gu Lee

PB26054 **Longitudinal fecal microbiota dynamics in Holstein calves and comparative analysis between Holstein and Jersey breeds**

Dohun Lee, Eun Tae Kim, Dong-Hyeon Kim, Dong-Hyun Lim, Tai-Young Hur, Sang-Bum Kim, Gi-Won Park, Myeong-Gwan Oh, Tansol Park

PB26055 **대용유 급여 횟수가 한우 송아지의 성장성적에 미치는 영향**

김호연, 신지호, 강유진, 임진현, 김태호, 김동연, 권원서, 최한빈, 최용준

PB26056 **Effects of feeding system on growth performance and velvet antler productivity in deer**

Se Jin Lim, Sung June Byun

PB26057 **Evaluating milk protein conversion efficiency in Holstein dairy cows across lactation stages as a function of dietary crude protein level**

Young-Lae Kim, Dong-Hyun Lim, Seong-Min Park, Ji-Hoo Park, Jeong-hee Yun, Tae-Jeong Choi, Dong-Hyeon Kim

PB26058 **Evaluation of physiological and biochemical parameters according to different roughage sources in Hanwoo heifers**

······ Youl Chang Baek, Eunju Kim, Sung-Sik Kang, Yonghwan Kim, MyungSun Park, SungJin Moon, KyungHwan Um, Jun-Kyu Son

PB26059 **Major revisions in the 5th edition of Korean feeding standards for dairy cattle**

······ Sang-Yoon Kim, Da-Hyun Choi, In-Ki Kang, ji-sun Nam, Gui-Seck Bae, Chang-Hyun Kim

PB26060 **Effects of pectin-rich by-products (citrus pulp and apple pomace) on *in vitro* rumen fermentation: a meta-analysis**

······ Gyeongmok Kim, Byungho Chae, Inhyeok Cheon, Ji-Yoon Kim, Chang-Hyun Baeg, Sam-Churl Kim, Nag-Jin Choi

PB26061 **축산 분야 AI 자율 생성 논문의 학술적 활용 가능성 및 검증: 6개 연구 사례를 중심으로**

······ 문예진, 김경목, 한규진, 전무궁, 송수정, 남은주, 고하늘, 허선하, 신다원, 황인호

PB26062 **Effects of dietary crude protein levels and carcass weight GEBV groups on Hanwoo calves under summer heat stress**

······ Dae-Hee Jang, Xue-Cheng Jin, Won-Seob Kim, Keun-Kyu Park, Ki-Yong Chung, Hong-Gu Lee

PB26063 **Effects of dietary metabolizable energy, protein and essential amino acids on nitrogen utilization efficiency and milk production in dairy cows: a meta-analytic ensemble classifier**

······ Inhyeok Cheon, Byungho Chae, Gyeongmok Kim, Nag-Jin Choi

PB26064 **Implication of combined vitamin supplementation on reproductive capacity during the growing period in Holstein heifers under summer heat-stress conditions**

······ G. M. Back, J. U. Hwang, H. R. Nam, J. P. Oh, S. K. Kang

PB26065 **서방형 유기산 및 에센셜오일이 반추위 발효 특성에 미치는 영향 조사**

······ 한규진, 천인혁, 김경목, 전무궁, 손성민, 신명선,김채원, 안지선, 양예진, 조상범, 최낙진

PB26066 **Effects of hydrogen supplementation on protozoa-associated prokaryotic communities in rumen protozoal cultures**

······ Changbeen Jang, Geonwoo Kim, Tansol Park

PB26067 **Effects of coconut oil supplementation on methane emissions and feed intake in ruminants: a meta-analysis**

······ Xiaoshuang Nie, Byungho Chae, Inhyeok Cheon, Nag-Jin Choi

PB26068 **복합 미생물 처리가 TMR 발효 품질 및 반추위 *in vitro* 발효 특성에 미치는 영향**

······ 전무궁, 천인혁, 문예진, 정은경, 채병호, 이숙경, 조상범, 최낙진

PB26069 **Effects of dietary energy and *Lactiplantibacillus plantarum* LM1001 culture on fermentation characteristics and greenhouse gas emissions in the rumen**
…… Jun-Hee Lee, Ji-Yoon Kim, Chang-Hyun Baeg, Bu-Gil Choi, Arrynda R. D. Wardani, Jong-Jin Park, Tae-Woong Hur, Sam-Churl Kim

PB26070 **Evaluation of physiological and metabolic responses of goats under cold stress conditions**
…… Ji-Yun Hwang, Yun-Seo Song, Jang-Hoon Jo, Hong-Gu Lee

PB26071 **Feed values of ground corn and ramen by-products as the dietary energy sources for ruminant**
…… Chang-Hyun Baeg, Ji-Yoon Kim, Bu-Gil Choi, Arrynda R. D. Wardani, Jun-Hee Lee, Jong-Jin Park, Byungho Chae, Nag-Jin Choi, Sam-Churl Kim

PB26072 **Effects of plant extract mixture and extruded linseed supplementation on enteric methane emissions in mid lactation Holstein cows**
…… Jun-seo Kim, Jang-hoon Jo, Si-Hyeon Lee, Jeon-ji Young, Joon-pyo Oh, Hong-Gu Lee

PB26073 **Effects of maternal L-citrulline supplementation on growth performance and gene expression in Hanwoo calves**
…… Sung-Bin Chang, Xue-Cheng Jin, Hyeon-Jun Oh, Min-Ah Park, Hong-Gu Lee

PB26074 **Efficacy of a synbiotics complex on dairy cow productivity and calf gut health under Uzbekistan farming conditions**
…… Dong Wook Kim, Young Bin Park, Yeong Min Hwang, Sung Ho Lee

PB26075 **Effects of methanotroph-based probiotic (NC52PC) on milk production performance and milk composition in Holstein dairy cows**
…… Hyeon-Chae Ju, Jang-Hoon Jo, Jun-Hee Lee, Yu-Been Cho, Do-Hye Heo, Si-Hyeon Lee, So-Yul Lee, Seon-Won Kim, Hong-Gu Lee

PB26076 **Chemical composition and methane production of total mixed fermentation for different Hanwoo growth stages**
…… MinJung Ku, YoungSun Choi, YuJin Noh, Cheolhwan Nam, JaeEun Choi

PB26077 **Citrus peel-based *Bacillus subtilis* fermentation and surfactin: impacts on *in vitro* rumen fermentation characteristics and methane emissions**
…… Yong-Ho Jo, Yu-Bin Jo, Eung-Seok Kim, Mi-Ye Kwon, Won-Jong Yoon, Hwa-Seong Shin, Hong-Gu Lee

PB26078 **Effects of processing methods on ruminal fermentation characteristics and protein utilization of palm kernel meal**
…… S. J. Lee, H. W. Shin, B. S. Kim, G. H. Son, J. Y. Song, J. K. Seo

제3발표분야 : 동물생명공학

PC26001 Economic evaluation of ultrasonographic fetal sex prediction: implications for profitability and market dynamics in Hanwoo cattle
Ke Huang, Jiaxi Zhang, EunJi Seo, Myoung Ok Kim

PC26002 Isolation and characterization of a novel Stx1-converting temperate bacteriophage St1-gc
Seunghui Lee, Soojin Lim, Ji Hyung Kim

PC26003 Isolation and characterization of a novel bacteriophage KW1 infecting *Lactococcus lactis*
Gayoung Min, Soojin Lim, Ji Hyung Kim

PC26004 Breaking host barriers: a novel bacteriophage infecting hybrid strains of Enterotoxigenic/Shiga toxin-producing *Escherichia coli*
Seojeong Choi, Soojin Lim, Ji Hyung Kim

PC26005 Spirobenzofuran isolated from *Acremonium* mitigates the negative effects of Ochratoxin A in porcine intestinal epithelial cells
Jung Woong Yoon, Yo Han Lee, Suhyeon Yun, HaEun Han, Sang In Lee

PC26006 Standardized safety evaluation protocols for *Enterococcus* spp. as probiotic candidates
Haram Kim, Yejin Choi, Jinok Kwak, Juyoun Kang, Yeongjae Chae, Suyoung Lee, Sheena Kim, Hyeun Bum Kim

PC26007 Stress-associated cortisol elevation is associated with impaired nursing behavior and gut microbial alterations in periparturient sows
Sarbani Biswas, Jua Woo, Juho Lee, Cheolju Park, Minseok Kim, Jinhyeon Yun

PC26008 Comparison of electroporation conditions in mouse zygotes for improving CRISPR/Cas9-mediated ssODN knock-in efficiency
Ga-Yeon Kim, Hyeon-Seoung Kim, Eun-Ji Choi, Yun-Go, Man-Jong Kang

PC26009 *C. maltaromaticum*-derived factors enhance white adipose beiging and lipolysis, ameliorating metabolic dysfunction in an HFD-induced obese mouse model
Junsung Kim, Hyun A Song, Junkoo Yi

PC26010 Protective effects of Stanniocalcin 2 against oxidative stress in muscle cells
Sarang Choi, Yeongeun Kim, Daeun Lee, Sangsu Shin

PC26011 Artepillin C triggers mitochondria-dependent apoptosis in canine osteosarcoma cell lines

Eunseo Hwang, Wan Lim, Minha Jeong, Jiyeon Ham

PC26012 Effect of calving season on postpartum ovarian activity in Holstein cows

Gyeonglim Ryu, Jihwan Lee, Hyeonguk Baek, Seulgi Lee, Sungwoo Kim, Tae-Jeong Choi

PC26013 Effects of nonylphenol on oxidative stress and implantation-related functions in porcine luminal epithelial cells

Jaeha Hwang

PC26014 Adenovirus-mediated CRISPR/Cas9 system for efficient knockout of the ovalbumin gene in chicken cells

Jae-Yeong Lee, Sangeun Kim, Hyeon Yang, Jingu No, Seunghoon Lee, Seokho Kim, Keon Bong Oh

PC26015 Development of bta-miR-375 biomarker associated with intramuscular fat deposition in Korean Native cattle

김다현, 이충수, 김형록, 전주민, 전민욱, 김영석, 김지윤, 최시연, 정수한, 이동규, 이윤석

PC26016 Preliminary deep learning-based image analysis for segmentation-assisted measurement of jejunal mucosal morphology of weaning pigs under different nutritional conditions

Min Chul Jeon, George Kalaivanan Michelle Aquilera Costa, Sunbo Cho

PC26017 Effects of commercial feed additive on methane reduction and microbial communities in Korean Native cattle

J. Jeon, M. Jeon, Y. Kim, H. Kim, S. Baek, H. Kim, S. Kang, K. Kim, Y. Lee

PC26018 Development of a prediction model for methane emission in Korean Native cattle

Y. Kim, H. Kim, J. Jeon, J. Kim, S. Moon, Y. Baek, S. Lee, K. Kim, J. Oh, H. Lee, Y. Lee

PC26019 Effects of vitamin E and glutamine on stress-responsive and myogenic gene expression in heat-stressed bovine skeletal muscle-derived cells

Bo-Mi Kim, Xue-Cheng Jin, Jun-Hee Lee, Yu-Been Cho, Won-Seob Kim, Jae-Sung Lee, Hong-Gu Lee

PC26020 Heat stress-induced temporal shifts in the fecal microbiome and predicted functional pathways of laying hens using 16S rRNA gene sequencing

M. M. Hossain, S. Lee, Y. Park, Y. Ko, W. Park, H. Kim, J. E. Park

PC26021 Comparative analysis of physiological and transcriptomic responses to heat stress in laying hens in different time period using RNA-seq

……… Y. Park, M. M. Hossain, S. Lee, Y. Ko, W. Park, H. Kim, J. E. Park

PC26022 Immunoinformatics-based design and *in silico* evaluation of a multi-epitope vaccine candidate against porcine reproductive and respiratory syndrome virus

……… Guneswar Sethi, Sang Eun Kim, Keon Bong Oh, Young-Jin Jang, Jeong Ho Hwang

PC26023 Engineering the delta-9 pathway for *de novo* synthesis of eicosapentaenoic acid (EPA) in *Yarrowia lipolytica*

……… H. R. Nam, J. U. Hwang, G. M. Back, S. H. Kang, S. K. Kang

PC26024 Evaluation of antioxidant probiotic potential of lactic acid bacteria isolated from swine feces and fermented foods

……… Suhong Jeon, Sejong Oh

PC26025 Identifying time-dependent molecular adaptations to heat stress in finishing pigs through longitudinal blood transcriptome profiling

……… Nak-Won Ma, Chiwoong Lim, Min-Jae Jang, Young-Jun Seo, Ji-Young Lee, Nae-Ho Park, Jun-Mo Kim

PC26026 전사체 분석(RNA-seq)을 통한 돼지 고환 탈장 관련 차등발현유전자 및 조절 네트워크 발굴

……… 이건혁, 박연희, 조인철, 강용준, 고유진, Mortuza Hossain, 이상훈, 박종은

PC26027 Effect of *Cordyceps militaris* powder on dextran sulfate sodium-induced colitis in mice

……… Won Vin Choi, Gyu Seong Kim, Hae Cheol Lee, Ji Eun Lee, Ye Lin Lee, Seok Ju Kim, Min Ju Kim

PC26028 Modeling interferon-associated transcriptomic dynamics following kidney xenograft transplantation through gene regulatory network inference and time-lagged dynamical modeling

……… Won-Jae Lee, Chiwoong Lim, Min-Jae Jang, Do-Young Kim, Jun-Mo Kim

PC26029 Transcriptomic and microbiome profiling of heat stress responses in the broiler jejunum

……… Chang-Hyeon Ham, Young-Jun Seo, Ji-Yeong Lee, Sang-Hyeop Lee, Chiwoong Lim, Jun-Mo Kim

PC26030 Multi-tissue longitudinal transcriptomics identifies adaptive immunity and lymphoepithelial homeostasis as drivers of interindividual PRRSV susceptibility in weaning piglets

……… Sang-Hyeop Lee, Byeonghwi Lim, Chiwoong Lim, Young-Jun Seo, Min-Jae Jang, Jun-Mo Kim

PC26031 **Application of exosomes as a functional culture supplement for bovine muscle satellite cells in cultured meat production**

Yoonji Shin, Bosung Kim, Jehyeon Lee, Minjae Shin, Nayoung Yun, Sungkwon Park

PC26032 **Development of gelatin-based edible scaffolds for muscle satellite cell culture in cultured meat production**

Yuna Jeong, Bosung Kim, Cui Shuo, Sungkwon Park

PC26033 **CRISPR/Cas9-mediated knockout of ISG15 and IDO1 in porcine alveolar macrophages for PRRSV resistance studies**

Sunirmal Sheet, Seokho Kim, Poongyeon Lee, Chaemin Yu, Ara Cho, Dahye Kim

PC26034 **Comparative molecular docking and dynamics analysis of milk β-casomorphin binding across opioid receptor family**

Tae-Hong Min, Min-Jae Jang, Arvind Kumar Yadav, Chiwoong Lim, Jun-Mo Kim

PC26035 **Lipopolysaccharide-induced alterations in barrier integrity and inflammatory signaling in porcine small intestinal organoids**

Sumin Park, Boram Lee, Dahye Kim, Sheet Sunirmal, Min Gook Lee, Haesun Lee, Sun A Ock, Jae Gyu Yoo

PC26036 **Sustained lactogenic differentiation of bovine mammary epithelial cells through RAC1 overexpression**

Hyun Su Jung, Jong Hyeon Han, Byeong Jun Choi, Keun Woo Kang, Eun Seo Min, Hyejung Kim, Beomsik Kim, Sung Gu Han

PC26037 **Dynamic molecular transitions of sperm storage tubules are associated with long-term sperm retention after artificial insemination in chickens**

Mi-Ryung Park, Se Young Lee, Gyeong Eun Oh, Chang Jun Lee, Youngcheol Cho, Yeoung-Gyu Ko

제4발표분야 : 번식 및 생리

PD26001 Multigenerational effects of gestational BBP exposure on sperm function in mice

Woo-Jin Lee, Won-Hee Kim, Jin Yeon Park, Claudine Uwamahoro, Jae-Hwan Jo, Seung-Ik Jang, Eun-Ju Jung, Jeong-Won Bae, Joon hee Lee, Woo-Sung Kwon

PD26002 Seasonal effect on the morphological and viability parameters of Hanwoo spermatozoa

Jae-Hwan Jo, Won-Hee Kim, Jin-Yeon Park, Claudine Uwamahoro, Seung-Ik Jang, Eun-Ju Jung, Woo-Jin Lee, Jeong-Won Bae, Woo-Sung Kwon

PD26003 Male reproductive toxicity induced by metal components of PM2.5 from pig house exposure in mice

Chae Rim Kim, Zhibin Liu, JaYoung Won, Ryu Hyeon Seo, Myoung Ok Kim

PD26004 Effects of dimethyl sulfoxide on the pluripotency and differentiation ability of mouse embryonic stem cells

Geun Hye Park, Nangwon Yee, Myoung Ok Kim

PD26005 Defatted *Tenebrio molitor* extract alleviated LPS-induced cytotoxicity and oxidative stress in porcine endometrium

Juhyeong Seo, Jiyeon Ham

PD26006 Carbendazim induces G2/M phase arrest and mitochondrial dysfunction in bovine mammary epithelial cells

Minha Jeong, Jiyeon Ham

PD26007 Effects of Ashwagandha extract on testicular dysfunction caused by gut dysbiosis

Ayanthi Ahishcharya, Malavi Arachchi Gamage Nayodya DMAG, Wijesooriya Mudhiyanselage Nadeema Dissanayake, Young-Joo Yi, Seung-Tae-Moon

PD26008 Analysis of effects of feeding systems and body condition score on serum metabolic profiles and pregnancy rate in Hanwoo cows

Sung-Sik Kang, Yonghwan Kim, Myung Sun Park, Youl Chang Baek, Hanwool Do, Joo Young Lee, Dong Gyun Jang, Jun Kyu Son

PD26009 Association between microplastic-induced gut dysbiosis and testicular dysfunction in mammals

Wijesooriya Mudhiyanselage Nadeema Dissanayake, Malavi Arachchi Gamage Nayodya Dananjanee Malavi Arachchi Gamage, Jung Min Heo, Young-Joo Yi

PD26010 **흑염소 암·수 합사 방법에 따른 번식 특성 분석**

남철환, 최재은, 최영선, 구민정, 노유진

PD26011 **한우 번식우의 임신 유무와 혈중 대사체 농도의 관계**

도한울, 김용환, 손준규, 이명숙, 진실, 강성식

PD26012 **Narciclasine induces apoptosis in canine osteosarcoma cells via ROS-mediated mitochondrial dysfunction**

Jinhyeon Son, Seojeong Hwang, Juhyeong Seo, Jiyeon Ham

PD26013 **Immunomodulatory ability of porcine peripheral blood-derived mesenchymal stem cells**

Ji Woo Shin, Jeong Ho Hwang

PD26014 **Preliminary evaluation of *in vitro* embryo development using sex-sorted Jersey semen compared with conventional Hanwoo embryo production**

Jihwan Lee, Hyeonguk Baek, Gyeonglim Ryu, Seulgy Lee, Sung Woo Kim, Seong-Min Park, Dong-Hyeon Kim, Dong-Hyun Lim, TaeJeong Choi

PD26015 **Effects of heat stress on motility of dairy bull frozen-thaw Jersey and Holstein spermatozoa**

Sung Woo Kim, Jihwn Lee, Gyeonglim Ryu, Hyeonguk Baek, Taejeong Choi

PD26016 **Antifreezing gold colloids rescue developmental competence after bovine blastocyst vitrification**

Sehyeon Park, Dong June Ahn, Junkoo Yi

PD26017 **Hematological and metabolic responses of Hanwoo calves to early and conventional weaning**

HyeonJun Yang, Daejin Jung, Youngho Joo, Junkoo Yi

PD26018 **Integrated analysis of subclinical endometritis, uterine microbiota dysbiosis, and conception rate in dairy heifer**

J. U. Hwang, G. M. Back, H. R. Nam, J. P. Oh, S. H. Kang, S. K. Kang

PD26019 **Runs of homozygosity analysis reveals candidate genomic regions underlying spontaneous abortion in Hanwoo**

Jihye Baek, Dohyun Kim, Inseo Lee, Hak-Kyo Lee, Woncheoul Park, Donghyun Shin

PD26020 **Associations of mating body weight and lactation feed intake with reproductive performance and piglet growth in gilts**

Gyu Seong Kim, Won Vin Choi, Hae Cheol Lee, Ji Eun Lee, Ye Lin Lee, Seok Ju Kim, Min Ju Kim

PD26021 한우 생체 난소 내 난자 생검 기술 활용 분만 유래 거세우 도체 성적에 관한 연구

…… 이준선, 유대중, 최재은, 최영선, 김대현

PD26022 Effect of recipient age in months on conception rate in Hanwoo OPU-derived embryo transfer

…… Dae-joong Yu, Jun-sun Lee, Young-sun Choi, Jae-eun Choi, Dae-hyun Kim, Hee-mang Song

PD26023 Effects of sow-specific pheromone on body weight gain in weaned pigs

…… Yubin Song, Junyoung Kim, Minjung Yoon

PD26024 Effectiveness of an ovarian ultrasonography centric practical training program for Hanwoo embryo transfer technicians

…… Jisu Kim, Mirae Kim, Jongil Jeong, Hyeonho Lee, Seoyeong Park, Daehyun Kim

제5발표분야 : 축산물 이용 및 가공

PE26001 Emergence and genomic characterization of carbapenem-resistant *Morganella morganii* carrying bla_{NDM-1} isolated from a Korean commercial livestock farm
Soojin Lim, Seojeong Choi, Tae Seon Cha, Ye Bin Kim, Ji Hyung Kim

PE26002 Isolation and characterization of a novel bacteriophage vB_SenP-GCUTh1 infecting *Salmonella enterica* serovar Thompson
Yejin Seo, Tae Seon Cha, Ji Hyung Kim

PE26003 Effects of fattening starting age and slaughter age on carcass traits and meat quality of Hanwoo steers
Oni Faith Oluwaseyi, Shine Htet Aung, Phyo Htet Htet Kyaw, Madiththe Gedara Asela Sandaruwan Abeyrathna, Byeolee Kang, DongGyu Lee, Ki-Chang Nam

PE26004 Quality and volatile changes of Korean native black goat meat by refrigerated storage and cooking
Jeong Beom Ju, Dongheon Lee, Seokjun Lee, Jinyi Che, Cheorun Jo

PE26005 Development and validation of a refined automated muscle fiber analysis algorithm for immunohistochemistry images
Jaehoon Baek, Junyoung Park, Sumin Song, Huilin Cheng, Hyun-Jun Kim, Gap-Don Kim

PE26006 The effect of intramuscular fat content in beef on the bioaccessibility of protein and lipids
Minkyung Woo, Seul-Ki-Chan Jeong, Hayeon Jeon, Soeun Kim, Seokhee Han, Seonmin Lee, Samooel Jung

PE26007 Identification of proteins associated with quality changes in beef during aging
Junyoung Park, Sumin Song, Huilin Cheng, Jaehoon Baek, Hyun-Jun Kim, Gap-Don Kim

PE26008 Comparison of peptide profile similarity between fresh and spoiled pork cuts
Sumin Song, Junyoung Park, Huilin Cheng, Jaehoon Baek, Hyun-Jun Kim, Gap-Don Kim

PE26009 From pig feces to functional feed additives: Development of multi-strain probiotics for gut health in pigs
Saeyoun Shin, Sua Jin, Subin Kim, Ayeong Jo, Kiyeop Kim, Suhong Jeon, Sejong Oh

PE26010 Association of postmortem metabolic characteristics and ultimate pH in *longissimus dorsi* of Korean native black goat
Kang-Jin Jeong, Jeong-Uk Eom, Jin-Kyu Seo, Han-Sul Yang

PE26011 Effects of initial chilling rate on the oxidative stability and volatile compound profiles of Korean native black goat loin under different storage conditions

Jun-Won Sung, Jeong-Uk Eom, Jin-Kyu Seo, Han-Sul Yang

PE26012 Effect of initial carcass chilling conditions on oxidative stability of *Longissimus dorsi* in Korean native black goats

Jae-Hyeok OK, Jeong-Uk Eom, Jin-Kyu Seo, Han-Sul Yang

PE26013 Impact of dietary betaine supplementation on the quality characteristics of refrigerated and frozen–thawed pork loin

Nayeem Mia, Jeong-Uk Eom, Kang-Jin Jeong, Jin-Kyu Seo, Han-Sul Yang

PE26014 Detection of foreign materials in chicken meat using SWIR hyperspectral imaging

Juntae Kim, Lorna Bridget Alal, Yun-Kil Kwon, Sun-Moon Kang, Byoung-Kwan Cho

PE26015 Handheld NIR spectrometer for beef carcass composition and oleic acid prediction

Juntae Kim, Woo-Sung Chu, Hae-Seong Jeong, Byoung-Kwan Cho

PE26016 Anaerobic isolation and identification of *Propionibacterium freudenreichii* and lactic acid bacteria from commercial emmental cheese and their potential cross-feeding interactions

Yuri Kim, Joon Pyo Oh, Seungha Kang

PE26017 Microbial succession and proteolytic activity during high-temperature fermentation of traditional wheat-based nuruk

Gyeong-seok Kang, Jeong Woong Park, Seungwoo Son, Jaeyoung Heo, Donghyun Shin

PE26018 Impact of different black soldier fly powder supplementation levels on broiler chicken breast meat quality

Hyeon-Yeop Kim, Dong-Ju Moon, Kang-Jin Jeong, Jin-Kyu Seo, Han-Sul Yang

PE26019 Effect of packaging method on physicochemical quality traits in goat meat during storage

Keonhui Kim, Inchan Back, Seohyeon Kong, Seokchan Lee, Junseong Hwang, Donggyun Yim

제6발표분야 : 유전 및 육종

PF26001 Comparison of genomic prediction methods for carcass traits in Hanwoo (Korean Brown Cattle) using genomic best linear unbiased prediction and machine learning approaches

…… Seungwon Oh, Duhak Yoon

PF26002 Genomic characterization of Korean native chickens compared with Kyrgyz populations using genome-wide SNPs

…… Seungchang Kim, Huimang Song, In-Cheol Cho

PF26003 Genetic evaluation of milk yield and heat tolerance in Korean Holstein cattle using a random regression model

…… SuBin Han, SangHoon Han, GyeongLim Ryu, JiHwan Lee, TaeJeong Choi, SeongWoo Kim, JungJae Lee

PF26004 Comparison of growth curve models for Hanwoo cattle: a simulation analysis of sample size and measurement interval

…… Ji Min Kang, Jeong Il Won, Shil Jin, Sung-Sik Kang, Hanwool Do, Yonghwan Kim, Jun Kyu Son

PF26005 Meta-GWAS reveals hidden shared genetic signals for meat quality traits across the Korean chicken populations

…… Eunjin Cho, Hyojun Choo, Jun Heon Lee

PF26006 Microsatellite markers for parentage testing in Korean native black goats: a review

…… Unudbayasgalan Zunduibaatar, Eunjin Cho, Jinhyeong Kim, Jaewon Kim, Hilal Ahmed, Jun Heon Lee

PF26007 First haplotype-resolved assembly of Korean Jeju Black cattle using a trio-binning approach with nanopore sequencing

…… Jaewon Kim, Miyoung Won, Jongan Lee, Sang-Min Shin, In-Cheol Cho, Jun Kim, Jun Heon Lee

PF26008 Genomic characterization of Holstein–Jersey crossbred cattle in Korea using genome-wide SNP data

…… Seulgy Lee, Gyeonglim Ryu, Mi-Na Park, Chang Gwan Dang, Tae-Jeong Choi

PF26009 Blood transcriptome-based cell deconvolution for dissecting intrinsic gene expression changes in pigs

…… Ga-Hyeon Jeong, Jeong-Woo Han, Chiwoong Lim, Young-Jun Seo, Dajeong Lim, Jun-Mo Kim, Kyu-Sang Lim

PF26010 Glycobiology-based engineering of O-linked glycans in monkey FSH

Gisung You, Kyeong-Hoon Phi, Jae Won Lee, Eunyeong Park, Dabin Jeong, Munkhzaya Byambaragchaa, Kwan-Sik Min

PF26011 Validation of an in-house SNP quality control pipeline using pedigree- and genomic-based relationship matrices

GwangTaek Lim, YoonJae Han, YeonHo Kim, YeonWoo Kim, DeukMin Lee

PF26012 Evaluation of single-step genomic best linear unbiased prediction integrating transformer embeddings in a closed nucleus herd

YoonJae Han, DongKyu Lee, GwangTaek Lim, YeonHo Kim, YeonWoo Kim, GyeSik Lee, DeukMin Lee

PF26013 Single-cell transcriptomic atlas of Hanwoo *longissimus dorsi* muscle reveals marbling-associated cellular and molecular features

YoungSun Choi, Minseo Kim, Chan ho Lee, Hyunsoo Lee, Minseo Yang, Cabuloy Amylin Jay Eunice, Taeyeoung Go, Gayeon Heo, SungHak Kim

PF26014 Wnt signaling pathway associated *cis*-lncRNA-mRNA crosstalk in Ogye breast muscle

Jae-rung So, Ki-Duk Song

PF26015 Visualization of GEBV–phenotype relationships in Hanwoo steers for precision feeding

Sung-yeon Kwon, Do-Hyun Kim, Ji-suk Yu, Hak-kyo Lee

PF26016 Genome-wide association study of coat color traits in Korean brindled cattle using genotype

R. Kim, H. Seung, J. Hong, C. Dang, J. Cha, W. Park, S. Lee, H. Ko, E. Kim, S. Maeng, C. Lee, M. Park

PF26017 Evaluation of oleic acid and physicochemical meat quality in Hanwoo cattle

D. Lee, M. Alam, M. Park, H. Seong, J. Cha, C. Dang, S. Lee, E. Kim, H. Ko, W. Park, J. Lee, J. Hong, E. Ryu, C. Lee, A. Jang, C. Cho

PF26018 젖소 산유능력 평가를 위한 신규 305일 보정계수 개발 및 정확도 검증

안성영, 홍준기, 당창권, 김은호

PF26019 Comparison of genetic evaluation models for meat quality pH traits in a Korean Duroc pigs

Ji-Won Kim, Sang-Min Lee, Eun-Ho Kim, Jaebeom Cha, Mahboob Alam, Ha-Seung Seong, Chang-Kwon Dang, Hae-Su Ko, Woncheoul Park, Suyeon Maeng, Dongkyu Lee, Joon-Ki Hong

PF26020 Engineering of O-linked glycan modification in recombinant bovine FSH

Jae Won Lee, Ye Rin Yu, Eunyeong Park, Dabin Jeong, Gisung You, Munkhzaya Byambaragchaa, Kwan-Sik Min

PF26021 Genomic selection and metabolite profiling for quality differentiation of Goheung Hanwoo

…… Young-Gyu Cho, Na-kyung An, Ji-eun Baek, Min-Ji Hong, Kang-Seok Seo

PF26022 Genetic analysis of stage-specific survivability traits in Korean Holstein cattle

…… M. Alam, C. Dang, J. Cha, H. Seong, E. Kim, S. Lee, D. Lee, H. Ko, W. Park, J. Lee, J. Kim, R. Kim, C. Lee, E. Ryu, M. Park, J. Hong

PF26023 Microsatellite Marker 기반 국내 소형견 품종의 개체식별 및 유전적 다양성 분석

…… 공홍식, 이광현, 서길종, 성지연

PF26024 Estimation of genetic parameters for carbon emission intensity in dairy cattle based on milk production performance in Korea

…… Dohyun Kim, JeongWoong Park, Dajeong Lim, SeongWon Seo, Donghyun Shin

PF26025 Genome-wide association analysis of insulin function phenotypes reveals distinct genetic architecture in Koreans

…… Ju-Hyun Baek, Min-Jae Jang, Jun-Mo Kim

PF26026 Integrative network propagation analysis of GWAS candidate genes for carcass traits in Hanwoo

…… Serin Lee, Junyoung Park, JaeDon Oh, Hong Sik Kong

PF26027 Accuracy of genomic estimated breeding values for carcass traits in Hanwoo cattle

…… Azizul MD Haque, Jong-Joo Kim

PF26028 제주마의 혈통 분석 및 유효집단크기 추정

…… 장찬우, 고유진, 송지연, 박연희, 이상훈, 박종은

PF26029 Assessment of genetic structure, diversity, and inbreeding in a conserved line-breeding Hanwoo population

…… Shil Jin, Hyoun Ju Kim, Jeong Il Won, Hanwool Do, Sung-Sik Kang, Jun Kyu Son

PF26030 Blood type diagnostic method using the GGTA1 gene structure differences in pigs

…… In-Cheol Cho, Hee-Mang Song, Sung-Chang Kim, Young-Jun Kang, Hyun-A Kim

PF26031 Evaluation of single-step genomic BLUP for milk production traits in Korean Holstein cattle

…… Jeyran Jabbari Tourchi, Monira Akter Mou, Yewon Shin, Yurim Kim, Hui-Eun Lee, Jong-Joo Kim

제7발표분야 : 초지 및 환경

PG26001 착유우의 물리적, 감각적 환경 풍부화의 유형과 효과에 대한 고찰
…… 이우도, 김찬호, 문예진, 김수미, 방한태, 양가영, 차지혜

PG26002 Effect of negative pressure on exhaust fan performance and determination of critical ventilation rate in pig housing
…… Sungwon Park, Seungyoon Lee, Minjae Bae, Seung-rok Yoon

PG26003 제주 지역에서 한·난지형 목초 및 사료작물 혼파에 따른 초지 식생 구성 및 생산성 비교
…… 정진우, 고하늘, 박형수, 우제훈, 양승학, 정종성

PG26004 이유자돈 환경풍부화물 선택을 위한 문헌 기반 효과 분석
…… 김수미, 김찬호, 이우도, 문예진, 양가영, 방한태

PG26005 Adaptive ventilation control strategy based on heat balance modeling for improved microclimate management in broiler housing
…… Chae-rin Lee, Se-yeon Lee, Ji-yeon Park, Jinseon Park, Rial Arifin Rajagukguk, Se-woon Hong

PG26006 A comprehensive framework for monitoring and enhancing animal welfare and environmental safety in livestock transport systems
…… Rial Arifin Rajagukguk, Jinseon Park, Chae-rin Lee, Ji-yeon Park, Se-yeon Lee, Se-woon Hong

PG26007 Estimation annual nitrogen excretion from gestating and lactating sow
…… Donghyeon Lee, Beob Gyun Kim

PG26008 저전력 엣지 환경에 최적화된 비육염소 행동 분류 Transformer-CNN 모델 개발
…… 이지훈, 허태준, 김주현, 최윤철, 유흥종, 신민용, 김나연, 김성진

PG26009 IMU 센서 기반 젖소 헐떡임 탐지를 통한 고온 스트레스 모니터링 기술 개발
…… 허태준, 이지훈, 김주현, 최윤철, 유흥종, 신민용, 김나연, 김성진

PG26010 Evaluation of methane reduction effects in swine farm slurry by application of a methane reducing agent
…… YuJin No, YoungSun Choi, MinJung Ku, CheolHwan Nam, JaeEun Choi, ChangDae Jung

PG26011 Evaluation of odor reduction effects of microorganisms isolated from swine feces, slurry, and wastewater
…… Sunjoon Lee, Eun Ryul Oh, Ko Eun Jeong, Woong Ji Lee, Hyun-Jun Jang

PG26023 **Comparison of popular YOLO's (YOLOv5 & YOLOv8) for the detection of postures, feeding and drinking behaviors of pig**

Hong-Seok Mun, Eddiemar B. Lagua, Md Sharifuzzaman, Hasan Md Kamrul, Ahsan Mehtab, Jin-Gu Kang, Hae-Rang Park, Young-Hwa Kim, Chul-Ju Yang

PG26024 **Farm-scale pig posture and behavior monitoring: a critical review of vision-based technologies**

Hong-Seok Mun, Ahsan Mehtab, Eddiemar B. Lagua, Md Sharifuzzaman, Md Kamrul Hasan, Hae-Rang Park, Jin-Gu Kang, Young-Hwa Kim, Yoon Sung, Chul-Ju Yang

PG26025 **A systematic literature review on the uses, benefits, challenges and prospects of digital twins in livestock farm management**

Hae-Rang Park, Md Kamrul Hasan, Hong-Seok Mun, Keiven Mark Bigtasin Ampode, Eddiemar Baguio Lagua, Young-Hwa Kim, Md Sharifuzzaman, Jin-Gu Kang, Ahsan Mehtab, Na-Rim Kim, Chul-Ju Yang

PG26026 **Limitations of combined posture and nutritive behaviors for a comprehensive detection model in group-housed pigs using YOLO architectures**

Eddiemar B. Lagua, Hong-Seok Mun, Md Sharifuzzaman, Md Kamrul Hasan, Ahsan Mehtab, Jin-Gu Kang, Hae-Rang Park, Young-Hwa Kim, Chang-Min Park, Chul-Ju Yang

PG26027 **Computer vision-based detection of agonistic behaviors in pigs: advances and applications for precision livestock farming**

Md Kamrul Hasan, Hong-Seok Mun, Ahasan Mehtab, Jin-Gu Kang, Md Sharifuzzaman, Eddiemar B. Lagua, Young-Hwa Kim, Hae-Rang Park, Ha-Eun Ahn, Chul-Ju Yang

PG26028 **Effects of construction noise stress on growth performance and behavior in growing pigs**

Jin-Gu Kang, Hong-Seok Mun, Eddiemar Lagua, Shariffuzzaman MD, Md Kamrul Hasan, Ahsan Mehtab, Young-Hwa Kim, Hae-Rang Park, Tae-Eun Go, Chul-Ju Yang

포스터 발표회 초록

단위영양

PA26001

Effects of various dietary fiber sources on growth performance, hematological parameters, and fecal score in weaning pigs

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Yongdae Jeong, Chaibin Lim, Yohan Choi

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This study was conducted to evaluate the effects of different dietary fiber sources on the growth performance, hematological parameters, and fecal score of weaning pigs. A total of 150 weaning pigs (7.64 ± 0.068 kg) were assigned to 5 treatments with 6 replicates per treatment (5 pigs per pen). The treatments included: 1) CON: basal diet (corn-SBM based diet), 2) BB: basal diet + 4% barley bran, 3) OB: basal diet + 4% oat bran, 4) WB: basal diet + 4% wheat bran, 5) RB: basal diet + 4% rice bran. Notably, all fiber-supplemented groups exhibited significantly higher average daily gain and feed efficiency compared to the CON group ($p < 0.01$). Specifically, the BB group recorded the lowest fecal score during the early phase after weaning among all treatments ($p < 0.01$). Regarding blood profiles, pigs fed fiber sources maintained significantly higher red blood cell-related parameters in PhaseII compared to the CON group ($p < 0.01$). In conclusion, while various fiber sources provide benefits, the inclusion of barley bran is the most effective nutritional strategy to simultaneously enhance growth performance and reduce the incidence of diarrhea. The results of this study suggest that barley bran can be successfully incorporated into weaning pig diets to mitigate post-weaning diarrhea and optimize productivity.

Key words : various fiber sources, barley bran, growth performance, post-weaning diarrhea, weaning pigs

PA26002

Eggshell quality in brown laying hens: formation, challenges, and nutritional strategies

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The eggshell serves as an essential protective barrier that determines egg quality during storage and transport. Eggshell integrity depends on complex formation processes involving protoporphyrin IX (PPIX) synthesis for pigmentation and calcium carbonate ($CaCO_3$) mineralization for structural strength and thickness. Hen age, environmental challenges, and nutritional deficiencies compromise these formation mechanisms. These factors impair calcium metabolism, disrupt acid-base balance, and elevate oxidative stress, ultimately resulting in weakened shell structure and compromised egg quality. Therefore, nutritional and physiological strategies are essential to restore disrupted formation pathways and optimize eggshell mineralization efficiency. Enhanced calcium utilization and strategic phytase supplementation improve mineral deposition and shell structural integrity. Gut microbiota modulation enhances calcium absorption by promoting short-chain fatty acid and lactic acid production. These metabolites lower intestinal pH and improve gut integrity, thereby facilitating mineral utilization and eggshell mineralization. Additionally, antioxidant interventions protect pigment synthesis pathways and maintain cellular homeostasis during shell formation. These approaches suggest synergistic effects in restoring eggshell quality parameters. Therefore, this review suggests that comprehensive restoration of shell formation requires integrated approaches that simultaneously modulate multiple physiological pathways.

Key words : calcium utilization, eggshell quality, gut health, laying hen, nutritional strategies, protoporphyrin IX

PA26003

Interactive effects of *in ovo* β-hydroxy-β-methylbutyrate and different embryonic day on hatching performance and intestinal morphology in Japanese quail

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The objective of this study was to investigate the effects of *in ovo* feeding (IOF) of β-hydroxy-β-methylbutyrate (HMB) on hatching performance and jejunal morphology in Japanese quail. The present experiment was conducted using a 2 × 2 factorial arrangement including 2 IOF days (embryonic day 7 or 11; E7 or E11) and 2 IOF treatments (1× PBS or 1% HMB), administered into the air cell at a volume of 50 μL per egg. A total of 520 eggs from 16-week-old Japanese quail breeder flocks were allotted to 4 treatments with 10 replicates. Results indicated a significant interaction ($p < 0.05$) between IOF day and treatment for hatching performance. On E7, IOF of HMB showed greater ($p < 0.05$) body weight (BW), chick yield, and less ($p < 0.05$) hatch window than the IOF of PBS. On E11, IOF of HMB decreased ($p < 0.05$) pipped shell compared to IOF of PBS. For the main effect of IOF days, no significant effect of IOF day was observed on hatching performance and jejunal morphology. Regarding the main effect of IOF treatment, IOF of HMB increased ($p < 0.05$) hatch of set, hatch of fertile, BW, chick yield, villus height, villus width, and villus height to crypt depth ratio compared to IOF of PBS. IOF of HMB decreased ($p < 0.05$) hatch window and late embryo mortality compared to IOF of PBS. In conclusion, IOF of HMB on E7 resulted in effective hatching performance. Furthermore, HMB improved hatching performance and jejunal morphology, although its effects varied depending on the IOF day.

Key words : β-hydroxy-β-methylbutyrate, embryonic day, hatching performance, *in ovo* feeding, Japanese quail

PA26004

Differential heat stress responses in chicken breast and leg muscle satellite cells: implications for oxidative stress and apoptosis

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Heat stress is a major environmental factor affecting poultry production, yet its cellular mechanisms in muscle satellite cells remain incompletely understood. This study investigated the time-dependent responses of chicken breast and leg muscle satellite cells to heat stress (43°C), focusing on oxidative stress, apoptosis, and mitochondrial adaptation. Cells were exposed to heat stress for 1, 6, and 24 h, and the expression of HSP60, HSP70, SOD1, IL6, BAX, BCL2, and PGC1α was analyzed using RT-PCR. Heat stress rapidly induced heat shock protein expression in both cell types, with significantly greater upregulation of HSP60 and HSP70 in leg muscle cells at 1 h. Early increases in SOD1 and PGC1α were observed only in leg muscle cells, indicating faster activation of oxidative and mitochondrial responses. At later time points, both cell types showed increased apoptosis-related gene expression; however, leg muscle cells exhibited a higher BAX/BCL2 ratio, suggesting greater susceptibility to apoptosis, whereas breast muscle cells maintained higher anti-apoptotic capacity. These findings suggest that leg muscle satellite cells respond more rapidly to heat stress but are more prone to oxidative damage and apoptosis, while breast muscle satellite cells exhibit delayed yet more protective adaptive responses. These differences may be associated with intrinsic muscle fiber characteristics and mitochondrial activity.

This research was supported by Korea Institute of Planning and Evaluation for Technology in Food, Agriculture and Forestry (IPET) through the ‘High Value-added Food Technology Development Program’ and was funded by the Ministry of Agriculture, Food and Rural Affairs (MAFRA) (322006-05-CG000).

Key words : apoptosis, chicken satellite cells, heat stress, mitochondrial adaptation, oxidative stress

PA26005

Analysis of key determinants and correlations of productivity in laying hens during the mid-laying period

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Laying hen productivity is determined by the complex interaction of management practices and environmental factors. The mid-laying period is a critical time for maintaining productivity and managing feed intake; therefore, elucidating the quantitative relationships among key factors is essential for developing effective management strategies. However, our understanding of the quantitative relationships among major productivity factors during the mid-laying period remains limited. This study collected weekly data on egg production, egg weight, feed intake, and temperature from laying hens aged 40–48 weeks. Based on this data, indicators such as Egg mass, Feed intake, Feed Conversion Ratio (FCR), and Temperature (Temp) were calculated to analyze the correlations among the variables. Pearson correlation analysis was used to evaluate the relationships among the variables, and statistical significance was tested at the 0.05 level. The results showed that Feed intake and Temp were significantly correlated with Egg mass ($r = 0.14$, $p < 0.05$; $r = 0.21$, $p < 0.001$), but the strength of these correlations was generally limited. In contrast, a strong negative correlation was observed between FCR and Egg mass ($r = -0.85$, $p < 0.001$), and regression analysis also showed high explanatory power ($R^2 = 0.72$). This suggests that FCR is a key indicator explaining mid-laying productivity. Therefore, it was confirmed that, to improve mid-lay productivity, a precise feeding management strategy based on FCR tailored to each age group is more important than simply increasing feed intake. However, as this study is based on mid-lay data, its application to the pre- and post-lay periods is limited, and further research reflecting the entire production cycle and various environmental conditions is needed.

This work was supported by Korea Institute of Planning and Evaluation for Technology in Food, Agriculture and Forestry (IPET) and Korea Smart Farm R&D Foundation (KosFarm) through Smart Farm Innovation Technology Development Program, funded by Ministry of Agriculture, Food and Rural Affairs (MAFRA) and Ministry of Science and ICT (MSIT), Rural Development Administration (RDA) (RS-2025-02314059).

Key words : laying hens, feed conversion ratio, feed intake, egg mass, precision feeding

PA26006

A comprehensive analysis of breed-associated predispositions in canine metabolic disorders

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With the expansion of the companion animal market, a wider variety of canine breeds are being raised, leading to an increased demand for customized healthcare. To effectively support this demand, identifying the most frequently associated metabolic disorders with breeds is essential. This study aimed to establish a frequency-based reference for metabolic disorders by investigating the distribution of 30 metabolic diseases reported across 64 canine breeds. Data regarding breed-disease associations were systematically collected and analyzed based on WSAVA guidelines and major academic databases, including PubMed and ScienceDirect. The analysis of reported cases revealed that hypothyroidism (21.9%) was the most prevalent metabolic disorder, followed by nephrolithiasis (14.1%), and both diabetes mellitus and hyperlipidemia (12.5% each). Regarding breed-specific vulnerabilities, the Doberman Pinscher (23.3%) exhibited the highest frequency of documented metabolic disease associations, followed by the Dachshund and German Shepherd (20.0% each). Additionally, the Labrador Retriever, Golden Retriever, Yorkshire Terrier, and West Highland White Terrier (16.7% each) showed identical frequencies of association. These findings highlight the associations between metabolic diseases and canine breeds, indicating differences in disease susceptibility across breeds. Accordingly, such patterns may be considered in the development of breed-specific, personalized health management strategies.

Key words : canine, canine metabolic diseases, breed susceptibility

PA26007

산란계 복지 및 생산지표에 대한 환경 풍부화물 제공 효과와 영향 요인

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현재 국내외 동물복지 인증기준에서는 산란계의 행동 욕구 충족 및 복지 문제 경감의 수단으로 환경 풍부화물 제공을 권장하고 있다. 그러나 환경 풍부화물 제공 효과는 산란계의 유전적 특성 및 제공 조건에 따라 상이한 바, 일관되지 않은 연구 결과로 인해 과학적 근거에 기반한 적정 제공 기준을 수립하기 어려운 실정이다. 이에 본 고찰에서는 산란계에 횃대, 알팔파 및 부석을 제공한 총 28편의 연구 논문을 대상으로 그 효과와 영향 요인을 검토하여, 향후 산란계 환경 풍부화물 제공 기준 및 근거 마련을 위한 기초자료로 활용하고자 한다. 횃대 제공을 통해 산란계의 공포 반응 및 이상행동 감소, 인지능력 향상, 골밀도 및 근육량 증가 등 행동 및 근골격계 지표 개선이 보고되었으나, 생산성과 생리학적 지표에 대한 효과는 상대적으로 제한적인 것으로 나타났다. 알팔파와 부석은 대체로 산란계의 깃털 및 물체 쪼기 감소, 스트레스 호르몬 감소 등 행동 및 생리학적 지표에 긍정적인 영향을 미쳤으나, 생산성과 깃털 상태에 대한 효과는 일관되지 않았다. 다만 일부 연구에서 알팔파와 부석을 함께 제공할 경우, 산란계의 피부와 깃털 상태가 개선되는 것으로 나타났다. 한편, 이들 효과는 제공 시기, 종류, 설치 형태 등 환경 풍부화물의 제공 조건을 비롯해 품종, 사육 조건 및 지표 측정 시점 등 다양한 요인의 영향을 받는 것으로 보인다. 본 고찰에서는 제공 조건 및 실험 설계의 이질성으로 인해 산란계 환경 풍부화물 제공 효과의 직접적인 비교에 한계가 있음을 확인하였다. 보다 효과적인 제공 기준 마련을 위해서는 연구 설계 및 평가 방법의 이질성을 줄이기 위한 지속적인 노력이 필요할 것으로 사료된다.

Key words : 산란계, 동물복지, 환경풍부화물, 횃대, 알팔파, 쪼는 물질

PA26008

Impact of dietary crude protein and fiber levels during the early weaning on growth performance, blood profiles, and fecal score in weaning pigs

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This study was conducted to evaluate the effects of dietary crude protein (CP) and fiber (barley bran, BB) levels on the growth performance, blood profiles, and fecal score of weaning pigs. A total of 180 weaning pigs (7.24 ± 0.155 kg) were assigned to 6 treatments with 6 replicates per treatment (5 pigs per pen). The treatments consisted of: 1) PC: 18% CP + 2,000 ppm ZnO, 2) NC: 18% CP, and 3–6) T1–T4, which received different CP and BB levels (18% or 16% CP; 0% or 4% BB) only during PhaseI, followed by a common diet (18% CP + 4% BB) in PhaseII. Notably, the overall gain-to-feed ratio was significantly higher in T1 (18% CP + 0% BB) than in the PC and NC groups (ANOVA, $p = 0.032$), showing optimized feed efficiency. In blood profiles, a significant CP × BB interaction was observed for lymphocyte counts during PhaseI (CP × BB, $p = 0.008$). Regarding fecal score, while the PC group showed the lowest score, lowering the dietary CP level from 18% to 16% significantly reduced fecal score (CP, $p = 0.009$), effectively mitigating post-weaning diarrhea. In conclusion, while growth performance was maintained across treatments, providing 18% CP without barley bran in the immediate post-weaning phase maximized feed efficiency. Furthermore, reducing the dietary CP level to 16% served as an effective nutritional strategy to mitigate post-weaning diarrhea in weaning pigs.

Key words : crude protein levels, barley bran, growth performance, fecal score, weaning pigs

PA26009

Comparative effects of different dietary fiber sources on ileal and colonic health: Insights into gut integrity and microbial interactions in weaning pigs

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This study aimed to investigate the effects of different dietary fiber sources on intestinal morphology, mRNA expression of genes related to gut integrity, and microbial composition of weaning pigs. A total of 60 weaning pigs (age 28 d, initial body weight 7.64 ± 0.365 kg, n = 6) were assigned to 5 treatments: 1) CON: corn-SBM based diet, 2) BB: basal diet + 4% barley bran, 3) OB: basal diet + 4% oat bran, 4) WB: basal diet + 4% wheat bran, and 5) RB: basal diet + 4% rice bran. Thirty pigs were euthanized at the end of PhaseI and PhaseII, respectively. The results showed that dietary fiber supplementation, particularly BB and WB, significantly increased large intestinal crypt depth and total goblet cells during PhaseII compared to the CON group ($p < 0.05$). In the ileum, the mRNA expression of *ZO-1* was significantly upregulated in the BB group during PhaseI ($p < 0.01$), although *MUC2* expression was lower in all fiber-supplemented groups than in the CON group ($p < 0.01$). The expression of *Ki-67,* a cell proliferation marker, was significantly higher in all fiber groups than in the CON group ($p < 0.01$), whereas *ODC1* expression was significantly downregulated by fiber supplementation ($p < 0.01$). Regarding immune response, BB group tended to lower the mRNA expression of *CD8* in PhaseII ($p = 0.015$). According to LEfSe analysis, BB supplementation specifically enriched beneficial biomarkers, including Butyricicoccaceae and Prevotellaceae in the cecum, as well as *Faecalibacterium* in the feces. In conclusion, barley bran is the most effective strategy to improve intestinal structures and promote a favorable microbial environment by modulating gut barrier-related genes in weaning pigs.

Key words : dietary fiber sources, intestinal morphology, tight junction proteins, gut microbiome, weaning pigs

PA26010

Effects of dietary calcium and phosphorus supply levels based on total versus standardized ileal digestible specifications on growth performance of broiler chickens

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The present study was conducted to evaluate the effects of dietary calcium (Ca) and phosphorus (P) levels on growth performance of broiler chickens, comparing diets formulated based on total Ca and non-phytate phosphorus (NPP) versus standardized ileal digestible (SID) Ca and P. A total of 210 10 day-old birds were allocated to five dietary treatments with six replicate cages of seven birds per cage in a randomized complete block design based on body weight. Treatments consisted of 1) CON1, formulated based on SID Ca and P, 2) CON2, formulated based on total Ca and NPP, 3–4) LOW1 and LOW2 reducing Ca and P levels of CON1 and CON2 by 30%, respectively, and 5) HIGH, increasing SID Ca and P of CON1 by 30%. On day 14, body weight and feed leftovers were recorded to calculate body weight gain, feed intake, gain-to-feed ratio. Data were analyzed using the MIXED procedure of SAS software 9.4, and the experimental unit was the cage. Birds fed diets formulated on a total Ca and NPP basis (CON2 and LOW2) exhibited superior growth performance compared to those fed SID-based diets ($p < 0.001$). In conclusion, these findings indicate that the nutrient specification system significantly affects broiler growth performance. Furthermore, the observed performance differences between total and SID-based formulations suggest that further research is needed to precisely determine the optimal Ca and P inclusion levels under each specification system.

Key words : broiler, calcium, growth performance, nutrient specification, phosphorus

PA26011

Evaluation of antioxidant activity of ergothioneine using a co-culture microfluidic chip with canine skeletal muscle and liver cells

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Co-culture microfluidic chip systems are *in vitro* platforms that integrate multiple cell types within a controlled microfluidic environment, enabling dynamic inter-organ interactions. Ergothioneine (EG) is a naturally occurring thiol-histidine betaine found in foods, particularly mushrooms, and functions as an antioxidant by scavenging reactive oxygen species (ROS). In this study, the antioxidant activity of EG was evaluated using a co-culture microfluidic chip integrating canine skeletal muscle and liver cells. Oxidative stress was induced by hydrogen peroxide via the inlet, while EG was administered through the outlet. After 24 h, cells were collected for mRNA expression analysis. Compared with the oxidative stress-induced control, EG treatment altered the expression of genes related to antioxidant defense, apoptosis, and inflammatory responses, suggesting enhanced cellular defense against oxidative stress. In conclusion, EG exerted protective effects by regulating gene expression associated with oxidative stress responses. These results demonstrate the utility of the co-culture microfluidic chip system for evaluating bioactive compounds.

Key words : antioxidant, canine liver cell, canine muscle cell, co-culture chip, ergothioneine

PA26012

In vitro digestibility of cat diets varying in carbohydrate source

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Carbohydrate sources are widely used as ingredients in cat diets; however, their digestibility varies depending on starch structure and fiber composition. Although *in vivo* trials are considered the gold standard, ethical and practical limitations have increased the need for reproducible *in vitro* methods. This study evaluated the *in vitro* dry matter (DM) and crude protein (CP) digestibility of cat diets containing six carbohydrate sources: rice, corn, potato, tapioca, sweet potato, and wheat. All diets met the nutrient requirements for adult cats based on AAFCO guidelines. *In vitro* digestion was performed using a two-step enzymatic model simulating gastric and intestinal phases. Digestibility was calculated according to Biagi et al. (2016) as follows: DM (%) = 100 − (residue weight / sample weight × 100); CP (%) = 100 − [(CP % in residue × (100 − DM digestibility %)) / CP % in diet]. Potato- and tapioca-based diets showed significantly higher ($p < 0.05$) DM and CP digestibility than corn-, sweet potato-, and wheat-based diets. These findings provide reference data for selecting carbohydrate sources in nutritionally optimized cat diets.

Key words : cat, carbohydrate source, *in vitro* digestibility

PA26013

Arginine supplementation enhances intestinal barrier integrity via jejunal microbiota modulation in broiler chickens raised under multiple stress conditions

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This study aimed to investigate the effects of dietary concentrations of arginine (Arg) on jejunal microbiota composition and predicted functional profiles in broiler chickens raised under multiple stress (MS) conditions. A total of 2,052 21-d-old Ross 308 broiler chickens were randomly allotted to 6 treatments with 6 replicates in a 2 × 3 factorial arrangement. Birds were raised under normal (N) conditions (23.0 ± 0.7°C; 9 birds/m^2) and MS conditions (29.9 ± 0.7°C for 10 h and 23.1 ± 0.9°C for 14 h; 18 birds/m^2). The experimental diets were prepared with digestible Arg levels of 1.17, 1.35, and 1.52%. Treatment groups were named as N-1.17%, N-1.35%, N-1.52%, MS-1.17%, MS-1.35%, MS-1.52%. Four samples per treatment group were included in the microbial analysis. Results indicated that Pielou's evenness was less ($p < 0.05$) in MS-1.35% and MS-1.52% groups than in N-1.17%, N-1.35%, and MS-1.17% groups. At the genus level, *Ligilactobacillus* was the most abundant, followed by *Campylobacter*, *Staphylococcus*, and *Enterococcus*. Arg-related metabolic pathways were increased under MS conditions at 1.35% and 1.52% Arg groups. *Ligilactobacillus* was the largest contributor to multiple KEGG Orthologys (KOs) enriched in 1.52% Arg groups compared with 1.17% Arg groups. Arg deiminase pathway-related KOs showed the same directional correlations ($p < 0.05$) and increased with dietary Arg levels. In conclusion, increasing dietary Arg levels enhances *Ligilactobacillus*-associated functions and Arg-related metabolic pathways in broiler chickens raised under MS conditions.

Key words : arginine, broiler chicken, gut microbiota, multiple stress, predicted functional profile

PA26014

Nutritional composition and antioxidant properties of young alfalfa as a functional feed additive for dogs

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Plant-based functional ingredients for canine diets require comprehensive evaluation of their nutritional and antioxidant properties. Accordingly, this study evaluated the nutritional composition and antioxidant activity of hydroponically grown, dried young alfalfa powder. Proximate composition analysis revealed a high protein content (41.89%; 45.70% on a dry matter basis), along with moderate fiber (11.05%) and low fat (1.77%). The powder demonstrated a robust amino acid profile, particularly rich in aspartic acid (8.99%) and key essential amino acids, including leucine (1.81%), lysine (1.78%), and valine (1.31%), supporting its value as a high-quality plant-based protein source. Antioxidant assays showed a total phenolic content of 9.30 ± 0.09 mg GAE/g and a total flavonoid content of 5.48 ± 0.96 mg QE/g. Furthermore, the extract exhibited strong, concentration-dependent ABTS radical scavenging activity, reaching 86.42 ± 0.88% at 10 mg/mL (444.86 μM AAE). These findings indicate that young alfalfa powder is a potent source of essential nutrients and natural antioxidants, with significant potential as a multifunctional ingredient to enhance the nutritional value and metabolic health of canine diets.

Key words : alfalfa, antioxidant activity, functional feed additive, dog, nutritional composition

PA26015

Effects of dietary supplementation with *Gloiopeltis tenax* on gut microbiota composition and functional profiles in dogs

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Dietary components play a key role in modulating gut microbiota and are increasingly considered in the development of functional feed ingredients for companion animals. This study investigated the effects of dietary supplementation with *Gloiopeltis tenax* on gut microbial composition and predicted functional profiles in dogs. Ten adult dogs (Maltese and Poodle) were fed a diet containing 1% *G. tenax* for 4 weeks following AAFCO guidelines. Gut microbiota was analyzed using 16S rRNA gene sequencing, and functional potential was predicted using PICRUSt2. *G. tenax* supplementation significantly altered gut microbial community structure (beta diversity), with notable changes in genera associated with polysaccharide degradation. Functional prediction analysis indicated shifts in pathways related to glycan degradation and carbohydrate metabolism. These results suggest that *G. tenax* supplementation modulates gut microbiota and metabolic potential in dogs, providing foundational evidence for its application as a functional feed ingredient.

Key words : *Gloiopeltis tenax*, dog, gut microbiome, 16S rRNA, sequencing, functional feed ingredient

PA26016

Contribution of compromised feed intake and feed efficiency to growth reduction in nursery pigs challenged with F18$^+$ *E. coli*

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The first objective of this study was to quantify how much F18$^+$ *E. coli* challenge reduces growth performance in nursery pigs based on meta-analysis. The second objective was to quantify how much of the reduction in weight gain in nursery pigs challenged with F18$^+$ *E. coli* could be explained by the reduction in feed intake and feed efficiency. Data were collected from 23 peer-reviewed papers in which nursery pigs were challenged with F18$^+$ *E. coli*. Percent changes (%) in average daily gain (ADG), average daily feed intake (ADFI), and gain-to-feed ratio (G:F) of F18$^+$ *E. coli*-challenged nursery pigs, relative to non-challenged pigs, were defined as ΔADG, ΔADFI, and ΔG:F, respectively. The PROC MIXED of SAS was used to compare ADG, ADFI, and G:F between non-challenged and F18$^+$ *E. coli*-challenged nursery pigs with F18$^+$ *E. coli* challenge as a fixed effect and paper (individual study) as a random effect. The PROC REG of SAS was used to regress ΔADG on ΔADFI or ΔG:F. The ADG (444 vs. 368), ADFI (689 vs. 614), and G:F (0.676 vs. 0.615) of non-challenged pigs were greater ($p < 0.05$) compared with pigs challenged with F18$^+$ *E. coli*. Regression lines for ΔADG were generated as follows: $\Delta ADG = 7.40 + 0.89 \times \Delta ADFI$ ($R^2 = 0.54$) and $\Delta ADG = 11.72 + 0.71 \times \Delta G{:}F$ ($R^2 = 0.41$). In conclusion, F18$^+$ *E. coli* challenge reduces ADG, ADFI, and G:F by an average of 17%, 11%, and 9%, respectively, and the reduction in ADG by F18$^+$ *E. coli* challenge can be attributed 54% to compromised ADFI and 41% to compromised G:F.

Key words : F18$^+$ *E. coli*, feed efficiency, feed intake, nursery pigs, weight gain

PA26017

Comparison of nutritional characteristics of protein hydrolysates derived from different sources and evaluation of *in vitro* ileal digestibility in dog diets

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As the pet food market grows, interest in protein hydrolysates has increased, yet comparative studies on hydrolysates derived from different source materials remain limited. This study compared the nutritional characteristics of commercially available protein hydrolysates from plant (soybean meal, HSM), insect (mealworm, HMW), and marine (shrimp, HSP) sources, and evaluated the *in vitro* ileal digestibility (IVID) of commercial dog diets formulated with each hydrolysate as the primary protein source: soybean meal hydrolysate diet (HSMD), mealworm hydrolysate diet (HMWD), and shrimp hydrolysate diet (HSPD). Crude protein content was similarly high in HMW (72.18%) and HSP (72.50%), while HSM (54.60%) was significantly lower ($p < 0.05$). Ether extract and crude fibe contents were highest in HMW ($p < 0.05$). Regarding essential amino acid (EAA) composition, HSP showed the highest total EAA content ($p < 0.05$). The NPN-to-CP ratio was highest in HSP (93.47%), and free amino group content was also highest in HSP (24.27 g/100 g DM), indicating the greatest degree of hydrolysis among the three hydrolysates. In the diet, total EAA content was highest in HSMD, though *in vitro* crude protein digestibility was highest in HSPD (93.47%), followed by HSMD (90.19%) and HMWD (88.41%), and HSPD also showed the highest digestibility across all essential amino acids ($p < 0.05$). These findings suggest that protein source and processing characteristics should be considered in the selection of hydrolysate ingredients for dog diet formulation.

This work was carried out with the support of “Strategic Export Activation Program (Project No. RS-2025-02304950)” Korea Institute of Planning and Evaluation for Technology in Food, Agriculture and Forestry (IPET).

Key words : dog diet, *in vitro* ileal digestibility, protein hydrolysate, protein source

PA26018

Effects of breed-specific feeding programs on growth performance of Hy-Line Brown and Lohmann Brown-Lite pullets

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This study evaluated the effects of breed-specific feeding programs on growth performance, nutrient digestibility, fecal characteristics, and manure gas emissions in Hy-Line Brown and Lohmann Brown-Lite pullets during the growing phase. A total of 600 one-day-old pullets were assigned to four dietary treatments for 16 weeks in a completely randomized design. The treatments included conventional and transition feeding programs based on the Daehan Feed Series (Daehan Feed Co., Ltd., Incheon, Republic of Korea). Overall growth performance, nutrient digestibility, fecal score, and ammonia emission were not significantly different among treatments ($p > 0.05$). However, transition feeding programs showed numerical improvements in final body weight and feed conversion ratio, particularly in Lohmann Brown-Lite pullets compared to Hy-Line Brown. In addition, the phase-adjusted feeding strategy maintained stable fecal scores, which was associated with a numerical reduction in ammonia emissions. In conclusion, breed-specific transition feeding programs may contribute to improved growth performance and environmental conditions by supporting gut stability and reducing ammonia emissions, suggesting potential benefits for pullet welfare and productivity.

Key words : ammonia emission, fecal score, growth performance, laying hens, phase feeding, pullet

PA26019

상업농장 현장 비교를 통한 이유자돈 사료내 감미제 급여의 생산성 개선 가능성 평가

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본 연구는 양돈농장의 생산성 향상을 목적으로 감미제 급여가 이유 후 돼지의 성장 및 출하일령에 미치는 영향을 상업농장 조건에서 평가하고자 수행되었다. 1차 평가는 2023년 9월부터 12월까지 용인지역 비육농장 1,000두를 대상으로 실시하였으며, A동 340두에는 감미제를 급여하고 B동 660두는 비급여 비교구로 설정하였다. 감미제 급여구는 비교구에 비해 출하종료일이 10일 단축되었고 폐사율은 1.5% 감소하였다. 2차 평가는 2025년 3월부터 9월까지 논산지역 명현농장 이유자돈 600두를 대상으로 실시하였으며, 이유 후 20일간 감미제를 급여한 후 80일령 전출체중을 측정하고 동일 농장의 2024년 기록과 비교하였다. 2025년 급여군의 80일령 전출체중은 전년 대비 3.5 kg 증가하였다. 결론적으로, 감미제의 초기 급여는 상업농장 조건에서 이유 후 성장 개선, 폐사율 감소 및 출하일령 단축에 긍정적 가능성을 보였다. 다만 본 결과는 일반 사육농장에서 수행된 현장 비교 자료이므로, 효과의 명확한 검증을 위해서는 추가적인 통제실험이 필요하다.

Key words : 감미제, 이유자돈, 성장성적, 폐사율, 출하일령

PA26020

Effects of dietary amino acids and chromium picolinate supplementation on growth performance and meat characteristics in Woori Heukdon pigs

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This study evaluated the effects of phase-specific dietary supplementation with amino acids and chromium picolinate on growth performance, nutrient digestibility, and meat characteristics in Woori Heukdon (WHD) pigs. A total of 104 WHD pigs (initial body weight, 31.5 ± 0.24 kg; 40 gilts and 64 barrows) were assigned to either a control diet or a treatment diet containing 4% higher amino acid levels during the growing period and 400 ppb chromium picolinate during the finishing period. Growth performance, backfat thickness, and nutrient digestibility were assessed throughout the feeding trial, and meat proximate composition was analyzed in 20 pigs per treatment after slaughter. Dietary supplementation did not significantly affect body weight, backfat thickness, or nutrient digestibility. However, average daily feed intake increased in the treatment group during the growing and overall periods, with a concomitant decrease in feed efficiency during the growing period ($p < 0.05$). Regarding meat proximate composition, the treatment group showed higher fat and lower protein contents in the loin and ham, whereas the belly showed lower fat and higher moisture contents ($p < 0.05$). Overall, phase-specific supplementation with amino acids and chromium picolinate had limited effects on growth performance and nutrient digestibility but altered meat compositional characteristics in WHD pigs.

Key words: Woori Heukdon, amino acids, chromium picolinate, growth performance, meat characteristics

PA26021

Behavioural and affective responses of heat-stressed weaned pigs supplemented with anandamide or citric acid

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Heat stress during post-weaning alters behavioural responses and may impair adaptation in pigs. This study evaluated whether dietary anandamide (AEA) or citric acid (CA) influence behavioural and affective responses in weaned pigs exposed to heat stress.A total of 600 weaned piglets were randomly allocated to four dietary treatments: NC, A1 (1,000 ppm AEA), A2 (2,000 ppm AEA), and CA (2,000 ppm CA). Behavioural responses were evaluated using the novel object test (NOT), human-animal relationship test (HART), forced human approach test (FHAT), and voluntary human approach test (VHAT), while affective state was assessed using qualitative behaviour assessment (QBA). A1 pigs showed higher HART scores than those in the other groups on day 2 ($p < 0.05$). No significant differences were detected for NOT latency, VHAT, or FHAT. QBA revealed a temporal shift across all groups from a more tense/fearful state at day 0 to a calmer state from day 2 onward. Behavioural tests and QBA provided complementary measures for evaluating heat stress adaptation in weaned pigs. While AEA supplementation was associated with transient alterations in early behavioural responses, QBA revealed a consistent time-dependent shift toward a calmer affective state following weaning across all treatments.

Key words : behavioural response tests, thermal stress, weaned piglets, qualitative behaviour assessment, stress response

PA26022

Dietary coated omega-3 supplementation modifies egg fatty acid profile without impairing performance or egg quality in late-phase Hy-Line Brown laying hens

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This study evaluated the effects of dietary coated omega-3 (REI3) supplementation on productive performance, egg quality, blood profile, and nutrient digestibility in late-phase laying hens. A total of 96 Hyline Brown laying hens at 70 weeks of age were randomly assigned to four dietary treatments, including six replicates with four hens in each for 15 weeks fed: CON, basal diet; TRT1, basal diet + 0.1% REI3; TRT2, basal diet + 0.2% REI3; and TRT3, basal diet + 0.3% REI3. The data were subjected to statistical analysis using version SAS 9.4 (SAS Institute Inc., Cary, NC, USA) based on a completely randomized design with four dietary treatments. Productive performance, egg quality, egg yolk fatty acid composition, blood profile and nutrient digestibility were analyzed by one-way ANOVA. Linear and quadratic effects of increasing dietary coated omega-3 levels were assessed using orthogonal polynomial contrasts. $p < 0.05$ was set as significant. Dietary coated omega-3 supplementation did not significantly affect body weight, downgraded egg percentage, feed conversion ratio, average daily feed intake, egg quality traits, or nutrient digestibility. Blood total cholesterol, LDL, white blood cell count, and lymphocyte percentage were also not significantly altered. However, hens fed 0.2% and 0.3% REI3 showed numerically higher egg production and lower FCR during the late phase of the trial. In addition, serum triglyceride concentration showed a linear tendency to decrease ($p = 0.0671$), whereas HDL showed a linear tendency to increase ($p = 0.0520$) with increasing REI3 levels. In conclusion, moderate coated omega-3 supplementation had limited effects on performance-related traits but effectively enhanced the nutritional quality of egg lipids in aging hens.

Key words : coated omega-3, Hyline Brown laying hens, late laying period, egg quality, blood lipid profile, nutrient digestibility.

PA26023

Dietary glycozyme supplementation enhances reproductive performance in sows and pre-weaning growth in piglets

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The reproductive performance of lactating sows is critical for swine productivity, but reduced feed intake during lactation can lead to energy imbalance, impairing sow health and piglet growth. Glycozyme, a mixture of simple sugar, β-glucan, exogenous enzymes, and probiotics, has been developed as a potential antibiotic alternative to enhance immune function and nutrient utilization. This study was conducted to evaluate the effects of Glycozyme supplementation on reproductive performance, nutrient digestibility, milk composition, and blood profiles of lactating sows, as well as growth and health status of their suckling piglets. A total of 21 lactating sows (Landrace × Yorkshire; average parity of 3.3) were randomly assigned to one of three dietary treatments for a 5-week trial, with seven replicates per treatment and one sow per replicate. The dietary treatments consisted of : 1) CON (basal diet), 2) TRT1 (basal diet + 0.25% Glycozyme), and 3) TRT2 (basal diet + 0.50% Glycozyme). Data were analyzed using the General Linear Model procedure of SAS (2013), and means were compared via Duncan's multiple range test. Linear and quadratic effects of Glycozyme levels were also evaluated. Statistical significance was declared at $p < 0.05$. In lactating sows, average daily feed intake (ADFI), milk yield, milk composition (protein, lactose, and solids-not-fat), and serum glucose levels were significantly higher in TRT2 than in CON ($p < 0.05$). Conversely, blood cortisol levels were significantly higher in CON than in TRT2 ($p < 0.05$). However, no significant differences were observed in nutrient digestibility and skin color among the dietary treatments ($p > 0.05$). Similarly, in suckling piglets, body weight and average daily gain were significantly higher in TRT2 than in CON ($p < 0.05$). In contrast, parameters such as fecal score, skin color, and blood profiles in piglets did not show any treatment-related deviations. In conclusion, dietary supplementation with Glycozyme, particularly at 0.50%, improved reproductive performance, milk production, and metabolic status in lactating sows, which subsequently enhanced the growth performance of suckling piglets without negatively affecting health-related parameters. These results suggest that Glycozyme can be used as a functional feed additive to improve both sow productivity and piglet growth during lactation.

Key words : glycozyme, growth performance, lactating sows, reproductive performance, suckling piglets

PA26024

Variation in social interaction following regrouping is associated with neuromodulation-related gut microbial functions in growing pigs

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Social interaction is essential for pigs to form structured group relationships and establish dominance hierarchies. In commercial farms, however, pigs have limited early-life social experiences and are abruptly regrouped into unfamiliar social groups, resulting in social instability, prolonged aggression and physiological stress. Given the emerging role of the gut microbiome in modulating behavioural regulation, this study investigated gut microbial functional profiles associated with variation in social interaction following regrouping. After a 2-h transport period and subsequent random regrouping, a total of 319 pigs were allocated to six pens across two batches. Based on the total proportion of pigs engaged in affiliative and agonistic interactions during the 24 h post-regrouping period, pens were classified into low social interaction (LS, n = 9) and high social interaction (HS, n = 9) groups. Faecal samples collected on days 1–2 post-regrouping were analysed using 16S rRNA sequencing to determine microbial composition and predicted functions. In LS pigs, taxa such as Terrisporobacter were positively correlated with functions related to excitatory neuromodulation (r = 0.50 to 0.60, $p < 0.01$), whereas HS-associated taxa such as *Lactobacillus* were negatively correlated with these functions (r = −0.74 to −0.62, $p < 0.001$). Conversely, HS-associated taxa, including Treponema, were positively correlated with functions related to inhibitory neurotransmission (r = 0.43 to 0.50, $p < 0.01$), while LS-associated taxa such as *Faecalibacterium* showed negative correlations (r = –0.66 to -0.51, $p < 0.01$). Consistently, pro-inflammatory taxa and excitatory neuromodulation-related functions were more abundant in LS pigs, whereas anti-inflammatory taxa and inhibitory neuromodulation-related functions were more abundant in HS pigs. These findings suggest that variation in social interaction following regrouping is associated with distinct gut microbiota–function profiles, with directional divergence in relationships between taxa and functions, particularly in relation to neuromodulation. These patterns support a potential role of the gut microbiome in behavioural adaptation to social stress.

Key words : gut microbiota-brain axis, microbial metabolism, neurotransmission, social behaviour, social stress

PA26025

Dietary microbial bioactive complex improves feed efficiency by modulating gut microbial fermentation in weaned piglets

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Improving feed efficiency while maintaining gut stability is a key nutritional objective during the post-weaning period in piglets. This study investigated the effects of dietary supplementation with a microbial bioactive complex (MBC), composed of *Pediococcus pentosaceus* CACC616, *Lactobacillus reuteri* CACC607, *L. dextrinicus* CACC889, *L. pentosus* CACC891, and *Saccharomyces cerevisiae* CACC699, on feed efficiency and gut microbial fermentation in weaned piglets. The complex was produced via solid-state fermentation (SSF), enabling the co-delivery of viable microorganisms and fermentation-derived metabolites. A total of 34 piglets were randomly assigned to either a basal diet (control) or the same diet supplemented with MBC for 33 days. The MBC contained approximately 2.4×10^9 CFU/g of lactic acid bacteria and 5.17×10^6 CFU/g of yeast and was included in the diet at 0.5%. MBC supplementation significantly improved feed conversion ratio ($p < 0.05$) and reduced average daily feed intake, indicating enhanced feed utilization efficiency without adverse effects on health-related blood parameters. The constituent strains exhibited acceptable safety characteristics, including the absence of hemolytic activity and low biogenic amine production. Microbial analysis revealed that taxa enriched in the MBC-treated group, including *Succinivibrio* and *Succinivibrionaceae UCG-001*, are associated with carbohydrate fermentation and succinate-producing pathways. Collectively, these findings demonstrate that dietary inclusion of MBC improves feed efficiency and reshapes gut microbial fermentation by modulating fermentation-associated metabolic pathways in weaned piglets, supporting its potential application as a functional feed additive in swine production.

Key words : microbial bioactive complex, weaned piglets, feed efficiency, feed conversion ratio, gut microbiota, propionate

PA26026

Growth performance and fecal characteristics of growing-finishing pigs fed a DDGS-palm kernel meal-based diet in mash or crumble form

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Feed formulation remains one of the major determinants of profitability and sustainability in pig production, as feed accounts for the largest share of total production costs. Therefore, increasing attention has been directed toward reducing reliance on conventional protein sources through the inclusion of lower-cost agro-industrial co-products without impairing growth performance or carcass quality. This study aims to evaluate the effects of partial replacement of soybean meal (SBM) with palm kernel meal (PKM) and distillers dried grains with soluble (DDGS), offered in mash or crumble feed forms, on growth performance and fecal characteristics of growing-finishing pigs. A total of 210 growing pigs ([Landrace × Yorkshire] × Duroc), weighted 30 ± 3.5 kg, were placed into three dietary treatments with fourteen replicates and five animals in each pen and fed TRT1, a mash diet based on corn-SBM; TRT2, a mash diet based on corn-SBM-DDGS-PKM; and TRT3, a crumble diet based on corn-SBM-DDGS-PKM. Data was analyzed using SAS 9.4 (SAS Institute Inc., Cary, NC, USA). Body weight, fecal moisture, and fecal score were analyzed using repeated-measures mixed model with treatment, time, and treatment × time as fixed effects. ADG, ADFI, and FCR were analyzed using PROC MIXED. Growth performance was evaluated during the growing and finishing periods. Moreover, fecal score and fecal moisture were recorded as indicators of digestive stability. The results showed that during the growing phase, body weight, average daily gain, average daily feed intake, and feed conversion ratio did not differ significantly among mash or crumble treatments. Likewise, no significant treatment effects were observed on fecal score or fecal moisture in mash or crumble treatments. Similar results were obtained during the finishing phase, where growth performance parameters remained unaffected significantly by treatment under mash or crumble form, and fecal traits also showed no significant differences. These results indicated that PKM and DDGS can partially replace SBM in growing-finishing pig diets without detrimental effects on growth performance or fecal consistency under the present conditions. The findings also suggest that crumble feed did not confer a clear advantage over mash feed when used in PKM- and DDGS-containing diets.

Key words : growing-finishing pigs, palm kernel meal, DDGS, crumble, mash, fecal characteristics

PA26027

Evaluation of ileal amino acid digestibility in bakery and biscuit by-products fed to growing pigs

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Rising feed costs and increasing sustainability demands driven with climate change have intensified interest in identifying alternative feed ingredients to replace corn as the primary energy source in swine diets. In particular, the reutilization of food by-products as feed ingredients has gained considerable attention as part of circular feed resource utilization strategies. Bakery and biscuit by-products are considered promising alternatives to corn due to their high energy density and palatability. However, their practical application is limited by variation in nutrient composition, highlighting the need for evaluation based on standardized ileal digestibility (SID) for precise diet formulation. Thus, this study was conducted to evaluate the apparent ileal digestibility (AID) and SID of amino acids in bakery by-products, including plain bread meal (PBM) and sweet bread meal (SBM), as well as biscuit meal (BM), and to compare these values with those of corn in growing pigs. A total of five barrows ([Landrace × Yorkshire] × Duroc) with an initial body weight of 17.22 ± 1.17 kg were assigned to a 5 × 5 Latin square design. Experimental diets consisted of a corn-based control diet (CON), diets containing the PBM, SBM, or BM, and a nitrogen-free diet used to estimate basal endogenous amino acid losses. All pigs were surgically fitted with a T-cannula at the distal ileum, and ileal digesta were collected for 2 days via the cannula. The SID of most indispensable amino acids in the PBM, SBM and BM did not differ from those in corn. These findings indicate that bakery and biscuit by-products may serve as an alternative feed ingredient in pig diets based on comparing SID basis.

Key words : ileal digestibility, bakery meal, biscuit meal, pigs

PA26028

Effect of *Agastache rugosa* Kuntze (Korean mint) extract supplementation on growth performance, nutrient digestibility, blood profile in beagles

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Agastache rugosa Kuntze, commonly known as Korean mint, is a medicinal and functional herb widely cultivated in Northeast Asian countries, including Korea, Japan, and China. Earlier studies reported its various pharmacological activities, including antifungal, antiviral, anti-inflammatory, and antioxidant effects. However, its potential role in modulating the immune system in dogs has not yet been investigated. Therefore, this study aimed to evaluate the effects of dietary supplementation with *Agastache rugosa* extract on growth performance, nutrient digestibility, fecal microbiota, and blood profiles in beagles. Eight healthy beagles with an initial body weight of 12.47 ± 0.05 kg were enrolled in a 10-week crossover study consisting of two experimental phases: Phase 1 (weeks 0–4) and Phase 2 (weeks 6–10), separated by a 2-week washout period. Dogs were assigned to receive either a control (CON) commercial diet or the CON diet supplemented with *Agastache rugosa* Kuntze extract at a dose of 120 mg/day. Growth performance, blood profiles, nutrient digestibility, fecal moisture and pH, and fecal microbiota were assessed at the end of each phase. Data was analyzed using linear mixed models for growth performance, nutrient digestibility, fecal pH, and hematological parameters, with dietary treatment and experimental period as fixed effects and individual dogs as a random effect using SPSS version 22.0 (SPSS Inc., Chicago, IL, USA). Our results showed that inclusion of 120mg/day plant extract into beagles' diet had no significant effects either on growth performance, nutrient digestibility, or overall fecal microbiota composition; however, significantly ($p < 0.05$) increased immunoglobulin G and lymphocyte concentrations compared with the CON group. Based on these results, dietary supplementation with *Agastache rugosa* extract at 120 mg/day may enhance immune responses in beagles without adversely affecting growth performance, nutrient utilization, or gut microbial balance, indicating its potential as a functional feed additive for canine health.

Key words : probiotic, growth performance, nutrient digestibility, gut health

PA26029

Optimization of phase-feeding programs to improve pork belly thickness in growing-finishing pigs

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The growing-finishing phase accounts for 80% of total feed consumption, where inappropriate protein levels often lead to excessive fat deposition and environmental pollution. Recently, low-crude protein (CP) diets supplemented with essential amino acids have emerged as a strategy to improve nitrogen utilization and gut health. Particularly in Korea, managing pork belly quality by controlling intermuscular fat is economically crucial. Therefore, this study evaluated the effects of phase-feeding programs using low-CP diets on growth performance, nutrient digestibility, fecal gas emissions, fecal score, meat quality, and carcass traits in growing-finishing pigs. A total of 200 growing pigs (initial body weight: 25.10 ± 1.76 kg) were randomly assigned to four dietary treatments for a 16 week trial: TRT1, growing diet (G, 4 wk) → early finishing diet (EF, 8 wk) → late finishing diet (LF, 4 wk); TRT2, G (4 wk) → EF (12 wk); TRT3, G (4 wk) → EF (8 wk) → G (4 wk); and TRT4, G (16 wk). For statistical analysis, all data were analyzed using the General Linear Model (GLM) procedure of SAS (2013). The significant differences among treatment means were determined by Duncan's multiple range test. No significant differences ($p > 0.05$) were detected between the treatment groups across all parameters, such as growth performance, nutrient digestibility, fecal gas emissions, fecal score, or meat quality. However, carcass traits analysis revealed that backfat thickness was significantly lower in TRT1 compared to TRT4 ($p < 0.05$). Furthermore, TRT4 resulted in a significantly higher fat proportion in the pork belly, particularly in the posterior rib region, whereas TRT1 exhibited the lowest fat proportion ($p < 0.05$). These findings demonstrate that phase-feeding programs using low-CP diets can successfully reduce dietary protein intake without compromising growth performance, nutrient utilization, or overall meat quality. Moreover, these programs effectively modulate fat deposition, offering a strategic approach to achieving desirable carcass characteristics in growing-finishing pigs.

Key words : growth performance, growing-finishing pig, low-crude protein diet, phase-feeding programs, pork belly

PA26030

Establishment of a meta-regression approach for predicting performance model in pigs

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This study was conducted to develop and validate a meta-regression–based predictive model for growth performance in grower–finisher pigs by integrating nutritional, environmental, and management factors. Correlation analysis revealed that ADG was strongly associated with BW (r = 0.75), CP (r = 0.55), and key essential amino acids, particularly Thr, Trp, and Val (r = 0.60). In addition, AA ratios, including Lys:Thr, Lys:Trp, and Lys:Met, showed significant correlations with both ADG (r = 0.30) and FCR (r = 0.55), while environmental factors such as TEMP (r = –0.30) and DEN (r = –0.50) were negatively correlated with growth performance.

Key words : swine, meta-regression approach, performance prediction, phase feeding, low protein, nitrogen

PA26031

Evaluation of nutrient and amino acid digestibility by age group in small-breed dogs: maltese and poodles

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This study evaluated life stage–dependent differences in nutrient and amino acid utilization in two representative dog breeds in Korea, Maltese and Poodles. Current data on nutrient requirements and digestibility in dogs are largely based on medium- and large-sized breeds, resulting in limited information for small-breed dogs. In this study, dogs were classified into puppies, adults, and seniors, and the apparent total tract digestibility (ATTD) of nutrients and amino acids was evaluated. In Poodles, the digestibility of dry matter, crude protein, nitrogen-free extract, and metabolizable energy was higher in adults and seniors than in puppies ($p < 0.05$), with most amino acids also showing significant age-related differences ($p < 0.001$). In Maltese dogs, crude protein and metabolizable energy digestibility were higher in adults, whereas nitrogen-free extract digestibility was lower in seniors ($p < 0.01$), and age-related differences in amino acids were limited. These findings indicate that nutrient and amino acid utilization varies across life stages and differs between breeds. This study provides fundamental data for precision nutrition and dietary formulation in companion dogs.

Key words : apparent total tract digestibility (ATTD), amino acids, age group, dog breeds

PA26032

Evaluation of the nutritional composition of food additive by-products as potential alternative feed resources for broilers

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This study was conducted to analyze the nutritional composition of by-products generated during the manufacturing process of food additives (e.g., amino acids), and to evaluate their feasibility as alternative feed resources for broilers.

The primary objective of this research is to present a circular livestock production model and reduce feed costs by recycling food industry by-products into high-value-added feed resources. Compositional analysis revealed that the crude protein content of the by-products ranged from 45.0% to 62.5%, which is comparable or superior to that of soybean meal. The Metabolizable Energy (ME) was measured between 2,800 and 3,200 kcal/kg, possessing an energy value similar to corn, the primary ingredient in broiler diets. Notably, the amino acid profile showed that levels of Glutamic Acid, Lysine, and Methionine were 2 to 3 times higher than those found in typical cereal by-products. The analysis confirms that these food additive by-products possess exceptional nutritional value as ‘high-protein concentrated feed resources.’ The results suggest that they can effectively replace synthetic amino acids and conventional protein sources in broiler diets. Future feeding trials are expected to establish optimal inclusion rates, enabling the development of an economically efficient feeding system.

Key words : food additive by-products, broiler feed, crude protein

PA26033

Energy availability and nitrogen utilization of cheese by-products in growing pigs

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Cheese by-products, including trimming losses, processing residues, and off-specification products, are generated during dairy production and may serve as a potential feed ingredient for swine diets. However, their nutritional value can vary considerably depending on the type of cheese, salt content, and the extent of whey removal, necessitating a quantitative evaluation of energy and nitrogen utilization prior to their practical application. Therefore, this study was designed to evaluate the energy and nitrogen utilization of three cheese by-products (mozzarella, gouda, and cheddar) in growing pigs, with corn used as a reference ingredient. A metabolism trial was conducted to determine the apparent total tract digestibility (ATTD) of gross energy (GE), including digestible energy (DE), metabolizable energy (ME), and nitrogen balance parameters. Feces and urine were quantitatively collected, and GE and nitrogen contents were analyzed to calculate energy and nitrogen utilization. The results showed that three types of cheese by-products had higher DE and ME values than those of corn, suggesting their potential as alternative energy sources in swine diets. In conclusion, cheese by-products may be viable alternative energy sources in swine diets, and their nutritional value should be further validated to support practical feed formulation.

Key words : cheese by-products, energy utilization, metabolizable energy, nitrogen balance, pigs

PA26034

Capsaicin, Piperine, Sinigrin이 Salmonella thompson의 SPI-1 유전자 발현 및 마우스 장 상피세포 침투에 미치는 억제 효과

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살모넬라균에 의한 식중독은 계란 및 가금육을 매개로 지속적으로 발생하고 있어 식품 안전 분야에서 위협이 되고 있다. 특히 항생제 내성 균주의 증가로 인해 병원성 인자를 직접 표적하는 항독성 전략이 새로운 접근법으로 부각되고 있다. 본 연구에서는 Capsaicin, Piperine, Sinigrin이 Salmonella Thompson(S. Thompson)의 제3형 분비 시스템(T3SS-1) 조절 유전자 및 숙주 세포 침투에 미치는 영향을 평가하여 S.Thompson에 의한 수직전파 억제제로서의 가능성을 확인하고자 하였다. 3가지 화합물의 최소 억제 농도(MIC)는 Capsaicin과 Sinigrin이 1.5 mM, Sinigrin은 1.0 mM으로 확인되었으며, MIC 이하 농도(500 μM)에서 S. Thompson의 증식, 운동성 및 마우스 장 상피세포에 영향을 미치지 않았다. 세포 부착과 달리 세포 침투는 농도 의존적으로 유의하게 억제되었으며, 대조군 대비 500μM에서 Capsaicin은 60.7%, Piperine은 68.6%, Sinigrin은 65.2%의 침투 억제 효과를 나타내었다. Q-PCR 분석 결과, 3가지 화합물 모두 hilD-hilC-rtsA-hilA 조절 네트워크 내 주요 유전자의 전사 수준을 유의적으로 억제하였으며, Capsaicin과 Sinigrin은 hilD의 발현을 각각 87.5%, 88.9%, Piperine은 hilC의 발현을 약 92.4% 억제하여 T3SS-1의 활성을 효과적으로 감소시켰다. 또한 효과 단백질 유전자인 sipA, sipB, sipC의 발현도 유의적인 감소가 확인되었다. 이는 3가지 화합물이 살모넬라의 증식에 직접적인 관여없이 T3SS-1의 활성을 저해하여 S. Thompson의 수직전파 제어에 활용될 수 있는 천연 항독성 억제제의 가능성을 시사한다. 본 연구 결과는 향후 식품 및 사료용 차세대 항생물질로서의 실용화를 위한 기초 자료가 될 수 있다.

Key words : Salmonella thompson, anti-virulence strategy, SPI-1, cell invasion, phytochemical

PA26035

Plasma metabolic responses to reduced dietary crude protein and graded lysine supplementation in finishing pigs

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This study was conducted to evaluate the effects of reducing dietary crude protein (CP) by 1 percentage point and supplementing lysine (Lys) at graded levels on growth performance, carcass traits, meat quality, nitrogen utilization, blood parameters, and plasma metabolites in finishing pigs. The dietary treatments consisted of a control diet containing 14% CP and 0.91% Lys, and three reduced-CP diets containing 13% CP with 0.91%, 0.98%, or 1.06% Lys. Two experiments were conducted using the same dietary treatments. In the feeding trial, 48 finishing pigs with an initial body weight of 85 ± 5 kg were allotted to four dietary treatments for 35 days, with three pigs per pen. In the metabolism trial, 12 pigs were assigned to the four treatments for 7 days in metabolism cages, with three pigs per treatment. In the feeding trial, reducing dietary CP improved feed efficiency, expressed as the gain-to-feed ratio (G:F; $p < 0.001$), with the greatest responses observed in pigs fed the 13% CP diets supplemented with 0.98% or 1.06% Lys. However, carcass yield decreased as dietary Lys concentration increased ($p = 0.011$). In the metabolism trial, body weight gain increased linearly with increasing dietary Lys concentration ($p = 0.044$). Meanwhile, reducing dietary CP by 1 percentage point significantly decreased retained nitrogen ($p = 0.038$) and absorbed nitrogen ($p = 0.005$). Regarding blood parameters, blood glucose increased linearly with increasing dietary Lys concentration ($p = 0.018$), whereas neutrophil counts showed a quadratic response to dietary Lys level ($p = 0.029$). In addition, increasing dietary Lys levels increased plasma metabolites associated with energy metabolism and the TCA cycle, including glucose-6-phosphate, pyruvate, citrate, and succinate ($p < 0.05$). Overall, these results suggest that reducing dietary CP by 1 percentage point, when accompanied by appropriate Lys supplementation, may maintain or improve growth performance and nitrogen utilization in finishing pigs without adversely affecting carcass weight or meat quality.

Key words : lysine, pig, protein

PA26036

Effects of replacing animal protein with *Bacillus*-fermented soybean meal-based functional protein on gut microbiota of weaned pigs

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This study investigated the effects of replacing animal protein with *Bacillus*-fermented soybean meal-based functional protein (FSBM) on gut microbiota of weaned pigs. Ninety-six newly-weaned pigs (initial body weight [BW] = 7.75 ± 1.12 kg; 28 days of age) were randomly allotted to four dietary treatments (seven replicates/ treatment; four pigs/pen) in a randomized complete block design. Initial BW considered as a blocking factor. Pigs were fed for 35 days in two-phase feeding programs (phase 1, day 1–14; phase 2, day 15–35). Dietary treatments included positive control (PC, basal diet with blood plasma 3% and fish meal 5% for phase 1 and phase 2, respectively); negative control (NC, basal diet based on corn and soybean meal); FSBM1 (basal diet with FSBM replacing 5% and 5% of animal protein for phase 1 and phase 2, respectively); FSBM2 (basal diet with FSBM replacing 5% and 3% of animal protein for phase 1 and phase 2, respectively). At the end of the study, fecal samples were collected from six pigs per treatment to evaluate gut microbial diversity and relative abundance. Bray-Curtis distance showed a difference ($r^2 = 0.19$; $p < 0.05$) among dietary treatments. Pigs fed FSBM2 had higher ($p < 0.05$) the relative abundance of *Clostridium* than those fed PC. In conclusion, dietary FSBM replacing animal protein modulated the gut microbial community of weaned pigs.

Key words : gut microbiota, functional protein, weaned pigs

PA26037

Evaluation of *Bacillus*-fermented soybean meal based functional protein substitute for animal-derived protein on growth performance and intestinal morphology of weaned pigs

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The study was conducted to evaluate the effects of *Bacillus*-fermented soybean meal based functional protein (BFSBM) on growth performance and intestinal morphology of weaned pigs. Weaned pigs [n = 112; 7.43 ± 0.82 kg of initial body weight(BW)] were randomly assigned to four dietary treatments (4 pigs/pen; 7 replicates/ treatment) in a randomized complete block design (block: initial BW) for 5 weeks. The 35-day feeding trial was divided into two phases (phase 1: day 1–14; phase 2: day 15–35). The dietary treatments were: 1) a basal corn-soybean meal diet (NC), 2) basal diet with 3% plasma protein and 5% fish meal during phase 1 and 2, respectively (PC), 3) basal diet with 3% dried porcine solubles (DPS), and 4) basal diet with 5% and 3% BFSBM during phase 1 and 2, respectively (BFSBM). All pigs and the amount of pen feed residual were weighed and recorded on days 1, 14 and 35 for growth performance. After euthanizing the pigs, a 3 cm segments from each of the duodenum, jejunum, and ileum were collected for intestinal morphology analysis. Pigs fed the NC diet had lower ($p < 0.05$) average daily gain compared with other treatments during overall period. The number of goblet cells in the ileum was significantly higher ($p < 0.05$) in the BFSBM group compared to the NC and DPS groups. These results indicated that the dietary BFSBM without impairing on growth performance and also enhance intestinal health of weaned pigs. In conclusion, BFSBM can be an effective substitute for protein sources in nursery diet.

Key words: feed, functional protein, growth performance, intestinal morphology, weaned pigs

PA26038

Evaluation of *Bacillus*-fermented soybean meal as a functional protein substitute for animal-derived sources on diarrhea frequency, blood profiles, and immune responses

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This study was conducted to investigate the effects of *Bacillus*-fermented soybean meal based functional protein (BFSBM) on diarrhea incidence, blood profiles, and immune responses of weaned pigs. A total of 112 weaned pigs (initial body weight [BW]: 7.43 ± 0.82 kg) were allotted to four dietary treatments in a randomized complete block design (block: initial BW) for 5 weeks, with 4 pigs per pen and 7 replicates per treatment. The 35-day feeding trial was divided into two phases (phase 1: day 1–14; phase 2: day 15–35). The dietary treatments were: 1) a basal corn-soybean meal diet (NC), 2) basal diet including 3% plasma protein and 5% fish meal during phase 1 and 2, respectively (PC), 3) basal diet with 3% dried porcine solubles (DPS), and 4) basal diet with 5% and 3% BFSBM during phase 1 and 2, respectively (BFSBM). Daily fecal score from 1 to 5 (1 = hard feces and 5 = watery diarrhea) was visually evaluated and recorded by two independent examiners for the first two weeks after weaning. The frequency of diarrhea was calculated as the average number of pen days with a fecal score of 4 or higher. Blood samples were collected for analyzing blood profiles and immune responses. On day 14, the BFSBM group showed lower ($p < 0.05$) hematocrit compared with the NC and DPS groups. Both PC and BFSBM groups had higher ($p < 0.05$) IgG levels compared with the NC group. Furthermore, IgA levels were significantly higher ($p < 0.05$) in the PC group than in the NC and DPS groups. In conclusion, BFSBM shows potential as a viable alternative protein source that supports immune responses without adversely affecting the blood profiles of weaned piglets.

Key words: blood profiles, diarrhea, functional protein, immune responses, weaned pigs

PA26039

Effects of fermented soybean meal-based functional protein on growth performance, nutrient digestibility, and intestinal morphology of weaned pigs

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The objective of this study was to evaluate the effects of a fermented soybean meal (FSBM)-based functional protein as an alternative protein source on growth performance, nutrient digestibility, and intestinal morphology of weaned pigs. A total of 112 weaned pigs (7.75 ± 1.12 kg of initial body weight; 28 days of age) were assigned to 4 treatments in a randomized complete block design for 35 days with a two-phase feeding program (phase 1, day 1–14; phase 2, day 15–35). Dietary treatments included positive control (PC, basal diet containing 3% plasma protein during phase 1 and 5% fish meal during phase 2); negative control (NC, corn and soybean meal based diet); FSBM1 (basal diet containing 5% FSBM); FSBM2 (basal diet containing 5% and 3% FSBM during phase 1 and phase 2). The NC group showed lower ($p < 0.05$) average daily gain from day 1 to 35 than the other treatments. Dietary FSBM1 and 2 groups improved ($p < 0.05$) apparent ileal digestibility of energy, crude protein, and dry matter compared with the NC group. Dietary FSBM 1 and 2 also improved ($p < 0.05$) apparent total tract digestibility of crude protein compared with the NC diet. In the ileum, pigs fed FSBM2 had higher ($p < 0.01$) goblet cell numbers than those fed PC and NC diets. In conclusion, dietary FSBM can be used as an effective alternative protein source to improve growth performance and intestinal health in weaned pigs.

Key words : functional protein, gut health, weaned pigs

PA26040

Effects of fermented soybean meal-based functional protein on immune responses and diarrhea incidence of weaned pigs

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The present study investigated the potential of a fermented soybean meal (FSBM)-based functional protein as an alternative protein source by evaluating frequency of diarrhea, blood profiles, and immune responses of weaned pigs. A total of 112 weaned pigs (7.43 ± 1.12 kg of initial body weight; 28 days of age) were assigned to 4 treatments in a randomized complete block design for 35 days with a two-phase feeding program (phase 1, day 1–14; phase 2, day 15–35). Dietary treatments included positive control (PC, basal diet containing plasma protein during phase 1 and fish meal during phase 2); negative control (NC, corn and soybean meal based diet); FSBM1 (basal diet containing 5% FSBM); FSBM2 (basal diet containing 5% and 3% FSBM during phase 1 and phase 2). Dietary FSBM1 and 2 improved ($p < 0.05$) total antioxidant capacity and reduced ($p < 0.05$) TNF-α and IL-8 concentrations on day 14 compared with the NC diet. Pigs fed FSBM 1 and 2 diets had higher ($p < 0.05$) IgG concentration on day 14 and 35 than those fed NC diet. In addition, FSBM 1 and 2 groups had increased ($p < 0.05$) IgA concetration on day 35 compared with the NC group. In conclusion, dietary FSBM can be used as an effective alternative protein source to improve immune responses and systemic health in weaned pigs.

Key words : alternative protein, immune response, weaned pigs

PA26041

Effects of dietary bacteriophage supplementation on growth performance, jejunal morphology, and cecal bacterial population in broiler chickens raised under multiple stress conditions

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This study aimed to investigate the effect of dietary bacteriophage (BP) supplementation as an alternative to antibiotics on growth performance, jejunal morphology, and cecal bacterial population in broiler chickens under multiple stress (MS) conditions. A total of 2,280 one-d-old Ross 308 broiler chickens were randomly allotted to 8 treatments with 5 replicates per treatment in factorial arrangements of 2 environment conditions and 4 dietary treatments. Birds were raised under either heat stress (HS) conditions (31 ± 1.0°C for 8 h/d and 28 ± 2.0°C for 16 h/d) and normal stocking density (SD; 9 birds/m^2) or MS conditions of both HS and high SD (18 birds/m^2). Dietary treatments included a basal diet (CON) or the basal diet supplemented with 0.05% ampicillin (AB), 0.05% BP (BP5), or 0.10% BP (BP10). Experiment lasted for 35 d. Results indicated that an interaction ($p < 0.05$) was observed for feed conversion ratio (FCR) because no effect of dietary treatments was detected under HS and normal SD, whereas under MS conditions, the AB diet decreased FCR compared with the CON and BP5 diets ($p < 0.05$) with the BP10 diet showing the similar FCR to the AB diet. Despite no interaction for jejunal morphology, villus height:crypt depth ratio was decreased by MS conditions with no main effects of dietary treatments. For cecal bacterial population, *Lactobacilli:Enterobacteriaceae* ratio (L:E ratio) tended to be greater ($p = 0.057$) in the AB and BP diets than in the CON diet although interaction and the main effects of environment conditions on L:E ratio were insignificant. In conclusion, although no clear interactive effects are identified, MS conditions impair broiler performance and jejunal morphology, whereas dietary BP supplementation regardless of environmental stress shows a beneficial effect on intestinal bacterial populations as similar to AB supplementation despite little benefits on growth performance and intestinal morphology in broiler chickens.

Key words : broiler chickens, bacteriophage, antibiotics, jejunal morphology, multiple stress condition

PA26042

Meta-analysis of the effect of reducing crude protein levels in diets on growth performance in broiler chickens during growing and finishing phases

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The current meta-analysis was conducted to investigate the effect of reducing crude protein (CP) levels in diets on growth performance in broiler chickens during growing and finishing phases. A total of 44 studies published between 2007 and 2026 were selected for each growing (11–24 d of age) and finishing (25–42 d of age) phase to evaluate the responses of broiler performance, including average daily gain (ADG), average daily feed intake (ADFI), and feed conversion ratio (FCR), to feeding diets with varying CP levels. Regression analysis was conducted to generate the linear, quadratic, broken-line linear plateau (BLL), and broken-line quadratic plateau (BLQ) models to identify performance responses with decreasing CP levels. For ADG, linear and BLQ models were significant ($p < 0.05$) in the growing phase, whereas the linear and BLL models were significant ($p < 0.05$) in the finishing phase. For FCR, only linear and BLL models were significant in both growing and finishing phases. No significant models were verified for ADFI in both phases. Finally, the BLL models for FCR were used to estimate the breaking points, which were considered minimal CP levels in diets to maintain FCR. Accordingly, the minimal CP levels in broiler diets were estimated to be 22.2% CP for the growing phase and 18.8% CP for the finishing phase. Furthermore, it was also predicted that every 1% reduction in dietary CP below these minimal CP levels increased FCR by 0.02 and 0.04 units for growing and finishing phases, respectively. In conclusion, the estimated minimal CP levels in low-CP diets and their predicted performance change from this meta-analysis may offer a practical and applicable strategy to produce low-CP diets without sacrificing growth performance in broiler chickens.

Key words : broiler chicken, crude protein, growth performance, meta-analysis, regression model

PA26043

Monitoring and detection characteristics of 327 pesticide residues in animal feed distributed in South Korea

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Continuous surveillance of pesticide residues in animal feed is imperative for ensuring the safety of livestock products and bolstering consumer confidence. This study investigated the prevalence and detection characteristics of pesticide residues in 301 samples of animal feed collected from the South Korean market between 2023 and 2025. Multiresidue analysis targeting 327 pesticide components was performed using GC-MS/MS and LC-MS/MS, in accordance with the official ‘Standard Analysis Methods for Feeds’ (MAFRA) and the ‘Multiresidue Method’ (NAQS). The results demonstrated that pesticide residue levels in all examined samples complied with the maximum residue limits (MRLs) established by the official ‘Criteria and Standards for Feeds’ (MAFRA), indicating a robust safety profile. However, nine pesticide components were consistently detected throughout the three-year study period, albeit at concentrations below the MRLs. Notably, the detection frequency of piperonyl butoxide (PBO), a pesticide synergist, exhibited a significant annual upward trend. Furthermore, distinct patterns of co-occurrence were observed between PBO, insecticides (pirimiphos-methyl and deltamethrin), and a herbicide (glyphosate). In conclusion, although pesticide residues in animal feed consistently demonstrated compliance with safety standards throughout the study period, the rising prevalence of synergists signifies a transition in pest management strategies necessitated by evolving agricultural conditions, such as climate change. The identified patterns of co-detected components provide a comprehensive basis for establishing novel strategic directions in future feed safety management. These findings emphasize the imperative to implement rigorous surveillance systems adaptable to emerging pesticide usage trends and to develop proactive risk management frameworks substantiated by longitudinal data.

Key words: animal feed, pesticide residues, detection characteristics, pesticide synergist, piperonyl butoxide

PA26044

Monitoring and occurrence of pesticide residues in complete pet food distributed in the Korean market: a three-year study (2023-2025)

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Given the sustained growth in pet-owning households, ensuring the safety and enhancing the risk management frameworks for pet food have become increasingly important. This study was conducted to evaluate the occurrence and residue levels of pesticides in pet food and to establish a baseline for the development and refinement of regulatory standards. Between 2023 and 2025, a total of 463 samples of complete pet food were collected from the Korean market for longitudinal monitoring. In accordance with the 'Official Standard Analysis Methods for Feeds' (MAFRA) and the 'Multiresidue Method' (NAQS), 327 pesticides were analyzed using GC-MS/MS and LC-MS/MS. The analytical results indicated that all 463 samples complied with the Maximum Residue Limits (MRLs) defined by the 'Criteria and Standards for Feeds' (MAFRA), with concentrations remaining within regulatory limits. Although 22 pesticide residues were consistently detected throughout the three-year study period, their concentrations were present at trace levels below the MRLs, and no instances of non-compliance were identified among the tested samples. These findings demonstrate that complete pet foods distributed in the Korean market are appropriately managed within established regulatory safety systems. In conclusion, the levels of pesticide residues in pet food distributed in Korea appear to be within safe levels relative to current regulatory standards. However, given the consistent annual detection of specific pesticide residues, continued monitoring and the implementation of a proactive risk management system incorporating evolving ingredient supply chains and residue patterns are recommended to further enhance pet food safety.

Key words : complete pet food, pesticide residues, monitoring

PA26045

Development of an LC-MS/MS-based simultaneous analytical method for vitamins A and D in pet feeds

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This study aimed to develop an analytical method for evaluating nutritional coompliance in pet feeds following the establishment of new labeling regulations for dog and cat feeds. However, the current HPLC-based vitamin analysis method has limitations in analyzing trace vitamins in compound pet feeds. Therefore, a pretreatment procedure and an LC-MS/MS-based analytical method were developed for the simultaneous quantification of vitamins A and D. The proposed method simplified the conventional multi-step extraction process involving saponification and hexane extraction, thereby improving pretreatment efficiency. A high-sensitivity mass spectrometry system enabled the simultaneous analysis of vitamins A and D. Additionally, post stable isotope dilution (SID) was applied to correct matrix-induced interferences, ensuring reliable quantification. Method validation demonstrated excellent linearity, with correlation coefficients (R^2) of 0.99 or higher for both vitamins A and D, satisfying the validation criterion of $R^2 \geq 0.98$. The limits of detection (LOD) and quantification (LOQ) were 17–18 ng/mL and 51–53 ng/mL, respectively. Furthermore, accuracy evaluation using certified reference materials (NIST SRM 1869 and 1849b) and AAFCO reference standards yielded recovery rates ranging from 73.1% to 108.8%, meeting the acceptance criteria of the official feed analysis methods. Compared with conventional HPLC methods, this approach improved sensitivity and selectivity while reducing pretreatment time, demonstrating its applicability for evaluation of nutritional compliance and quality control of pet feeds.

Key words : LC-MS/MS, vitamin A, vitamin D, pet feed, stable isotope dilution, method validation

PA26046

Effects of combined synbiotic and benzoic acid supplementation on short-chain fatty acid profiles and fecal microbiota in swine

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This study investigated the effects of 0.1% combined synbiotic and benzoic acid supplementation on short-chain fatty acid (SCFA) profiles and fecal microbiota in swine. A total of 23 pigs were assigned to two dietary groups: control (CON, n = 12) and synbiotic plus benzoic acid supplementation (SYN, n = 11). After a 7-week feeding period, fecal samples were collected for SCFA profiling using liquid chromatography-tandem mass spectrometry (LC-MS/MS), and fecal microbiota were analyzed by 16S rRNA gene sequencing. The mean concentrations of all analyzed SCFAs were lower in the SYN group than in the CON group, with significant reductions in acetic, butyric, lactic, and valeric acids ($p < 0.05$). Microbiota analysis showed that the SYN group had a significantly lower Chao1 richness index than the CON group ($p < 0.05$), while microbial composition differed between groups. LEfSe and correlation analyses indicated that specific bacterial taxa were associated with altered SCFA profiles. These findings suggest that combined synbiotic and benzoic acid supplementation is associated with reduced fecal SCFA concentrations and altered microbial richness and composition in swine.

Key words : feces, microbiota, short-chain fatty acids, swine, synbiotics, benzoic acid

PA26047

Monitoring and characterization of multi-component pesticide residue patterns in single-ingredient feed

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The monitoring of pesticide residues in plant-based single-ingredient feed, the foundational raw material for animal feed, is essential for ensuring safe livestock production and effective feed risk management. This study monitored pesticide residues in plant-based single-ingredient feed randomly collected from the Korean market from 2023 to 2025 to characterize the occurrence and residue patterns of pesticide contaminants. A total of 411 samples were analyzed for 327 pesticide components using GC-MS/MS and LC-MS/MS, in accordance with the official 'Standard Analysis Methods for Feeds' (MAFRA) and the 'Multiresidue Method' (NAQS). The analysis demonstrated that 14 pesticide components were consistently detected over the three-year study period. Notably, the study identified frequent instances of pesticide co-occurrence, where multiple residues were present in specific feed samples. In particular, co-detection of two pesticides was observed in 34 cases (8.3%), and multiple residue occurrences involving three or more pesticides were found in 7 cases (1.7%). The analysis of these co-detected pesticides by functional category and purpose revealed the concurrent detection of insecticides and synergists (e.g., Piperonyl butoxide) and the combined detection of multiple fungicides (e.g., Azoxystrobin + Propiconazole), reflecting multi-target pest and disease management during crop cultivation and storage. In conclusion, the multi-component residue patterns of pesticides observed in this study suggest a potential association with the pest control history during the cultivation and storage stages of plant-based single-ingredient feed. These findings highlight the importance of continuous monitoring and data accumulation regarding the identified co-occurrence patterns, alongside existing single-substance assessments. This study provides baseline data that can contribute to the development of more precise safety management strategies for feed ingredients in the future.

Key words : plant-based single-ingredient feed, pesticide residues, monitoring, synergist, multi-residue patterns

PA26048

Effects of crude protein reduction and a moderate increase in metabolizable energy on growth performance, digestibility, and blood metabolites in pigs

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Reducing dietary crude protein (CP) with essential amino acid (AA) supplementation can improve nitrogen utilization; however, it may compromise growth performance if nitrogen supply becomes limiting. This study evaluated the effects of dietary CP reduction on growth performance and metabolic responses in growing–finishing pigs. Two 28-day feeding trials were conducted using pigs with initial body weights of 55 and 70 kg. In Experiment 1, pigs were fed diets containing 15.5% or 13.5% CP, and in Experiment 2, CP levels were 13.5% or 11.5%. Reducing dietary CP decreased average daily gain in growing pigs whereas feed intake and gain-to-feed ratio were not affected. Low-CP diets reduced apparent total tract CP digestibility and blood urea nitrogen, and altered circulating proline and serine concentrations, while most essential AA were maintained. In finishing pigs, low-CP feeding downregulated jejunal AA transporter and mammalian target of rapamycin gene expression. However, fecal fermentation characteristics, microbial composition, and carcass traits were not significantly affected by dietary treatments. Overall, dietary CP reduction influenced growth performance and metabolic responses in growing–finishing pigs, suggesting that adequate nitrogen supply remains important even when essential AA requirements are met.

Key words : pigs; crude protein; metabolizable energy; amino acids

PA26049

Effects of feed processing and different energy and protein level in lactating sows under hot ambient

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This study evaluated the effects of feed processing and dietary energy-protein strategies on physiological responses, productive performance, stress biomarkers, and fecal microbiota of lactating sows exposed to heat stress. Fifty multiparous Landrace × Yorkshire sows were assigned to five dietary treatments differing in feed form, metabolizable energy, crude protein, and amino acid supplementation. Feed processing did not significantly affect rectal temperature, sow feed intake, body weight change, reproductive performance, stress biomarkers, or fecal microbial populations. Respiratory rate was mostly unaffected by dietary treatment, although it increased during late lactation in sows fed the high-ME, low-CP pelleted diet with AA supplementation. Sow body weight at weaning was higher in sows fed higher-CP diets, and piglet weaning weight and average daily gain were improved by higher dietary ME and CP. Inflammatory cytokines, antioxidant capacity, hair cortisol, and fecal microbiota were not affected by the treatments, but malondialdehyde concentration increased with higher dietary ME. Overall, pelleted diets containing higher ME and adequate CP improved sow body weight at weaning and supported better piglet growth performance under heat stress.

Key words : cortisol, homeostasis, lactation, lipid peroxidation, microbiota

PA26050

Host-derived *Limosilactobacillus reuteri* supplementation improves piglet growth and gut integrity in heat-stressed sows

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Heat stress (HS) severely compromises sow productivity during lactation by disrupting feed intake, endocrine regulation, and gut integrity, ultimately impairing offspring growth. This study evaluated the effects of dietary probiotic supplementation (*Lactobacillus reuteri*) on performance, systemic responses, and fecal microbiota modulation in lactating sows under HS conditions. Forty multiparous sows (Landrace × Yorkshire) were assigned to four treatments: thermoneutral (TN), heat stress without supplementation (CN), HS + *L. reuteri* MP1 (L1), and HS + *L. reuteri* MP3 (L2). Results showed that HS elevated hair cortisol concentrations, whereas L2 supplementation significantly improved average daily feed intake and restored serum prolactin levels compared to the CN group. Although HS increased inflammatory markers (TNF- α, IL-1β) and oxidative stress, L2 treatment effectively lowered TNF-α and enhanced antioxidant capacity. Interestingly, gut barrier markers showed distinct responses, with L2 affecting serum zonulin levels and CN increasing occludin concentrations. Microbiota analysis revealed that L2 supplementation increased the relative abundance of beneficial taxa, such as Christensenellaceae and its R-7 group, at the family and genus levels. These findings demonstrate that *L. reuteri* supplementation, particularly the MP3 strain, alleviates HS-induced physiological disturbances by improving immune balance, endocrine regulation, and gut microbiota composition. Consequently, probiotic supplementation represents an effective nutritional strategy to enhance lactational resilience and offspring growth performance under heat stress conditions.

Key words : heat stress, lactating sows, *Lactobacillus reuteri*, probiotics, litter performance, gut microbiota, oxidative stress

PA26051

Strategic nutritional restriction followed by refeeding induces compensatory growth, improves jejunal morphology, and modulates the gut microbiome in weaning pigs

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This study investigated whether short-term dietary protein and energy restriction followed by balanced refeeding could induce compensatory growth and modulates physiological, intestinal morphological and gut microbial responses in weaning pigs. A total of 80 YLD weaning pigs were randomly assigned to two treatments, with 10 replicates per treatments. The dietary program consisted of two phases: TRT1 pigs received a balanced diet during both Phase 1 and 2 (week 0–3,3–6), whereas TRT2 pigs received a low-protein and low-energy (LP-LE) diet during Phase 1 followed by a balanced diet during Phase 2. During the restriction phase, TRT2 pigs exhibited lower body weight, average daily gain (ADG), and gain-to-feed ratio (G:F) than TRT1, despite a higher average daily feed intake (ADFI). Plasma ghrelin level was higher in TRT2 pigs, indicating an adaptive hormonal response to nutritional restriction. During recovery, TRT2 pigs exhibited compensatory growth and no significant differences in final body weight, ADG, ADFI, or G:F between treatments by week 6. At week 6 TRT2 pigs showed greater villus height, lower crypt depth, and a higher villus-to-crypt ratio than TRT1 indicating improved jejunal morphology. Gut microbiome analysis showed no significant differences at week 3, whereas TRT2 pigs had lower richness and evenness at week 6. Beta-diversity revealed distinct clustering between treatments at both Week 3 and 6, indicating treatment-related shifts in bacterial community composition. In conclusion, the strategic nutritional restriction followed by balanced refeeding may be a useful nutritional approach for modulating intestinal development and physiological adaptation in weaning pigs.

Key words : compensatory growth, nutritional restriction, gut microbiome, intestinal morphology, weaning pigs

PA26052

Dietary supplementation with *Limosilactobacillus reuteri* enhances lactational performance and mitigates heat stress induced physiological disturbances in sows

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This study was conducted to evaluate the effects of dietary supplementation with *Limosilactobacillus reuteri (L. reuteri)* on sow performance, litter growth, inflammatory and oxidative stress status, intestinal barrier function, endocrine responses, and fecal microbial composition under heat stress conditions. A total of 40 multiparous sows (Landrace × Yorkshire) were assigned to three treatments: thermoneutral condition (TN), heat stress without supplementation (CN), and heat stress with 0.05% L. reuteri supplementation (LR5). Heat stress increased hair cortisol concentrations and reduced average daily feed intake (ADFI), litter weight at weaning, and piglet body weight. In addition, serum concentrations of TNF-α, IL-10, and IL-1β were elevated in heat-stressed sows compared to those under thermoneutral conditions. Although no significant differences were observed, the LR5 treatment numerically improved ADFI and reduced TNF-α concentrations, indicating a partial mitigation of the negative effects induced by heat stress. Overall, L. reuteri supplementation showed protective effects against heat stress–induced metabolic, inflammatory, and microbial changes in lactating sows. Probiotic supplementation may improve feed intake, regulate immune responses, and enhance lactation performance and litter growth under heat stress conditions.

Key words : probiotics, climate change, stress, antioxidant, lactating sows

PA26053

Classification and market analysis of commercial prescription diets in Korea according to PARNUTs particular nutritional purposes

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Commercial prescription diets distributed in Korea are marketed for various disease management purposes; however, systematic guidelines and classification frameworks for these products remain insufficient, and they are currently regulated as “other pet foods” in Korea. In this study, a purpose-oriented classification system based on the EU’s PARNUTs (Particular Nutritional Purposes) was applied to 213 commercial prescription diet products distributed in Korea, and their market characteristics according to species, formulation type, and nutritional purposes were analyzed. Dog products accounted for 64.06% and cat products for 35.94% of the market. Dry formulations represented 64.13%, whereas wet formulations accounted for 35.87%, indicating a market structure predominantly centered on dog and dry-formulated diets. Among all products evaluated, 61 were classified as single-function diets and 152 as multifunctional diets, demonstrating a high prevalence of multifunctional formulations. The most frequently identified nutritional purposes were “Support of renal function in case of chronic renal insufficiency” (33), “Reduction of ingredient and nutrient intolerances” (29), and “Compensation for maldigestion” (21). In contrast, categories such as “Reduction of iodine levels in feed in case of hyperthyroidism” (1) showed extremely low representation, while no products corresponding to “Reduction of acute intestinal absorptive disorders” were identified. These findings may provide foundational data for the future establishment of regulatory standards and management systems for companion animal prescription diets in Korea.

Key words : companion animal, prescription diet, pet food, PARNUTs

PA26054

Cytotoxic effects of deoxynivalenol and fumonisin B1 in porcine ileum-derived organoids

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Deoxynivalenol (DON) and Fumonisin B1 (FB1) are major *Fusarium*-derived mycotoxins frequently co-contaminate swine feed, raising concerns about combined toxicological effects on intestinal health. This study investigated the single and binary cytotoxic effects of DON and FB1 on porcine ileum-derived organoid and single-cell cultures using the CCK-8 assay. DON alone exhibited potent dose-dependent cytotoxicity, reducing organoid viability to approximately 30% at 2 μM, while FB1 alone showed negligible cytotoxicity up to 200 μM. Binary co-treatment significantly reduced viability to 47–57% in organoids and 16–33% in single-cell cultures compared to the control. Short-term exposure (0–10 hours) produced no significant acute cytotoxic effects, indicating a time-dependent toxicity profile. These findings demonstrate that DON is the primary driver of cytotoxicity in porcine intestinal cells, while FB1 alone is non-cytotoxic but may potentiate DON-induced intestinal damage under binary co-exposure conditions. The results underscore the importance of considering mycotoxin co-contamination in feed safety risk assessments for swine.

Key words : cell viability, deoxynivalenol, fumonisin B1, mycotoxin co-contamination, porcine intestinal organoids

PA26055

Fatty acid composition and anti-inflammatory activity of black soldier fly (*Hermetia illucens*) larval oil

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Black soldier fly (*Hermetia illucens*) larvae (BSFL) are nutrient-dense, containing 25.8%–33.0% fat. Despite its rich fatty acid profile, BSFL oil is often discarded as a byproduct. However, anecdotal evidence in aquaculture and poultry sectors suggests that BSFL oil promotes growth and enhances disease resilience. This study evaluates the anti-inflammatory potential of BSFL oil (HIO) to establish its value as a functional feed additive. HIO was extracted via screw press at 120°C after hot-air drying larvae at 60°C. Cytotoxicity on RAW 264.7 macrophages was assessed using MTS assays (1.58%–12.5% v/v). Anti-inflammatory activity was evaluated by measuring nitric oxide (NO) production and pro-inflammatory cytokine levels (TNF-α, IL-1β, and IL-6) in lipopolysaccharide (LPS)-stimulated cells. HIO showed no cytotoxicity up to 6.25 % (LC_{50}: 10.3 ± 0.45%). While LPS stimulation significantly induced NO and cytokine expression, HIO treatment effectively suppressed these markers in a dose-dependent manner. HIO effectively attenuates key inflammatory markers without significant cytotoxicity. These findings suggest that HIO is a promising nutraceutical feed additive that can enhance animal health and inflammatory resilience, providing a scientific basis for the high-value utilization of insect-derived oils.

Key words : *Hermetia illucens*, black soldier fly larvae oil, fatty acid, anti-inflammation, nutraceutical, feed additive

PA26056

Effects of *Lactobacillus amylovorus* supplementation dosage on lactation performance and physiological responses in heat stressed sows

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This study evaluated *Lactobacillus amylovorus* (LA) supplementation on lactating sow performance and physiological responses under heat stress (HS). Forty multiparous sows (240.34 ± 11.57 kg) were assigned to a 2 × 3 factorial design: thermoneutral (TN), HS without supplementation (HSNS), HS + 0.01% LA (HL1), and HS + 0.05% LA (HL5). Chronic stress was assessed via hair cortisol alongside performance, immunity, antioxidant capacity, and fecal microbiota. Compared with TN, HSNS increased hair cortisol and reduced average daily feed intake (ADFI), litter weight, and piglet ADG ($p < 0.05$). In contrast, LA supplementation (HL1 and HL5) restored ADFI ($P < 0.05$). TNF-α and IL-1β were lower in TN than other groups ($p < 0.05$), while IL-10 was higher in HSNS and HL1 vs. TN and HL5 ($p < 0.05$). Superoxide dismutase activity was lower in HSNS compared with HL1 and HL5 ($p < 0.05$). No treatment effects were observed for body weight, backfat, zonulin, or occludin. Fecal *Lactobacillus* spp. abundance was greater in HSNS and HL1 than TN ($p < 0.05$). In conclusion, dietary *Lactobacillus amylovorus* supplementation (0.05%) mitigates heat stress impairments by improving productive performance and physiological resilience in lactating sows.

Key words: feed intake, immune response, gut integrity, oxidative status, probiotics, performance, sows

PA26057

Correlation analysis of bioactive compounds with antioxidant and anti-inflammatory properties in black soldier fly (*Hermetia illucens*) larval oil

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Black Soldier Fly (*Hermetia illucens*) oil (HIO) is rich in bioactives, yet the relationship between its antioxidant and anti-inflammatory properties remains poorly defined. This study investigated the correlations between bioactive compounds, factors related with antioxidant and anti-inflammatory activities of HIO. Antioxidant capacity was quantified through total phenolic content (TPC), total flavonoid content (TFC), and ABTS/DPPH radical scavenging assays. Anti-inflammatory activity was evaluated in LPS-stimulated RAW 264.7 cell by measuring nitric oxide (NO) production and pro-inflammatory cytokines (IL-1β, IL-6, and TNF-α). Pearson correlation analysis was carried out by using SPSS S/W ver. 29.0. Correlation analysis revealed that antioxidant factors (TFC, TPC, ABTS, and DPPH) exhibited significant negative correlations with both NO production and pro-inflammatory cytokine expression. In contrast, strong positive correlations were observed among cytotoxicity, NO production, and cytokine levels, suggesting that HIO could potentially modulate the synergistic inflammatory cascade. The observed correlations suggest that antioxidant properties of HIO may contribute to its anti-inflammatory performance. These findings imply that HIO could serve as a promising nutraceutical feed additive to potentially improve animal health and physiological resilience.

Key words : *Hermetia illucens*, black soldier fly larvae oil, correlation, antioxidant, anti-inflammation, nutraceutical

PA26058

Meta-analysis of the effect of reducing crude protein levels in diets on nitrogen excretion rate in broiler chickens during growing and finishing phases

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The current meta-analysis was conducted to investigate the effect of reducing crude protein (CP) levels in diets on the nitrogen (N) excretion rate (NER) in broiler chickens during growing and finishing phase. A total of 16 broiler studies with varing treatment levels of dietary CP, which were published between 2007 and 2026, were selected for the growing and finishing (11–42 d of age) phases. Regression analysis was conducted to generate the linear, quadratic, broken-line linear plateau (BLL), and broken-line quadratic plateau (BLQ) models to identify the responses of NER (%) with decreasing CP levels (%) in diets. Among these regression models, the linear model was only verified ($p < 0.05$) with a significant linear coefficient (estimate = 0.88; SE = 0.396; $p < 0.05$) and intercept (estimate = 13.35; SE = 1.691; $p < 0.05$). Based on model evaluation criteria, the linear model also showed the least AIC and BIC values among the evaluated models, indicating its best relative fit for NER. These results clearly indicate that decreasing CP levels in diets linearly decrease NER in broiler chickens. In addition, this linear model of [$Y = 0.88X + 13.35$, where X represents dietary CP level (%) and Y represents NER (%)] demonstrates that every 1 percentage point reduction in dietary CP levels decreases NER by 0.88 percentage point in broiler chickens during growing and finishing phases. In conclusion, our meta-analysis suggests a linear prediction model for NER and approximate reducing extents of NER with decreasing CP levels in broiler diets, which may aid in formulating low-CP diets to decrease N excretion from broiler production.

Key words : broiler chicken, crude protein, meta-analysis, nitrogen excretion rate, regression model

PA26059

Effects of black soldier fly (*Hermetia illucens*) larvae oil on blood glucose, serum lipids, and liver enzyme: a meta-analysis

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Black soldier fly (*Hermetia illucens*) larvae oil (HIO) is rich in fatty acids, particularly lauric acid, which is recognized as a representative functional fatty acid. Recently, HIO as a health-functional material has increased due to its rich content of lauric acid and various bioactive compounds. Previous studies have reported that HIO exhibits beneficial effects on blood glucose regulation, serum lipid metabolism, antioxidant activity, anti-inflammatory activity, immune modulation, and liver function protection. In this study, a meta-analysis was conducted using studies published between 2017 and 2026 that investigated the effects of HIO on blood glucose, serum lipids, and liver enzyme. A total of 19 studies were included in the meta-analysis, with an overall effect size of 0.760, indicating a moderate-to-large effect. The effect sizes for blood glucose (ES = 0.817), serum lipids (ES = 1.038), and liver function (ES = 1.235) were all found to be large. The results of the meta-analysis demonstrated that HIO had significant beneficial effects on blood glucose, serum lipids, and liver enzyme. In particular, large effect sizes were observed for serum lipid and liver function improvement, suggesting that HIO has strong potential as a functional food ingredient and bioactive material. Furthermore, HIO may have considerable industrial value in the functional food and biotechnology industries because it is an eco-friendly and sustainable resource.

Key words : *Hermetia illucens*, black soldier fly larvae oil, blood glucose, serum lipid, liver enzyme, meta-analysis

PA26060

Research trend analysis of swine nutrition and feed studies in Korea from 2023 to 2025

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This study systematically classified recent research trends by analyzing 237 abstracts in the field of swine nutrition and feed published by Korean researchers from 2023 to 2025. The abstracts were classified into eight research categories. Among them, functional feed additives accounted for the largest proportion (18.6%), followed by energy, amino acid, and digestibility prediction (16.9%). Other/integrated studies, including ICT, AI, and animal welfare, accounted for 14.8%, followed by gut microbiota and omics-based mechanistic studies (13.9%), low-protein diets, precision nutrition, and nitrogen reduction (11.8%), sow and piglet nutrition management (9.3%), environmental impact, odor, and manure reduction (7.6%), and feed ingredient evaluation (7.2%). These results indicate that recent swine nutrition research in Korea has mainly focused on evaluating functional feed additives and precisely estimating the nutritional value of feed ingredients, while expanding toward microbiome research, omics-based approaches, environmental impact reduction, and smart feeding management. The findings of this study may provide basic information for selecting future research topics and applying research outcomes to the swine industry.

Key words : swine nutrition, feed additives, nutrient digestibility, gut microbiota, research trend analysis

PA26061

Characterization and bioactive potential of oils from edible and industrial feed-grade insects

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Insects are recognized as sustainable bioresources, with their protein being widely utilized while the lipid fraction remains typically discarded. This study evaluated the extraction yields, color profiles, and bioactive potential of oils from five edible species (*Tenebrio molitor, Zophobas atratus, Protaetia brevitarsis, Gryllus bimaculatus, Bombyx mori*) and one feed-grade species (*Hermetia illucens*). To ensure gut clearance, insects were starved for 24–48 hours, hot-air dried, and oils were extracted using a screw press at 120°C. *H. illucens* exhibited the highest oil yield (27.8%), followed by *Z. atratus* (25%) and *T. molitor* (21%). Bioactive screening (1.58–25%) revealed that total flavonoid and phenolic contents, along with antioxidant activities (ABTS/DPPH), increased dose-dependently, while nitric oxide production was significantly inhibited. *H. illucens*, *Z. atratus*, and *T. molitor* are identified as efficient oil sources with superior yields and potent anti-inflammatory efficacy at non-cytotoxic levels, making them ideal for functional feed additives. While *G. bimaculatus* and *B. mori* showed moderate yields and unique chromaticity suitable for specialized biomedical niches, *P. brevitarsis* exhibited low oil yield and limited bioactivity, suggesting that prioritizing its protein fraction is more economically advantageous. These findings provide a strategic framework for upcycling insect lipids, transforming discarded byproducts into high-value functional bioresources for animal nutrition and biomedical applications.

Key words : edible Insect, Industrial feed-grade insect, insect Oil, *Tenebrio molitor, Zophobas atratus, Hermetia illucens*

PA26062

Impact of intravaginal lactic acid administration on sow body condition indices and piglet growth after farrowing

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This study investigated the effects of intravaginal lactic acid (LA) administration on sow body condition indices and piglet growth performance after farrowing under heat stress (HS). A total of 40 LY lactating sows were assigned to treatments in a 2 × 2 factorial arrangement: thermoneutral (TN) or heat stress (HS) conditions, with 0%, 0.1%, or 0.3% intravaginal LA administration. Heat stress significantly reduced average daily feed intake (ADFI; 6.44 vs. 5.79 kg/d, $p < 0.05$), whereas LA administration tended to improve ADFI in HS sows (6.07 and 6.24 kg/d for 0.1% and 0.3% LA, respectively; $p = 0.026$). Litter weight at weaning was significantly lower in HS sows (52.64 vs. 60.15kg; $p < 0.05$), and piglet average daily gain was reduced under HS (0.207 vs. 0.221 g/d; $p < 0.05$). LA administration showed numerical improvements in litter weight at weaning (54.70 and 56.79 kg for 0.1% and 0.3% LA). Body weight, backfat thickness, and litter size at birth were not significantly affected by temperature or LA administration. These findings suggest that LA administration may partially mitigate the negative effects of heat stress on feed intake and litter performance in lactating sows.

Key words : heat stress, lactating sows, organic acid, body condition, lactating performance

PA26063

Effects of probiotic feeding on productivity, immune system, and viral antibody titency in piglets after porcine reproductive and respiratory syndrome infection

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Previous studies have shown that feeding probiotics to piglets increases productivity and that serum analysis revealed significantly higher values in the probiotic-fed group, indicating that probiotics influence the immune system of pigs. This study was conducted to investigate the effects of probiotics on productivity, the immune system, and viral antibody titers following infection with Porcine Reproductive and Respiratory Syndrome Virus (PRRSV), a major disease in pigs. The experiment was conducted by dividing 56-day-old pigs, fed a control group, commercial probiotics, and two types of proprietary probiotics for 28 days, into four groups of 10 (CTR, CMP, JB, and VET); five pigs were infected with PRRSV, and five were normal. Regarding pig productivity, changes in average daily body weight and daily weight gain were analyzed. Serum indicators were analyzed to examine changes in the immune system, and Enzyme-Linked Immunosorbent Assay (ELISA) and real-time quantitative PCR (RT-qPCR) were performed to assess changes in PRRSV antibody titers. Among the PRRSV-infected groups, average body weight and daily gain were higher in the probiotic-fed group; conversely, between the PRRSV-infected group and the normal group, no significant difference was found in daily gain in the CMP probiotic group. Serum analysis results showed higher levels of neutrophil (Neu) and Total Protein (TP) in the probiotic-fed group compared to the control group, indicating enhanced immunity against the virus; however, the ELISA and RT-qPCR results did not show significant differences. Overall, the results indicated that feeding probiotics to piglets infected with PRRSV improved productivity and immunity.

Key words : PRRSV, probiotic, ELISA, RT-qPCR

PA26064

Changes in fecal organic acid profiles and odor-related indicators following dietary supplementation with *Latilactobacillus curvatus* CACC879 in finishing pigs

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This study evaluated the effects of dietary supplementation with *Latilactobacillus curvatus* CACC879 on fecal fermentation-related characteristics, odor-related indicators, and fecal microbiota in finishing pigs. A total of 60 finishing pigs were used in a 10-week feeding trial and assigned to either a basal diet or the basal diet supplemented with *L. curvatus* CACC879 at 0.25% (1.2×10^{10} CFU/g). Growth performance, nutrient digestibility, and fecal score were measured, and fecal samples collected from 10 pigs per treatment were used for 16S rRNA gene-based microbiota analysis, organic acid quantification, and fecal slurry malodor analysis. Dietary supplementation with *L. curvatus* CACC879 did not significantly affect growth performance or fecal score, although energy digestibility tended to increase. The supplemented group showed higher concentrations of butyric acid, propionic acid, valeric acid, isobutyric acid, isovaleric acid, and 2-methylbutyric acid, together with lower fecal slurry concentrations of hydrogen sulfide and methyl mercaptan. Microbiota analysis showed limited differences at the overall community level, but treatment-associated genus-level changes were observed at week 10. These results indicate that *L. curvatus* CACC879 may improve fermentation-related and odor-associated outcomes in finishing pigs without compromising productive performance.

Key words : *Latilactobacillus curvatus*, fecal microbiota, malodor, sulfur compounds, probiotics

PA26065

Effects of dietary dehydrated alfalfa hay supplementation on body condition and reproductive performance in late-gestating sows

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This study was conducted to investigate the effects of dietary dehydrated alfalfa hay supplementation during late gestation on body condition and reproductive performance in sows. A total of 27 Yorkshire × Landrace crossbred pregnant sows were assigned to a completely randomized design with three dietary treatments: T1, basal diet (control); T2, 5% dehydrated alfalfa hay inclusion; and T3, 10% dehydrated alfalfa hay inclusion (n = 9 per treatment). Sows were fed experimental diets from day 80 of gestation to farrowing. Body weight and backfat thickness were measured at day 80 and 110 of gestation, and at farrowing. Reproductive parameters including litter size, litter weight, individual piglet birth weight, number of piglets weaned, and weaning weight were recorded. Data were analyzed by one-way ANOVA using the general linear model (GLM) procedure of SAS, and treatment means were separated by Duncan's multiple range test. Significance was declared at $p < 0.05$. Results showed that dietary dehydrated alfalfa hay supplementation significantly increased gestational body weight gain ($p < 0.05$), with values of 8.0, 14.3, and 20.0 kg for T1, T2, and T3, respectively, indicating a significant linear response to inclusion level. However, no significant differences were observed in backfat thickness change among treatments. Litter size, litter weight, individual piglet birth weight, number of piglets weaned, and weaning weight were not affected by dehydrated alfalfa hay inclusion ($p > 0.05$). In conclusion, dietary supplementation with up to 10% dehydrated alfalfa hay during late gestation effectively enhanced gestational weight gain without adverse effects on reproductive performance, suggesting its potential as a nutritional strategy for improving sow body condition in late gestation.

Key words : dehydrated alfalfa hay, late gestation sow, body condition, reproductive performance

PA26066

Prediction equations for *in vitro* nutrient disappearance of tropical plant-derived ingredients from Vietnam in pigs

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The objectives were to determine *in vitro* total tract disappearance (IVTTD) of nutrients in tropical plant-derived ingredients and to develop prediction equations for IVTTD of dry matter (DM) and organic matter (OM) using their chemical composition for pigs. Nine tropical ingredients (pineapple peel, dragon fruit peel, passion fruit peel, banana peel, mangosteen peel, wild daisy leaves, white leadtree leaves, cassava leaves, and green tea leaves) were analyzed for chemical composition. The IVTTD of nutrients in 9 ingredients were determined using a 3-step *in vitro* procedure. The ash and lignin contents ranged from 2.9% to 12.6% and from 2.5% to 28.4%, respectively. The IVTTD of DM and OM in dragon fruit peel were the greatest (79.6% and 78.9%; $p < 0.05$) among 9 ingredients. The IVTTD of DM and OM was positively correlated with ash ($r > 0.73$; $p < 0.05$) whereas negatively correlated with lignin ($r < -0.79$; $p < 0.01$). The prediction equations for IVTTD of DM and OM were: IVTTD of DM = 58.78 – 1.19 × lignin + 2.21 × ash ($R^2 = 0.881$; $p < 0.001$), and IVTTD of OM = 55.48 – 0.83 × lignin + 2.37 × ash – 1.08 × ether extract ($R^2 = 0.919$; $p = 0.001$). All chemical compositions in test ingredients were expressed on % as-is basis. In conclusion, the IVTTD of DM and OM for pigs varies among the tropical plant-derived ingredients and can be estimated based on ash and lignin.

Key words : *in vitro* nutrient dissapearance, lignin, prediction equation, tropical plant-derived ingredients

PA26067

Effects of environment temperature on reproductive performance, piglet growth, and colostrum composition in first parity sows

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This study investigated the effects of environment temperature on reproductive performance, piglet growth, and colostrum composition in first-parity sows. A total of 28 sows were randomly assigned to either termoneutral (TN) or heat stress (HS) conditions. The TN condition was maintained at approximately 24℃ using air conditioning, whereas the HS condition was maintained at approximately 30℃ using heaters. The experimental temperatures were maintained from 5 days from 5 days after into the farrowing room until weaning. Average daily feed intake (ADFI) during lactation was significantly lower in HS sows than in TN sows (4.44 vs. 5.48 kg/d; p = 0.001). However, no significant differences were observed in body weight or backfat thinkness at the initial or weaning periods between the two groups. Litter size parameters, including total born, stillbirths, born alive, and number of piglets weaned, were not significantly affected by treatment. Similarly, litter weight, piglet birth weight (1.37 vs. 1.43 kg), weaning weight (5.63 vs. 6.00 kg), and average daily gain (0.20 vs. 0.22 kg/day) did not differ significantly between the HS and TN groups. Placental weight and placental efficiency were also not affected by heat stress. Regarding colostrum characteristics, colostrum yield (3.76 vs. 4.25 kg) and all compositional parameters, including fat, protein, lactose, and total solids, showed no significant differences between the HS and TN groups. In conclusion, although heat stress significantly reduced feed intake during lactation, it did not markedly impair reproductive performance, piglet growth, or colostrum composision in first-parity sows under the conditions of this study.

Key words : heat stress, sow, reproductive performance, colosturm, piglet growth

PA26068

Intestinal microbiome characteristics of piglets classified by early growth performance

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This study aimed to characterize gut microbial profiles associated with growth performance in piglets using full-length 16S rRNA sequencing. Piglets were classified into robust and non-robust groups based on average daily gain (ADG) at 4 weeks of age, and 25 animals were selected for each group at 8 weeks of age based on body weight. Digesta samples were collected from the jejunum, ileum, cecum, and colon. No significant differences in alpha- or beta-diversity were observed between groups across intestinal regions. Exploratory differential abundance analysis using the top and bottom five piglets based on body weight identified several gut microbial taxa showing compositional differences between groups. In particular, the *Ruminococcus*-related group and *Catenibacterium* showed relatively greater abundance in the cecum and colon, whereas *Olsenella* showed greater abundance in the colon of heavier piglets. These findings suggest that specific gut microbial taxa may be associated with growth-related phenotypes in piglets and provide preliminary insight into microbial candidates linked to piglet robustness.

Key words : piglet, microbiome, ADG

PA26069

In vitro nutrient disappearance can be predicted using fiber contents in fibrous ingredients for pigs

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The objective was to develop prediction equations for *in vitro* nutrient disappearance of various fiber sources for pigs using chemical composition. *In vitro* assay was employed to determine *in vitro* total tract disappearance (IVTTD) of dry matter (DM) and organic matter (OM). Six fibrous ingredients were used: defatted rice bran, wheat bran, sugar beet pulp, soybean hulls, corn cobs, and sawdust. Amylase-treated neutral detergent fiber (aNDF) contents in test ingredients ranged from 26.1% in defatted rice bran to 89.8% in sawdust, acid detergent fiber (ADF) ranged from 9.3% to 73.6%, and insoluble dietary fiber (IDF) ranged from 22.5% to 88.7%. The IVTTD of DM and OM in sugar beet pulp was greatest ($p < 0.05$) among the 6 fiber sources, followed by defatted rice bran, wheat bran, soybean hulls, corn cobs, and sawdust. The IVTTD of OM was negatively correlated with aNDF ($r = –0.94$; $p < 0.01$), ADF ($r = –0.82$; $p < 0.05$), and IDF ($r = –0.87$; $p < 0.05$). The equations for predicting the IVTTD of OM in fibrous ingredients based on fiber contents were: IVTTD of OM (%) = 113.74 – 1.20 × aNDF with $r^2 = 0.89$; IVTTD of OM (%) = 84.79 – 1.11 × ADF with $r^2 = 0.68$; IVTTD of OM (%) = 110.00 – 1.09 × IDF with $r^2 = 0.75$ (all variables are based on % as-is). In conclusion, the IVTTD of OM can be predicted using fiber contents in fibrous ingredients for pigs.

Key words : fiber sources, *in vitro*, nutrient, swine

PA26070

Determinants of piglet survival from birth to weaning: a comprehensive review

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Pre-weaning piglet mortality has turned out to be a major concern in modern swine operations. To keep up with enhanced piglet welfare and economic viability, a comprehensive understanding of the factors influencing piglet survival rate is essential. This review paper examines the factors affecting piglet survival and discusses the latest advancements in technology and research aimed at improving survival rates. Through an extensive analysis of relevant literature and research studies across major databases, extracted data were analysed and graphically represented. Data from the studied literature showed a relatively higher heritability for piglet birth weight, indicating genetic selection could improve survivability. For the sake of statistical comparison, piglet birth weight, a major determinant of survivability, was classified into five categories. It was found to have 24%, 62.15%, 89.70%, 90.63% and 97% of piglet pre-weaning survivability with the birth weight categories of < 0.7 kg, < 1.1 kg, ≥ 1.1 kg, > 1.6 kg, and ≥ 2.40 kg, respectively. For other traits like stillborn, mummified piglet, survival to day 5, and pre-weaning mortality, the heritability estimates are low, indicating these are more influenced by management and environment. So, genetic selection for higher birth weight (≥ 1.1 kg) and improved nutrition, housing, and farrowing supervision are recommended after evaluating the existing data.

Key words : piglets, colostrum intake, birth weight, pre-weaning mortality, pre-weaning survivability

PA26071

Dietary antioxidants and postbiotics modulate the gut microbiota-redox axis in broiler chickens: implications for intestinal health, growth performance and meat quality

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Modern broiler production exposes birds to nutritional, environmental, and biological stressors that promote oxidative stress, intestinal dysfunction, reduced growth efficiency, and deterioration of meat quality. This review examines the conceptual basis of this axis in broiler chickens, including microbiota development, common biomarkers of redox homeostasis, tight-junction disruption, and the signaling pathways that connect intestinal oxidative stress with whole-bird outcomes. It then critically evaluates major stressors that destabilize this system and the roles of dietary antioxidants and postbiotics as complementary nutritional interventions. Across heat stress, high stocking density, oxidized lipids, mycotoxins, lipopolysaccharide challenge, and enteric disease models, these interventions have been associated with improved antioxidant status, modulation of Nrf2/Keap1 and inflammatory pathways, preservation of intestinal morphology and tight-junction function, and favorable shifts in microbial composition and metabolite production, particularly short-chain fatty acids. These gut-level effects can translate into better nutrient utilization, feed efficiency, growth performance, and meat oxidative stability. However, current evidence remains heterogeneous with respect to experimental models, biomarker panels, microbiome methods, product characterization, and the definition of postbiotics.

Key words : broiler chickens, gut microbiota, oxidative stress, redox homeostasis, dietary antioxidants

PA26072

Audio-based artificial intelligence for respiratory health and welfare monitoring in broiler chickens

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Respiratory diseases and welfare impairments impose economic and ethical burdens on broiler production, driven by high stocking density, rapid pathogen transmission, and limited sensitivity of conventional monitoring. Because respiratory pathology and stress alter vocal behavior, acoustic monitoring has emerged as a non-invasive tool for flock-level surveillance. This manuscript synthesizes the anatomical basis of sound production in broilers, key vocal categories related to health and welfare, and recording strategies, datasets, acoustic features, machine-learning and deep-learning models, and evaluation metrics in poultry sound analysis. Evidence indicates that broilers are especially vulnerable to respiratory stress at early and late production stages; respiratory sounds such as coughing, sneezing, and rales are mainly associated with disease, while distress calls and silence patterns inform welfare and environmental interpretation. Advanced deep-learning and transformer-based models can outperform classical machine-learning approaches, especially with optimized feature–model combinations. Overall, AI-based acoustic systems can detect respiratory sounds, stress, and welfare changes and support earlier intervention. However, noise, data imbalance, limited multi-farm validation, interpretability, and deployment challenges remain barriers to wider application.

Key words : broiler chickens, respiratory disease, acoustic monitoring, artificial intelligence, animal welfare

PA26073

Effects of dietary *Salmonella*-specific bacteriophage supplementation in broiler chickens

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The present study investigated the antibacterial effects of Salmonella-specific bacteriophages and their influence on gut(intestinal) health in broiler chickens challenged with *Salmonella Typhimurium*. Prior to the feeding trial, bacteriophage L and bacteriophage B were evaluated for lytic activity against *Salmonella gallinarum* and *Salmonella enteritidis* using agar plate assays, where clear antibacterial activity was confirmed. A total of 960 one-day-old Arbor Acres broilers were assigned to 12 treatment groups in a 2 × 6 factorial design based on challenge status and dietary treatment. Birds were orally inoculated with *S. Typhimurium* at 4 days of age and fed experimental diets for 35 days. As expected, Salmonella challenge negatively affected growth performance and increased mortality ($p < 0.05$). Dietary treatments did not markedly influence overall growth performance. However, birds receiving bacteriophage supplementation showed lower cecal Salmonella counts at day 28 and improved villus height and villus height-to-crypt depth ratio at day 32 ($p < 0.05$). In addition, several cecal volatile fatty acid parameters were affected by the interaction between Salmonella challenge and dietary supplementation. Overall, the results suggest that dietary bacteriophage supplementation could help reduce intestinal Salmonella colonization and support gut health in broiler chickens under Salmonella challenge conditions.

Key words : bacteriophage, *Salmonella Typhimurium*, broiler, gut health

PA26074

A comprehensive review of bump-feeding strategies during late gestation in sows: nutritional and behavioral implications for farrowing performance and reproductive outcomes

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Bump feeding is a late-gestation nutritional strategy that increases feed allowance or nutrient density, usually from day 90 to farrowing, to support fetal growth and prepare sows for lactation. This review summarizes current evidence on the effects of bump feeding on sow body condition, feeding behavior, farrowing outcomes, and piglet viability. Previous studies suggest that increased late-gestation feed intake may improve litter characteristics, piglet survival, and sow energy reserves, as reflected by backfat thickness and body condition score. However, responses vary depending on dietary energy, amino acid balance, parity, and sow feeding behavior. Inconsistent findings remain, particularly regarding reproductive benefits versus excessive fat deposition. Optimized parity-specific bump-feeding strategies are needed to improve farrowing performance, piglet survival, sow welfare, and production efficiency.

Key words : bump feeding, late gestation, piglet birth weight, feeding behavior, backfat thickness

PA26075

Effects of dietary co-contamination of deoxynivalenol and fumonisin B1 on growth performance and fecal microbiota in weaned piglets

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Mycotoxin contamination in feed, particularly deoxynivalenol (DON) and fumonisin B1 (FB1), is a major concern in swine production as these toxins negatively affect gut health. This study evaluated the effects of combined DON and FB1 exposure on growth performance and fecal microbiota in weaned piglets. A total of 15 male piglets were assigned to five treatments with three pigs per group for 4 weeks: Control (CON), T1 (DON 0.1 ppm + FB1 0.1 ppm), T2 (DON 0.1 ppm + FB1 4 ppm), T3 (DON 4 ppm + FB1 0.1 ppm), and T4 (DON 4 ppm + FB1 4 ppm). Fecal samples collected at the end of the experiment, and fecal microbiota was analyzed using 16S rRNA sequencing. T4 showed the lowest final body weight and average daily gain, as well as the highest feed conversion ratio among treatments ($p < 0.05$). Fecal microbial composition differed among treatments based on beta-diversity analysis ($p = 0.018$). Spirochaetota was predominant in T4 ($p = 0.047$), while *Prevotella* abundance increased under high FB1 exposure ($p = 0.037$). In contrast, *Roseburia hominis* was most abundant in CON ($p = 0.042$). Carbohydrate metabolism pathways, including galactose metabolism ($p = 0.043$) and starch/sucrose metabolism ($p = 0.029$), were enriched in CON compared with mycotoxin-treated groups. These results suggest that dietary DON and FB1 co-contamination negatively affected growth performance and altered fecal microbiota and metabolic functions in weaned piglets.

Key words : deoxynivalenol, fumonisin B1 fecal microbiota, growth performance, weaned piglets

PA26076

Nutritional evaluation and *in vitro* digestibility of novel feed ingredients for swine diets

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This study evaluated the nutritional composition and *in vitro* digestibility of four novel by-product feed ingredients ramen by-product (RBP), spent mushroom substrate (SMS), black soldier fly larvae (BSFL), and cabbage (CAB) as potential alternatives in swine diets. Dry matter (DM), organic matter (OM), gross energy (GE), and ether extract (EE) were analyzed, and *in vitro* digestibility was assessed using a two-step enzymatic method (Boisen & Fernandez, 1997; pepsin followed by pancreatin, n = 6). Nutritional composition differed significantly among ingredients, with BSFL showing the highest GE and EE, and CAB the highest OM content. *In vitro* digestibility ranked BSFL > RBP > CAB ≥ SMS across all measured parameters ($p < 0.05$). In a second experiment, RBP and SMS were included as partial corn replacements at 5, 7.5, and 10% levels in complete piglet diets. DM, OM, and EE digestibility were not significantly affected by either ingredient or inclusion level ($p > 0.05$), whereas GE digestibility was affected by SMS inclusion level ($p < 0.05$). These results suggest that RBP and SMS can partly replace corn without substantially reducing *in vitro* digestibility, supporting their potential as cost-effective and domestically available feed ingredients for swine production, and further *in vivo* studies are needed to confirm their practical nutritional value.

Key words : novel feed ingredients, swine diets, *in vitro*, nutrient digestibility

PA26077

Effects of fat content and aging time on flavor precursors and volatile flavor compounds in beef

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Minced round aged for 3 days and 14 days was blended with 0%, 5%, 10%, 15%, and 20% back fat to create mixed meat preparations. This investigated material changes during aging and the effect of fat content on the formation mechanism of volatile flavor compounds in Hanwoo beef. Gas Chromatography–Mass Spectrometry (GC-MS) was used to analyze the fatty acid composition, metabolites, and volatile flavor compounds in the meat mixtures, while ultra-high-performance liquid chromatography (UHPLC) was employed to detect free amino acids. Results showed that the 14-day aged round meat contained higher abundances of amino acids, sugars, fatty acids, and organic acid metabolites compared to the 3-day aged round meat. The 14-day aged round meat blended with backfat sample exhibited 17 additional detected aroma compounds, primarily aldehydes (e.g., Hexanal, Heptanal), ketones, furans, and pyrazines, with aldehydes being the main differentiating variable. PCA and PLS-DA clearly distinguished flavor compounds in blended meat mixtures with varying backfat ratios. Key differential variables included hexanal, octanal, heptanal, 2-butanone, furan, and 2-pentyl-based compounds across different backfat sample groups. Fatty acid analysis revealed changes in unsaturated fatty acids during aging. Adding back fat increased the ruminant fatty acid spectrum (C15:0, C17:0) characteristics in the minced meat's fatty acid composition. Spearman correlation analysis between fatty acids and flavor compounds indicated that C17:1n7, C20:1n9, C12:0, C14:0, C15:0, C16:1n7, and C14:1n5 showed significant correlations ($p < 0.05$) with flavor compounds such as Butanal, 3-methyl-, 2-Butanone, Butanal, 2-methyl-, 1-Pentanol, Hexanal, Pentanal, and 2,3-Butanedione.The increased fat content produces a simple dilution effect and increases lipid oxidation substrates, thereby altering the formation pathways of volatile flavor compounds. The aging process increases the content of protein, carbohydrates, and nucleic acid precursors, while butter increases the content of lipid precursors. These two factors together contribute to the different flavor profiles of cooked beef.Furthermore, volatile flavor characteristics also reflect these biochemical changes.

Key words : Hanwoo beef, aging, backfat, volatile flavor components

PA26078

Validation of the prediction model for estimating gross energy concentrations of pig urine using Brix value

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Determination of metabolizable energy of swine feeds requires an analysis of urinary gross energy (GE). A prediction equation for estimating GE of pig urine based on Brix value: urinary GE (kcal/kg) = 11.96 × Brix (%) + 2.33 ($r^2 = 0.87$; $p < 0.001$). However, the prediction equation has not been validated. Therefore, the present study aimed to validate the prediction equation using pig urine samples that were not used for developing the equation. A total of 117 urine samples from pigs were analyzed for GE concentrations using an adiabatic bomb calorimeter and Brix values using a digital refractometer. The measured GE concentrations of the urine samples ranged from 12.9 to 172.4 kcal/kg and Brix values ranged from 1.1% to 12.0%. The predicted GE concentrations of the urine samples were calculated using the equation with measured Brix value. A regression analysis was performed for measured GE minus predicted GE on predicted GE minus average of predicted GE. The intercept was 1.68 (standard error = 1.66; $p = 0.315$), indicating that there was no mean bias. The slope was 0.102 (standard error = 0.065; $p = 0.117$), indicating that there was no linear bias. Therefore, urinary GE concentrations in pigs can be fairly well estimated using the previously developed prediction equation based on Brix value.

Key words : Brix, gross energy, swine, urine, validation

PA26079

Gene set enrichment-based reanalysis of hepatic transcriptomic responses to feed restriction and refeeding in pigs differing in birth weight

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This study reanalyzed a publicly available hepatic transcriptome dataset to characterize pathway-level responses to early postnatal feed restriction and subsequent refeeding in pigs differing in birth weight (BW). Normal-BW (N) and low-BW (U) pigs were compared between control-fed (K) and feed-restricted (R) groups at day 98, immediately after restriction, and day 131, after five weeks of refeeding. Gene Set Enrichment Analysis was performed for Gene Ontology biological process, cellular component, and molecular function categories, with adjusted $p < 0.05$ considered significant. At day 98, NK versus NR showed 125 biological process, 99 cellular components, and 45 molecular function terms, involving ribosome biogenesis, rRNA processing, preribosome, and catalytic activity acting on RNA. UK versus UR showed broader enrichment, with 282 biological process, 67 cellular component, and 80 molecular function terms. In low-BW pigs, restriction-associated terms included rRNA metabolic process, ribosome biogenesis, mitotic sister chromatid segregation, mitotic spindle organization, and chromosomal region, suggesting coordinated regulation of RNA metabolism, translational capacity, and cell-cycle processes. At day 131, significant terms were greatly reduced, with four biological process terms in NK versus NR and one protein folding term in UK versus UR. These findings indicate that feed restriction induces acute hepatic transcriptomic remodeling, particularly in low-BW pigs, while most pathway-level signals are attenuated after refeeding, providing insight into compensatory growth mechanisms and BW-dependent nutritional programming in the juvenile swine liver during the postnatal development period.

Key words : pig, birth weight, feed restriction, liver transcriptome, GSEA, compensatory growth

PA26080

반려동물 사료와 동물성 원료의 칼슘·인 분석 정확도 향상을 위한 ICP-OES 파장 조건 비교 연구

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반려동물은 사람과 달리 다양한 식품 섭취를 통한 영양 보완이 제한적이며, 주식인 사료를 통해 필수 영양소가 균형 있게 공급되어야 한다. 특히 칼슘(Ca)과 인(P)은 골격 형성, 대사 및 생리 기능 유지에 핵심적인 무기질로, 함량뿐 아니라 상호 비율 또한 매우 중요하다. 이에 따라 AAFCO는 반려동물 사료 내 칼슘과 인의 비율을 1:1–2:1 범위로 권장하고 있다. 따라서 사료의 영양학적 품질 평가를 위해서는 칼슘과 인 분석의 정확성과 재현성을 확보하는 것이 필수적이다. 이러한 칼슘과 인을 분석하는 ICP-OES는 다원소 및 다파장 동시 분석이 가능한 장비로, 적은 시료량으로 짧은 시간 내 정성 및 정량 분석이 가능하다는 장점이 있다. 그러나 장비 구성, 분광 특성, 적용 파장에 따라 동일 시료에서도 결과값의 편차가 발생할 수 있다. 특히 칼슘과 인은 원소 특성상 파장 선택에 따른 감도 및 간섭 영향이 크며, 분석 조건에 따라 결과 재현성이 달라질 수 있다. 또한 반려동물 사료의 주요 원료인 육분과 같은 동물성 원료는 골 함량 및 회분 조성 변동성이 크기 때문에 칼슘과 인 함량 또한 변동성이 크다. 따라서 ICP-OES 분석 시에는 여러 파장을 비교하여 특성을 분석하고 가장 대표적인 파장을 선정하는 것이 중요하다. 본 연구에서는 반려동물 사료와 동물성 원료를 대상으로 칼슘과 인의 ICP-OES 분석을 수행하고, 파장 조건 별 편차를 비교 후, 원료에 따른 변동성을 평가하였다. 이를 통해 반려동물 사료의 칼슘 및 인 분석 시 발생 가능한 주요 편차 요인을 확인하여, 분석 정확성과 재현성을 확보하였다.

Key words : ICP-OES, 칼슘, 인, 반려동물 사료, 동물성원료

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PB26001

Effects of different dietary crude protein and energy levels on growth performance of post-weaning Hanwoo calves: sex-based differences

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This study investigated the effects of increased dietary nutrient levels on the growth performance of post-weaning Hanwoo calves, with particular emphasis on differences in growth responses between sexes. A total of 120 Hanwoo calves (3–6 months of age; 60 males and 60 females) were allocated to two treatments: a Control group (CP 18%, TDN 72%) and a Treatment group (CP 20%, TDN 73%). Formula feed was provided based on body weight, while forage (Klein grass hay) was restricted to 2 kg/day. Overall, the Treatment group tended to show higher average daily gain (ADG) and final body weight (BW) compared to the Control group. When analyzed by sex, female calves in the Treatment group showed significantly higher final BW than those in the Control group ($p < 0.05$). ADG also tended to improve in both females (1.08 vs. 1.14 kg/d) and males (1.16 vs. 1.26 kg/d) fed the high-nutrient diet. The feed conversion ratio (FCR) was numerically improved in both sexes. In conclusion, feeding a high-protein and high-energy diet (CP 20%, TDN 73%) to post-weaning Hanwoo calves significantly improved early growth performance in females and showed a tendency toward improved productivity in males, suggesting its potential application in sex-specific precision feeding strategies.

Key words : Hanwoo calves, dietary nutrients, average daily gain, female, sex difference

PB26002

반추위 보호 카르니틴 급여 수준이 거세 한우 도체 성적 및 비육기간에 미치는 영향

이기환[1], 이경근[1], 이대동[1], 이상민[2], 김경진[3], 김은중[3,4]

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본 연구는 사료 내 반추위 보호 카르니틴(Rumen-Protected Carnitine; RPC) 첨가 수준이 거세 한우의 도체 성적 및 비육기간에 미치는 영향을 규명하고자 수행되었다. 거세 한우 60두를 공시하여 RPC 첨가 수준에 따라 대조구(n = 20), RPC 0.0125% 첨가구(n = 16), RPC 0.025% 첨가구(n = 24)의 3처리로 배치하고, 각 처리구가 출하 기준에 도달할 때까지 사양 실험을 실시하였다. 결과에 대한 통계 분석은 일원분산분석으로 수행하였다. 도체중, 등지방두께, 배최장근 단면적, 근내지방도, 일당증체량 및 사료요구율은 처리구 간 유의적 차이가 없었다($p > 0.05$). 반면, 비육기간은 대조구 237.5일에 비해 RPC 0.0125% 첨가구 223.4일, RPC 0.025% 첨가구 210.0일로 RPC 첨가 수준이 증가할수록 유의적으로 단축되었다($p < 0.05$). 이상의 결과를 종합하면, 사료 내 RPC 0.025% 첨가는 도체 품질을 대조구와 동등한 수준으로 유지하면서 비육기간을 약 28일 단축하는 효과가 있어, 거세 한우 비육 농가의 출하 회전율 향상 및 생산비 절감에 실질적으로 기여할 수 있을 것으로 판단된다.

Key words : Hanwoo steer, rumen-protected carnitine (RPC), carcass characteristics, finishing period, production efficiency

PB26003

Effect of feeding hot-air dried alfalfa hay on the productivity of growing Holstein heifers

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This study evaluated the effects of domestically produced hot-air dried alfalfa hay on the productivity of growing Holstein heifers. Eleven heifers were assigned to a control (n = 5) or treatment group (n = 6) and fed experimental diets for 28 days (7-day adaptation, 21-day feeding trial). Animals were selected based on age (7.1 ± 0.4 months) and body weight (208.7 ± 37.7 kg), and diets were formulated by substituting imported with domestic alfalfa hay to meet target ADG (0.8 kg/day) and metabolizable energy requirements (14.1 Mcal/day). Body weight, dry matter intake (DMI), and ADG were measured weekly, and economic analysis was assessed. No significant differences in body weight, DMI, or ADG were observed between treatment groups or across weeks, indicating no adverse effects of the dietary substitution. Domestic alfalfa hay reduced feed costs by 370 KRW per head per day compared to imported hay. These results suggest that hot-air dried alfalfa hay can effectively replace imported alfalfa hay in growing heifer diets without negatively affecting growth performance or palatability, though further studies accounting for seasonal variation are warranted.

Key words : hot-air dry system, alfalfa, growing Holstein heifers

PB26004

Circadian-aware and individualized activity modeling improves early estrus prediction in dairy cows

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This study developed an estrus prediction model that incorporates circadian rhythms and individualized baselines to improve early detection in dairy cows. Five-year activity data from 164 cows (about 2.3 million records) were used to construct a balanced dataset of 5,120 samples comprising 7-day windows preceding estrus or non-estrus periods. Features included time-of-day Z-score normalization using each cow's 30-day historical baseline and a moving activity index comparing recent 24-hour activity with a 6-day baseline. A Random Forest classifier was trained and evaluated at 4, 8, and 12 hours before estrus onset. The proposed model achieved 70.8% accuracy 8 hours pre-estrus, outperforming a conventional raw-activity model lacking individualized temporal normalization that reached only 51.1% and required a shorter lead time of 6 hours to achieve comparable performance. Improvements stemmed from enhanced detection of subtle nighttime activity increases and reduced misclassification during naturally high-activity daytime periods. Error analysis showed reduced false positives—by filtering normal daytime spikes—and false negatives—by accentuating early low-activity deviations. Feature importance identified maximum Z-score, absolute activity peaks, and sustained upward trends as the dominant predictors. These results demonstrate that circadian-aware, individualized feature design enables earlier and more reliable estrus alerts, providing a ≥2-hour improvement in actionable lead time and contributing to more efficient reproductive management in precision dairy farming.

Key words : estrus detection, circadian rhythm, random forest, wearable sensor data, precision dairy farming

PB26005

유전체 육종가 수준이 거세 한우의 성장과 도체 성적 및 육질 특성에 미치는 영향

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본 연구는 유전체 육종가 수준이 거세 한우의 성장 성적과 도체 성적 및 육질 특성에 미치는 영향을 규명하기 위해 수행하였다. 거세 한우 36두를 마블링스코어 유전체 육종가(genomic estimated breeding value of marbling score, gMS) 수준에 따라 상위그룹과 하위 그룹으로 배치하였다. 상위그룹이 마블링스코어, 도체중 및 등심단면적 유전체 육종가가 높았다($p < 0.01$). 시험축은 평균 10개월령부터 출하 시까지 육성기, 비육전기, 비육후기별로 구분하여 농후사료와 조사료를 두 그룹에 동일하게 급여하였다. Blood free fatty acid 농도는 상위그룹에서 높았으며($p < 0.01$), urea nitrogen과 glucose 농도는 차이가 없었다. 29개월령 체중은 하위그룹 대비 상위그룹에서 17% 높았다($p < 0.01$). 시험축은 30개월과 33개월 2시기로 나누어서 출하하였다. 2시기 평균 도체중은 하위그룹 대비 상위그룹에서 20% 높았다($p < 0.01$). 도체의 마블링스코어와 등심단면적은 하위그룹 대비 상위그룹에서 각각 100% 및 22% 높았다($p < 0.01$). 도체 경락 단가와 두당 지육가격은 하위그룹 대비 상위그룹에서 각각 34% 및 59% 높았다($p < 0.01$). 등심의 마블링 섬세도와 관능 평가에 의한 연도, 풍미 및 palatability가 모두 하위그룹보다 상위그룹에서 우수하였다($p < 0.05$). 결론적으로 유전능력이 우수한 개체를 선정하여 사육하는 것이 한우 농가의 소득 증대와 고품질 한우육 생산에 기여함을 확인하였다. 유전능력에 기반한 맞춤형 영양·사양을 통하여 추가적인 소득 증대가 기대된다.

Key words : 거세 한우, 유전체 육종가, 성장 성적, 도체 성적, 경란 단가, 지육 단가, 연도, 풍미

PB26006

경산우 고에너지 급여에 따른 비육기간별 생산성 및 수익성 평가

박명선, 장선식, 문성진, 엄경환, 김재성, 백열창

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경산우에서 에너지 수준이 비육기간별 생산성 및 수익성에 미치는 영향을 구명하고자 본 시험을 수행하였다. 시험은 비육기간(5개월, 8개월)과 관행(TDN 75%), 고에너지(TDN 80%)에 따라 처리구를 구성하고 일당증체량, 건물섭취량 및 도체특성을 조사하였다. 결과적으로, 5개월 비육에서 고에너지 급여구는 관행에 비해 일당증체량과 육량지수가 높게 나타났으나, 도체중이 상대적으로 낮아 수익이 낮게 나타나는 경향을 보였다. 또한, 8개월 비육에서는 고에너지 급여구의 증체 효율이 낮고 사료비가 증가하는 경향을 보였다. 두당 수익 분석 결과, 관행 5개월 비육구가 가장 높은 수익을 나타냈으며, 고에너지 5개월 비육구는 가장 낮은 수익을 보였다. 이는 에너지 수준을 높일 경우 증체 효율은 향상되나, 도체중 증가로 충분히 이어지지 않아 수익성 개선으로 연결되지 않을 수 있음을 의미한다. 따라서, 경산우 비육 시 수익성은 육량지수보다 도체중과 같은 절대량에 크게 영향을 받는 것으로 사료된다.

Key words : 경산우, 고에너지 사양, 비육기간, 도체중, 수익성

PB26007

Impact of palm oil supplementation on growth performance, rumen fermentation, and methane emissions in Hanwoo steers

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This study evaluated the effects of graded levels of palm oil inclusion in concentrate on growth performance, rumen fermentation, and methane emissions in Hanwoo steers. Twelve steers (571.00 ± 65.09) were assigned to a replicated 3 × 3 Latin square design with three 21-day periods and three dietary treatments: CON (0% palm oil), T1 (1.5% palm oil), and T2 (2.0% palm oil). Growth performance parameters were measured alongside ruminal pH, ammonia nitrogen (NH_3-N), volatile fatty acids (VFA), and methane emissions. Growth performance was not affected by palm oil supplementation ($p > 0.05$). Ruminal pH differed significantly among treatments ($p < 0.05$), whereas NH_3-N and total VFA concentrations remained unchanged ($p > 0.05$). The molar proportion of propionate was higher in the T2 group, resulting in a reduced acetate-to-propionate ratio compared to CON and T1 ($p < 0.05$). Methane emissions decreased significantly in steers fed palm oil-supplemented diets ($p < 0.05$), with the T2 group showing the greatest reduction in methane production (13.27%), yield (10.33%), and intensity (13.43%). In conclusion, palm oil supplementation altered rumen fermentation patterns and reduced methane emissions without negatively affecting growth performance in Hanwoo steers. These findings support that palm oil can be used as a dietary strategy to improve rumen efficiency and mitigate enteric methane emissions in beef production systems.

Key words : palm oil, methane emission, Hanwoo, rumen, growth performance

PB26008

Evaluation of kaolinite-based feed additive and fumarate supplementation on *in vitro* rumen fermentation and methane production

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This study evaluated the interaction of kaolinite-based feed additive (K) and disodium fumarate (F) supplementation on *in vitro* rumen fermentation and methane (CH_4) production. The experimental followed a 5 × 2 factorial arrangement design, consisting of five supplementation levels of kaolinite (0%, 1%, 1.5%, 2.0%, and 3.0%) with or without 15 mM disodium fumarate in a substrate containing a 70:30 concentrate-to-forage ratio. Rumen fluid was obtained from a ruminally cannulated Holstein cow and used as the inoculum for the *in vitro* experiment. Batch culture incubations were conducted for 12 and 24 h. Data were analyzed using the MIXED procedure of SAS, with kaolinite dose (K), fumarate (F), and their interaction (K × F) included in the model as fixed effects. For gas production parameters, the K × F interactions were significant for total gas production and CH_4 production (mL) at both 12 and 24 h of incubation ($p < 0.05$). At 12 h of incubation, CH_4 production was 32.0%, 42.8%, 46.1%, and 40.7% lower in $K_{1.5}$, $K_{2.0}$, $F_{1.0}$ and $F_{3.0}$, respectively, compared with K_0 ($p < 0.05$). At 24 h, CH_4 production was 11.9%, 26.9%, 25.2% lower in $K_{1.5}$, $F_{1.0}$, and $F_{1.5}$, respectively, relative to K_0 ($p < 0.05$). Propionate, butyrate, and the acetate-to-propionate ratio showed significant K × F interactions at both 12 and 24 h of incubation ($p < 0.05$), whereas total volatile fatty acids (VFA) and ammonia-nitrogen exhibited significant K × F interactions only at 12 h. These findings indicate that kaolinite and disodium fumarate exert interactive effects on rumen fermentation and methane production, with both additives contributing to reductions in CH_4 production. The combination of kaolinite and fumarate modulated fermentation characteristics, particularly VFA profiles, suggesting a shift in rumen metabolic pathways. Overall, this strategy shows potential as an effective dietary approach for mitigating enteric methane emissions while influencing rumen fermentation dynamics, warranting further *in vivo* validation.

Key words : kaolinite, disodium fumarate, *in vitro*, methane, rumen

PB26009

Effects of sodium sulfite on methane mitigation in goats

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This study was conducted to evaluate the effects of sodium sulfite (SS) supplementation on enteric methane emission and rumen fermentation in goats. Ten goats (58.7 ± 9.57 kg) were used in this study. The experimental design was a randomized block design, with treatments allocated to control (no supplementation) and 0.5% SS supplementation, based on body weight (BW). Tall fescue and concentrate were offered as the basal diet at 2% of BW on a dry matter basis. The adaptation period of the feed and the respiration chamber was 14 days and 3 days, respectively. CH_4 exhaled by goats was measured for 3 days using a methane analyzer (Airwell + 7) equipped with tunable diode laser absorption spectroscopy, while collecting feces for digestibility analysis. Thereby, blood and rumen fluid samples were collected after 3 h of morning feeding to assess rumen fermentation and blood biochemical parameters. Compared with the control, SS 0.5% significantly reduced CH_4 emissions by 21% ($p < 0.05$) without altering dry matter intake or nutrient digestibility. Molar proportion of propionate was significantly increased in SS 0.5%, while that of acetate was significantly decreased compared to the control ($p < 0.05$). No differences were observed in other rumen fermentation or blood biochemical parameters in goats. Collectively, supplementing sodium sulfite can mitigate enteric CH_4 in goats. Further studies are warranted to examine the effects of SS on animal performance, including carcass characteristics.

Key words : methane, sodium sulfite, goat, rumen fermentation

PB26010

Effects of thiamine diphosphate (ThDP) supplementation on methane emissions and milk productivity in lactating Holstein cows

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Methane produced during the digestive process of dairy cows is not only a greenhouse gas but also represents a loss of unutilized dietary energy. Therefore, mitigating methane emissions can simultaneously reduce greenhouse gases and improve livestock growth performance. Thiamine diphosphate (ThDP), the active coenzyme form of vitamin B1, was previously found to reduce *in vitro* methane production by 32% at 720 ppm. Building on these findings, the present study investigated the effects of dietary supplementation with 720 ppm ThDP on the productivity and methane emissions of lactating Holstein cows. Supplementation did not significantly affect overall productivity ($p > 0.5$), with no statistical differences between the control and treatment groups in body weight (734.61 vs. 740.53 kg), dry matter intake (20.13 vs. 20.29 kg/d), milk yield (30.65 vs. 31.20 kg/d), milk fat (4.53% vs. 4.30%), milk protein (3.60% vs. 3.53%), and lactose (4.80% vs. 4.72%). Similarly, *in vivo* methane emissions showed no significant difference, with the control group producing 17.92 g/kg^{DMI} compared to 18.03 g/kg^{DMI} in the treatment group. The lack of *in vivo* efficacy, contrary to *in vitro* findings, is likely due to continuous ruminal saliva flow hindering ThDP's ability to regulate metabolism or compete with coenzyme M (CoM). Further research, such as modifying the feeding method or adjusting the dosage, is needed to overcome these *in vivo* limitations.

Key words : methane reduction, ruminant, ThDP, dairy cow, Holstein cow

PB26011

Synergistic influence of exogenous fibrolytic enzymes and probiotics on *in vitro* rumen fiber digestion in Korean native black goats

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The use of bio-supplements to enhance fiber degradation and stabilize rumen fermentation has gained increasing attention in animal industry of South Korea. An *in vitro* experiment was conducted to evaluate the effects of a fibrolytic enzyme blend (cellulase + xylanase) with or without the probiotic *Clostridium butyricum* on rumen fermentation and selected microbial groups using rumen fluid from Korean native black goat. Four treatments were tested: control (CON), fibrolytic enzymes (FE), *C. butyricum*(CB) and a combination (FECB). Across incubation times (24 and 48 h), all treatments increased *in vitro* dry matter digestibility compared to the CON ($p < 0.05$). The treatments showed higher levels of propionic and butyric acids than CON ($p < 0.05$), its indicative of their distinct ruminal fermentation pathways that prioritize rapid energy availability and gut health. Quantitative PCR (qPCR) results ($\log_{10}$ gene copy numbers/mL) showed that the treatment groups had a notable increase in protozoa and anaerobic fungi compared to the CON ($p < 0.05$). This reflects the unique dependence on these microbes for fiber degradation and nutrient recycling. Therefore, it is considered that these shifts in the microbial community led to increased fiber degradation and improved ruminal fermentation efficiency. [This work was supported by IPET through Agriculture and Food Convergence Technologies Program for Research Manpower Development Program or Project, funded by MAFRA (grant number RS-2024-00400922)].

Key words : probiotics, cellulase, xylanas, *Clostridium butyricum*, rumen fermentation, Hanwoo

PB26012

제주흑우 수소(비거세우)의 생후 초기 성장특성 연구

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제주흑우는 유전적 보존 가치가 높은 재래축종이지만, 한우 대비 지육량이 적고 1등급 이상 출현율이 낮아 경제성이 낮은 품종으로 평가받고 있다. 또한 사육 두수 감소로 산업 기반이 약화되고 있으며, 특히 씨수소 개체 부족으로 우량 개체 선발과 세대교체를 위한 체계적 사양관리 및 성장 자료 확보가 시급한 실정이다. 더불어 생후 초기 성장단계의 체형 발달 특성에 대한 정량적 자료가 부족하여, 초기 성장 특성 구명과 예측모델 구축의 필요성이 제기되고 있다. 본 연구는 제주흑우 수소의 생후 초기 성장단계별 체형 변화를 조사하고, 이를 바탕으로 최적 성장 예측모델을 제시하고자 수행되었다. 난지축산연구센터 등에서 사육 중인 제주흑우 수소(비거세우)를 대상으로 생시부터 6개월령까지 매월 체중과 11개 체형 항목(체고, 체장, 흉위, 십자부고 등)을 정기 측정하였다. 수집된 데이터를 바탕으로 품종 간(제주흑우 vs 한우) 성장 양상을 비교하였으며, 선형 및 비선형(Logistic, Gompertz) 회귀모델을 적용하여 체형지표와 체중 간의 상관관계 및 성장 예측 가능성을 분석하였다. 제주흑우 수소의 평균 생시 체중은 26.0 kg이었으며, 2–3개월령에 이유 및 급이 조건 변화로 인해 일당증체량(ADG)이 일시적으로 감소(0.53 kg/일)했으나 이후 회복되는 경향을 보였다. 체형지표와 체중 간의 상관관계 분석 결과, 흉위(Chest Girth)와의 결정계수(R^2)가 0.987로 가장 높게 나타나 체중 예측을 위한 핵심 지표임을 확인하였다. 성장모델 적용 결과, 제주흑우는 한우에 비해 초기 성장률은 높으나 성장이 일찍 안정화되는 경향을 보였다. 특히 Gompertz 모델은 생후 6개월까지의 데이터로 18개월령까지의 성장을($R^2 = 0.933$) 예측할 수 있는 것으로 나타났다. 본 연구에서 구축한 제주흑우 수소의 초기 성장자료와 예측모델은 희소축종의 효율적 사양관리 기준 수립과 씨수소 선발을 위한 기초자료로 활용될 것으로 판단된다. 향후 통계적 신뢰도 향상을 위해 공시축 두수 확대와 장기 반복측정이 필요하다.

Key words : 제주흑우, 성장특성, 영양사료, 흉위, Gompertz 모델

PB26013

The effects of mixture of thiamine pyrophosphate and plant oils on the *in vitro* methane production and rumen fermentation characteristics

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The present study was conducted to evaluate the effects of a mixture of thiamine pyrophosphate (TPP) and plant oils (canola, sunflower, and soybean) on *in vitro* rumen fermentation characteristics and methane production. TPP was added at 0 or 480 ppm (DM basis), and each plant oil was added at 0 or 4 % (DM basis). The substrate used was a mixture of ground concentrate and forage in a 7:3 ratio. Rumen fluid was collected from two cannulated cows and mixed with McDougall's buffer at a ratio of 1:3. A total of 50 mL of the buffered rumen fluid and 0.5 g of the substrate were dispensed into 125 mL serum bottles, which were then incubated at 39℃ for 24 h. After incubation, each gas sample was collected for methane analysis, and rumen fluid was sampled to evaluate fermentation characteristics. Methane production (% digested DM) showed a interaction effect between TPP and plant oils ($p = 0.018$), with the TPP and plant oil mixture groups showing the lowest production ($p < 0.05$) compared with the single (TPP or oil) treatments. In addition, the acetate-to-propionate ratio increased in the plant oil treatments due to a decrease in propionate concentration, but the TPP and plant oil mixture improved these values through an interaction effect ($p < 0.001$). *In vitro* dry matter digestibility and total volatile fatty acid concentrations did not differ significantly among all treatments ($p > 0.05$). In conclusion, the mixture of TPP and plant oil was demonstrated to improve methane inhibition and the acetate-to-propionate ratio in rumen fluid.

Key words : methane, thiamine pyrophosphate, plant oils

PB26014

Development of an automatic feeder-specific calf milk replacer through analysis of its physical and chemical properties

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This study was conducted to establish development criteria for calf milk replacers suitable for automatic milk feeders (AMF) by comparing the chemical and physical properties of four commercial milk replacers (A, B, C, D) with whole milk powder (WMP). Proximate analysis showed that WMP had the highest dry matter (97.13%), whereas C had the lowest (96.92%) ($p < 0.05$). Crude protein was highest in A (25.09%) and lowest in B (21.62%), while ether extract was highest in WMP (30.16%) and lowest in A (8.28%) ($p < 0.05$). Crude ash was highest in A (7.61%) and lowest in C (6.74%) ($p < 0.05$). Particle size distribution analyzed by laser diffraction showed that D had the lowest SPAN value (1.81), indicating more uniform particle size, whereas A had the highest SPAN value (2.82). SPAN is a measure of the width of particle size distribution. Accordingly, D exhibited more uniform particle size, whereas A showed greater heterogeneity. Solubility analysis revealed that D exhibited superior solubility, whereas A showed lower solubility and a higher possibility of insoluble residue formation after reconstitution ($p < 0.05$). These findings suggest that the suitability of calf milk replacers for AMF depends not only on nutritional composition but also on physical properties such as particle uniformity and solubility. Therefore, both nutritional value and rehydration stability should be considered in establishing quality criteria for AMF-specific calf milk replacers.

Acknowledgement: This work was supported by Korea Institute of Planning and Evaluation for Technology in Food, Agriculture and Forestry (IPET) through Smart Farm Multi-Ministry Package Innovation Technology Development Project, funded by Ministry of Agriculture, Food and Rural Affairs (MAFRA). (RS-2025-02263116).

Key words : calf, milk replacer, automatic feeder, particle size, solubility

PB26015

Effects of dietary L-citrulline supplementation on adipogenic and arginine metabolism-related gene expression in finishing Hanwoo steers

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This study aimed to investigate the effects of dietary L-citrulline (L-Cit) supplementation on the mRNA expression of adipogenic and arginine metabolism–related genes in finishing Hanwoo steers. Thirty-four Hanwoo steers (age: 25.0 ± 0.6 mo) were assigned to two dietary treatments: a control group (0% L-Cit; n = 17) and an L-Cit group (0.4% L-Cit on a dry matter basis via top dressing; n = 17). Following a 6-mo treatment period, the steers were slaughtered. Samples of the liver, kidney, and *longissimus lumborum* (LL) muscle were collected for mRNA expression analysis. Statistical analyses were performed using the TTEST procedure in SAS 9.4. In the liver, *OTC* expression was higher ($p < 0.05$) in the L-Cit group than in the control group, whereas *ARG1*, *ASS*, *ASL*, and *GAMT* expression did not differ between groups. In the kidney, *AGAT* expression was lower ($p < 0.05$) in the L-Cit group than in the control group, whereas *ASS* and *ASL* expression did not differ between groups. In the LL muscle, *ZNF423*, *CD36*, *FABP4*, and *SNAP23* expression was higher ($p < 0.05$) in the L-Cit group than in the control group, whereas *PPARG*, *LPL*, *SCD*, *DGAT2*, and *BSCL2* expression did not differ between groups. Overall, dietary supplementation with 0.4% L-Cit in finishing Hanwoo steers induced tissue-specific transcriptional responses in renal and hepatic arginine metabolism and up-regulated intramuscular adipogenic gene expression, warranting further investigation with phenotypic measures of carcass quality.

Key words : finishing Hanwoo steer, L-citrulline, arginine metabolism, adipogenic gene expression

PB26016

Growth performance, nutrient intake, and digestibility in female goats fed low versus high levels of different type of alfalfa

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This study evaluated the effects of low (1.5% of body weight) and high (2.0% of body weight) feeding levels of local and imported alfalfa on growth performance, nutrient intake, and nutrient digestibility in female crossbred goats (Boer × Korean native, *Capra hircus*). Twelve female goats with initial body weight of 38.7 ± 1.3 kg were assigned to a 4 × 4 Latin square design with four dietary treatments (L1: local alfalfa at 1.5% BW; L2: imported alfalfa at 1.5% BW; H1: local alfalfa at 2.0% BW; H2: imported alfalfa at 2.0% BW) over four periods of one month each period.

Final body weight was numerically higher in the high feeding level groups, reaching up to 43.17 kg, compared to the low feeding level groups. Body weight gain ranged from 1.63 kg (lowest in H1) to 3.08 kg (highest in H2), while average daily gain ranged from 58.04 g/day (lowest in H1) to 110.12 g/day (highest in H2). Dry matter intake was higher in the high alfalfa level treatments ($p < 0.0001$). Nutrient intake values for dry matter, organic matter, crude protein, crude fiber, acid detergent fiber, and neutral detergent fiber were generally higher in the high feeding level groups. In contrast, digestibility coefficients for all measured nutrients remained similar across treatments, ranging from approximately 71% to 84%.

These results indicate that both local and imported alfalfa performed similarly in female crossbred goats when fed at either 1.5% or 2.0% of body weight. Notably, the highest body weight gain (3.08 kg) and average daily gain (110.12 g/day) were observed in H2 (imported alfalfa at 2.0% BW), suggesting that the combination of imported alfalfa at the high feeding level supported the strongest numerical growth performance while maintaining comparable nutrient digestibility.

Key words : alfalfa, female goats, low feeding level, high feeding level, growth performance, nutrient intake, digestibility

PB26017

Effects of feeding level on nutrient intake, digestibility and nitrogen balance in hybrid goats offered a locally produced alfalfa

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This study investigated the effects of feeding level (1.5% vs 2.0% of body weight) of locally produced alfalfa on growth performance, nutrient intake, digestibility, and nitrogen balance in hybrid goats (Boer × Korean native, *Capra hircus*). Twenty-four goats (12 females and 12 males; initial body weight 38.1 ± 1.1 kg for females and 40.3 ± 1.1 kg for males) were used in a 2-period crossover design with a 2 × 2 factorial arrangement (sex × feeding level) over 12 weeks (cage and diet adaptation: 4 weeks + experiment diet adaptation: 8 weeks) with four treatments: F1 (1.5% BW in female), F2 (2.0% BW in female), F3 (1.5% BW in male), and F4 (2.0% BW in male). Males exhibited higher body weight gain and ADG than females, with the highest value recorded in F4. Dry matter intake was clearly higher in the high feeding level groups (2.0% BW), particularly in males ($p < 0.05$). Nutrient intake, especially crude protein intake, was substantially higher in male goats compared to females, reaching the highest level in F4. Digestibility coefficients for most nutrients were generally similar between feeding levels. Male goats exhibited significantly higher nitrogen intake, body nitrogen retention, and nitrogen utilization efficiency than females, while feeding level (1.5% vs 2.0% BW) had limited impact on nitrogen balance parameters. Nevertheless, both sexes maintained positive nitrogen balance across all treatments.

These findings suggest that male hybrid goats responded to higher feeding levels of locally produced alfalfa with greater growth and crude protein intake, while females showed relatively better nitrogen utilization efficiency despite lower overall intake.

Key words : local alfalfa, hybrid goats, feeding level, sex difference, nutrient intake, digestibility, nitrogen balance

PB26018

Early growth performance, feed intake, and phenotypic traits of uncastrated Jeju black bulls

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Jeju Black cattle, a native Korean breed, possess distinct genetic and phenotypic characteristics; however, early growth in uncastrated bulls remains insufficiently characterized, and feeding standards are largely derived from Hanwoo. This study aimed to evaluate early growth performance, feed intake, and phenotypic development in uncastrated Jeju Black bull calves and generate baseline data for breed-specific management. Three uncastrated Jeju Black bull calves were monitored from birth to 12 weeks. Body weight, daily feed intake, and morphometric traits (height, body length, and heart girth) were recorded at regular intervals. Growth patterns were assessed using repeated measurements, and relationships between body weight and body-size traits were analyzed by regression. Body weight increased from approximately 20–37 kg at birth to 71–108 kg at 12 weeks, showing consistent growth with gradual acceleration. Daily feed intake rose from 0.1 to 2.5 kg/day, reflecting increasing nutritional demand. Morphometric traits increased steadily and were positively associated with body weight, indicating coordinated development. Compared with Hanwoo references, Jeju Black calves exhibited slightly lower body weights, suggesting breed-specific growth patterns. These findings provide baseline data on early growth, feed intake, and phenotypic development in uncastrated Jeju Black bulls, supporting breed-specific feeding strategies and future large-scale and genetic studies.

Key words : Jeju black cattle; early growth; feed efficiency; morphometric traits; growth dynamics

PB26019

Development of a body condition score prediction algorithm for dairy cows using 3D point cloud data based on a pointpillar model

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This study aimed to develop an artificial intelligence-based model for the automatic estimation of Body Condition Score (BCS) in dairy cows using 3D point cloud data. A total of 605 3D point cloud datasets were utilized, and BCS labels were defined as the average scores from three independent observers. For datasets with temporal gaps, linear interpolation was applied assuming that changes in BCS occurred linearly over time. During preprocessing, data with insufficient point counts were excluded to ensure data quality. Data augmentation techniques, including random sampling, rotation, and noise addition, were applied. The dataset was divided into training (80%) and validation (20%) sets. The model was developed based on the PointPillar architecture, converting 3D point cloud data into a 2D grid representation. Spatial features were extracted using a convolutional neural network (CNN). This approach enabled effective learning of individual cow characteristics for BCS prediction. Model performance was evaluated using MSE, RMSE, MAPE, and SMAPE metrics. t-SNE analysis showed clear separation among individual cows, indicating effective feature extraction. Cosine similarity analysis further suggested the potential for estimating BCS across different individuals.

Key words : body condition score, 3D point cloud, PointPillar, dairy cow

PB26020

Rumen protozoal and fungal community composition in Hanwoo steers with divergent residual feed intake phenotypes

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This study aimed to evaluate the association between RFI phenotype and rumen protozoal and fungal communities in early fattening Hanwoo steers. Sixty-four Hanwoo fattening steers (16 months of age; 528.5 ± 44.4 kg body weight) were divided into two extreme phenotypic groups: low RFI (L-RFI; efficient; top 10%, n = 6) and high RFI (H-RFI; inefficient; bottom 10%, n = 6). Metagenomic DNA was extracted from rumen samples (n = 12), and the protozoal 18S rRNA gene and fungal ITS region were amplified and sequenced on the Illumina MiSeq platform. Bioinformatic analysis was performed using QIIME 2, and differential abundance was assessed using the ANCOM-BC method. Alpha diversity metrics (observed ASVs, Shannon, and Simpson) did not differ in the protozoal community between RFI groups, whereas significant differences were observed in the fungal community ($p < 0.05$). Principal coordinate analysis based on Bray-Curtis dissimilarity revealed significant differences in both protozoal and fungal community composition between the two RFI groups. In the protozoal community, *Dasytricha, Polyplastron*, and *Entodinium* were significantly enriched in the H-RFI group ($q < 0.05$), whereas *Eudiplodinium* and *Ostracodinium* were predominant in the L-RFI group ($q < 0.05$). Additionally, *Anaeromyces* was the only fungal genus with higher abundance in the L-RFI group ($q < 0.05$). Taxa associated with fiber degradation, including *Eudiplodinium* and *Ostracodinium* in the protozoal community and *Anaeromyces* in the fungal community, were enriched in efficient steers, suggesting their potential association with improved energy utilization from structural carbohydrates.

Key words : Hanwoo cattle, rumen microbiota, residual feed intake

PB26021

Site-specific microbiome features reveal functional specialization of fecal and vaginal microbiomes in Holstein dairy cows

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Fecal and vaginal microbiomes are closely associated with digestive and reproductive physiology in ruminants, but their site-specific ecological and predicted functional characteristics in Holstein dairy cows remain insufficiently understood. This study investigated the diversity, taxonomic composition, predicted pathway-level functions, and temporal microbial dynamics of fecal and vaginal microbiomes in Holstein dairy cows using 16S rRNA gene sequencing. Fecal samples exhibited higher alpha diversity than vaginal samples, and both taxonomic and predicted functional profiles showed clear separation according to anatomical site. The fecal microbiome showed higher predicted contributions to secondary bile acid biosynthesis, lysosome-related pathways, and sphingolipid metabolism, whereas the vaginal microbiome was characterized by the enrichment of Actinomycetota, Mycoplasmoidaceae, *Blautia*, and predicted pathways related to phosphotransferase system and ketone body metabolism. Longitudinal analysis further indicated that fecal Prevotellaceae showed an increasing trend over time, suggesting temporal taxonomic responsiveness of the fecal microbiome. These findings highlight site-specific ecological and predicted functional differentiation between fecal and vaginal microbiomes and suggest their potential as microbial indicators for nutritional management and reproductive health monitoring in dairy cows.

Key words : dairy cows, feces, metabolic pathways, microbiota, vagina

PB26022

Low versus high forage levels of alfalfa: effects on growth performance and morphological characteristics of male Korean Crossbred Goats

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This study investigated the effects of low (1.5% of body weight) versus high (2.0% of body weight) forage levels of local and imported alfalfa on growth performance and morphological characteristics in male Korean crossbred goats (Boer × Korean native, *Capra hircus*). Twelve goats with an initial body weight of 39.1 ± 1.2 kg were assigned to a replicated 4 × 4 Latin square design with four dietary treatments: T1 (local alfalfa at 1.5% BW), T2 (imported alfalfa at 1.5% BW), T3 (local alfalfa at 2.0% BW), and T4 (imported alfalfa at 2.0% BW) over four 1-month periods.

High forage levels (2.0% BW) resulted in numerically higher total dry matter intake compared to the low forage levels ($p < 0.05$). Final body weight was higher in the high forage groups, particularly in goats fed local alfalfa at 2.0% BW. Body weight gain and average daily gain were also numerically highest in the high forage level with imported alfalfa (T4). In terms of morphological characteristics, withers height was greater in the high forage level groups, with the highest value observed under high local alfalfa feeding (T3, $p < 0.05$). Other body measurements such as body length, chest width, and chest girth showed modest numerical increases in the high forage level groups.

These results suggest that increasing the forage level from 1.5% to 2.0% of body weight with either local or imported alfalfa improved dry matter intake and supported better final body weight and withers height in male crossbred goats. High forage feeding, especially with local alfalfa, appeared advantageous for certain morphological traits, while both alfalfa types performed comparably overall in growth performance.

Key words : alfalfa, low forage, high forage, male goats, growth performance, morphological characteristics

PB26023

성장단계별 육용 염소의 혈중 대사물질 및 생리적 지표 변화 분석

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국내 염소 산업은 건강식에 대한 수요 증가에 따라 전업화 및 규모화가 진행되고 있으나, 사료비 상승과 표준화된 사양관리 체계의 부재로 인해 농가 경영 부담이 심화되고 있다. 특히 성장 단계별 염소의 영양 요구량 충족 여부를 평가할 수 있는 생리적 지표에 대한 연구는 여전히 부족한 실정이다. 따라서 본 연구는 육용 염소의 주요 성장 단계 (3, 6, 9, 및 13개월령)에 따른 혈중 대사물질의 변화를 추적하여 시기별 대사적 특성을 규명하고자 수행되었다. 보어 교잡종 염소 18두를 공시하였으며, 성장 특성 조사를 위해 시험 기간 동안 체중을 매월 측정하였다. 또한 혈중 대사물질 분석을 위해 혈액은 각 성장 단계에서 경정맥을 통해 채취하였으며, 에너지·단백질·간 기능 관련 지표를 자동생화학분석기를 이용하여 분석하였다. 성장 단계에 따라 체중은 3개월령 14.97 kg에서 13개월령 51.22 kg까지 완만하게 증가하였으며, 혈중 대사물질 지표에서 유의적인 시기적 변화가 관찰되었다. 혈중 BUN 농도는 3개월령(17.30 mg/dL) 대비 13개월령(34.10 mg/dL)에서 약 2배 가까이 증가하였고, glucose 농도는 3개월령에 가장 높았으나, 이후 감소 되어(Min: 56.00–Max: 117.00) 범위를 유지하였다. 혈중 NEFA 및 cholesterol 농도는 3개월령에서 일시적으로 높게 나타난 후 6개월령에 감소하였으며, 이후 점진적으로 증가하는 경향을 보였다. 간 기능 지표인 GGT 및 AST 또한 성장 단계에 따라 유의적인 변동을 나타냈다. 본 연구 결과, 성장 단계에 따라 육용 염소의 단백질 및 지질 대사 특성이 다르게 나타났으며 혈중 대사산물의 변화 양상은 성장 단계별 적정 영양 공급 기준 마련과 생리적 이상 판정을 위한 기초 자료로 활용될 수 있을 것으로 판단된다.

Key words : 육용 염소, 보어, 성장 단계, 혈중 대사산물, 생리적 지표

PB26024

Effects of nutrient levels in concentrate feed on rumen fermentation characteristics, growth performance, plasma metabolites, and carcass characteristics in Hanwoo steers

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This study evaluated the effects of concentrate feed nutrient levels on rumen fermentation characteristics, growth performance, plasma metabolites, and carcass characteristics in Hanwoosteers. A total of 157 Hanwoosteers (269.5 ± 37.5 kg; 8 months of age) were assigned to two dietary treatments differing in concentrate feed nutrient levels during the growing, early fattening, and late fattening periods: Control (CP 16.5–18.5%, TDN 81–83%) and Treatment (CP 17–19%, TDN 82–84%). Rumen pH values and NH_3-N concentrations were higher in the Control group than in the Treatment group ($p < 0.05$), whereas propionate concentration was higher in the Treatment group than in the Control group ($p < 0.05$). The relative abundances of *Acetitomaculum* and *Saccharofermentans* were lower in the Treatment group than in the Control group ($p < 0.05$), while no significant differences were observed in the relative abundances of other genera. Body weight did not differ between treatments at any age. During the late fattening period (22–26 months of age), average daily gain was higher and feed conversion ratio was lower in the Treatment group than in the Control group ($p < 0.01$). Plasma NEFA concentration was lower, whereas triglyceride concentration was higher, in the Treatment group than in the Control group ($p < 0.05$). Concentrate feed nutrient levels had no significant effects on carcass yield or meat quality characteristics. The results of this study suggest that raising CP and TDN levels in concentrate feed by 0.5 and 1.0 percentage points, respectively, may improve late-fattening growth performance and favorably affect energy-related plasma metabolites, although the effects on carcass characteristics were limited.

Key words : Hanwoo steers, nutrient levels in concentrate feed, rumen fermentation characteristics, growth performance, plasma metabolites, carcass characteristics

PB26025

Effects of nano-formulated vitamin supplementation on milk production characteristics in lactating Holstein cows

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This study was conducted to evaluate the effects of nano vitamin supplementation on milk production characteristics in lactating Holstein cows and to assess the field applicability and feeding efficiency of nano-formulated vitamins. A total of 40 lactating Holstein cows with an average milk yield of 33.4 ± 0.5 kg/day were used and assigned to three treatment groups: T1, regular vitamin; T2, nano vitamin; and T3, regular vitamin plus organic selenium. Milk yield, somatic cell count, and milk fat content did not differ significantly among treatments. However, solids-not-fat content was higher in T1 and T3 than in T2 ($p < 0.05$), and milk urea nitrogen concentration increased in the order of T1, T2, and T3 ($p < 0.05$). Stearic acid content in milk tended to be lower in T2 and T3 than in T1, whereas lauric acid and myristic acid contents tended to be higher in T3 than in T1 and T2. Milk vitamin D_3 content tended to be higher in T2 than in T1 and T3, and vitamin A content was higher in T2 than in T3 ($p < 0.05$). The results of this study suggest that nano vitamin supplementation did not significantly affect milk yield or major milk components but may favorably affect milk vitamin D_3 and vitamin A contents, as well as some fatty acid profiles, indicating the potential field applicability of nano-formulated vitamins.

Key words : lactating Holstein cows, nano-formulated vitamin, milk production characteristics, milk fatty acids, milk vitamins

PB26026

Effects of genetic potential and dietary soybean meal-to-lupin ratio on growth performance, plasma metabolites, and carcass characteristics in Hanwoo steers

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This study was conducted to evaluate the effects of genetic potential and dietary ingredient ratios on growth performance, plasma metabolites, and carcass characteristics in Hanwoo steers under identical TDN and CP levels. A total of 22 Hanwoo steers (314.5 ± 49.2 kg, 10.4 ± 1.8 months of age) were assigned to four groups: YC, yield-type control; QC, quality-type control; YT, yield-type treatment; and QT, quality-type treatment. The control diet contained soybean meal (SBM) and lupin at 3% and 6%, respectively, during the growing period and at 0% and 5%, respectively, during the fattening period. The treatment diet contained SBM and lupin at 6.5% and 2%, respectively, during the growing period and at 6% and 2%, respectively, during the fattening period. Average daily gain tended to be higher in the yield-type group than in the quality-type group. A significant interaction effect between genetic potential and dietary ingredient ratio was observed for feed conversion ratio, with the lowest value observed in the QT group ($p < 0.05$). Most plasma metabolite concentrations did not differ significantly among treatments throughout the experimental period; however, plasma BUN and cholesterol concentrations at 13, 16, and 28 months of age were higher in the control diet groups than in the treatment diet groups ($p < 0.05$). Carcass weight was higher in the YT group, whereas rib-eye area, marbling score, and the proportion of carcasses graded 1^+ or higher for meat quality tended to be higher in the control diet groups than in the treatment diet groups. In conclusion, although the effects of genetic potential and dietary ingredient ratios on plasma metabolites and carcass characteristics were limited under identical TDN and CP levels, adjusting soybean meal and lupin ratios may partially improve growth performance and carcass weight, particularly in yield-type Hanwoo steers.

Key words : Hanwoo steers, soybean meal, lupin flakes, genetic potential, growth performance, carcass characteristics

PB26027

Effects of genetic potential on growth performance, plasma metabolites, and carcass characteristics in Hanwoo steers under a 28-month production system

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This study was conducted to evaluate the effects of genetic potential, classified as yield-type and quality-type, on growth performance, plasma metabolites, and carcass characteristics in Hanwoo steers raised under a 28-month rearing system from birth to slaughter. A total of 157 Hanwoo steers (269.5 ± 44.3 kg; 8 months of age) were used, and SNP genotyping was performed using hair follicle samples to classify the animals into yield-type and quality-type groups. Body weights at 21 and 28 months of age and average daily gain during the overall experimental period were higher in the yield-type group than in the quality-type group ($p < 0.05$). Plasma albumin and calcium concentrations at 8 months of age and magnesium concentration at 21 months of age were higher in the yield-type group, whereas plasma phosphorus concentration at 12 months of age was higher in the quality-type group ($p < 0.05$). Carcass weight and rib-eye area were higher in the yield-type group than in the quality-type group ($p < 0.01$), but yield grade distribution did not differ between groups. Marbling score and the proportion of carcasses graded 1^{+}or higher for meat quality were numerically higher in the quality-type group than in the yield-type group, although the differences were not significant. The results of this study suggest that yield-type Hanwoo steers may have advantages in growth performance and carcass yield-related characteristics, whereas quality-type Hanwoo steers may have relative advantages in marbling score and producing high-quality meat-quality grade carcasses under a 28-month rearing system form birth to slaughter.

Key words : Hanwoo steers, genetic potential, growth performance, plasma metabolites, carcass characteristics

PB26028

Effects of genetic potential on growth performance, plasma metabolites, and carcass characteristics in Hanwoo Steers under a 26-month short-term fattening system

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This study investigated the effects of genetic potential (yield-type vs. quality-type) on growth performance, plasma metabolites, and carcass characteristics in Hanwoo steers slaughtered at 26 months of age under a shortened fattening system. A total of 157 Hanwoo calves (269.5 ± 37.5 kg; 7 months of age) were classified into yield-type (n = 84) and quality-type (n = 73) groups and raised until slaughter at 26 months of age. Body weights at 12, 21, and 26 months of age, as well as average daily gain during the overall experimental period and dry matter intake, were higher in the yield-type group than in the quality-type group ($p < 0.05$), whereas feed conversion ratio was higher in the quality-type group than in the yield-type group ($p < 0.05$). At 21 months of age, plasma NEFA concentration was higher in the yield-type group than in the quality-type group, whereas insulin concentration was higher in the quality-type group than in the yield-type group ($p < 0.05$). At 26 months of age, plasma BUN concentration was higher in the quality-type group than in the yield-type group ($p < 0.01$). Carcass weight, rib-eye area, and the proportion of carcasses with yield grade A were higher in the yield-type group than in the quality-type group ($p < 0.01$). Marbling score and the proportion of carcasses graded 1+ or higher for meat quality tended to be higher in the quality-type group than in the yield-type group. In conclusion, yield-type Hanwoo steers showed greater growth performance and carcass yield characteristics, whereas quality-type Hanwoo steers showed a higher marbling score and greater potential for producing high meat-quality grade carcasses under a shortened fattening system with slaughter at 26 months of age.

Key words : Hanwoo steers, genetic potential, growth performance, carcass characteristics, short-term fattening system

PB26029

Effects of dietary soybean protein by-product meal supplementation levels on rumen fermentation characteristics, growth performance, and carcass characteristics in Hanwoo steers

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This study was conducted to evaluate the effects of soybean protein by-product meal (SPM) supplementation levels on rumen fermentation characteristics, growth performance, and carcass characteristics in Hanwoo steers. A total of 16 Hanwoo steers (488.6 ± 48.5 kg; 16.5 ± 1.6 months of age) were assigned to four treatments: control (no SPM supplementation), T1 (1% SPM), T2 (2% SPM), and T3 (3% SPM). *In vitro* rumen pH values and NH_3-N concentrations at 8, 12, 24, and 48 h of incubation were higher in T1, T2, and T3 than in the control group ($p < 0.01$). Acetic acid concentration was higher in T2 than in the control group and T1 at 24 h ($p < 0.05$), and was higher in T2 and T3 than in the control group and T1 at 48 h ($p < 0.05$). Butyric acid concentration was highest in the control group at all incubation times ($p < 0.01$). At 4 h, total VFA concentration was higher in the control group, T1, and T2 than in T3 ($p < 0.01$), whereas at 8, 12, and 24 h, total VFA concentration was lower in T1, T2, and T3 than in the control group ($p < 0.05$). Average daily gain was higher in T1 than in the control group and T2 ($p < 0.01$), and feed conversion ratio was numerically lowest in T1. Marbling score was higher in T3 than in the control group ($p < 0.05$), whereas meat texture was lower in T3 than in the control group ($p < 0.05$). The proportion of carcasses with meat quality grade 1+ or higher was numerically highest in T3.The results of this study suggest that dietary supplementation with 3% SPM may contribute to increasing the proportion of carcasses with meat quality grade 1+ or higher by increasing marbling score in Hanwoo steers.

Key words : Hanwoo steers, soybean protein by-product meal, rumen fermentation characteristics, growth performance, carcass characteristics

PB26030

Effects of thiamine diphosphate and soybean oil supplementation on rumen fermentation and methane production in Hanwoo steers

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This study investigated the effects of thiamine diphosphate (ThDP) and soybean oil (SBO) supplementation on rumen fermentation and methane production in Hanwoo steers. Eight Hanwoo steers (average body weight 740.18 kg; 31 month olds) were used in a 2 × 2 crossover design consisting of two treatments and two experimental periods. Each period lasted three weeks. The treatments were: a control diet without a supplementation (CON) and a diet supplemented with 480 ppm of ThDP and 4% of SBO (TRT) on a dry matter (DM) basis. Diets were formulated with a concentrate-to-forage ratio of 7:3, and offered level equivalent to 2% of body weight (DM basis) and provided twice daily at 10:00 and 15:00. Methane production was monitored using the GreenFeed system, and end of each experimental period, rumen fluid and blood samples were collected four hours after morning feeding. All data were analyzed using the GLIMMIX procedure in SAS. The results showed that, average daliy gain, body weight$^{0.75}$ and dry matter intake were not significantly affected ($p > 0.05$). In addition, methane production were significantly lower in the TRT group than in the CON group ($p < 0.05$). These results demonstrate that a dietary supplementation with 480 ppm of ThDP and 4% of SBO effectively reduced methane production without negatively affecting rumen fermentation in Hanwoo steers.

Key words : Hanwoo, methane production, rumen fermentation, soybean oil, thiamine diphosphate

PB26031

Effects of genomic estimated breeding values and sucrose supplementation on growth performance, rumen fermentation, blood profiles, and meat quality traits in Hanwoo steers

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This study evaluated the effects of genomic estimated breeding value (gEBV) and sucrose supplementation on growth performance, rumen fermentation characteristics, blood metabolites, hormones, and meat quality traits in 34 Hanwoo steers (26 months, 725 kg) over 24-week period. Animals were assigned to a 2 × 2 factorial design: gEBV for marbling score (gMS; high vs. low) and sucrose supplementation (control vs. treatment). The animals were fed a basal diet consisting of concentrate (1.1% of body weight/day) and oat hay (1 kg/day) on an as-fed basis. The treatment group received an additional 150 g/day of sucrose on an as-fed basis. High gMS groups exhibited greater ($p < 0.01$) body weight than low gMS groups, whereas sucrose had no effect. Average daily gain, dry matter intake, and feed efficiency remained unaffected by either factor. Sucrose treatment tended ($p = 0.05$) to decrease ruminal iso-butyric acid, while other VFAs and ammonia were not influenced. While the high gMS groups exhibited higher ($p < 0.01$) plasma free fatty acid, other plasma metabolites and hormones were not affected by gMS or sucrose. Most meat quality traits were influenced ($P < 0.05$) by gMS. Notably, a tendency for an interaction ($p = 0.06$) and a significant ($p < 0.01$) gMS effect were observed for eye muscle area. These findings confirm genetic potential as the primary driver of economically important traits in Hanwoo.

Key words : Hanwoo, genomic estimated breeding value (gEBV), sucrose, growth performance, carcass trait

PB26032

Distinct effects of oleic and palmitic acid on intramyocellular lipid accumulation in bovine myotubes under heat stress

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Intramyocellular lipid (IMCL) in skeletal muscle serves as an energy reservoir and contributes to intramuscular fat deposition and metabolic flexibility. This study evaluated the effects of oleic acid (OA) and palmitic acid (PA) on IMCL accumulation, and on myogenic and lipogenic responses, in bovine myotubes under thermoneutral (TN; 38°C) and HS (41°C) conditions. We hypothesized that OA would promote greater IMCL accumulation than PA under HS. Myotubes were treated with 100 μM OA, PA, or BSA (vehicle control) under TN or HS for 48 h. Gene expression (RT-qPCR), protein abundance (Western blot), IMCL content (immunofluorescence), and mtDNA copy number were analyzed by two-way ANOVA with Šidák post hoc correction ($p < 0.05$). *MYH7*, *PGC-1α*, *PPARγ*, *FAS*, and *SCD* mRNA showed treatment × temperature interactions ($p < 0.05$); PA upregulated these genes under TN, but the responses were attenuated under HS. *MYOD* and *MYOG* mRNA increased under HS as a main effect ($p < 0.01$). At the protein level, PA did not increase FAS or PPARγ, and mtDNA copy number was unaffected. SCD protein was greatest in OA- and PA-treated cells under TN and decreased under HS ($p = 0.01$). IMCL accumulation showed main effects of treatment and temperature ($p < 0.01$) without an interaction ($p = 0.15$); OA-treated cells accumulated more IMCL than PA-treated cells at both temperatures, despite the elevated lipogenic mRNA in PA-treated cells. Although PA activated lipogenic transcription, OA more effectively promoted IMCL accumulation in bovine myotubes, indicating that OA is a more effective substrate for intramuscular lipid deposition, including under heat stress.

Key words : bovine myotube, heat stress, intramyocellular lipid, oleic acid, palmitic acid

PB26033

Effects of glycerol monolaurate supplementation on growth performance, blood metabolites, and disease incidence in Hanwoo and Holstein calves

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This study was conducted to evaluate the effects of glycerol monolaurate (GML) supplementation on growth performance, blood metabolites, and disease incidence in Hanwoo and dairy calves. A total of 49 Hanwoo calves (27 calves without artificial colostrum, 10 calves fed artificial colostrum, and 12 calves fed artificial colostrum supplemented with 0.1% GML) and 40 dairy calves (20 calves fed milk replacer and 20 calves fed milk replacer supplemented with 0.1% GML) were used in the experiment. Although no significant differences were observed in average daily gain (ADG) of Hanwoo calves, ADG tended to increase numerically with artificial colostrum and GML supplementation. In dairy calves, body weight and ADG were significantly increased in the milk replacer+GML treatment group ($p < 0.05$). No significant effects of treatment were observed on blood metabolites in Hanwoo calves; however, most parameters were significantly affected by sampling time ($p < 0.05$). Immunoglobulin concentrations were not significantly different among treatments at any sampling time, but numerically increased in response to GML supplementation. The proportion of prolonged diarrhea was lower in the GML-supplemented groups. Therefore, GML supplementation may improve immune status in young calves, thereby reducing the persistence of diarrhea and improving growth performance.

Key words : Hanwoo calf, Holstein calf, glycerol monolaurate, immune status, blood metabolites, IgG, growth performance, diarrhea

PB26034

Effects of different injection levels of vitamins A, D_3, and E on blood metabolites and growth- and adipogenesis-related gene expression in Hanwoo calves

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This study investigated the effects of different injection levels of vitamins A, D_3, and E on growth performance, blood metabolites, and growth- and adipogenesis-related gene expression in Hanwoo calves. Twenty-two calves were assigned to four groups: control (no injection, n = 6), T1 (vitamin A 300,000 IU, vitamin D_3 100,000 IU, vitamin E 50 mg; n = 6), T2 (vitamin A 600,000 IU, vitamin D_3 200,000 IU, vitamin E 100 mg; n = 5), and T3 (vitamin A 900,000 IU, vitamin D_3 300,000 IU, vitamin E 150 mg; n = 5). Vitamin injections did not significantly affect growth performance. Total protein concentration at 1 month was lower in T3 than in the control group ($p < 0.05$), while triglyceride concentration at 3 months was higher in T2 ($p < 0.05$). Serum leptin concentration at 6 months decreased as vitamin A injection levels increased ($p < 0.05$), whereas insulin concentration was not affected. Gene expression analysis showed that MYOG and PAX7 expression levels were lower in T3 and T2, respectively ($p < 0.05$). FABP3 and PDGFRA expression levels were higher in the treatment groups, whereas KLF2, STAT6, and VEGFA expression levels were lower compared with the control group ($p < 0.05$). These results suggest that early administration of vitamins A, D_3, and E may influence lipid metabolism and energy metabolism-related physiological mechanisms in Hanwoo calves.

Key words : vitamin A, D_3, and E administration, growth performance, fat-related genes, Hanwoo calves.

PB26035

Effects of vitamins A, D_3, and E injection at birth on growth and expression of genes related to adipogenesis and angiogenesis across different feeding stages in Hanwoo steers

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This study investigated the effects of neonatal injection of vitamins A, D_3, and E on the expression of growth-, adipogenesis-, and angiogenesis-related genes during different growth stages in Hanwoo steers. Eighteen calves were assigned to either a control group (n = 9) or a treatment group injected with vitamin A (300,000 IU), vitamin D_3 (100,000 IU), and vitamin E (50 mg) at birth (n = 9). In the treatment group, the expression of growth-related genes, including MYF5, MYOG, PAX3, and PGC1A, and adipogenesis-related genes, including ACACA, FABP3, SREBF1, and ZNF423, significantly changed according to growth stage ($p < 0.05$). In particular, MYF5, MYOG, ACACA, and FABP3 expression levels were higher during the early and late fattening stages than during the growing stage, whereas PAX3 expression gradually increased as growth stage progressed ($p < 0.001$). In addition, PPARA expression was significantly higher in the treatment group than in the control group during the growing stage ($p < 0.05$). Overall, the expression of growth-, adipogenesis-, and angiogenesis-related genes changed according to growth stage, whereas treatment effects were limited. These findings suggest that neonatal vitamin administration may be associated with stage-dependent metabolic and developmental regulation in Hanwoo steers.

Key words : vitamin A, D_3, and E administration, growth stage, adipogenesis-related genes, Hanwoo calves.

PB26036

한우 미경산우의 성성숙 개시 시기 및 생리적 변화 평가

조현진, 정신용, 강계원, 전서영, 이민경, 강하민, 서성원

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본 연구는 한우 미경산우의 성성숙 개시 시기와 이와 관련된 체중, 체형, 호르몬(에스트로겐, 프로게스테론, IGF-1, 렙틴)의 변화를 평가하고자 수행되었다. 육성기 한우 미경산우 30두(281 ± 23.2 kg; 9개월령)를 공시하고, 체중이 유사한 2두씩 1개 우방(5 m × 5 m)에 배치하였다. 모든 동물에게 9개월령부터 한달간 동일한 섬유질배합사료를 급여하였으며, 10개월 이후에는 조사료와 배합사료의 비율 및 중성세제불용섬유소의 사료원에 차이가 있는 3종류의 완전혼합사료 중 하나를 급여하였다. 사료는 개체별 섭취량을 측정할 수 있는 사료조에 1일 2회(0800, 1800) 직접 급여하여 자유채식토록 하였다. 섭취량은 매일 수집하였으며, 체중 및 체형 측정과 혈액 채취는 4주 간격으로 실시하였다. 채취한 혈액에서 혈청을 분리하여 효소결합면역흡착검사를 통해 호르몬 농도를 분석하였다. 성성숙은 초음파로 측정한 난소 크기 및 구조물(난포 크기 및 황체 유무)을 기반으로 산출한 생식기 점수(reproductive tract score, RTS)를 통해 매주 평가하였다. 체고를 제외한 체중 및 체형(흉위, 배둘레, 체장)은 월령이 지남에 따라 유의적으로 증가하였다($p < 0.05$). 에스트로겐 및 IGF-1의 농도는 월령이 증가함에 따라 유의적으로 감소하였으며($p < 0.05$), 프로게스테론 농도는 월령에 따른 유의적인 차이가 없었다($p > 0.05$). 렙틴 농도는 월령이 증가함에 따라 유의적으로 증가하였다($p < 0.05$). RTS는 9개월령 3.2점에서 10개월령 4.3점, 11개월령 4.7점으로 유의하게 증가하였으며($p < 0.05$), 10개월령에 성성숙 도달 기준인 4점 이상을 충족하였다. 결론적으로 한우 미경산우는 10개월령 이전, 체중 282–298 kg 정도에서 성성숙에 도달하였다.

Key words : 성성숙, 체중, 체형, IGF-1, 렙틴, 한우

PB26037

Effects of alfalfa produced in Korea at different inclusion levels in TMR on rumen fermentation and methane production *in vitro*

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This study was conducted to evaluate the effects of different inclusion levels of domestically produced alfalfa in total mixed ration (TMR) (0%, 13%, and 27% on a dry matter basis) on rumen fermentation characteristics *in vitro*. Total gas production (TGP) differed significantly among treatments at all incubation times (12, 24, and 48 h; $p < 0.05$), with values of 110.66, 144.66, and 171.94 mL/g DM, respectively. Methane production in the 27% alfalfa treatment was 17.51, 25.56, and 36.33 mL/g DM at 12, 24, and 48 h, respectively, representing an increase of 28–51% compared to the 0% alfalfa treatment. At the end of incubation (48 h), ruminal pH was 6.59 across all treatments, indicating that a stable environment for microbial activity was maintained. Ammonia nitrogen (NH_3-N) concentrations were 173.8, 149.3, and 217.4 mg/dL for the 0%, 13%, and 27% alfalfa treatments, respectively, with no significant differences among treatments. *In vitro* dry matter digestibility (IVDMD) increased significantly ($p < 0.05$) with increasing alfalfa inclusion levels, with values of 71.88%, 76.00%, and 79.66% for the 0%, 13%, and 27% treatments, respectively. The increases in TGP and IVDMD with higher alfalfa inclusion levels suggest enhanced availability of fermentable substrates for rumen microbes. The relatively high digestibility and readily fermentable components of alfalfa may have contributed to the increased fermentation rate.

Key words : Hanwoo, alfalfa, total mixed ration (TMR), rumen fermentation, *in vitro* dry matter digestibility (IVDMD)

PB26038

Comparison of DNA, PMA-treated DNA, and RNA-based rumen microbial profiles in Hanwoo steers fed low-protein diets

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This study evaluated the effects of a low-protein diet during the late fattening period of Hanwoo steers and compared rumen microbial profiles derived from total DNA (tDNA), Propidium monoazide-treated DNA (vDNA), and RNA. Hanwoo steers (n = 6; 26 months of age) were assigned to either a control diet (CON, 17.2% CP; n = 3; 793 ± 91 kg) or a low-protein treatment diet (TRT, 14.9% CP; n = 3; 748 ± 56 kg) and were fed under the same housing and management conditions until 30 months of age. Growth performance, carcass characteristics, and rumen microbial communities were assessed to evaluate the effects of dietary protein level and nucleic acid source. Feeding a low-protein diet did not markedly affect growth performance or carcass characteristics. Although dietary treatment influenced overall rumen microbial community structure, its effects on individual genera were limited, suggesting a modest impact on taxonomic composition under the present conditions. In contrast, differences according to nucleic acid type were more apparent, indicating that the choice of nucleic acid source can influence the interpretation of rumen microbiota. These findings suggest that a low-protein diet during late fattening may be feasible in Hanwoo steers, while nucleic acid source should be carefully considered in rumen microbiome analysis.

Key words : Hanwoo steer, low-protein, average daily gain, feed conversion ratio, carcass traits, propidium monoazide, deoxyribonucleic acid, ribonucleic acid, microbiome, alpha diversity, beta diversity

PB26039

Imported alfalfa at two feeding levels: impacts on nutrient utilization and body conformation in female and male crossbred goats

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This study evaluated the effects of two feeding levels (1.5 and 2.0% BW) of alfalfa from abroad on growth performance, nutrient utilization, and body conformation in female and male crossbred goats (Boer × Korean native, *Capra hircus*). Twenty-four goats (12 females and 12 males; initial body weight 39.4 ± 1.1 kg for females and 38.0 ± 1.4 kg for males) were used in a 4 × 4 Latin square design with four dietary treatments over four 4-week periods (total 16 weeks).

Males showed higher dry matter intake at the high feeding level (2.0% BW), reaching the highest value among all groups ($p = 0.0003$). Females recorded higher final body weight and body weight gain at the low feeding level (1.5% BW), with the highest body weight gain observed in females fed 1.5% imported alfalfa. Nutrient intake (dry matter, organic matter, crude protein, crude fiber, ADF, and NDF) was generally higher in the high feeding level groups, particularly in males. Digestibility of most nutrients tended to be higher in females at the low feeding level, with crude protein digestibility reaching its highest value in females fed 2.0% BW.

Body conformation measurements, including body length, withers height, chest width, and chest girth, were numerically higher in the high feeding level groups for both genders, though differences remained modest.

Therefore, the results indicate that imported alfalfa at 1.5–2.0% of body weight supported good growth and nutrient utilization in both female and male crossbred goats. However, females performed better in body weight gain and nutrient digestibility at lower feeding levels, while males showed higher nutrient intake at the high feeding level, suggesting gender-specific responses to imported alfalfa feeding levels.

Key words : imported alfalfa, crossbred goats, feeding level, gender difference, nutrient utilization, body conformation

PB26040

Effect of TMR feeding compared to conventional feeding during the performance testing period of growing Hanwoo bull

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Residual Feed Intake (RFI) is a key economic trait in Hanwoo. However, measuring intake in ruminants is often challenging when concentrate and forage are fed separately, as it requires individual monitoring of both components. This study was conducted to compare the effects of conventional feeding (separate supply of concentrate and forage) and Total Mixed Ration (TMR) feeding on feed efficiency and performance during the growing period. Twenty growing Hanwoo bulls were assigned to either a conventional feeding group (n = 10) or a TMR feeding group (n = 10). Initial body weights for the conventional and TMR groups were 250.7 ± 29.0 kg and 259.6 ± 18.3 kg, respectively. The Total Digestible Nutrients (TDN) content was 73.99% for concentrate, 55.71% for forage, and 63.25% for TMR. The results showed that metabolic body weight was 69.9 ± 5.9 kg for the conventional group and 73.3 ± 4.0 kg for the TMR group, while TDN intake was 358.1 ± 40.1 kg and 406.5 ± 33.1 kg, respectively. No significant differences were observed between the two groups in actual feed intake (5.190±0.581 vs. 5.891±0.480 kg) or predicted feed intake (5.362±0.565 vs. 5.712±0.337 kg). The RFI values were analyzed as –0.172±0.350 kg for the conventional group and 0.173±0.347 kg for the TMR group. Overall, no statistical significance was found across all traits ($p > 0.05$). These findings suggest that TMR feeding provides a level of testing accuracy equivalent to conventional methods while significantly enhancing the convenience and efficiency of intake data collection during Hanwoo performance testing.

Key words : feed efficiency, residual feed intake (RFI), conventional feeding, total mixed ration (TMR) feeding, Hanwoo

PB26041

Evaluation of carcass and meat quality traits under methane-mitigation feeding strategies

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This study was conducted to evaluate the effects of methane-mitigation feeding strategies on carcass characteristics and meat quality traits in beef cattle under commercial production conditions. A total of 542 animals were analyzed after excluding cattle older than 45 months at slaughter. Animals were classified into three feeding groups: conventional feeding (n = 109), synthetic compound-based methane-mitigating feed additive supplementation (n = 145), and plant-based methane-mitigating feed additive supplementation (n = 288). In addition, exploratory analyses were performed according to supplementation duration within methane-mitigating feeding groups. The evaluated traits included carcass weight, backfat thickness, loin area, yield index, and marbling score. The synthetic compound-based methane-mitigating feed additive group showed average marbling score, loin area, and carcass weight values of 6.90, 98.71 cm^2, and 464.57 kg, respectively, whereas the plant-based methane-mitigating feed additive group showed values of 6.28, 93.66 cm^2, and 435.81 kg, and the conventional feeding group showed values of 5.71, 91.44 cm^2, and 427.61 kg, respectively ($p < 0.05$). In contrast, yield index did not show substantial differences among feeding groups. Furthermore, long-term supplementation of methane-mitigating feed additives did not show detrimental effects on carcass or meat quality traits under field production conditions.

Key words : beef cattle, low-carbon livestock production, meat quality, methane-mitigating feed

PB26042

Effects of hot water-extracted plant materials on *in vitro* ruminal fermentation and methane production

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This study investigated the effects of hot water-extracted plant materials on *in vitro* ruminal fermentation and methane (CH_4) production. Hot water extract was prepared by extracting 10 g of plants sample with 200 mL distilled water at 90°C for 2 h while stirring at 400 rpm. The extract was cooled for 5 min, centrifuged at 4,500 rpm for 22 min at 4°C, and concentrated using a rotary evaporator at 65°C and 100 rpm. The substrate was prepared at a 3:7 concentrate-to-forage ratio on a dry matter (DM) basis and incubated with rumen fluid and McDougall's buffer at 39°C and 110 rpm for 24 and 48 h. Treatments consisted of CON (control), turmeric at 0.5% and 1.0%, chrysanthemum at 0.5% and 1.0%, deodeok at 0.5% and 1.0%, and Dunggulle at 1.0%. At 24 h, total gas production did not differ among treatments (p = 0.0612), although Dunggulle 1.0% showed a was numerically lower than that of CON (44.25 and 52.00 mL, respectively). *In vitro* dry matter digestibility (IVDMD), CH_4 concentration, and CH_4 production did not differ among treatments at 24 h ($p > 0.05$). However, CH_4 production per g digested DM was significantly lower in Dunggulle 1.0% than in CON (p = 0.0305). The values were 15.40 and 17.56 mL/g digested DM, respectively, corresponding to a 12.3% reduction. These results indicate that Dunggulle 1.0% reduced methane production per g digested DM after 24 h of *in vitro* ruminal incubation without decreasing IVDMD, but this effect was not observed after 48 h.

Key words : hot water-extract, *in vitro*, methane, plant, rumen fermentation

PB26043

Impact of heat stress on metabolic changes and the effects of heat-treated fermented soybean meal supplementation on lactation performance in Holstein cows under heat stress environmental condition

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Heat stress induces abnormal metabolism and impairs lactation performance in dairy cows. This study aimed to understand heat stress-induced metabolic alterations and evaluate a potential dietary mitigation strategy. The metabolomic analysis revealed severe disruptions in both carbohydrate and amino acid metabolism by heat stress. We evaluated heat-treated fermented soybean meal (HFSBM) as a targeted nutritional intervention to recover protein metabolism in heat stressed dairy cows. HFSBM was produced by fermenting soybean meal (SBM) with *Enterococcus faecium* (EF) and *Lactobacillus plantarum* (LP), followed by heating at 130°C. Nutritional evaluation confirmed that HFSBM possessed higher crude protein and amino acid contents than raw SBM. *In vitro* rumen fermentation assays demonstrated that HFSBM significantly enhanced digestibility and propionate production while decreasing ammonia nitrogen levels compared to SBM. To assess *in vivo* efficacy, a field trial was conducted where heat-stressed dairy cows were fed a TMR supplemented with 0.1% HFSBM for two weeks. Although heat stress dramatically depressed overall milk production, dietary supplementation with HFSBM significantly increased the average daily milk yield by 1.3 kg/day. In conclusion, HFSBM supplementation is an effective nutritional management strategy to counteract metabolic abnormalities and improve productivity in heat-stressed dairy cows.

Key words : by-pass protein, fermented soybean meal, heat stress, Holsteins, metabolites

PB26044

Effects of creatinolfosfate supplementation level on *in vitro* rumen fermentation characteristics and methane production

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This study evaluated the effects of different inclusion levels of Creatinolfosfate (CRE) on *in vitro* ruminal fermentation characteristics and methane production. An *in vitro* batch culture system was used in which rumen fluid was incubated for 24 and 48 h with the following treatments: a negative control without additives, a positive control containing 120 ppm of 3-nitrooxypropanol, and CRE supplemented at 480, 600, and 720 ppm. After 48 h of incubation, total gas production and methane production decreased linearly with increasing CRE supplementation levels. In addition, acetate concentration decreased, whereas propionate concentration increased linearly as CRE inclusion levels increased, suggesting a shift in ruminal fermentation patterns. The greatest reduction in methane production was observed at 720 ppm, indicating a dose-dependent inhibitory effect on methanogenesis. However, dry matter digestibility and ammonia nitrogen concentration were not affected by CRE supplementation. These results suggest that CRE has the potential to mitigate ruminal methane emissions without negatively affecting nutrient digestibility under the conditions of the present study. Further *in vivo* studies are required to evaluate the efficacy, safety, and long-term applicability of CRE supplementation in practical ruminant production systems.

Key words : ruminant, methane, rumen fermentation, creatinolfosfate

PB26045

Effects of synbiotics-based FTMR on rumen fermentation and host metabolism in ruminants

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Methane emissions from ruminants are a major environmental concern. In this study, a synbiotics-based fermented total mixed ration (FTMR) was developed using *Komagataeibacter intermedius* and *Zygosaccharomyces parabailii* (KZ). Genome-scale metabolic model analysis identified selective prebiotic candidates that enhanced KZ growth and showed methane-reducing potential. To evaluate its effects, in vitro rumen fermentation and in vivo feeding were conducted. Although methane reduction was not statistically significant, FTMR improved digestibility and reduced ammonia production. qNMR-based metabolomic analyses revealed distinct metabolic alterations in rumen fluid and blood after FTMR feeding. In rumen fluid, methanogenesis-associated metabolites including formate and methylamine-related compounds decreased, whereas metabolites related to substrate utilization and microbial activity increased. Blood metabolomic profiles showed increased creatine, creatinine and antioxidant-related metabolites, indicating improved energy metabolism and physiological stability. In contrast, trimethylamine N-oxide, associated metabolic imbalance, decreased following FTMR supplementation. Overall, synbiotics-based FTMR modulated rumen microbial metabolism and host metabolic responses, suggesting its potential as a strategy through coordinated modulation of rumen microbial metabolism and host metabolic responses.

Key words : synbiotics, FTMR, metabolomics

PB26046

Effects of *Bjerkandera adusta* on *in vitro* rumen fermentation and methane production

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Methane produced during enteric fermentation in ruminants is recognized as a major contributor to agricultural greenhouse gas emissions and represents a loss of dietary energy. This study aimed to evaluate the effects of *Bjerkandera adusta* on *in vitro* rumen fermentation and methane production. Rumen fluid was collected from three Hanwoo cattle for the *in vitro* incubation. To prepare the incubation medium, rumen fluid was mixed with McDougall's buffer at a 1:2 ratio. A diet with a concentrate-to-forage ratio of 8:2 was used as the basic substrate. *B. adusta* were supplemented at 0% (control), 1%, 3%, and 5% of the substrate. After 24 h incubation at 39°C, *in vitro* dry matter digestibility was significantly greater in all supplementation groups than in the control group ($p < 0.05$), whereas pH was not affected by supplementation ($p > 0.05$). Methane production (mL/g DM) was significantly reduced in both the 3% and 5% supplemented groups compared with the control group ($p < 0.05$). These findings suggest that the supplementation of *B. adusta* may serve as a potential feed additive for methane mitigation in ruminants while maintaining stable rumen fermentation and improving feed digestibility.

Key words : Hanwoo cattle, rumen fermentation, methane production, *Bjerkandera adusta*

PB26047

The effects of additional pressure processing of lupin flake on protein degradation characteristics

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Lupin imports have shown an increasing trend over the past decade in Korea. Lupin has high crude protein (CP) and energy content, it can used in livestock diets. However, lupin contains a high proportion of rumen degradable protein (RDP), resulting in rapid degrdation within the rumen and reduced protein utilization by the host animal. The processing methods like heat and flaking were applied to modulate protein degradability of grain, also physical press affect protein denaturation. This study aimed to evaluate the effects in *in situ* degradability of additional pressure processing of lupin flake . In the experiment, three treatments were evaluated: CON (control, no processing), lupin flake (LF, heated at 110°C for 900 s), lupin flake with press (LFP, heated at 110°C for 900 s, pressurized). All *in situ* experiments were conducted using two cannulated Hanwoo cattle for 120 h. Degradability was measured at 0, 3, 6, 12, 24, 48, 72, 96, and 120 h. In the dry matter fractional value, soluble fraction (A fraction) was higher in LF than CON ($p < 0.05$). The potentially degradable fraction (B fraction; % CP) was lower in the LF than CON ($p < 0.05$). There was no significant difference between CON and LF in rumen undegradable protein (RUP; % CP) ($p > 0.05$). As a result of additional pressure treament, B fraction (% CP) was highest in LFP ($p < 0.0001$). RUP (% CP) was higher in LFP than LF ($p < 0.05$), also $\mathrm{MP}_{\mathrm{feed}}$ (% CP) was higher in LFP than LF ($p < 0.05$). In conclusion, an additional pressure treatment of lupin flake can increase the proportion of $\mathrm{MP}_{\mathrm{feed}}$ by increasing RUP proportion of lupin thereby improving protein availability of the ruminant.

Key words : feed evaluation, lupin flake, rumen degradability, metabolizable protein, *in situ*

PB26048

Analysis of genomic estimated breeding value (GEBV) application based on growth traits in Hanwoo steers

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This study was conducted to evaluate the potential of Genomic Estimated Breeding Values (GEBV) for predicting growth and carcass traits using genomic and feeding management data from Hanwoo farms. Genomic information from 199 newborn calves raised on three Hanwoo farms was analyzed. Hanwoo 50K SNP markers were used for individual identification and estimation of carcass weight (CW)-related GEBV. The results showed that birth weight ($p < 0.05$) and carcass weight ($p > 0.05$) were higher in the high-GEBV group, indicating the potential of genomic information for predicting growth-related traits. These differences became more distinct when comparing the upper and lower 25% groups ($p > 0.05$). In contrast, weaning weight and several carcass traits were strongly influenced by farm-specific feeding environments and management systems. Furthermore, genomic prediction accuracy was higher in integrated breeding farms with well-established genetic improvement programs, whereas lower accuracy was observed in feedlot farms with limited pedigree information. In conclusion, CW-related GEBV showed considerable potential for predicting growth traits in Hanwoo cattle and could be effectively applied to farm-level precision breeding programs.

Key words : genomic estimated breeding value (GEBV), carcass weight, Hanwoo steers

PB26049

Integrative metagenomic characterization of the bovine colostrum virome and candidate bacteria-virus interactions

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Bovine colostrum is essential for neonatal calf adaptation, yet its viral community and host-associated interactions remain poorly understood. This study characterized the colostrum-associated virome and candidate host–virus linkages using shotgun metagenomic data from 44 postpartum colostrum samples collected from 7 Holstein and 4 Jersey cows at 0 h, 12 h, 24 h, and 5 d postpartum. Host-unmapped reads were co-assembled, and viral contigs were identified using VirSorter2, followed by CheckV-based quality assessment and geNomad, VIBRANT, and DRAM-v annotation. Bacterial metagenome-assembled genomes (MAGs) were reconstructed, classified using GTDB-Tk, and quantified with viral contigs using CoverM. Candidate host–virus association were evaluated by integrating iPHoP-based host prediction, MAG taxonomy, and co-variation analysis. Among 1,315 candidate viral contigs, six core *Caudoviricetes* contigs were selected, including one *Enterococcus*-linked contig that showed a nominally significant positive co-variation with an *Enterococcus* B lactis MAG (Spearman $p < 0.05$). Functional annotation detected putative nucleotide metabolism-related genes, including dUTPase and thymidylate synthase, in two core contigs. Temporal patterns were more pronounced in viral or integrated MAG-viral profiles, particularly in Holstein samples, whereas Holstein–Jersey differences were mainly reflected in MAG abundance profiles. These findings provide a framework for bovine colostrum virome analysis and suggest that phage-bacterial host interactions may be associated with temporal restructuring of the colostrum microbial ecosystem.

Key words : bovine colostrum, virome, metagenomics, host-virus linkage, MAG, *Caudoviricetes*, dairy cow

PB26050

Effects of enzyme, probiotic supplementation and fermentation period on the fermentation characteristics and quality of total mixed ration under summer temperature conditions

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This study investigated the effects of fermentation conditions on the quality of the fermented total mixed ration (TMRf) at 27°C, simulating summer conditions on a farm in South Korea. A 3 (probiotics level: Low 0.05%, Medium 0.1% and High 0.2%) × 2 (enzyme supplementation: 0.05% or non-supplemented) × 4 (fermentation period: 3, 7, 14 and 28 days) factorial design with 3 replicates per treatment was used in this study. The probiotic complex consisted of *Lactobacillus plantarum* and *Saccharomyces cerevisiae* (10^8 colony-forming units (CFU)/mL). The enzyme treatment included a commercial mixture (cellulase, amylase and protease). As fermentation progressed, pH and ammonia-N decreased, while total volatile fatty acids (VFA) and acetate increased ($p < 0.001$). Lactic acid bacteria enumeration significantly declined from 9.07 log CFU/mL at day 3 to 6.68 log CFU/mL at day 28. In addition to time-dependent effects, probiotic concentration and enzyme treatment showed significant main effects and two-way interactions on pH, ammonia-N and total VFA ($p < 0.05$). Probiotics significantly influenced dry matter, crude ash (CA) and neutral detergent fiber (NDF), while enzymes affected CA, crude fiber and NDF ($p < 0.05$). Notably, butyrate was not detected in any treatment, indicating stable fermentation without clostridial putrefaction. These findings suggest that probiotic concentration, enzyme application and fermentation period are critical factors for optimizing TMRf production.

Key words : TMRf, probiotics, enzyme, fermentation period, summer conditions

PB26051

Effects of carcass weight genomic estimated breeding values (GEBV) on productivity and carbon reduction in Hanwoo steers

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This study evaluated the effects of carcass weight-related Genomic Estimated Breeding Values (GEBV) on productivity, carcass traits, and carbon reduction potential in Hanwoo steers. Genomic information from Hanwoo cattle raised on five farms was analyzed using the Hanwoo 50K SNP chip, and animals were classified into high (Bv H) and low (Bv L) GEBV groups. Growth performance, carcass characteristics, and economic traits were compared according to farm and GEBV group.

The high-GEBV group showed greater carcass weight than the low-GEBV group across most farms, indicating the usefulness of GEBV for predicting growth performance ($p > 0.05$). However, marbling score tended to decrease in the high-growth group, suggesting a trade-off between growth and meat quality traits. Despite lower carcass prices associated with reduced marbling, total income was maintained due to increased carcass weight. Furthermore, the high genomic breeding value group demonstrated a 4.6% reduction in carbon emissions per unit of production, showing positive results in terms of production efficiency and environmental sustainability. In conclusion, carcass weight-related GEBV may be effectively applied to improve growth performance and reduce carbon emissions in Hanwoo production systems. However, balanced breeding strategies considering both growth and meat quality traits are necessary to maximize farm profitability.

Key words : genomic estimated breeding value (GEBV), carcass weight, carbon reduction effects, Hanwoo steer

PB26052

Storage stability of glucose and ketone in blood samples from Korean native cattle

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Accurate measurement of blood glucose and ketone concentrations is important for evaluating energy metabolism and diagnosing metabolic disorders in cattle. However, delayed sample processing after blood collection may affect analytical results due to ongoing cellular metabolism and changes in sample stability. Under field conditions, there is often a delay between blood sample collection and laboratory analysis, and storage conditions during this period may affect the measured values. This study evaluated the storage stability of glucose and ketone concentrations in serum and whole blood samples from Hanwoo cattle. Materials and Methods: Blood samples were collected from clinically healthy Hanwoo cattle and divided into serum and whole blood samples using serum separator tubes and anticoagulant tubes. Samples were stored under room-temperature (20–25°C) and refrigerated (4°C) conditions. Glucose and ketone concentrations were measured at 0, 1, 2, 4, 6, 8, 12, and 24 h after blood collection. The measured values were statistically analyzed to evaluate the effects of sample type and storage condition over time. Results: Glucose concentrations in serum samples stored at room temperature decreased from 74.5 mg/dL at 0 h to 39.2 mg/dL at 6 h, whereas refrigerated samples showed a smaller decrease from 74.5 mg/dL to 62.8 mg/dL during the same period. In contrast, there were no significant differences in ketone concentrations between room-temperature and refrigerated storage conditions. Conclusions: The results of this study indicate that storage conditions and elapsed time after blood collection significantly affect glucose concentrations in Hanwoo blood samples, whereas ketone concentrations remain relatively stable. Immediate refrigeration and rapid serum separation following blood collection are recommended to minimize analytical errors. These findings provide useful information for establishing standardized sample handling procedures for metabolic profile testing in Hanwoo cattle.

Key words : Korean native cattle, blood glucose, ketone

PB26053

Effects of a microcurrent-generating mineral mixture on ruminal nitrogen utilization and microbial composition *in vitro*

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This study evaluated the effects of a microcurrent-generating mineral mixture (MC) on ruminal fermentation, nitrogen utilization, and microbial composition *in vitro*. Batch cultures were incubated for 6 h (n = 5), and microbial crude protein (MCP), NH_3-N, total gas production, volatile fatty acids (VFA), and pH were measured. Microbial composition was analyzed by 16S rRNA gene V3–V4 region sequencing. MC increased MCP and decreased NH_3-N concentrations ($p = 0.001$ and $p = 0.049$, respectively), with no significant changes in VFA profiles, total gas production, or pH ($p > 0.05$). Richness and overall diversity were unchanged, whereas Pielou's evenness and Simpson diversity increased with MC ($p = 0.010$ and $p = 0.028$, respectively). Weighted and unweighted UniFrac distances showed significant community separation ($p = 0.036$ and $p = 0.019$, respectively), whereas Bray–Curtis dissimilarity was unchanged. Differential abundance analysis showed enrichment of Prevotellaceae_UCG.003 ($q = 0.033$) and depletion of *Olsenella* and *Anaerobutyricum* ($q = 0.022$ for both) under MC. Functional beta diversity of predicted pathways was unchanged, but differential pathway abundance analysis indicated reduced upstream carbohydrate metabolism and enrichment of downstream carbon-routing, cofactor-, and vitamin-related pathways. These results suggest that MC may shift ruminal nitrogen utilization toward microbial biomass formation without increasing overall fermentation output or inducing broad community turnover.

Key words : rumen, microcurrent, nitrogen utilization, microbial crude protein, 16S rRNA sequencing

PB26054

Longitudinal fecal microbiota dynamics in Holstein calves and comparative analysis between Holstein and Jersey breeds

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This study investigated the developmental dynamics of the fecal microbiota in calves, focusing on age-related succession, weaning-associated transitions, and breed-related differences between Holstein and Jersey calves. In Holstein calves, both richness and evenness increased with age, and the overall microbial community underwent marked temporal shifts before 12 weeks, followed by relative stabilization. Multivariable association analysis showed that age was associated with increases in putatively plant polysaccharide-associated genera including *Treponema*, *Monoglobus*, and *Alistipes,* whereas early-life-associated genera such as *Bifidobacterium, Parabacteroides*, and *Faecalibacterium* decreased. Weaning was linked to additional taxonomic reorganization, with postweaning increases in Spirochaetaceae, Monoglobaceae, *Akkermansia*, and *Monoglobus* and decreases in Bacteroidaceae, Enterobacteriaceae, Bifidobacteriaceae, *Parabacteroides*, *Megasphaera*, and *Faecalibacterium*. Functional prediction suggested that postweaning microbial communities were enriched in pathways related to bacterial chemotaxis, flagellar assembly, and genetic information processing. Breed-related differences were comparatively limited, although Holstein calves showed higher richness and evenness than Jersey calves at several postweaning time points and distinct temporal developmental patterns in beta diversity. Together, Holstein calves showed pronounced age-dependent microbial maturation and marked transition across weaning toward a more mature, fermentation-oriented intestinal ecosystem, whereas breed-related differences mainly involved specific microbial groups rather than broad taxonomic differences.

Key words : dairy cows, breed differences, fecal microbiota, early-life microbiota, weaning, temporal microbial succession

PB26055

대용유 급여 횟수가 한우 송아지의 성장성적에 미치는 영향

김호연, 신지호, 강유진, 임진현, 김태호, 김동연, 권원서, 최한빈, 최용준*

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본 연구는 대용유 급여 횟수가 한우 송아지의 성장 성적, 설사발생률 및 혈액 성상에 미치는 영향을 규명하기 위해 수행하였다. 본 연구에서는 한우 송아지 18두(30.51 ± 3.31 kg; 암수 각 9두)를 공시하여 개별 팬에서 사육하였으며, 30일간 실험을 진행하였다. 본 연구는 15% 농도로 희석한 대용유를 모든 송아지에게 체중의 30%를 처리구별로 2회, 4회, 6회로 분할하여 30일간 급여하였다. 2회 급여 처리구는 06시와 18시에 4회급여 처리구는 6, 11, 16 및 21시에 6회 급여 처리구는 6, 9, 12, 15 18 및 21시에 대용유를 급여하였다. 실험 기간 동안 10일 간격으로 체중, 흉위를 측정하였고, 혈액을 채취하여 일반혈액성분 및 혈중 대사물질을 분석하였으며, 사료 섭취량은 매일 1회 측정하였다. 실험 결과, 총 건물 섭취량, 사료 요구율, 일반 혈액 성분 및 대사 지표는 급여 횟수에 따른 유의적인 차이를 나타내지 않았다. 반면, 증체량과 일당증체량은 대용유 급여 횟수가 증가함에 따라 유의하게 증가하였으며(p = 0.001), 설사 발생 빈도는 1일 6회 처리구에서 2회 및 4회 급여 처리구 대비 증가하는 경향이 나타났다(p = 0.097). 결과적으로 한우 송아지에게 다량의 대용유를 급여할 경우, 급여횟수를 늘릴수록 성장에 긍정적인 효과가 있으나, 설사발생률을 고려할 때 1일 4회 급여가 성장성적과 설사 예방 측면에서 가장 적합한 것으로 판단된다. 본 연구의 결과는 송아지에서 자동포유기를 활용한 대용유 인공포유시 일일 급여횟수를 설정하는데 기초자료로 활용할 수 있을 것으로 사료된다.

Key words : 한우 송아지, 대용유 급여 횟수, 성장성적, 설사발생률, 인공포유

PB26056

Effects of feeding system on growth performance and velvet antler productivity in deer

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This study was conducted to evaluate the effects of feeding systems on growth performance and velvet antler productivity in deer during the antler growth period. Ten deer were assigned to two dietary treatments: conventional feeding (concentrate and hay) or total mixed ration (TMR), with five animals per treatment. Animals were allocated to treatments considering age, previous velvet antler production, and initial body weight to minimize baseline variation between groups. The experiment was conducted from March to June 2026, from antler casting to velvet antler harvest. Experimental periods were standardized based on the day after completion of antler casting (Day 0). Body weight was measured weekly throughout the experimental period, and feed intake, behavioral characteristics, blood parameters, and velvet antler productivity were monitored. Preliminary results showed that body weight gradually increased during the antler growth period in all animals, although individual variation was observed. In the conventional feeding group, body weight gain during the currently monitored period ranged from 9 to 23 kg, whereas the TMR group showed gains ranging from 14 to 22 kg. Body weight fluctuations were observed in several individuals during the experimental period. Further analyses, including feed intake, behavioral responses, blood metabolites, and velvet antler productivity, are currently ongoing. These results may serve as preliminary data for future studies on feeding management and velvet antler productivity in deer.

Key words : deer, velvet antler, growth performance, feeding system

PB26057

Evaluating milk protein conversion efficiency in Holstein dairy cows across lactation stages as a function of dietary crude protein level

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This study was conducted to investigate the milk protein conversion efficiency of Holstein dairy cows according to their lactation stages and dietary crude protein (CP) supply levels. Fifteen Holstein dairy cows were assigned to three groups based on lactation stage: early lactation (n = 5; parity: 3.3 ± 1.9, DIM: 53 ± 11.9 d, milk yield: 29.1 ± 5.67 kg/d), mid-lactation (n = 5; parity: 2.4 ± 1.7, DIM: 114 ± 11.0 d, milk yield: 32.7 ± 3.96 kg/d), and late lactation (n = 5; parity: 2.2 ± 1.4, DIM: 272 ± 17.1 d, milk yield: 29.9 ± 3.10 kg/d). The experimental diets were formulated by adjusting the soybean meal content to provide 80%, 100%, and 120% of the CP requirements specified in the Korean Feeding Standard for Dairy Cattle. The results showed that milk protein conversion efficiency was highest in the early lactation stage across all CP levels and decreased linearly as lactation progressed. However, the 80% CP level resulted in lower milk protein conversion efficiency compared to the 100% level. At the 120% CP level, the highest conversion efficiency during early lactation, the inefficiency caused by excess protein became more pronounced as lactation advanced. In conclusion, to optimize milk protein conversion efficiency in Holstein dairy cows, it is recommended to increase the dietary protein level during early lactation and maintain appropriate protein levels as lactation progresses.

Key words : Holstein dairy cows, lactation stage, dietary crude protein level, milk protein conversion efficiency

PB26058

Evaluation of physiological and biochemical parameters according to different roughage sources in Hanwoo heifers

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Feed resources used in Hanwoo breeding farms can influence metabolic status and reproductive performance due to differences in nutrient composition. Hanwoo heifers were assigned to four dietary treatment groups according to roughage source: rice straw, corn silage, triticale, and Italian ryegrass (IRG). Body weight and body condition score (BCS) were measured to evaluate physiological responses to different feeding treatments. Blood samples were collected for the analysis of blood urea nitrogen (BUN), albumin (ALB), total protein (TP), and triglyceride concentrations. All collected data were statistically analyzed to compare differences among treatment groups. There were no significant differences in BCS among the feeding groups. BUN concentration was lowest in the IRG group at 11.14 mg/dL, whereas the triticale group showed the highest concentration at 16.89 mg/dL. Blood triglyceride concentration was significantly higher ($p < 0.05$) in the triticale-fed group at 154.21 mg/dL. Albumin and total protein concentrations were significantly lower in the IRG-fed group compared with the other feeding groups. Physiological indicators influenced by feed resources are important not only for evaluating growth performance but also for a comprehensive assessment of metabolic health. These indicators may provide fundamental information to improve productivity and economic efficiency in Hanwoo cattle breeding.

Key words : Hanwoo, roughage source, blood biochemical parameters, heifer, metabolic status

PB26059

Major revisions in the 5th edition of Korean feeding standards for dairy cattle

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The Korean Feeding Standards for Dairy Cattle have been revised on a 5-year cycle since their initial publication in 2002, with the 5th edition scheduled for release in 2027. This edition goes beyond improving productivity to address the dual challenges of achieving carbon neutrality and reducing environmental pollution, incorporating domestic empirical data into the revision process. Energy requirements have been adjusted upward to reflect the increasing milk yield and body weight trends of Korean dairy cattle, while maintaining the NE framework to ensure alignment with international standards such as NASEM (2021) and INRA (2019). In addition, Chapter 10 (Environmental Improvement) has been newly established to refine emission factors based on the IPCC Tier 2 methodology; application of the updated emission factors is projected to reduce greenhouse gas emissions from the Korean dairy sector by approximately 97,000 tonnes CO_2eq annually (an 8% reduction). For nitrogen emission reduction, the combined use of low-CP diets with rumen-protected amino acids has been presented as a core strategy, with evidence indicating that precision feeding utilizing ICT-based feeders can reduce nitrogen emissions by 10–20%. The 5th edition provides a scientific basis for simultaneously achieving the dual goals of maintaining productivity and reducing the environmental burden of Korean dairy cattle through the integration of precision nutrition design and greenhouse gas mitigation technologies.

This work was carried out with the support of “Cooperative Research Program for Agriculture Science & Technology Development (Project No. RS-2026-25517562)” Rural Development Administration, Republic of Korea.

Key words : Korean feeding standards, dairy cattle, methane, nitrogen, greenhouse gas

PB26060

Effects of pectin-rich by-products (citrus pulp and apple pomace) on *in vitro* rumen fermentation: a meta-analysis

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This study evaluated the effects of pectin-rich by-products, citrus pulp and apple pomace, on *in vitro* rumen fermentation through a meta-analysis. Following the PRISMA 2020 guidelines, 17 studies investigating citrus pulp and apple pomace as alternative carbohydrate sources were included from 419 articles in PubMed, Scopus, and Web of Science, yielding 10–30 comparisons per outcome after standardizing incubation time to 24 h. Standardized mean differences (SMD, Hedges' *g*) were calculated using a random-effects model, with subgroup analyses by type of by-product. Both by-products promoted fermentation: pH remained stable ($k = 17$, SMD = –2.840, $p = 0.109$), while ammonia-nitrogen decreased ($k = 10$, SMD = –1.093, $p = 0.010$), and gas production ($k = 30$, SMD = 0.932, $p < 0.001$) and propionate concentration ($k = 24$, SMD = 0.415, $p < 0.001$) significantly increased. Citrus pulp induced an acetate-enhancing pattern ($k = 12$, SMD = 0.728, $p < 0.001$), whereas apple pomace induced a propionate-enhancing pattern with increased propionate proportion ($k = 12$, SMD = 0.784, $p < 0.001$) and decreased acetate-to-propionate ratio ($k = 12$, SMD = –0.783, $p < 0.001$). Methane reduction was significant only with apple pomace ($k = 11$, SMD = –1.248, *p*-subgroup = 0.003). Pectin-rich by-products could partially replace corn grain in ruminant diets, promote acetate-centered fermentation without negative effects on ruminal fermentation.

Key words: citrus pulp, apple pomace, alternative carbohydrate source, rumen fermentation, meta-analysis

PB26061

축산 분야 AI 자율 생성 논문의 학술적 활용 가능성 및 검증: 6개 연구 사례를 중심으로

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최근 생성형 인공지능(Artificial Intelligence, AI)의 급속한 발전에 따라 국내 축산학계에서도 연구 전반에 걸쳐 이를 적용하려는 노력이 지속되고 있으나, AI 활용 방법 및 결과물의 신뢰성에 대한 명확한 기준과 윤리적 가이드라인은 미비한 실정이다. 본 연구는 인간의 개입을 최소화하고 실제 실험 없이 AI 도구만을 활용해 축산 분야 학술논문을 작성하고, AI 기반 연구의 가능성과 한계를 검토하였으며, 표절 검사를 통해 연구 결과의 신뢰성을 검증하고자 하였다. ChatGPT, Google Gemini, Claude, Perplexity 등 다양한 AI 플랫폼을 교차 활용하여 연구 주제 선정, 실험 설계, 데이터 분석 및 최종 논문 작성의 전 과정을 포함한 6편의 연구가 수행되었다. 표절률은 표절 검사 도구(CopyKiller) 및 AI 생성물 탐지 도구(GPT Killer)를 통해 검증하였다. 연구 유형은 (1) 문헌 기반형(반추위 마이크로바이옴, 한우 관능 품질, 착유우 유기산 급여 효과, 반추동물 스트레스 관련 메타분석 등 4편)과 (2) 데이터 기반형(합성 데이터 가상 실험, 공공데이터 기반 메탄 발생량 산정 등 2편)으로 분류하였다. 신뢰성 검증 결과, 프롬프트 반복 수정을 통해 문헌 표절률을 10% 이하 수준으로 유지할 수 있었으나, 초기 AI 생성물 탐지율은 60% 이상으로 나타나 추가적인 개선이 필요한 것으로 판단되었다. 결과적으로 AI는 축산 분야 학술 연구 및 문헌 작성의 보조 도구로서 실질적인 적용이 가능할 것으로 판단되나, 수집 및 합성 데이터의 투명한 공개, 인용 정확성 확보 및 연구 윤리 준수가 반드시 전제되어야 할 것으로 사료된다.

Key words : 생성형 인공지능, 축산학, 표절률, 연구 윤리

PB26062

Effects of dietary crude protein levels and carcass weight GEBV groups on Hanwoo calves under summer heat stress

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This study evaluated the effects of dietary crude protein (CP) and carcass weight genomic estimated breeding value (CW GEBV) on growth performance and stress-related responses in Hanwoo calves under summer heat stress. Thirty-six Hanwoo calves (initial BW 117.9 ± 24.3 kg; 3.9 ± 0.6 months of age) were assigned to a 2 × 2 factorial arrangement with initial BW as a blocking factor. Treatments comprised two CP levels (BCP, 15.0%; HCP, 17.5%) and two CW GEBV groups (LG, low; HG, high), yielding four groups: BCP-LG, BCP-HG, HCP-LG, and HCP-HG. Body weight and blood samples were collected at the start (initial), and after one (middle) and two (final) months of feeding. ADG tended to be greater in HCP than in BCP and in HG than in LG (both $p = 0.077$), whereas rectal temperature and respiration rate were unaffected. Blood urea nitrogen was higher in HCP than in BCP ($p < 0.05$). Lymphocyte counts were higher in LG than in HG at the middle time point and higher in HCP than in BCP at the final time point ($p < 0.05$). Granulocyte counts showed a CP × GEBV interaction at the final time point ($p = 0.009$); BCP-LG was lower than the other three groups ($p < 0.05$). In peripheral blood mononuclear cells (PBMCs), HSP27 expression showed a CP × GEBV interaction at the middle time point ($p < 0.05$), although means did not differ. HSP70 tended to be higher in HG than in LG at the middle time point ($p = 0.074$). In conclusion, increasing dietary CP to 17.5% tended to improve ADG in Hanwoo calves under summer heat stress, while immune and cellular stress responses to dietary CP appeared to be modulated by CW GEBV.

Key words : heat stress, Hanwoo calves, dietary protein level, heat shock protein

PB26063

Effects of dietary metabolizable energy, protein and essential amino acids on nitrogen utilization efficiency and milk production in dairy cows: a meta-analytic ensemble classifier

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This study developed a machine-learning ensemble to classify nitrogen utilization efficiency (NUE) in lactating dairy cows from dietary metabolizable energy (ME), metabolizable protein (MP) and metabolizable-protein essential amino acids (MP-EAA), and interpreted it with shapley additive expanations (SHAP). Following PRISMA 2020, control records were extracted from 1,175 peer-reviewed papers and standardized with the NASEM DairyFeed Library (2021); after quality screening, 1,217 records (1,142 studies) with NUE entered the analysis. NUE was dichotomized at 26.7%, the mean reported by Huhtanen and Hristov (2009). A soft-voting ensemble of logistic regression, random forest, and XGBoost validated by repeated stratified group 5-fold cross-validation (3 repeats; group = Study_ID) and cluster bootstrap resampling (1,000 study-level resamples) achieved ROC AUC = 0.840 (95% CI 0.809–0.886). In SHAP analysis, MP was the strongest negative contributor, whereas histidine retained a consistently leading positive contribution in both low- and high-CP diets, identifying it as a limiting amino acid independent of dietary crude protein level. High-NUE records further exhibited significantly greater milk yield (Hedges' g = 0.56), ECM (g = 0.69), milk protein (g = 0.26), and milk fat (g = 0.30) than low-NUE counterparts in linear mixed-effects models adjusting for between-study heterogeneity (Holm-adjusted $p < 0.001$). Together, these findings indicate that ME and MP-EAA profiles can identify lactating cows that are simultaneously higher in NUE and superior in lactational performance, contributing to sustainable dairy production.

Key words : nitrogen utilization efficiency, metabolizable energy, metabolizable amino acid, ensemble machine learning, dairy cows

PB26064

Implication of combined vitamin supplementation on reproductive capacity during the growing period in Holstein heifers under summer heat-stress conditions

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This study investigated whether combined vitamin supplementation alleviates physiological stress and sustains reproductive capacity in growing Holstein heifers under summer heat-stress conditions. We hypothesized that elevated summer Temperature-Humidity Index (THI) induces metabolic acceleration for homeostasis, triggers excessive ROS production, and leads to oxidative damage and inflammation that impairs reproductive capacity. Based on this hypothesis, vitamin C and E were selected for their expected role in alleviating oxidative stress, and vitamin A and D for immune function regulation. Sixteen heifers were assigned to four groups (RCBD, n = 4 per group). From June 5, moderate heat stress was induced in the heifers as the THI reached 72 or higher. The control group received 100% of vitamin A, D, and E according to the Korean Feeding Standard. T1 received vitamin A and D at 200%. T2 received vitamin E at 300% with vitamin C at 5 g/day. T3 combined both approaches, providing vitamin A and D at 200%, vitamin E at 300%, and vitamin C at 5 g/day. Multiple parameters of growth, physiology, reproduction, and behavior were analyzed. The T3 treatment effectively preserved SOD activity to mitigate final MDA accumulation, and stabilized key endocrine indicators including hair cortisol and estrogen. Multi-parameter integrated Z-score analysis showed that the synergistic T3 group scored the highest (12.22/20), followed by T2 (9.48), quantitatively confirming superior stability. In conclusion, combined supplementation of vitamins A, C, D, and E provides a meaningful nutritional intervention to maintain physiological homeostasis and reproductive capacity in heifers under summer heat stress.

Key words : heat stress, temperature-humidity index (THI), reactive oxygen species (ROS), vitamin, reproductive capacity

PB26065

서방형 유기산 및 에센셜오일이 반추위 발효 특성에 미치는 영향 조사

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본 연구는 서방형 유기산 제제(slow-release organic acid, SROA; 사과산·푸마르산)와 서방형 에센셜오일 제제(slow-release essential oil, SREO; 티몰·카바크롤)의 첨가가 반추위 발효 성상에 미치는 영향을 조사하고자 수행되었다. 시험군은 첨가 수준과 종류에 따라 기초사료(CON), SROA(0.20%, 0.40%: DM 기준) 및 SREO(0.20%, 0.40%: DM 기준)으로 설정하였다. 배양 9시간 및 24시간에 반추위 pH, 암모니아태질소(NH_3-N), 휘발성 지방산(VFA) 조성 및 발효 가스 발생량을 분석하였다. 반추위 발효 pH와 암모니아태질소 생성 수준을 통해 서방형 제제 첨가가 반추위 발효 안정성에 부정적인 영향을 미치지 않음을 확인하였다. 그러나 총 VFA 생성량은 SREO 첨가구가 대조구 대비 최대 37% 유의적으로 증가하였다($p < 0.001$). 또한 메탄 발생량은 배양 24시간에서 SROA 0.4% 첨가구가 대조구 대비 약 11% 유의적으로 감소하였다($p < 0.05$). 일련의 결과를 통해 서방형 에센셜오일 첨가가 반추위 미생물의 발효 활성을 촉진하는 것으로 나타났으며, 반추동물의 에너지 공급 개선 효과가 관찰되었다. 특히 서방형 유기산제제의 반추위 메탄 저감에 효과가 관찰되었다.

Key words : 서방형 유기산, 서방형 에센셜오일, 반추위 *in vitro* 발효, 휘발성지방산, 메탄

PB26066

Effects of hydrogen supplementation on protozoa-associated prokaryotic communities in rumen protozoal cultures

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Rumen ciliate protozoa harbor diverse prokaryotic communities, including bacteria and methanogenic archaea. These symbionts play a central role in ruminal hydrogen (H_2) metabolism and methanogenesis, yet it remains poorly understood how elevated H_2 partial pressure influences the stability of theses associations. Therefore, this study investigated whether H_2 supplementation (500 mbar) induces the redistribution or detachment of microbes from the protozoal fraction (PF) to the free-living fraction (FLF). Monoxenic *Epidinium ecaudatum* and meroxenic *Entodinium* spp. cultures, established via single-cell isolation, were incubated for 24 h with H_2 or N_2 (control) in a completely randomized design. Results showed that H_2 supplementation did not significantly affect overall fermentation characteristics, including VFA profiles, protozoal cell counts, and NH_3-N concentrations. Although H_2 supplementation successfully stimulated methanogenesis, evidenced by increased CH_4 proportions and reduced CO_2, 16S rRNA gene sequencing (V3-V4 region) revealed that the prokaryotic community structure was primarily stratified by niche fraction (PF vs. FLF) rather than gas supplementation in both the protozoal cultures. The absence of distinct redistribution patterns between fractions suggests that these microbial communities remain relatively stable under elevated H_2 conditions. These findings provide insight into the structural stability of protozoa-prokaryote associations. Ongoing analyses using fluorescence *in situ* hybridization (FISH) will further evaluate the spatial localization of associated prokaryotes across the separated fractions.

Key words : rumen protozoa, hydrogen partial pressure, symbiotic association

PB26067

Effects of coconut oil supplementation on methane emissions and feed intake in ruminants: a meta-analysis

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Coconut oil, rich in medium-chain fatty acids (MCFA), has been proposed as a natural lipid additive for reducing enteric methane emissions in ruminants. However, whether its methane-reducing effects are accompanied by negative impacts on feed intake and fiber utilization remains unclear. This meta-analysis evaluated the effects of dietary coconut oil supplementation on methane yield (g/kg of dry matter intake [DMI]), methane production (g/day), DMI, and neutral detergent fiber digestibility (NDFD) in ruminants, based on 20 *in vivo* studies identified through a systematic search following PRISMA 2020 guidelines. Coconut oil supplementation significantly reduced methane production (SMD = –1.82, $p < 0.001$) and methane yield (SMD = –1.51, $p < 0.001$) across both cattle and small ruminants. However, it also significantly decreased DMI (SMD = –1.39, $p < 0.001$) and NDFD (SMD = –1.47, $p < 0.001$). Paired-effect analysis further indicated that the reduction in NDFD remained positively associated with decreased DMI, suggesting that MCFA-induced impairment of rumen fiber digestion may partly underlie reduced feed intake. These findings highlight the biological trade-offs associated with coconut oil use, and its practical application should carefully consider the balance between methane mitigation and adverse effects on rumen fermentation.

Key words : coconut oil, methane emission, dry matter intake, ruminants, fiber digestibility, meta-analysis

PB26068

복합 미생물 처리가 TMR 발효 품질 및 반추위 *in vitro* 발효 특성에 미치는 영향

전무궁, 천인혁, 문예진, 정은경, 채병호, 이숙경, 조상범, 최낙진

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본 연구는 복합 미생물 제제의 첨가가 섬유질 완전 배합사료(TMR, total mixed ration)의 발효 품질과, *in vitro* 반추위 발효 특성에 미치는 영향을 평가하고자 수행하였다. *Pediococcus pentosaceus, Saccharomyces cerevisiae, Bacillus coagulans*를 동일한 비율로 혼합하여 복합 미생물 제제를 제작하였다. 실험 1에서는 복합 미생물 제제를 첨가한 TMR을 10일간 발효시킨 후 발효 전 TMR 대비 pH, 유기산 및 미생물 군집의 변화를 분석하였다. 실험 2에서는 복합 미생물제제를 분말 제형으로 가공한 후에 그 첨가 수준(건물 기준 0.5%, 1.0%) 이 반추위 발효 특성에 미치는 영향을 조사하였다. 발효 가스 조성(CH_4, H_2), pH, 휘발성 지방산 및 암모니아태 질소를 발효 지표로 분석하였다. 실험 1에서는 복합 미생물제 적용으로 TMR의 pH가 유의적으로 감소하였다(5.15 vs. 4.37)($p < 0.001$). TMR 내 젖산 함량도 15.4mM에서 53.2mM로 약 3.5배가 증가하였고($p < 0.001$), 초산은 1.70 mM에서 17.31 mM로 약 10.1배 증가하였다($p < 0.01$). 특히 mold와 대장균 군 및 살모넬라군의 검출은 관찰되지 않았다. 실험 2의 반추위 발효 특성에서는 총 휘발성 생산량, 초산 및 프로피온산 생성량이 유의적으로 증가하였다($p < 0.001$). 반면, 다른 발효 특성에서는 유의적인 차이가 관찰되지 않았다. 본 연구 결과, 복합 미생물 제제의 첨가는 TMR 발효 시 pH를 낮추고 젖산 및 초산 생성을 촉진하였으며, 곰팡이, 대장균 군 및 살모넬라의 증식을 억제하여 사료의 발효 품질과 위생적 안정성을 향상시키는 것으로 나타났다. 또한 반추위 *in vitro* 발효에서는 총 휘발성 지방산과 초산, 프로피온산 생성을 증가시켰다. 따라서 본 복합 미생물 제제는 TMR의 발효 품질 개선과 반추위 발효 효율에 기여할 수 있는 첨가제로서 활용 가능성이 있는 것으로 판단된다.

Key words : mixed microbial inoculant, fermented total mixed ration, fermentation quality, *in vitro* rumen fermentation, methane mitigation

PB26069

Effects of dietary energy and *Lactiplantibacillus plantarum* LM1001 culture on fermentation characteristics and greenhouse gas emissions in the rumen

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This study estimated the effects of dietary energy and *Lactiplantibacillus plantarum* LM1001 culture (LPC) on rumen fermentation characteristics and greenhouse gas (GHG) emissions of fermented total mixed ration. A 2 (dietary energy = low (LE) vs. high (HE)) × 3 (LPC = 0 vs. 10 vs. 20%) factorial design was used. Each diet (5 kg) was ensiled for 21 days. After that, the experimental diet (0.3 g) was incubated with rumen buffer (30 mL) (n = 4) for 24 h. After incubation, total gas emission was measured and sub-sampled for GHG analysis. The rumen buffer was centrifuged to separate the residue and the supernatant for nutrient digestibility and rumen fermentation characteristics. The HE group showed higher crude protein and *in vitro* digestibilities of dry matter (IVDMD) and organic matter (IVOMD) than the LE group. And these parameters in the HE group increased ($p < 0.05$) by increasing LPC supplementation levels. The HE group showed lower ($p < 0.01$) total gas, CH_4, and CO_2 than the LE group. These gases showed interaction ($p < 0.001$) between dietary energy and LPC, which increased in the LE group but decreased in the HE group by increasing LPC supplementation levels. Notably, the HE group with 20% LPC showed the highest crude protein and IVOMD, along with the lowest GHG emissions. Therefore, the HE with 20% of LPC supplementation could be a promising approach to enhance feed value and methane mitigation in Hanwoo.

Key words : dietary energy, fermentation characteristics, greenhouse gas emissions, *Lactiplantibacillus plantarum* LM1001 culture

PB26070

Evaluation of physiological and metabolic responses of goats under cold stress conditions

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The objective of this study was to evaluate the effects of winter ambient temperature on productivity, physiological indicators, and blood parameters (hematology, metabolite, and amino acids) in goats. This study was conducted using 16 goats (Korean native black × Boer crossbred, 8 months of age, initial body weight 29.0 ± 3.1 kg, ≥ 20% Korean native black) over a 30-day period with repeated sampling every 5 days (temperatures: 3.78, 2.13, 0.52, –1.47, –2.31, 1.00, and –3.67°C). The data were analyzed using repeated-measure Mixed procedure of SAS. Rectal and ear temperatures remained stable throughout the experimental period ($p < 0.01$); however, rectal temperature decreased at d30, and ear temperature reached the highest value at d25 and then decreased. Respiratory rate increased after d15, whereas water intake and average daily gain decreased, with the lowest values observed at d30 ($p < 0.01$). Hematological responses showed a decrease in granulocyte count and proportion and an increase in lymphocyte proportion at d25 ($p < 0.05$). Red blood cell indices (hemoglobin, and hematocrit) decreased from d15 to d25 and recovered by d30 ($p < 0.01$). Blood metabolites showed that blood urea nitrogen decreased during d10 to d20 and increased again at d30, whereas creatinine reached the lowest value at d10 and increased gradually ($p < 0.05$). These results indicate that cold exposure affected physiological indicators, blood parameters, and productivity in goats, as reflected by reduced water intake and growth performance. Meanwhile, the recovery of several blood parameters by d30, together with stable rectal temperature, suggests adaptation to prolonged winter conditions accompanied by the activation of physiological homeostatic mechanisms.

Key words : cold stress, growth performance, hematological parameters, metabolic and physiological response

PB26071

Feed values of ground corn and ramen by-products as the dietary energy sources for ruminant

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This study aimed to evaluate the feed value of corn meal and ramen by-products as the dietary energy sources for ruminants based on rumen fermentation characteristics and greenhouse gas emissions. Corn meal was used as a control (CON), while 4 ramen by-products (Shinramyun (SHR), Chapagetti (CPT), Anseongtangmyun (AST), and Neoguri (NGR) were assigned as the new energy sources. Each feed source (0.5 g) was incubated with rumen buffer (40 mL) in quadruplicate for 24 h. During the incubation period, gas pressure was measured every 5 min to generate the fermentation kinetics in the rumen. After incubation, gas samples were collected for CO_2 and CH_4. The bottle contents were centrifuged to collect the supernatant for fermentation characteristics. The AST had the highest crude protein ($p < 0.05$), while CON had the lowest ether extract ($p < 0.05$). All ramen by-product treatments had lower ($p < 0.05$) rumen pH, ammonia-N, acetate, and A:P ratio than CON. However, the total VFA and propionate were higher ($p < 0.05$) in CPT, AST, and NGR than in the other feed sources. The NGR showed the highest immediately degradable fraction (A) ($p < 0.05$), while the AST had the lowest total gas and CH_4 ($p <$ 0.05, per DMD) among the feed sources. Therefore, ramen by-products, particularly AST, showed potential as an alternative dietary energy source for CH_4 mitigation without negative effects on rumen fermentation characteristics.

Key words : corn meal, rumen fermentation characteristics, methane emissions, ramen by-product

PB26072

Effects of plant extract mixture and extruded linseed supplementation on enteric methane emissions in mid lactation Holstein cows

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This study investigated the effects of dietary supplementation with a plant extract mixture (PEM) additive and extruded linseed (EL) on enteric methane (CH_4) emissions, productivity, milk composition, and hematological characteristics of mid- to late-lactating Holstein cows. Nine multiparous cows were assigned to a 3 × 3 Latin square design consisting of three treatments: control, PEM (50 g/head/day), and EL (500 g/head/day). Cows were blocked according to CH_4 emission (300.8 ± 38.7 g/day), parity (1.67 ± 0.86), and milk yield (28.2 ± 5.08 kg/day). Cows were offered a total mixed ration (TMR) ad libitum and were additionally fed 2 kg of concentrate daily. CH_4 production was monitored using a GreenFeed system and calculated as CH_4 emission (g/day), CH_4 yield (g/kg of dry matter intake (DMI)), and CH_4 intensity (g/kg of milk yield). Statistical analysis was performed using the MIXED procedure of SAS 9.4. The statistical model included treatment as a fixed effect and cow and period as random effects. Dietary supplementation did not affect CH_4 emission, CH_4 yield, or CH_4 intensity ($p > 0.05$). Mean CH_4 emissions for the control, PEM, and EL treatments were 354.7, 369.9, and 368.9 g/day, respectively. No overall differences in DMI and milk yield were observed among treatments ($p > 0.05$). Milk composition and hematological parameters were unaffected by treatment. These findings suggest that fixed additive inclusion levels and ad libitum TMR feeding may have contributed to the lack of detectable supplementation effects.

Key words : GreenFeed system, Holstein, linseed, methane mitigation, plant extract

PB26073

Effects of maternal L-citrulline supplementation on growth performance and gene expression in Hanwoo calves

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This study aimed to evaluate the effects of maternal L-citrulline (L-cit) supplementation on blood metabolites in Hanwoo cows, as well as growth performance and gene expression in offspring calves. Forty-eight pregnant Hanwoo cows were stratified by experimental start date, sire, and parity, and randomly assigned to three groups: control (no supplementation, n = 15), T1 (0.5% L-cit of DM from mid-gestation until calving, n = 16), and T2 (0.5% L-cit of DM from late gestation until calving, n = 17). Maternal blood metabolites and postpartum interval to estrus were measured after calving. Calf birth weight, body weight at 60 days, and average daily gain (ADG), as well as postpartum interval to estrus in cows, were recorded. At 75 days of age, longissimus lumborum muscle and liver biopsies were collected from male calves, and mRNA expression was quantified by RT-qPCR. Data were analyzed using the GLM procedure of SAS 9.4, with Tukey's test. L-cit supplementation did not affect postpartum blood concentrations of aspartate aminotransferase, alanine aminotransferase, glucose, total cholesterol, total protein, triglycerides, or blood urea nitrogen in cows, nor postpartum interval to estrus. In calves, no significant effects were observed for birth weight, body weight at 60 days, or ADG. Similarly, mRNA expression of myogenic (*MYF5, MYOD, MYOG, MYF6*) and adipogenic (*PREF1, ZNF423, PPARG, CEBPA, CEBPB, FABP4*) genes in skeletal muscle, as well as hepatic *ASS1, OTC, ASL,* and *GAMT* expression, were not affected. However, hepatic *ARG1* expression was lower in T1 than in the control and T2 ($p = 0.006$). In conclusion, maternal L-cit supplementation initiated in mid-gestation, but not in late gestation, may influence hepatic arginine metabolism-related gene expressionin Hanwoo offspring. Long-term follow-up is warranted to determine whether these molecular changes translate into differences in growth performance and carcass traits in Hanwoo cattle.

Key words : Hanwoo cattle, L-citrulline, maternal nutrition, offspring calves, arginine metabolism

PB26074

Efficacy of a synbiotics complex on dairy cow productivity and calf gut health under Uzbekistan farming conditions

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This study was conducted to investigate a synbiotics complex (Syner-win plus®; *Bacillus licheniformis*, dietary fiber, benzoic acid) on early-lactation performance and calf growth and gut health in Uzbekistan. For lactating cows, the basal diet was formulated with a 50:50 forage-to-concentrate ratio on a dry matter (DM) basis. The treatment group received synbiotics supplemented at 0.1% of the DM, targeting a daily provision of 20 g/cow based on a target DMI of 20 kg/d. Over the first 105 days in milk, the daily average milk yield significantly increased by approximately 7% in the treatment group 33.6 kg/d compared to the control group 31.3 kg/d ($p < 0.05$). Milk fat 3.63% and milk protein 3.25% contents were maintained, indicating that the synbiotics improved absolute milk yield without negative effect on milk components. Furthermore, synbiotics supplementation in newborn calves significantly increased cumulative weight gain at 11 weeks of age by 6% (61.98 kg vs. 58.34 kg; $p < 0.05$). During the weaning transition period around 2 months of age, the average fecal score was maintained lower in the treatment group 0.11 compared to the control 0.20, suggesting improved gut health in diarrhea incidence. In conclusion, dietary supplementation with Syner-win plus® is a showed positive effects to enhance milk production in lactating cows and improve initial growth and gut health in calves.

Key words : calf performance, early lactation, fecal score, milk yield, synbiotics

PB26075

Effects of methanotroph-based probiotic (NC52PC) on milk production performance and milk composition in Holstein dairy cows

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This study evaluated the effects of a rumen-derived bacterial consortium (NC52PC) on milk production and composition in Holstein dairy cows. Sixty lactating cows were assigned to control (CON) and treatment (TRT) groups in a randomized complete block design based on milk yield, parity, days in milk, and milk composition. The TRT group received NC52PC at 0.5% of dry matter as a top-dressing on the total mixed ration for 35 days, including a 7-day adaptation period. Overall milk yield was not significantly affected, although significant effects of time and treatment × time interaction were observed ($p < 0.05$). Milk yield temporarily decreased during full-dose transition but recovered thereafter. Major milk composition traits were not significantly affected by NC52PC supplementation. However, fat percentage tended to be higher in the TRT group than in the CON group throughout the experimental period ($p < 0.1$), while milk urea nitrogen (MUN), C18:1, and long-chain fatty acids (LCFA) increased in the TRT group ($p < 0.05$). Monounsaturated fatty acids (MUFA), saturated fatty acids (SFA), differential somatic cell count (DSCC), medium-chain fatty acids (MCFA), and short-chain fatty acids (SCFA) tended to increase in the TRT group compared with the CON group ($p < 0.1$). Rumen fermentation characteristics remained stable throughout the experimental period, and ruminal bacterial diversity and community structure were not significantly affected by NC52PC supplementation. In conclusion, NC52PC supplementation did not compromise milk yield or major milk composition traits but influenced selected metabolic indicators and fatty acid profiles, suggesting its potential as a functional feed additive in lactating dairy cows.

Key words : rumen-derived bacterial consortium, feed additive, Holstein dairy cow, milk production, milk composition

PB26076

Chemical composition and methane production of total mixed fermentation for different Hanwoo growth stages

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This study evaluated the chemical composition and *in vitro* methane (CH_4) production of 26 total mixed fermentation (TMF) diets formulated for different Hanwoo production stages, including calves, growing, early fattening, late fattening, and breeding cattle. Chemical composition analysis revealed no significant differences ($p > 0.05$) in major nutritional components, such as crude protein, neutral detergent fiber, acid detergent fiber, ethanol-soluble carbohydrates, and total digestible nutrients, among TMF diets within each production stage. Principal component analysis (PCA) indicated that digestibility-related parameters and fatty acid content were the primary factors distinguishing the TMF diets. Among the evaluated diets, TMF16, TMF23, TMF24, TMF25, and TMF26 were identified as the most suitable TMFs for calves, growing, early fattening, late fattening, and breeding cattle, respectively, based on their chemical composition profiles. Several TMF diets also showed reduced CH_4 production after 24 h incubation, with particularly significant reductions ($p < 0.05$) observed in breeding TMFs. Overall, although the nutritional compositions of the TMF diets were generally similar, specific TMF diets demonstrated potential for mitigating methane production in Hanwoo cattle.

Key words : total mixed fermentation (TMF), methane production, Hanwoo

PB26077

Citrus peel-based *Bacillus subtilis* fermentation and surfactin: impacts on *in vitro* rumen fermentation characteristics and methane emissions

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Citrus peel is a valuable by-product, yet its application in ruminant diets remains limited. This study evaluated the effects of *Bacillus subtilis* cultured in a citrus peel-based medium specifically its liquid/solid fermentation products and the metabolite surfactin on *in vitro* rumen fermentation and methane (CH_4) production. Four batch culture experiments were conducted with graded inclusion levels of each component. Results showed that while *B. subtilis* and its fermentation products generally improved fermentability and nitrogen turnover (increasing volatile fatty acids and ammonia nitrogen), they had minimal impact on methane mitigation. In contrast, surfactin demonstrated a clear dose-dependent effect: at 0.01% of substrate DM, it reduced CH_4 production by 6.9% and shifted fermentation toward propionate without suppressing overall efficiency. However, a higher dose (0.02%) abolished these benefits. In conclusion, a citrus peel–*B. subtilis* platform serves as a viable strategy for value-added feed additives, with 0.01% surfactin identified as the optimal level for balancing methane reduction and rumen fermentation efficiency.

Key words : *Bacillus subtilis*, citrus peel, methane, rumen fermentation, surfactin

PB26078

Effects of processing methods on ruminal fermentation characteristics and protein utilization of palm kernel meal

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Palm kernel by-products are potential alternative protein sources for ruminants. However, their nutrient composition and protein availability may differ depending on the oil-extraction and processing method. Comparative information integrating ruminal fermentation characteristics, ruminal protein degradation, intestinal digestibility of rumen-undegraded protein (RUP), and metabolizable protein (MP) supply among different palm kernel by-products remains limited. Therefore, this study evaluated the ruminal fermentation characteristics and protein utilization of three palm kernel by-products: palm kernel meal (PKM), palm kernel expeller (PKE), and palm kernel extraction in bulk (PKEB). *In vitro* fermentation was conducted to determine dry matter degradability (IVDMD), pH, ammonia-N, volatile fatty acid (VFA), and gas production, which was measured at 6, 12, and 24 h. *In situ* was conducted using two rumen-cannulated Hanwoo heifers (BW: 450 ± 10 kg) to determine dry matter and crude protein degradability and to calculate rumen degradable protein (RDP) and RUP. After 12 h of ruminal in situ incubation, the residual samples were subjected to a separate *in vitro* intestinal digestibility assay to determine intestinal digestibility (ID) of rumen undegradable protein (RUP) and to calculate metabolizable protein from feed (MP_{feed}). *In vitro*, PKEB showed lower IVDMD than PKM and PKE ($p = 0.0002$) but a greater molar proportion of propionate and a lower acetate-to-propionate ratio ($p < 0.05$). *In situ*, PKM had higher soluble CP and RDP, whereas PKE and PKEB had higher RUP than PKM ($p < 0.0001$). Intestinal digestibility of RUP was greatest in PKEB, and MP_{feed} was higher in PKE and PKEB than in PKM ($p < 0.0001$). Considering both *in vitro* and *in situ* results, PKE appears to be the most effective palm kernel by-product for improving utilizable protein supply, owing to its relatively high IVDMD, greatest RUP, and greatest MP_{feed} supply. PKEB showed an advantage in intestinal digestibility of RUP and fermentation profile, but further *in vivo* studies are needed to confirm their practical feeding value.

Key words: palm kernel by-products, palm kernel by-products, palm kernel expeller, rumen undegradable protein, intestinal digestibility, metabolizable protein

동물생명공학

PC26001

Economic evaluation of ultrasonographic fetal sex prediction: implications for profitability and market dynamics in Hanwoo cattle

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This study aimed to evaluate the diagnostic accuracy and optimal timing of ultrasonographic fetal sex determination in Hanwoo cattle and to examine its economic implications for breeding farm profitability and market dynamics. Specifically, we investigated whether early fetal sex identification could affect the transaction price of pregnant cows and shift profit distribution between breeding and purchasing farms. A total of 107 pregnant Hanwoo cows were examined by transrectal ultrasonography between 55 and 100 days of gestation; after excluding indeterminate cases, 104 were included in the final analysis. Fetal sex was determined by identifying the position of the genital tubercle and external genital structures. Diagnostic performance was assessed across three gestational periods (55–70, 71–85, and 86–100 days). An economic scenario analysis was conducted to estimate changes in asset value, net profit, cost–benefit ratio, and return on investment under different pricing strategies reflecting male–female calf price differentials. Sensitivity analyses further evaluated the effects of ultrasound costs and market fluctuations. The economic analysis indicated that farms adopting this technology could increase profitability by differentiating market prices according to fetal sex, with male calves contributing substantially to herd asset value. However, the magnitude of economic benefit depended on market conditions, implementation costs, and sex ratio variation. Ultrasonographic fetal sex determination has strong potential as a management tool to improve profitability and long-term sustainability in Hanwoo production systems, although its economic effectiveness requires strategic adoption that accounts for associated costs and market variability.

Key words : particulate matter, metal, testis, sperm, reproductive toxicity

PC26002

Isolation and characterization of a novel Stx1-converting temperate bacteriophage St1-gc

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Shiga toxin-producing *Escherichia coli* (STEC) is a major foodborne pathogen responsible for hemorrhagic colitis and hemolytic uremic syndrome in humans. Shiga toxins are encoded by Stx-converting bacteriophages (phages), which facilitate horizontal gene transfer and drive the emergence of new pathogenic strains. As ruminants are recognized as major reservoirs of STEC, understanding the biological and genomic characteristics of Stx-converting phages is essential for food safety and sustainable livestock management. In this study, we report a novel temperate phage, St1-gc, induced from a STEC isolate by mitomycin C treatment. The phage exhibited siphovirus-like morphology and showed strong lytic activity against its indicator *E. coli* strain in both planktonic and biofilm states, along with high tolerance to environmental stresses. Notably, phage St1-gc successfully mediated transduction of the *stx1* gene into a non-STEC strain. Genomic analysis revealed that phage St1-gc possessed a double-stranded DNA genome (50,192 bp) encoding 85 predicted ORFs, and the stx1 subunits A and B were identified within the genome. These findings highlight the potential role of phage St1-gc in the dissemination of STEC virulence factors and provide insights into strategies for controlling STEC to support sustainable livestock production.

Key words : STEC (Shiga toxin producing *Escherichia coli*), Stx-converting bacteriophage, transduction

PC26003

Isolation and characterization of a novel bacteriophage KW1 infecting *Lactococcus lactis*

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Lactococcus lactis is a Gram-positive lactic acid bacterium widely used as a starter culture in dairy fermentation because of its roles in rapid acidification, curd formation, flavor development. However, bacteriophage (phage) infection can disrupt these processes, leading to fermentation failure and economic losses. Despite ongoing control efforts, phage infection remains a persistent challenge due to the diversity and adaptability of lactococcal phages, many of which remain poorly characterized. In this study, a *L. lactis*-infecting phage, KW1, was isolated and characterized. The phage formed clear plaques with distinctive halos on its host strain, consistent with a lytic lifestyle, and exhibited a high degree of host specificity. Morphological analysis identified KW1 as a siphovirus-like phage, and stability tests showed high tolerance to pH and thermal stress. Genome sequencing revealed the phage possessed a 29,600-bp genome with 35.8% GC content, encoding 44 ORFs with no tRNAs, with no identifiable virulence-associated or antibiotic resistant genes. Interestingly, Gp38-like protein associated with Abi (abortive infection) resistance and multiple recombination-related proteins were detected, suggesting potential anti-host defense mechanisms and genomic adaptability. These results provide insights into the biology of lactococcal phages and support the development of control strategies against phage contamination in dairy fermentation.

Key words : *Lactococcus lactis*, bacteriophage, lytic phage, characterization, genome analysis, dairy fermentation

PC26004

Breaking host barriers: a novel bacteriophage infecting hybrid strains of Enterotoxigenic/Shiga toxin-producing *Escherichia coli*

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Escherichia coli is a Gram-negative bacterium commonly found in the intestinal tract of humans and animals. Certain pathotypes possess distinct virulence factors and can cause enteric and extraintestinal disease in both humans and livestock. Among these, enterotoxigenic *E. coli* (ETEC) is a major cause of post-weaning diarrhea in piglets, while Shiga toxin-producing *E. coli* (STEC) is an important foodborne pathogen. Recently, hybrid ETEC/STEC strains carrying virulence factors from both pathotypes have been increasingly reported, complicating disease control in the livestock industry. In the context of ongoing efforts to reduce antibiotic use, bacteriophages (phages) have emerged as a promising biocontrol agent. Here, we isolated and characterized a novel phage, SJ25, capable of infecting a broad range of ETEC and ETEC/STEC hybrid strains. Transmission electron microscopy revealed that SJ25 exhibits myovirus morphotype with an icosahedral head and contractile tail. The phage also demonstrated strong bacteriolytic activity and typical lytic characteristics against several ETEC *E. coli* isolates. In addition, SJ25 remained stable across various pH and temperature conditions. Genomic analysis showed that SJ25 possessed a 166,101 bp double-stranded DNA genome with a G+C content of 35.5%, encoding 261 predicted ORFs and 8 tRNAs without virulence or antibiotic resistance genes. Phylogenetic analysis classified SJ25 within the genus *Tequatrovirus* of the class Caudoviricetes. Overall, SJ25 represents a promising biocontrol candidate for the control of both ETEC and ETEC/STEC hybrid strains, supporting its potential application as a sustainable alternative to antibiotics in livestock production under a One Health framework.

Key words : bacteriophage, enterotoxigenic *Escherichia coli* (ETEC), ETEC/STEC hybrid, post-weaning diarrhea, biocontrol

PC26005

Spirobenzofuran isolated from *Acremonium* mitigates the negative effects of Ochratoxin A in porcine intestinal epithelial cells

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In the pig industry, the consumption of feed exposed to Ochratoxin A (OTA) causes various adverse effects, and absorbed OTA particularly targets the small intestine, resulting in hindered intestinal function. Antimicrobial peptides (AMPs) are small peptides present in the immune system that are revealed various functions such as toxin neutralization, wound healing, and cell growth. We confirmed through RNA-seq that Beta-defensin 1 (DEFB1), one of the AMPs, is significantly reduced by OTA, and hypothesized that the recovery of OTA-induced reduction in beta-defensin 1 could have a mitigating effect. The present study evaluated the mitigating effect in porcine intestinal epithelial cells (IPEC-J2 cells) exposed to OTA through the construction of DEFB1 overexpressing cell line and discovery of DEFB1-induced natural product. The study results showed that OTA induced cytotoxicity in IPEC-J2 cells, reduced cell migration, and increased the expression of inflammatory marker mRNA. Importantly, the overexpression of DEFB1 and the administration of Spirobenzofuran, a DEFB1-inducing natural compound selected through high-throughput screening, significantly mitigated the cytotoxicity, reduced cell migration, and increased inflammatory marker expression induced by OTA. These findings provide insights into the molecular mechanisms by which mycotoxins affect the intestinal epithelium and can aid in the selection of feed additives in the pig industry.

Key words : Ochratoxin A, porcine intestinal epithelial cells, beta defensin 1, high-throughput screening, spirobenzofuran

PC26006

Standardized safety evaluation protocols for *Enterococcus* spp. as probiotic candidates

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Enterococcus spp., such as *Enterococcus faecium* (*E. faecium*) and *Enterococcus faecalis* (*E. faecalis*), are recognized for their ability to inhibit the growth of pathogens and exhibit strong adhesion to the intestinal mucosa, underscoring their potential as probiotics. However, their safety is highly strain-dependent, as certain strains are associated with opportunistic pathogenicity and specific virulence determinants. Nevertheless, no globally harmonized safety standards currently exist for these bacteria. Therefore, this study aimed to establish a scientific foundation for the standardization of safety criteria for *Enterococcus* spp. The proposed evaluation framework encompassed seven key safety aspects: antibiotic resistance, hemolytic activity, lactate dehydrogenase activity, antimicrobial substance production, and biogenic amine production, along with genotoxicity assessments, specifically the bacterial reverse mutation test and the micronucleus assay. Validation was conducted using type strains of *E. faecium* and *E. faecalis*. Our results demonstrated that these standardized protocols were highly accurate and suitable for the safety evaluation of *Enterococcus* spp., providing a reliable framework for future industrial applications.

Key words : *Enterococcus*, probiotic safety, safety assessment

PC26007

Stress-associated cortisol elevation is associated with impaired nursing behavior and gut microbial alterations in periparturient sows

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Parturition is accompanied by substantial physiological stress, which may influence maternal behavior and the composition of the gut microbiota in sows. This study investigated whether stress-associated variation in cortisol levels is associated with gut microbial composition and maternal behavior in periparturient sows. A total of 22 primiparous sows were classified into low-cortisol (LC, n = 12) and high-cortisol (HC, n = 10) groups based on postpartum cortisol concentrations. Fecal samples were collected on day 1 after farrowing and analyzed using full-length 16S rRNA sequencing (PacBio). The HC group showed higher total nursing termination and lower carefulness scores than the LC group ($p < 0.05$ for all). The relative abundance of *Campylobacter coli* was significantly higher in the HC group than in the LC group. Correlation analysis indicated that *C. coli* tended to be negatively correlated with total nursing duration ($r = -0.40$, $p = 0.06$), total nursing bout duration ($r = -0.40$, $p = 0.06$), and unsuccessful nursing bout duration ($r = -0.39$, $p = 0.07$). The results indicate that elevated cortisol levels around parturition are associated with altered maternal behavioral patterns and distinct gut microbial composition in sows. The correlation between *C. coli* abundance and impaired nursing behavior further suggests a potential involvement of gut microbiota in maternal performance during the periparturient period.

Key words : *Campylobacter coli*, carefulness score, maternal behavior, microbial changes, parturition

PC26008

Comparison of electroporation conditions in mouse zygotes for improving CRISPR/Cas9-mediated ssODN knock-in efficiency

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Successful gene editing is essential for the generation of disease model animals, functional validation of genes, and gene therapy applications. The CRISPR/Cas9 system induces artificial double-strand breaks (DSBs) in the genome, which are repaired through either homology-directed repair (HDR) or non-homologous end joining (NHEJ). Although NHEJ-mediated knock-out can be achieved relatively easily, HDR-mediated knock-in remains technically challenging. To generate genetically engineered mice using the CRISPR/Cas9 system, genome-editing components are delivered into zygotes. Single-stranded oligodeoxynucleotides (ssODNs) shorter than 200 nt have been reported to exhibit relatively high knock-in efficiency. Compared with microinjection, electroporation is easier to perform and enables efficient delivery of genome-editing components into embryos. Therefore, this study evaluated the electroporation efficiency of ssODNs in mouse zygotes using the NEPA21 electroporator. A 200-nt ssODN containing a 34-bp loxP sequence was used to assess knock-in efficiency. Overall, embryo developmental rates decreased following electroporation regardless of electrode type compared with the control group. However, knock-in efficiency at the right-arm target locus was significantly increased in the group treated with high concentrations of ribonucleoprotein (RNP) complex and ssODN using the CUY505P5 electrode.

Key words : CRISPR/Cas9, ssODNs, electroporation, knock-in efficiency

PC26009

C. maltaromaticum-derived factors enhance white adipose beiging and lipolysis, ameliorating metabolic dysfunction in an HFD-induced obese mouse model

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Obesity drives metabolic syndromes like type 2 diabetes and non-alcoholic fatty liver disease, making probiotics a compelling alternative to traditional pharmaceuticals for restoring metabolic homeostasis. This study investigated the therapeutic potential and molecular mechanisms of *Carnobacteria maltaromaticum* and its culture supernatant in a high-fat diet (HFD)-induced obese mouse model. C57BL/6L mice were fed an HFD for six weeks while receiving *C. maltaromaticum* or its medium, compared against *Lactobacillus gasseri* BNR17 and Semaglutide controls. Metabolic health was evaluated via glucose and insulin tolerance tests and serum lipid profiling, while molecular changes in adipose tissues were analyzed through histology and qPCR. *C. maltaromaticum*-derived factors significantly suppressed weight gain without affecting food intake, suggesting direct metabolic modulation rather than appetite suppression. Intervention reduced total cholesterol and triglycerides while improving insulin sensitivity. At the tissue level, treatment decreased adipocyte hypertrophy and ectopic lipid accumulation. Molecular analysis showed the downregulation of adipogenic factors (SREBP1C, FAS, ACC) and the upregulation of lipolytic enzymes (ATGL, HSL). Importantly, increased expression of UCP1 and PGC1α in both white and brown adipose tissues indicates promoted energy expenditure through WAT beiging and BAT activation. In conclusion, *C. maltaromaticum* comprehensively ameliorates obesity by inhibiting adipogenesis, promoting lipolysis, and activating thermogenic programs, establishing it as a promising probiotic candidate for metabolic syndrome management.

Key words : *C. maltaromaticum*, obesity, probiotics, adipogenesis, lipolysis, browning, beige adipocytes, thermogenesis, UCP1

PC26010

Protective effects of Stanniocalcin 2 against oxidative stress in muscle cells

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Excessive accumulation of reactive oxygen species (ROS) disrupts cellular homeostasis and contributes to muscle damage and atrophy. In poultry, rapid growth and high metabolic rates increase susceptibility to oxidative stress in skeletal muscle, leading to impaired muscle development and breast muscle abnormalities. Therefore, clarifying the cellular mechanisms related to oxidative stress is essential. *Stanniocalcin 2* (*STC2*) is known to be involved in stress-related cellular functions; however, its specific role in skeletal muscle under oxidative conditions remains unclear. This study examined the function of *STC2* in H_2O_2-induced oxidative stress in muscle cells. Upon H_2O_2 exposure, *STC2* expression was upregulated in the quail muscle cell line. To evaluate its functional role, *STC2*-overexpressing muscle cells were established, allowed to differentiate for 4 days, and subsequently exposed to oxidative stress. *STC2* overexpression significantly improved cell survival, suppressed ROS accumulation, reduced cell death, and preserved myotube structure compared to control cells. These findings suggest that *STC2* plays a protective role in skeletal muscle cells under oxidative stress and may serve as a potential target for preventing oxidative stress-related muscle damage.

Key words : Stanniocalcin 2, oxidative stress, QM7 cell line, muscle differentiation, myotube

PC26011

Artepillin C triggers mitochondria-dependent apoptosis in canine osteosarcoma cell lines

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Artepillin C (ARC) is a prenylated derivative of p-coumaric acid and a major phenolic constituent of *Brazilian green propolis*. This compound has been reported to exhibit diverse pharmacological activities, such as antioxidant, anti-inflammatory, immunomodulatory, and anticancer properties. As osteosarcoma (OS) is the most prevalent skeletal malignancy in dogs, we investigated the anticancer effects of ARC on the canine OS cell lines DSN and D17.

In this study, we demonstrated that ARC significantly inhibited cell proliferation and induced apoptosis by triggering excessive ROS generation. Mechanistically, ARC treatment decreased cytosolic Ca^{2+} levels while increasing mitochondrial Ca^{2+} accumulation, leading to a significant loss of mitochondrial membrane potential. These findings suggest that Artepillin C is a promising therapeutic agent for canine OS that acts by inducing mitochondria-mediated apoptosis.

Key words : Artepillin C, osteosarcoma, apoptosis, mitochondria

PC26012

Effect of calving season on postpartum ovarian activity in Holstein cows

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This study investigated the effect of calving season on postpartum resumption of ovarian activity in Holstein cows under Korean climatic conditions, hypothesizing that summer heat stress delays reproductive recovery in spring-calving cows. A total of 20 multiparous cows (spring: n = 9; summer: n = 7; autumn: n = 4) were evaluated. Blood samples were collected weekly from 10 to 100 days postpartum. Resumption of luteal activity was defined as progesterone (P4) ≥ 1 ng/mL, with ovulation estimated 5 days prior to this detection. Fisher's exact test revealed that the proportion of cows with delayed ovarian activity resumption (61–80 days postpartum) was significantly higher in spring-calving cows (55.5%) than in summer (14.3%) and autumn (0%) groups ($p < 0.05$). Conversely, spring-calving cows tended to show lower early resumption rates (within 40 days) compared to other seasons (22.2% vs. 63.6%; $p < 0.1$). In conclusion, calving season may influence postpartum reproductive recovery in Holstein dairy cows under Korean climatic conditions. These results suggest that heat stress during the summer breeding period could negatively affect reproductive performance in spring-calving cows.

Key words : dairy cattle, heat stress, Holstein, postpartum ovarian activity, progesterone

PC26013

Effects of nonylphenol on oxidative stress and implantation-related functions in porcine luminal epithelial cells

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Nonylphenol (NP) is a widely distributed environmental endocrine-disrupting chemical that may be associated with reproductive dysfunction. In this study, we investigated the effects of NP exposure on endometrial function and implantation-related cellular responses using porcine luminal epithelial (pLE) cells. NP treatment decreased pLE cell viability in a concentration-dependent manner, indicating NP-induced cytotoxicity. qPCR analysis showed altered expression of inflammation-related genes, including IL18, IL21, NFKBIA, TNFα, and TGFβ1. NP also changed the expression of implantation-, adhesion-, and cell function-related genes, including VCAM1, ICAM1, IGF1, FGF2, LOX, and CCND1. Changes in antioxidant-related genes, including GCLC, NQO1, GPX1, SOD1, and GPX4, suggest that NP may disrupt cellular redox homeostasis. Annexin V assay demonstrated that NP induced apoptosis. Spheroid culture showed that NP altered three-dimensional structure formation in pLE cells. In addition, pTr transwell assay and pTr/pLE co-culture transwell assay indicated that NP may affect trophoblast cell migration and endometrial–trophoblast cell interactions. Taken together, these results demonstrate that NP can induce cytotoxicity, inflammatory responses, apoptosis, and implantation-related functional impairment in pLE cells. These findings suggest that NP may negatively affect porcine endometrial function and early implantation processes. This study provides evidence that pLE- and pTr-based *in vitro* models can be useful for evaluating the reproductive toxicity of environmental endocrine-disrupting chemicals.

Key words : nonylphenol, pLE cell, pTr cell, endometrium, oxidative stress, implantation, reproductive toxicity

PC26014

Adenovirus-mediated CRISPR/Cas9 system for efficient knockout of the ovalbumin gene in chicken cells

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Ovalbumin (OVAL) is the major protein component of egg white and an important target in food allergy and biopharmaceutical research. In this study, we aimed to establish a CRISPR/Cas9-based knockout system targeting the chicken OVAL gene and evaluate its in vitro editing efficiency. To induce deletion of exon 2 in the OVAL gene, two guide RNAs (gRNAs) targeting intron 1 and two gRNAs targeting intron 2 were designed. A total of four gRNAs (cOVAL_int1_gR1, cOVAL_int1_gR2, cOVAL_int2_gR1, and cOVAL_int2_gR2) were generated, and a dual-gRNA strategy was applied to induce exon 2 deletion. Adenovirus-based CRISPR/Cas9 vectors containing paired gRNAs were constructed and transduced into chicken embryonic fibroblasts (CEFs). Initial in vitro validation confirmed cleavage activity for all four gRNAs using PCR-based analysis. Subsequently, genome editing efficiency was evaluated for each dual-gRNA combination. Expected deletion bands ranging from approximately 258 to 315 bp were detected, along with additional deletion products of various sizes in some combinations, suggesting diverse genomic rearrangements at the target locus. The present study demonstrated the feasibility of establishing an adenovirus-based OVA knockout system in chicken cells. Further analyses, including gel extraction and Sanger sequencing, will be performed to characterize the editing patterns.

Key words : CRISPR/Cas9, genome editing, adenovirus, ovalbumin, chicken

PC26015

Development of bta-miR-375 biomarker associated with intramuscular fat deposition in Korean Native cattle

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Although SNP markers have been widely used for genetic improvement, they have limitations in explaining complex economic traits. This study aimed to elucidate the important role of bta-miR-375 in bovine adipogenesis and to evaluate its potential as a miRNA biomarker. Preadipocytes were isolated from Hanwoo adipose tissue and transfected with bta-miR-375, followed by adipogenic differentiation. Total RNA extraction, cDNA synthesis and qRT-PCR were performed to analyze the expression of adipogenesis and lipid metabolism-related genes. For biomarker developemnt, Plasma bta-miR-375 was also quantified in Hanwoo blood samples using miRNA-specific qRT-PCR. These results demonstrated that bta-miR-375 significantly upregulated the expression of adipogenesis- and lipid metabolism-related genes, including PPARγ, CEBPα, ADIPOR2, and GPAM, in bta-miR-375-treated cells compared with the negative control at day 14 of differentiation. Furthermore, bta-miR-375 was stably detected in all plasma samples within a Ct range of 20–27, demonstrating its technical feasibility as a circulating miRNA biomarker. These findings indicate that bta-miR-375 promotes lipid accumulation during early adipogenic differentiation in Korean native cattle. Taken togather, these study suggests the potential application of bta-miR-375 as a biomarker for improving meat quality traits.

Key words : bta-miR-375, circulating biomarker, adipogenesis genes, intramuscular fat deposition, Korean native cattle

PC26016

Preliminary deep learning-based image analysis for segmentation-assisted measurement of jejunal mucosal morphology of weaning pigs under different nutritional conditions

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Nutritional imbalance can affect jejunal mucosal morphology and intestinal function in piglets. Accordingly, villus height (VH), crypt depth (CD), and the VH/CD ratio are widely used indicators of intestinal morphology, but these parameters are commonly measured manually from hematoxylin and eosin-stained tissue sections, which is time-consuming and may be affected by observer-dependent variability. This study aimed to develop a preliminary deep learning-based image analysis approach for segmentation-assisted measurement of VH and CD in porcine jejunal tissue under different nutritional conditions. A total of 223 jejunal tissue images were collected from weaning pigs at day 21 and day 42 after feeding either a basal diet (CON) or a restricted nutrition diet (TRT). Images were annotated using four mutually exclusive classes: background, villus, crypt, and lumen, with labeling focused on villus-crypt structures suitable for morphometric evaluation. A deep learning-based image analysis model was trained using the annotated dataset. Conventional morphology data showed that the TRT group had greater VH, lower CD, and a higher VH/CD ratio than the CON group. Mask-derived morphometric indices showed a similar biological pattern, particularly for the age-related increase in VH and the increased VH/CD ratio in the TRT group. The VH/CD ratio, which was the primary morphometric indicator in this study, was accurately showing a relative agreement of 89.0% compared to conventional morphology results. These preliminary findings suggest that deep learning-based image analysis has potential as an objective tool for intestinal morphometry in piglets.

Key words : piglet, jejunum, villus height, crypt depth, deep learning, image analysis, intestinal morphometry

PC26017

Effects of commercial feed additive on methane reduction and microbial communities in Korean Native cattle

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Recent implementation of national carbon-neutrality policies has increased interest in commercial feed additives for reducing enteric methane emissions from ruminants. Therefore, this study evaluated the methane mitigation effect of an allicin-containing commercial feed additive through *in vitro* rumen fermentation and field validation trials. *In vitro* fermentation was conducted using rumen fluid in the AnkomRF Gas Production System with a TMR substrate control, a monensin-supplemented control, and commercial methane-reducing feed additive treatments. Among the treatments, T4 showed the lowest methane production, corresponding to 92.35% of the control, and was selected for field validation. The selected additive was administered to 12 Korean Native cattle at 1% of dietary DM, and daily CH_4 emissions were significantly reduced from 140.4 g/d in the control group to 124.5 g/d in the treatment group, representing an 11.3% reduction ($p = 0.049$). Full-length 16S rRNA sequencing was performed using rumen fluid samples on the PacBio Sequel II platform, and microbial community analysis will be conducted based on non-chimeric ASVs. Taken together, these findings suggest that the allicin-containing commercial feed additive effectively mitigated methane emissions without compromising dry matter intake, indicating its potential as a practical methane mitigation strategy for Korean Native cattle.

Key words : Korean native cattle, ANKOM system, methane emission reduction, commercial feed additive, 16S rRNA full-length sequencing

PC26018

Development of a prediction model for methane emission in Korean Native cattle

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Methane (CH_4), a potent greenhouse gas 28 times more warming than CO_2, mainly originates from ruminant enteric fermentation. For its measurement, direct tools like respiration chambers and the Greenfeed system exist, yet limited sampling capacity hinders their use in diverse conditions. Therefore, multiple linear regression (MLR) equations have been widely utilized for indirect methane prediction due to their simplicity, interpretability, and applicability across datasets. The aim of this study was to develop a predictive equation capable of estimating CH_4 emissions (g/day) from Korean native cattle under field conditions. A MLR equation was constructed using body weight (BW), dry matter intake (DMI), and the CH_4/CO_2 ratio as input variables. Equation performance was estimated using adjusted R^2, root mean square error (RMSE), and the concordance correlation coefficient (CCC). The equation incorporating the three predictors achieved the highest accuracy, yielding an adjusted conditional R^2 of 0.860, an RMSE of 18.382 and a CCC of 0.951. The developed MLR equation demonstrates strong predictive performance and may serve as a practical tool for estimating CH_4 emissions from Korean native cattle. Furthermore, it is expected to contribute benchmark data and technical foundations for national methane mitigation strategies and the improvement of livestock GHG inventory systems in Korea.

Key words : methane emission, Korean native cattle, multiple linear regression, respiration chamber, ruminant greenhouse gas

PC26019

Effects of vitamin E and glutamine on stress-responsive and myogenic gene expression in heat-stressed bovine skeletal muscle-derived cells

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Heat stress (HS) impairs skeletal muscle development by inducing oxidative stress and disrupting myogenic programs. This study evaluated the individual and combined effects of vitamin E (Vit E; 0.1 or 1 μM) and L-glutamine (Gln; 1 or 10 mM) on antioxidant, apoptotic, and myogenic gene expression in bovine skeletal muscle-derived cells (BSMCs) isolated from three Korean native cattle. BSMCs were cultured at 37°C (control) or 41°C (HS) for 24 h at differentiation day 6 across six treatment groups. One-way ANOVA was performed using PROC GLM of SAS 9.4. HS elevated ($p < 0.05$) HSP70, SOD1, and MYOD while reducing FBXO32, an atrophy marker. Gln supplementation (1 and 10 mM) upregulated MYOG expression in a dose-dependent manner, suggesting enhanced terminal myogenic differentiation. Vit E (0.1 μM) and low Vit E + low Gln upregulated ($p < 0.05$) MYF5, an early myogenic regulator. The combination of high Vit E and high Gln uniquely upregulated ($p < 0.05$) NFE2L2 and GPX1, activating Nrf2-mediated antioxidant defense, and downregulated ($p < 0.05$) the apoptotic marker CASP3. These findings suggest that combined Vit E and Gln supplementation enhances antioxidant capacity and suppresses apoptosis in heat-stressed BSMCs.

Key words : heat stress, bovine skeletal muscle-derived cells, glutamine, vitamin E, myogenesis, antioxidants

PC26020

Heat stress-induced temporal shifts in the fecal microbiome and predicted functional pathways of laying hens using 16S rRNA gene sequencing

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Heat stress impairs productivity, immune function, and nutrient utilization in laying hens; however, its temporal effects on the fecal microbiome and associated functional pathways remain unclear. This study investigated time-dependent changes in the fecal microbiome and 16S rRNA-based predicted functional pathways during prolonged heat stress. A total of 48 Lohmann Brown laying hens (26 weeks old) were exposed to heat stress for 14 days at THI 82 (33°C, 66% relative humidity), and fecal samples were collected on day 0, day 7, and day 14. Fecal bacterial 16S rRNA V3–V4 sequencing data were processed with QIIME2, followed by alpha and beta diversity analyses, LEfSe-based discriminative taxa identification, and PICRUSt2-based functional prediction. Alpha diversity remained unchanged; however, PCoA based on Bray-Curtis, unweighted UniFrac, and weighted UniFrac distances revealed time-dependent shifts in microbial community structure during prolonged heat stress. LEfSe identified 50 discriminative taxa ($LDA > 3.5$); Lactobacillus, Enterobacteriaceae, Klebsiella, and Veillonella were enriched at day 14. PICRUSt2 predicted 39 functional pathways ($FDR < 0.05$), mainly involving carbohydrate utilization and fermentation at day 14. In summary, prolonged heat stress alters the fecal microbiome of laying hens by shifting microbial community composition and predicted metabolic functions, particularly pathways related to carbohydrate utilization and fermentation, which may be associated with microbial responses to prolonged heat stress.

Key words: laying hens, heat stress, fecal microbiome, gut microbiota, 16S rRNA sequencing, LEfSe, PICRUSt2

PC26021

Comparative analysis of physiological and transcriptomic responses to heat stress in laying hens in different time period using RNA-seq

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Increasing global temperatures and humidity associated with climate change have intensified heat stress as a major challenge in poultry production. This study evaluated the effects of different THI conditions on laying performance, physiological responses, and transcriptomic changes in laying hens over a 14-day period. Forty-eight 26-wk-old Lohmann Brown laying hens were assigned to THI 68 or THI 85 (24 birds / group) and blood samples for RNA-seq were collected on days 0, 7, and 14. RNA-seq analysis was performed to identify DEGs ($FDR < 0.05$, $|\log2FC| \geq 1$), followed by functional enrichment via DAVID. In the THI 85 group, feed intake, body weight gain, egg production, and egg quality traits decreased, while water intake, rectal temperature, and serum potassium levels increased. DEGs identified were 40 in Day 0 vs. 7 (12 up, 28 down), 292 in Day 0 vs. 14 (152 up, 140 down), and 22 in Day 7 vs. 14 (15 up, 7 down). At Day 7, upregulated *Hmox1* and *Jchain* linked to heme binding and detoxification-related pathways indicated acute oxidative stress. By Day 14, upregulation of *Oma1*, *Bnip3*, and *Acsl1* was associated with mitochondrial homeostasis and metabolic reprogramming (fatty acid biosynthesis and pentose phosphate pathway) for chronic stress adaptation. In summary, high THI impairs laying hen productivity and egg quality. Transcriptomic analysis suggests a time-dependent shift from acute oxidative stress toward long-term cellular adaptation. These findings provide insights into the importance of environmental management and future selection strategies for enhancing heat tolerance in laying hens.

Key words : laying hen, heat stress, RNA-seq, transcriptome, physiological response

PC26022

Immunoinformatics-based design and *in silico* evaluation of a multi-epitope vaccine candidate against porcine reproductive and respiratory syndrome virus

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Porcine reproductive and respiratory syndrome virus (PRRSV) causes significant economic losses in the global swine industry. As the high genetic variability of circulating strains limits the cross-protective efficacy of current modified-live and inactivated vaccines, we employed an immunoinformatics pipeline to design a multi-epitope subunit vaccine (MESV) targeting conserved and immunologically relevant regions of the PRRSV proteome. We prioritized three proteins (GP3, GP4, and RPP1TF) based on their antigenicity and immune accessibility. The MESV was then assembled by systematically screening and combining predicted B- and T-cell epitopes. Linkers (EAAAK, KK, and AAY) were incorporated to maintain epitope integrity and ensure optimal antigen processing. To enhance the immunostimulatory properties of the vaccine construct, the 50S ribosomal protein L7/L12, a well-characterized TLR4 agonist, was utilized as an adjuvant. Physicochemical characterization indicated favorable stability and antigenicity. The docking analyses revealed stable interactions with porcine Toll-like receptors (TLR3 and TLR4), which were further confirmed by molecular dynamics simulations and MM-GBSA binding free energy calculations. Immune simulations predicted robust activation of both humoral and cellular immunity. These in silico findings suggest that the proposed MESV is a promising candidate for further *in vitro* and in vivo validation to improve PRRSV control strategies.

Key words : porcine reproductive and respiratory syndrome virus (PRRSV), multi-epitope subunit vaccine, immunoinformatics, molecular docking, molecular dynamics simulation

PC26023

Engineering the delta-9 pathway for *de novo* synthesis of eicosapentaenoic acid (EPA) in *Yarrowia lipolytica*

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Eicosapentaenoic acid (EPA) is an omega-3 polyunsaturated fatty acid involved in inflammatory regulation and cardiovascular health, with broad applications in food, feed, and nutraceutical products. In particular, because mammals have a limited ability to biosynthesize omega-3 fatty acids, dietary intake is essential. However, current EPA production largely relies on fish oil, which raises concerns over marine resource depletion and heavy metal contamination. Thus, sustainable microbial production systems are needed as alternative sources of EPA. In this study, an EPA-producing strain (EPA strain) was constructed using the oleaginous yeast *Yarrowia lipolytica*, which naturally produces fatty acids only up to linoleic acid. To establish the EPA biosynthetic pathway, four heterologous pathway genes (*Δ9E*, *Δ8D*, *Δ5D*, and *Δ17D*), encoding one elongase and three desaturases, were sequentially integrated into the *A08* pseudogene locus at intervals of less than 500 nt using the CRISPR-Cas9 system. After establishing the EPA strain, *DGA1*, encoding diacylglycerol acyltransferase involved in neutral lipid synthesis, was inserted into the *PEX10* locus, which is involved in peroxisome biogenesis, to further improve EPA productivity. This one-step strategy was designed to increase fatty acid accumulation by enhancing neutral lipid synthesis while reducing peroxisomal fatty acid degradation. The engineered strains were analyzed by qRT-PCR, GC-FID, HPLC, and lipid body staining to evaluate gene expression, fatty acid composition and EPA content, carbon source consumption and organic acid production, and intracellular lipid accumulation. As a result, the *DGA1*-integrated EPA strain (EPA-DGA1 strain) showed approximately 3-fold higher total fatty acid content and 2-fold higher EPA content than the EPA strain. These findings support the use of engineered *Y. lipolytica* as a sustainable microbial EPA source, with potential food and feed applications to improve omega-3/omega-6 fatty acid balance in humans and livestock.

Key words : yeast, EPA, omega-3, CRISPR Cas-9, *Yarrowia lipolytica*

PC26024

Evaluation of antioxidant probiotic potential of lactic acid bacteria isolated from swine feces and fermented foods

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Lactic acid bacteria with antioxidant potential are considered useful candidates for improving gut health and maintaining redox balance. This study aimed to screen antioxidant probiotics candidates isolated from 3-week-old piglet feces and kimchi. Approximately 40 bacterial isolates were obtained by selective anaerobic culture, and 9 lactic acid bacterial strains were selected for evaluation. Their probiotic properties were assessed by acid tolerance, bile tolerance, intestinal adhesion ability, auto-aggregation, and cell surface hydrophobicity. Antioxidant activity was determined using DPPH and ABTS radical scavenging assays. Based on overall probiotic and antioxidant properties, three strains were selected as final candidates, and their safety was confirmed by hemolytic activity and bile salt hydrolase associated assessments. Among the candidates, kimchi-derived *Limosilactobacillus reuteri* showed excellent probiotic potential, including 94.95% acid tolerance, 93.05% bile tolerance, and 61.65% intestinal adhesion ability. It also showed the highest antioxidant activity, with 51.06% DPPH and 41.02% ABTS radical scavenging activity. In LPS-stimulated RAW 264.7 cells, this strain increased *Nqo1* expression at 3 h and strongly induced *Hmox1* expression at 6 h, indicating a possible association with NRF2/KEAP1-related antioxidant responses. These findings suggest that kimchi-derived *L. reuteri* is a promising antioxidant probiotic candidate.

Key words : *Limosilactobacillus reuteri*, antioxidant activity, NRF2/KEAP1 pathway

PC26025

Identifying time-dependent molecular adaptations to heat stress in finishing pigs through longitudinal blood transcriptome profiling

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Heat stress poses a major challenge to swine production by reducing feed intake, metabolic efficiency, and immune function. However, the molecular basis of metabolic adaptation to chronic heat exposure remains poorly understood. This study investigated time-dependent metabolic changes in finishing pigs exposed to heat stress for 14 days. Nine pigs [(Landrace × Yorkshire) × Duroc] were assigned to thermoneutral (TN, 23–24°C, n = 5) and heat-stressed (HS, 32–33°C, n = 4) groups, and whole-blood samples were collected at weeks 0, 1, and 2. RNA sequencing, differential expression, and functional enrichment analyses were performed to characterize longitudinal responses to heat stress. Using a linear mixed model with group × time interaction, differentially expressed genes (DEGs) were identified based on FDR < 0.05 and $|\log_2 FC| > 1$. A total of 257 DEGs were identified at week 1, 131 DEGs at week 2, and 608 DEGs from the interaction term, indicating a temporal shift in transcriptional responses. Early responses were enriched for cell cycle, heme biosynthesis, and porphyrin metabolism pathways, whereas later responses were associated with erythrocyte differentiation, AMPK signaling, and ferroptosis pathways. These findings suggest that chronic heat stress induces dynamic transcriptional changes associated with metabolic and homeostatic adaptation in finishing pigs, providing molecular insight into the biological processes underlying heat tolerance.

Key words : heat stress, finishing pigs, transcriptome, RNA-seq, longitudinal design, repeated measures

PC26026

전사체 분석(RNA-seq)을 통한 돼지 고환 탈장 관련 차등발현유전자 및 조절 네트워크 발굴

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돼지 고환탈장은 장기 탈출에 따른 성장 지연 및 폐사 등으로 농가에 경제적 손실을 초래하는 복합 유전 질환이다. 동일 사양 조건에서도 개체별 발생 차이가 뚜렷하나, 기존 특정 유전자 중심 연구로는 전반적인 기전 설명에 한계가 있다. 따라서 본 연구는 전사체 분석(RNA-seq)을 통해 정상 개체와 환축 간의 mRNA 발현 차이를 비교하여 분자 유전학적 발병 기전을 구명하고자 하였다. 제주 난지축산연구센터에서 사육한 랜드레이스와 제주재래돼지의 교배로 생산된 자돈을 대상으로 이유시점인 3주령에 표현형 조사를 실시하여 고환탈장 환축 6두와 정상축 10두를 사용하였다. 선별된 개체의 등심 조직에서 RNA를 추출하여 RNA-seq을 수행하였다. 추출된 발현 데이터는 edgeR 패키지 이용해 차등발현 유전자 분석하였고, Gene Ontology 및 Kyoto Encyclopedia of Genes and Genomes 네트워크 분석을 실시하였다. 정상축과 환축 간 총 3,218개의 유의한($FDR < 0.05$, $|\log_2 FC| \geq 1$) 차등발현 유전자를 확인하였다. 기능 분석(GO, KEGG, 네트워크) 결과, 세포 유착(cell adhesion), 세포외기질(ECM) 항상성, 국소 부착(focal adhesion) 및 조직 형태 형성(tissue morphogenesis) 등 결합조직 구조 조절 경로들의 복합적인 상호작용이 두드러지게 나타났다. 결론적으로, 이러한 구조적 네트워크 및 유전자 발현 패턴의 변화는 고환탈장의 해부학적 배경과 연관될 가능성을 시사한다. 발굴된 주요 차등 발현 유전자 신호전달 경로는 고환탈장 발생 기전 이해 및 추가연구를 위한 기초 자료를 넘어, 향후 양돈 산업에서 고환탈장 발생률을 낮추고 저항성 개체를 선별하기 위한 핵심 지표로 적극 활용될 수 있을 것이다.

Key words : 고환탈장, 제주재래돼지, 전사체 분석, 차등발현유전자, 세포외기질

PC26027

Effect of *Cordyceps militaris* powder on dextran sulfate sodium-induced colitis in mice

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This study evaluated the effects of *Cordyceps militaris* (CM) powder on intestinal inflammatory response, enteroendocrine cell hormone secretion, intestinal receptor expression, and intestinal barrier function using an *ex vivo* mouse model. The ileum was collected from 12-week-old male ICR mice (n = 6) and cultured in Krebs-Ringer Bicarbonate/HEPES (KRB/HEPES) buffer under two conditions: control (CON) and CM treatment (100 mg/kg) at 37°C with 5% v/v CO_2. Following incubation, glucagon-like peptide-1 (GLP-1) concentration in the culture medium was measured by ELISA, and the relative mRNA expression of GCG, Tas1r2, NfkB1, TNF-α, IL-6, ZO-1, OCLN and CLDN4 was analyzed by RT-qPCR. GLP-1 secretion did not differ significantly between the CON and CM groups ($p > 0.05$), as GLP-1 secretion in vivo involves complex regulatory mechanisms encompassing intestinal L cells, gut microbiota, short-chain fatty acids, and various luminal nutrients. CM treatment significantly improved the relative mRNA expression of inflammation-related genes compared to the control group ($p < 0.05$). These results suggest that the diverse bioactive compounds present in CM may attenuate intestinal inflammatory responses. Further in vivo studies are warranted to elucidate the mechanisms by which CM modulates intestinal endocrine function and inflammatory regulation.

Key words : *Cordeyceps militaris*, *ex vivo*, enteroendocrine cells, GLP-1, intestinal inflammation

PC26028

Modeling interferon-associated transcriptomic dynamics following kidney xenograft transplantation through gene regulatory network inference and time-lagged dynamical modeling

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Kidney xenotransplantation has emerged as a promising strategy to overcome donor organ shortage, yet its clinical application remains constrained by systemic immune and inflammatory dysregulation. This study investigated survival-associated temporal immune dynamics using longitudinal whole-blood transcriptomic profiles obtained from one recipient in each of three survival categories after pig-to-nonhuman-primate kidney xenotransplantation. Trajectory-based gene selection, functional enrichment analysis, Dynamic bayesian network inference, and delay differential equation modeling were integrated to characterize shared and group-specific expression dynamics. The transcriptomic response may reflect host recognition of the xenograft as a persistent foreign antigenic stimulus, leading to activation of interferon-stimulated antiviral defense programs. Representative interferon-stimulated genes showed earlier and sustained induction in short-term survival, whereas long-term survival exhibited delayed and attenuated activation. Network inference identified survival group-dependent regulatory edge patterns, and dynamic modeling achieved coefficients of determination greater than 0.8 for 18 of the 35 shared genes, with *USP18*, *DDX60*, and *OAS1* of exceeding 0.9. Permutation validation confirmed that temporal structure was essential for model performance. These findings suggest that longitudinal transcriptomic modeling can reveal dynamic risk signals and provide a framework for post-transplant host responses.

Key words : kidney xenotransplantation, longitudinal modeling, transcriptomics, gene regulatory network, interferon-stimulated genes

PC26029

Transcriptomic and microbiome profiling of heat stress responses in the broiler jejunum

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Heat stress (HS) disrupts intestinal physiology, host metabolism, and gut microbial balance in broiler chickens. Although transcriptomic and microbiome changes under HS have been widely studied, the regulatory interactions among long non-coding RNAs (lncRNAs), mRNAs, and gut microbiota remain unclear. In this study, RNA-seq-based jejunal transcriptome and microbiome data from four HS-exposed and four thermoneutral broilers were analyzed using an integrated multi-omics framework. Differential expression analysis (FDR < 0.05, $|\log_2 FC| > 1$) identified 139 mRNAs and 140 lncRNAs associated with HS, together with microbial features linked to stress conditions. Functional enrichment analysis indicated that HS-responsive genes were mainly involved in metabolic, membrane-associated, and immune-related pathways, including retinol metabolism and cholesterol-related processes. Several bacterial taxa associated with inflammatory responses, mucosal immune activity, and nutrient metabolism were enriched under HS conditions. In addition, opposite expression tendencies between mRNAs and lncRNAs may suggest potential lncRNA-mediated regulation of stress-responsive genes. Overall, these findings provide insight into host transcriptional and microbial alterations associated with HS in the broiler jejunum and improve understanding of host–microbiome interactions under heat stress conditions.

Key words : chicken, heat stress, jejunum, microbiome, transcriptome, lncRNA

PC26030

Multi-tissue longitudinal transcriptomics identifies adaptive immunity and lymphoepithelial homeostasis as drivers of interindividual PRRSV susceptibility in weaning piglets

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Porcine reproductive and respiratory syndrome virus (PRRSV) remains a major economic burden to the global swine industry due to its high genetic diversity and different virulence levels. Elucidating the biological basis of individual variation in clinical outcomes is crucial for disease control. To identify host factors underlying differential susceptibility, we performed longitudinal, multi-tissue RNA-seq based transcriptomic profiling of the lungs, bronchial lymph nodes (BLNs), and tonsils of PRRSV-infected 34 piglets. Animals were classified into non-susceptible and susceptible phenotypes based on average daily gain (ADG). While early innate antiviral responses were similar, non-susceptible pigs exhibited stronger, metabolically supported adaptive immunity in lymphoid tissues during later infection stages. Conversely, susceptible pigs showed upregulation of genes associated with epithelial damage and remodeling, particularly in the tonsils. Weighted gene co-expression network analysis (WGCNA) revealed that genes governing epithelial barrier integrity and keratinization—specifically *KRT78*, *IVL*, and *KLK10*—acted as central regulatory hubs distinguishing the susceptible phenotype. These findings demonstrate that PRRSV susceptibility depends on both robust adaptive immunity and the maintenance of lymphoepithelial homeostasis. This approach provides novel insights into the biological basis of disease resilience, offering potential host-directed strategies for PRRSV control.

Key words : PRRSV, susceptibility, RNA-seq, lymphoid tissues, epithelial homeostasis

PC26031

Application of exosomes as a functional culture supplement for bovine muscle satellite cells in cultured meat production

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Bovine muscle satellite cells (BMSCs) are a major cell source for cultured meat production because of their proliferation and myogenic differentiation capacity. However, continuous passaging can reduce their proliferative capacity and accelerate cellular aging, limiting their long-term use. This study evaluated the effects of exosome supplementation on the proliferation and long-term culture stability of BMSCs. Exosomes were analyzed using nanoparticle tracking analysis and transmission electron microscopy, which confirmed their particle characteristics and typical round vesicle-like morphology. Cell experiments were conducted at passages 5 and 10 using cell proliferation assay, live/dead staining, and immunofluorescence analysis. The comparison between P5 and P10 showed that 100 μg/mL exosome-treated BMSCs maintained significantly higher cell growth even at P10 compared with the control group ($p < 0.0001$). Live/dead staining showed continued cell growth in the 100 μg/mL exosome-treated group, and differentiated cells formed comparable myotube-like structures at both P5 and P10. These results suggest that exosome supplementation helps maintain the viability, proliferation, and myogenic differentiation potential of BMSCs during continuous passaging. Therefore, exosomes could be used as a functional culture supplement for cultured meat production.

Key words : exosome, cell culture, bovine muscle satellite cells, proliferation, long-term culture

PC26032

Development of gelatin-based edible scaffolds for muscle satellite cell culture in cultured meat production

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In cultured meat production, edible three-dimensional scaffolds with extracellular matrix (ECM)-like properties are needed to support cell adhesion, proliferation, and differentiation under in vitro culture conditions. In this study, wet-spinning-based edible composite scaffolds were fabricated using gelatin and plant-derived materials and applied to muscle satellite cell culture. The gelatin based composite solutions showed a gradual increase in viscosity as the content of plant-derived materials increased. Cell proliferation was compared on days 1, 3, 5, and 7, and cells cultured on the T2 scaffold showed a significantly higher growth rate than those cultured on the other scaffold groups ($p < 0.001$). Live/dead staining confirmed that cells were stably attached to the scaffold surface on day 1 and gradually proliferated by day 7. These results suggest that gelatin-based composite scaffolds can effectively support muscle satellite cell attachment and proliferation and may be used as edible three-dimensional scaffolds for cultured meat production.

Key words : scaffold, cell culture, bovine muscle satellite cells, proliferation, wet-spinning

PC26033

CRISPR/Cas9-mediated knockout of ISG15 and IDO1 in porcine alveolar macrophages for PRRSV resistance studies

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Porcine reproductive and respiratory syndrome virus (PRRSV) remains one of the most economically important viral pathogens in swine production, highlighting the need for host-directed strategies to improve resistance. In this study, we generated CRISPR/Cas9-mediated ISG15 and IDO1 knockout porcine alveolar macrophage (PAM) cell lines as candidate models for PRRSV resistance research. Four guide RNAs were designed for each target gene, and genome editing was followed by single-cell dilution cloning. Because both genes are inducible immune-related factors, protein expression was assessed after interferon stimulation. ISG15 protein was detected in parental cells after interferon treatment but was absent in ISG15-edited cells. Genotyping PCR and Sanger sequencing confirmed ISG15 clone 27 as a successfully edited clone harboring an approximately 254-bp deletion near the target region. Similarly, IDO1 protein expression was induced by IFN-γ in parental cells but was not detectable in IDO1-edited cells. Genotyping PCR and sequencing identified IDO1 clone 9 as a candidate edited clone with an approximately 105-bp deletion at the target site. These results confirm the successful establishment of ISG15- and IDO1-deficient PAM cell lines. Because both genes are closely linked to interferon-mediated antiviral and immunoregulatory pathways, these edited cells provide a useful platform for investigating host-gene-dependent modulation of PRRSV infection. Ongoing challenge studies will determine whether loss of ISG15 or IDO1 alters viral replication and macrophage antiviral responses.

Key words : PRRSV, CRISPR/Cas9, ISG15, IDO1, porcine alveolar macrophages, genome editing, antiviral immunity

PC26034

Comparative molecular docking and dynamics analysis of milk β-casomorphin binding across opioid receptor family

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β-Casomorphins (BCMs) are opioid-like peptides generated from β-casein during gastrointestinal digestion. Although BCM7 has been well studied for its interaction with the μ-opioid receptor (MOR), the binding properties of other BCM variants remain unclear. This study investigated the receptor-specific binding behavior of BCM3–BCM11 against MOR, δ-opioid receptor (DOR), κ-opioid receptor (KOR), and nociceptin/orphanin FQ peptide (NOP) receptors. Three-dimensional BCM structures were generated and docked to each opioid receptor subtype. Docking scores and binding poses were compared to identify receptor-preferred BCM variants by using Glide SP-Peptide docking. Selected high-affinity complexes were further analyzed using molecular dynamics simulations by 500ns. Docking analysis showed that BCM7 had the lowest docking score for MOR (−10.503 kcal/mol), whereas non-MOR receptors preferentially interacted with other BCM variants, including BCM11 for DOR (−9.039 kcal/mol) and KOR (−11.959 kcal/mol), and BCM9 for NOP (−10.798 kcal/mol). Molecular dynamics and protein –ligand contact analyses showed that representative BCM–receptor complexes reached equilibrated conformational states and maintained recurring receptor–peptide interaction networks supported by hydrogen bonding, hydrophobic contacts, ionic interactions. Overall, these findings suggest that BCM7 dominance is mainly MOR-specific, while other BCMs may preferentially bind non-MOR opioid receptors.

Key words : opioid receptor, β-casomorphins, peptide docking, molecular dynamics simulation

PC26035

Lipopolysaccharide-induced alterations in barrier integrity and inflammatory signaling in porcine small intestinal organoids

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Inflammation-associated diseases in pigs damage the intestinal tract and impair its function, posing a major threat to animal health and productivity. However, current *in vitro* models do not adequately replicate porcine physiological conditions. This study aimed to establish a novel inflammation model using porcine small intestinal organoids (pSIOs) derived from adult jejunum and stimulated with lipopolysaccharide (LPS). Inflammatory responses were evaluated through cytokine mRNA expression, intestinal barrier integrity, and changes in the expression and localization of nutrient transporters, receptors, and an enteroendocrine hormone associated with absorptive function using quantitative real-time PCR and immunofluorescence staining. Transcriptome analysis was also performed to identify LPS-responsive genes and enriched pathways. LPS successfully induced inflammation in pSIOs, as shown by increased cytokine expression, impaired barrier function, and altered nutrient transporter expression. Transcriptomic profiling further revealed broad transcriptional changes, including enrichment of immune- and inflammation-related pathways, as well as pathways associated with barrier maintenance and cellular adaptation to inflammatory stress. Collectively, these findings demonstrate that pSIOs represent a physiologically relevant *in vitro* model for studying porcine intestinal inflammation. This platform may be useful for investigating disease mechanisms and screening therapeutic candidates while supporting the 3Rs principles by reducing animal use.

Key words : lipopolysaccharide, inflammation, porcine, small intestinal organoid, disease model

PC26036

Sustained lactogenic differentiation of bovine mammary epithelial cells through RAC1 overexpression

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In the lactating mammary gland, mammary epithelial cells (MECs) are embedded within the extracellular matrix (ECM). Interactions between MECs and ECM activate RAC1, a Rho family small GTPase, which regulates signaling mechanisms involved in lactogenic differentiation. MEC–ECM interactions also regulate physiological processes, including cell polarization, differentiation, and reduced cell death, thereby facilitating long-term cell culture. This study aimed to investigate the effects of RAC1 activation in MAC-T cells on sustained lactogenic differentiation. MAC-T cells were transduced with lentiviral vectors to overexpress either GFP (GFPO) or RAC1 (RAC1O). To mimic an ECM-surrounding condition, GFPO cells were cultured on Matrigel-coated plates (M_GFPO). All cells were differentiated using lactation hormones. Increased active RAC1 levels, indicated by RAC1-GTP, were observed in both RAC1O and M_GFPO cells. In GFPO cells, cell viability and lactogenic differentiation persisted for only 10 days, after which cytotoxicity increased and differentiation capacity decreased. By comparison, RAC1O cells sustained cell viability and lactogenic differentiation for up to 20 days, whereas M_GFPO cells maintained these characteristics for up to 15 days. Collectively, these results demonstrate that RAC1 contributes to the prolonged maintenance of lactogenic differentiation and suggest that RAC1 activation may underlie ECM-mediated regulation of mammary gland function.

Key words : RAC1, matrigel, bovine mammary epithelial cell, lactogenic differentiation

PC26037

Dynamic molecular transitions of sperm storage tubules are associated with long-term sperm retention after artificial insemination in chickens

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Artificial insemination (AI) is an important reproductive technology in poultry breeding and production facilitating efficient genetic dissemination and reproductive management. In birds, AI enables prolonged fertility after a single insemination, largely due to sperm storage tubules (SST) located in the uterovaginal junction (UVJ). However, the molecular mechanisms by which SST support long-term sperm retention remain incompletely understood. In this study, we investigated time-dependent histological and transcriptomic changes in SST-containing UVJ tissues containing SST after AI. Histological analysis showed that sperm were absent before AI, became clearly detectable in SST at 3 days after AI, remained abundant at 7 days, and gradually declined thereafter, although sperm were still present in some SST at 21 days. No obvious structural damage to the SST epithelium was observed throughout the observation period. To characterize molecular responses during this process, RNA sequencing was performed on UVJ tissues containing SST collected at multiple post-AI time points. Among 8,522 expressed genes, distinct time-dependent expression patterns were identified, with the largest transcriptomic shift occurring at 3 days after AI (2,553 upregulated and 2,867 downregulated genes versus control), followed by persistent but gradually reduced transcriptional changes at later time points. Functional enrichment analyses revealed that genes showing gradual increases over time were associated with calcium, MAPK, and Wnt signaling, extracellular matrix interaction, focal adhesion, actin cytoskeleton regulation, and lipid-related metabolic pathways, whereas genes showing gradual decreases were enriched in immune-, inflammatory-, and defense-related pathways, including phagosome, necroptosis, and infection-associated terms. GO analysis further supported a transition from an early reactive state toward a more regulated functional state. Real-time RT-PCR validation of selected representative genes generally confirmed the major temporal trends identified by RNA-seq. Collectively, these findings indicate that long-term sperm storage after AI is accompanied by staged histological and transcriptomic reprogramming in UVJ tissues containing SST and suggest that prolonged sperm retention in birds is associated with dynamic molecular adaptation of the SST microenvironment.

Key words : uterovaginal junction, artificial insemination, sperm storage tubules, chicken

번식 및 생리

PD26001

Multigenerational effects of gestational BBP exposure on sperm function in mice

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Butyl benzyl phthalate (BBP), widely used in plastic manufacturing, is a potential endocrine disruptor and may pose a public health risk. However, its effects on male reproductive function across multiple generations (F2-F3) remain unclear. Therefore, this study investigated the multigenerational effects of gestational BBP exposure on sperm function, assessing generation-specific alterations. Pregnant female mice (F0) were orally administered BBP at doses of 0, 100, 250, and 500 mg/kg/day from gestation day (GD) 7 to 20 (until parturition). Male offspring from F1 to F3 generations were evaluated without additional exposure. The testis index of offspring mice was measured at postnatal day (PND) 78, along with sperm parameters, including sperm motility, capacitation status, and cell viability. The results showed that BBP exposure significantly decreased body weight in F1 and F2 offspring and reduced testis weight and anogenital distance (AGD) in all treated groups (F1-F3) compared with controls. In addition, sperm motility and motion parameters were significantly impaired in all treatment groups. Although no significant differences were observed in capacitation patterns and cell viability, BBP exposure induced abnormal alterations in the acrosome reaction. In conclusion, these findings suggest that gestational BBP exposure induces multigenerational effects on male reproductive function, potentially through heritable mechanisms, and highlight the long-term reproductive risks associated with BBP exposure.

Key words : butyl benzyl phthalate (BBP), multigenerational effects, gestational exposure, sperm function, male fertility

PD26002

Seasonal effect on the morphological and viability parameters of Hanwoo spermatozoa

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Seasonal effects are closely associated with reproductive efficiency in Hanwoo cattle. In particular, seasonal effects may influence spermatogenesis and, in turn, affect sperm morphology and function. Therefore, this study aimed to investigate seasonal changes in sperm morphology and cell viability in Hanwoo cattle in different seasonal conditions. Semen was collected from 16 Hanwoo bulls via electroejaculation, with two consecutive ejaculates obtained per session from four bulls each week over a one month period. This collection was conducted over a period from October to March to observe the recovery from or transition between seasonal thermal conditions. In the present study, sperm morphology was examined via microscopic observation, while cell viability was evaluated using the hypo-osmotic swelling test (HOST). Morphological analysis showed that the normal sperm morphology rate significantly increased in February and March. Additionally, abnormalities in the midpiece and tail significantly decreased during the same period. Furthermore, HOST results showed that swelled spermatozoa significantly increased from January to March. Consequently, these results suggest that seasonal variation influences Hanwoospermatozoa morphology and viability, with significant differences observed among seasons.

Key words : Hanwoo, spermatozoa, seasonal effects, sperm morphology, hypo-osmotic swelling test

PD26003

Male reproductive toxicity induced by metal components of PM2.5 from pig house exposure in mice

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This study aimed to investigate the effects of major metal components associated with particulate matter (PM2.5) on the male reproductive system, sperm function, and embryo development. PM2.5 samples were collected from a porcine farm and administered to male mice via intratracheal instillation. The mice were exposed to various concentrations of metal components, including calcium oxide (CaO), iron oxide (Fe_2O_3), aluminum oxide (Al_2O_3), zinc oxide (ZnO), lead oxide (PbO), and a combination of these metals. Fourteen days after exposure, testicular inflammation and abnormal sperm morphology were observed in the treated groups. Histopathological and biochemical analyses revealed elevated expression of inflammatory cytokines and oxidative stress-induced apoptosis in testicular tissue. Additionally, metal exposure adversely affected sperm morphology, capacitation status, serum testosteronelevels, and testosterone biosynthesis. Notably, decreased sperm fertilizing capacity resulted in impaired embryo development. These findings demonstrate that PM2.5-associated metal components derived from pig farming environments exert detrimental effects on male reproductive health in mice and may pose reproductive risks in agricultural settings.

Key words : metal, particulate matter, reproductive system, sperm, testis

PD26004

Effects of dimethyl sulfoxide on the pluripotency and differentiation ability of mouse embryonic stem cells

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The objective of this study was to investigate whether dimethyl sulfoxide (DMSO), a commonly used solvent in drug testing, influences the pluripotency and differentiation of mouse embryonic stem cells (mESCs) in the absence of leukemia inhibitory factor (LIF). In this study, 4-day-old mESC cultures were exposed to various concentrations of DMSO (0.1%, 0.5%, 1.0%, and 2.0%) to determine the safest and most effective dose for use as a solvent. mESCs maintained under standard pluripotency conditions without LIF were treated with DMSO. As a differentiation control, mESCs were also cultured in the absence of LIF alone. DMSO treatment increased the mRNA expression levels of pluripotency-associated markers. In contrast, DMSO significantly decreased the mRNA expression of the ectodermal marker β-tubulin3, the mesodermal marker Hand1, and the endodermal markers Foxa2 and Sox17 in mESCs. These findings suggest that DMSO enhances pluripotency while inhibiting the differentiation of mESCs. Furthermore, we demonstrate that members of the Tet oncogene family play an essential role in suppressing differentiation and DNA methylation in mESCs. Our results indicate that DMSO is suitable for maintaining mESC pluripotency in the absence of LIF and can preserve mESCs in an undifferentiated state. Therefore, DMSO may partially serve as a functional substitute for LIF.

Key words : mESCs, DMSO, LIF, pluripotency markers

PD26005

Defatted *Tenebrio molitor* extract alleviated LPS-induced cytotoxicity and oxidative stress in porcine endometrium

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This study investigated the protective effects of defatted *Tenebrio molitor* (TM-DF), an extract obtained through optimized aqueous extraction and defatting processes, against lipopolysaccharide (LPS)-induced inflammation and oxidative stress in porcine luminal epithelial (pLE) cells. Based on cell viability analysis, the optimal concentrations for the further experiments were established at 5 μg/mL for TM-DF and 50 μg/mL for LPS. The results demonstrated that pre-treatment with TM-DF not only significantly mitigated the LPS-induced decrease in cell viability but also inhibited the generation of reactive oxygen species (ROS) and prevented the loss of mitochondrial membrane potential (MMP). Furthermore, TM-DF effectively suppressed the expression of heat shock proteins (HSPs) that were sharply increased by LPS treatment. Collectively, these findings suggest that TM-DF possesses potent bioactivity against oxidative damage in pLE cells, highlighting its potential for use as a functional feed additive or a therapeutic candidate.

Key words : *Tenebrio molitor*, LPS, porcine endometrium, ROS, heat shock proteins

PD26006

Carbendazim induces G2/M phase arrest and mitochondrial dysfunction in bovine mammary epithelial cells

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Carbendazim, a benzimidazole-class fungicide, is widely used to control fungal infections in crops, fruits, and vegetables. Due to its broad agricultural application, both its residues and metabolites are commonly found in environmental compartments such as soil and water, raising concerns regarding its embryotoxic, reproductive, and potential carcinogenic effects. However, the impact of carbendazim on bovine mammary epithelial cells (MAC-T) remains unclear. In the present study, we demonstrated that carbendazim decreased MAC-T cell viability in a dose-dependent manner and significantly promoted early apoptotic cell death, and further induced G2/M phase arrest. Carbendazim also markedly increased cytosolic and mitochondrial calcium ion levels in MAC-T cells. In addition, carbendazim disrupted mitochondrial function and generated excessive oxidative stress, as evidenced by the loss of mitochondrial membrane potential. Collectively, these results indicate that carbendazim causes cytotoxic effects in bovine mammary epithelial cells through the disturbance of mitochondrial homeostasis and the modulation of cell cycle progression.

Key words : carbendazim, MAC-T cells, cytotoxicity, mitochondrial dysfunction, cell cycle arrest

PD26007

Effects of Ashwagandha extract on testicular dysfunction caused by gut dysbiosis

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Ashwagandha is rich in bioactive withanolides, which provide potent antioxidant and anti-inflammatory effects. Given these benefits, the present study aimed to evaluate the potential of Ashwagandha extract (ASH) in reversing reproductive damage caused by antibiotic-induced dysbiosis in male mice. Nine-week-old male mice were randomly assigned to treatment groups: WT (control), WA (antibiotics), WA200 (antibiotics + 200 mg/kg ASH), WA300 (antibiotics + 300 mg/kg ASH), and ASH300 (ASH only). Antibiotics were administered for 4 weeks to induce dysbiosis, followed by oral ASH for 2 weeks. After sacrifice, serum and organ samples were collected to analyze hepatotoxicity markers, pro-inflammatory cytokines, spermatogenesis and reproductive hormones. Dysbiosis significantly elevated the hepatotoxicity, pro-inflammatory cytokines, and HMGB1 levels in serum, while significantly decreasing reproductive hormone levels ($p < 0.05$) compared to the control group. Genes related to spermatogenesis were significantly upregulated after treatment ($p < 0.05$). ASH treatment markedly reduced inflammation caused by dysbiosis and helped restore hormonal balance. It also improved sperm quality and fertility competence. These results demonstrate that ASH effectively restores reproductive function impaired by dysbiosis by lowering oxidative stress and inflammation, highlighting its potential as a therapeutic agent for male infertility.

Key words : dysbiosis, Ashwagandha, testis, inflammation, spermatogenesis

PD26008

Analysis of effects of feeding systems and body condition score on serum metabolic profiles and pregnancy rate in Hanwoo cows

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This study investigated the effects of feeding systems and body condition score (BCS) on serum metabolic profiles and pregnancy rates in 590 Hanwoo cows from Hoengseong-gun and the Hanwoo Research Center at Pyeongchang-gun. Cows were monitored from May to July, including repeat breeding, with blood samples collected in September to evaluate metabolic status. The high BCS (4.0–5.0) group showed a significantly lower pregnancy rate (61.2%) than the low (74.5%) and medium (74.4%) groups ($p < 0.05$). The TMR group had higher BCS (3.1 ± 0.7 vs. 2.6 ± 0.8), albumin (3.4 ± 0.2 vs. 3.2 ± 0.2 g/dL), and total cholesterol (147.8 ± 30.8 vs. 116.7 ± 20.4 mg/dL) than the separate feeding group ($p < 0.05$). Blood urea nitrogen (BUN) was also markedly higher in the TMR group (18.0 ± 3.1 mg/dL), suggesting high metabolic concentration. Non-pregnant cows exhibited higher ALT (24.6 ± 5.2 U/L) and BUN (15.2 ± 4.3 mg/dL) than pregnant cows ($p < 0.05$). Specifically, non-pregnant cows in the TMR group showed elevated AST (68.9 ± 21.4 U/L) and phosphorus (6.9 ± 0.9 mg/dL). These findings suggest that maintaining optimal BCS and monitoring nitrogen metabolism are critical for enhancing reproductive efficiency in Hanwoo cows.

Key words : body condition score, feeding system, Hanwoo, pregnancy rate, serum metabolic profiles

PD26009

Association between microplastic-induced gut dysbiosis and testicular dysfunction in mammals

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Male reproductive dysfunction, characterized by impaired spermatogenesis and reduced sperm quality, is closely associated with immune and inflammatory dysregulation. In this context, microplastics (MPs) have emerged as a potential environmental factor contributing to these effects, possibly through the induction of gut dysbiosis; however, the underlying mechanisms remain poorly understood. Therefore, this study investigated the impact of MP-induced dysbiosis on reproductive function and inflammatory signaling in male mice. Five groups were used: control, 0.5 μm low (100 μg/L; 0.5L), 0.5 μm high (1,000 μg/L; 0.5H), 50 μm low (100 μg/L; 50L), and 50 μm high (1,000 μg/L; 50H). MPs were administered via drinking water for 8 weeks, followed by serum, testis, and fecal analysis. MP exposure increased hepatotoxicity markers and pro-inflammatory cytokines (IL-1β, IL-6, TNF-α), with the greatest changes in the 0.5H group ($p < 0.05$). Reproductive performance declined, as shown by reduced sperm motility, count, and mating ability, particularly in 0.5H. Testicular expression of inflammatory mediators (TLR4, RAGE, HMGB1, TIRAP, IRAK1, RelA) and macrophage markers (CD68, F4/80, CD14), along with calprotectin proteins (S100A8/A9), were significantly elevated. Fecal analysis confirmed gut dysbiosis. Overall, smaller particle size and higher concentration enhanced inflammation via the gut–testis axis, leading to impaired reproductive function.

Key words : dysbiosis, microplastics, testis, inflammation, spermatogenesis

PD26010

흑염소 암·수 합사 방법에 따른 번식 특성 분석

남철환, 최재은, 최영선, 구민정, 노유진

전라남도농업기술원 축산연구소

흑염소 자연교배 합사 기준은 정립되어 있지 않아 농가별 사육 규모와 환경에 따라 다양하게 운영되고 있다. 이에 본 연구는 선도농가 설문조사를 바탕으로 암컷 25두당 수컷 1두를 기준으로 설정하고, 암컷 25두당 수컷 1두 처리구와 암컷 50두당 수컷 2두 처리구를 비교하여 번식 성적을 분석하였다. 시험 결과, 암컷 50두당 수컷 2두 처리구의 첫 발정주기 수태율은 91%로 암컷 25두당 수컷 1두 처리구(75%)보다 16% 높았고, 평균 산자수도 2.3두로 0.2두 많았다. 농장 현장실증에서도 첫 발정주기 수태율은 각각 90%와 76%로 14% 높게 나타났고, 평균 산자수는 각각 2.6두와 2.5두로 유사한 경향을 보였다. 이는 수컷을 2두 이상 합사할 경우 개체별 교배 능력 차이나 일시적인 체력 저하를 상호 보완할 수 있으며, 교배 기회가 분산되어 전체 수정 성공률 향상에 긍정적으로 작용할 수 있음을 시사한다. 또한 복수의 수컷이 존재할 경우 발정이 집중되는 시기에도 교배 실패 가능성을 줄여 번식 성적의 안정성을 높이는 데 유리할 것으로 판단된다. 암컷 24두에 발정동기화 처리 후 수컷 1두와 자연교배한 결과 첫 발정주기 수태율은 45%로 나타나, 발정 집중 시 단일 수컷의 교배 능력에는 물리적·생리적 한계가 있을 가능성을 확인하였다. 이상의 결과는 자연교배 시 일정 규모 이상의 암컷 집단에서는 수컷 2두 이상을 합사하는 방식이 수태율 향상과 번식 성적 안정화에 효과적일 수 있음을 시사한다.

Key words : 흑염소, 자연교배, 합사방법, 수태율

PD26011

한우 번식우의 임신 유무와 혈중 대사체 농도의 관계

도한울, 김용환, 손준규, 이명숙, 진실, 강성식

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본 연구는 한우 번식우의 임신 여부와 혈중 대사체의 연관성을 탐색하고, 수태 예측을 위한 후보 지표를 도출하고자 수행되었다. 한우연구센터의 번식우 90두를 본 연구에 공시하였고, 인공수정 후 약 130일에 경정맥에서 혈액을 채취하였다. 이후 직장검사법을 통해 임신 여부를 확인한 결과, 임신우는 60두, 비임신우는 30두로 분류되었다. 전체 90두를 대상으로 혈액 생화학 성분과 혈중 레티놀 농도를 분석하였으며, 이 중 19두(임신 10두, 비임신 9두)에 대해서는 가스크로마토그래피-질량분석기를 이용하여 아미노산 및 유기산을 정량 분석하였다. 번식우 90두의 혈액 생화학 성분 및 레티놀 농도에 대한 개별 로지스틱 회귀분석을 수행한 결과, 임신 여부와 유의한 관련성을 보인 변수는 확인되지 않았다. 번식우 19두 자료에서도 개별 로지스틱 분석에서는 유의한 단일 대사체가 확인되지 않았으나, 단계적 변수선택을 통해 류신과 티로신이 최종 후보 변수로 도출되었다. 이후 2변수 모형에 대해 Firth 보정 로지스틱 회귀분석을 적용한 결과, 류신은 임신 odds 증가와 관련되었고(OR = 1.12, 95% CI = 1.03–1.29, $p < 0.001$), 티로신은 임신 odds 감소와 관련되었다(OR = 0.80, 95% CI = 0.59–0.95, $p < 0.001$). 최종 모형은 전체적으로 유의하였으며($p < 0.001$), leave-one-out cross-validation 결과 AUC 0.82, 정확도 84.2%, 민감도 80.0%, 특이도 88.9%를 나타내어 비교적 양호한 내부 판별 성능을 보였다. 이상의 결과는 류신과 티로신이 번식우의 임신 여부를 반영하는 잠재적 혈중 후보 지표일 가능성을 시사하나, 아미노산 분석 대상이 19두로 제한된 탐색적 결과이므로 향후 더 많은 개체를 대상으로 한 추가 검증이 필요하다.

Key words : 번식우, 임신율, 대사체

PD26012

Narciclasine induces apoptosis in canine osteosarcoma cells via ROS-mediated mitochondrial dysfunction

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Canine osteosarcoma is a highly malignant tumor with limited treatment options due to chemotherapy resistance and adverse effects. While Narciclasine (NAR) has shown anticancer activity in various human cancers, its efficacy in canine OSA remains unexplored. This study investigated the anticancer effects of NAR on D17 and DSN cells. In our results, NAR treatment significantly reduced cell viability and induced G2 phase arrest in a concentration-dependent manner. Also, through flow cytometry analysis, we confirmed that NAR caused apoptotic cell death and decreased both cytosolic and mitochondrial Ca^{2+} levels. Moreover, NAR induced the collapse of the mitochondrial membrane potential and excessive generation of reactive oxygen species (ROS). Therefore, NAR might induce apoptosis in canine osteosarcoma cells by triggering mitochondrial dysfunction and disrupting intracellular homeostasis.

Key words : narciclasine, osteosarcoma, ROS, mitochondria, calcium flux

PD26013

Immunomodulatory ability of porcine peripheral blood-derived mesenchymal stem cells

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Mesenchymal stem cells (MSCs) have been reported as promising candidates for modulating immune responses and promoting immune tolerance. Specifically, bone marrow-derived MSCs (BM-MSCs) have demonstrated significant immunomodulatory capabilities, however, obtaining BM-MSCs remains challenging due to its invasive nature. As an alternative, peripheral blood-derived MSCs (PB-MSCs) can be harvested through a minimally invasive method, however, their characterization and immunomodulatory function remain poorly understood. In this study, PB-MSCs isolated from peripheral blood mononuclear cells (PBMCs) of healthy porcine donors expressed MSC markers CD44, CD73, CD90, and CD105, while lacking hematopoietic markers CD11b and CD45, with comparable multi-lineage differentiation potential to BM-MSCs. Human monocyte-derived M1-like macrophages were indirectly co-cultured with MSCs. As a result, PB-MSCs more effectively suppressed pro-inflammatory cytokines IL-1β, TNF-α, and IL-6, enhanced anti-inflammatory IL-10, and promoted M2 macrophage polarization compared to BM-MSCs. These findings suggest that porcine PB-MSCs possess robust immunomodulatory capacity, which may contribute to modulating the maternal immune environment during reproduction in porcine.

Key words : peripheral blood-derived mesenchymal stem cells (PB-MSCs), immune-modulation, macrophage polarization, xenotransplantation, CD73, adenosine signaling

PD26014

Preliminary evaluation of *in vitro* embryo development using sex-sorted Jersey semen compared with conventional Hanwoo embryo production

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As the utilization of Jersey cattle in the Korean dairy industry increases, the use of sex-sorted semen for securing superior female calves has gained attention. However, information regarding *in vitro* embryo production (IVP) using Jersey sex-sorted semen remains limited in Korea. Therefore, this study evaluated embryo development using Jersey sex-sorted semen and compared the results with conventional Hanwoo IVP data. Jersey ovary-derived oocytes were subjected to *in vitro* maturation (IVM), *in vitro* fertilization (IVF), and *in vitro* culture (IVC). Embryonic development was evaluated at the 2-cell, 8–16 cell, and morula-blastocyst stages. In Hanwoo embryo production, morula-blastocyst development rates were 27.3%, 40.0%, and 52.0%, respectively, whereas Jersey sex-sorted semen-derived embryos showed development rates of 28.6%, 33.3%, and 32.6%, respectively. Normal embryonic development to the morula-blastocyst stage was observed in the Jersey groups. These results demonstrate that IVP using Jersey sex-sorted semen is feasible and may provide preliminary data for securing female Jersey calves and expanding the reproductive foundation of Jersey cattle in Korea.

Key words : Jersey, sex-sorted semen, *in vitro* embryo production (IVP), Hanwoo, blastocyst development

PD26015

Effects of heat stress on motility of dairy bull frozen-thaw Jersey and Holstein spermatozoa

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The decline in artificial insemination efficiency of dairy cattle during hot seasons is reportedly more severe in Holstein than in Jersey cows. Given that cow body temperatures can reach up to 41.5°C under extreme heat, this study evaluated the reduction in sperm motility under induced heat stress using Jersey and Holstein bull spermatozoa. The motile sperm was isolated with Percoll gradient method from the frozen straws of four Jersey and three Holstein bulls. Following incubation in BO medium at 41.5°C for 1, 3, and 6 hours, sperm motility was assessed by CASA system. Holstein sperm motility rapidly decreased to 45.2% at 1 hour, 15.7% at 3 hours, and 3.5% at 6 hours. In contrast, Jersey sperm maintained higher motility at 85.2%, 52.6%, and 32.5% at 1, 3, and 6 hours, respectively. These results demonstrate that the impaired summer fertility of Holstein cows is primarily due to the inherent thermal vulnerability of their spermatozoa, highlighting the need for future studies to improve sperm longevity.

Key words : dairy bull semen, heat stress, motility, Holstein, Jersey

PD26016

Antifreezing gold colloids rescue developmental competence after bovine blastocyst vitrification

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Bovine *in vitro*-produced (IVP) embryos are valuable resources for genetic preservation, embryo transfer, and reproductive biotechnology. However, cryopreservation remains limited by cryo-warming injury caused by osmotic imbalance, cryoprotectant-associated toxicity, oxidative stress, cellular structural disruption, and ice crystallization- or recrystallization-associated physical damage. Although vitrification minimizes ice crystal formation by inducing a glass-like state, insufficient stability during warming may impair membrane integrity, cytoskeletal organization, and trophectoderm function, reducing developmental competence. This study evaluated whether threonine-functionalized gold nanoparticles (AuNPs) could mitigate cryo-warming injury in bovine IVP blastocysts. AuNP physicochemical properties and stability in vitrification- and warming-related media were assessed. Bovine IVP blastocysts were assigned to control and AuNP-treated groups, vitrified, warmed, and evaluated for morphological survival, re-expansion, developmental progression, and degeneration. Cellular and molecular assessments related to oxidative stress, apoptosis, cytoskeletal stability, and trophectoderm integrity were further performed. This study provides an integrated evaluation of AuNP-based cryoprotection as a physical and chemical strategy to improve bovine embryo cryopreservation.

Key words : bovine IVP embryo, vitrification, gold nanoparticle, cryopreservation, developmental competence

PD26017

Hematological and metabolic responses of Hanwoo calves to early and conventional weaning

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This study evaluated the effects of weaning age on growth performance and physiological adaptation in Hanwoo calves under natural suckling conditions. Calves were assigned to either a 60-day (W60) or 90-day (W90) weaning group, and hematological and serum biochemical parameters were analyzed before and after weaning. No significant differences were observed in body weight or average daily gain between groups. However, calves in the W60 group showed greater alterations in hematological and metabolic parameters after weaning. Hematocrit, hemoglobin-related indices, glucose, calcium, and total cholesterol transiently decreased following weaning, with more prolonged changes observed in W60 calves. In contrast, AST, ALT, and BUN remained within normal physiological ranges. These findings suggest that early weaning at 60 days does not impair growth performance but may increase physiological adaptation stress compared with conventional weaning at 90 days. The results indicate that evaluation of weaning strategies should consider both growth and metabolic adaptation responses in calves.

Key words : Hanwoo calf, weaning age, hematology, metabolism, adaptation stress

PD26018

Integrated analysis of subclinical endometritis, uterine microbiota dysbiosis, and conception rate in dairy heifer

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Reduced reproductive efficiency in dairy cattle causes substantial economic losses, and subclinical endometritis (SCE) is difficult to diagnose due to the absence of overt symptoms. While most studies have examined multiparous cows, research on SCE in heifers remains limited. Early detection in the heifer stage may enable a healthy transition to breeding and improve conception. This study investigated eight dairy heifers to explore associations among uterine polymorphonuclear neutrophil percentage (PMN%), inflammatory markers (IL-6, TNF-α, and IL-1β) , hematological indices (CBC), uterine microbiota (16S rRNA-based microbiota profiling) and embryo transfer (ET) pregnancy outcome. Heifers with PMN% ≥ 5% were classified as SCE, whereas those with PMN% < 5% were classified as healthy controls (HC). The SCE group showed higher PMN% and a higher mean IL-6 level, while TNF-α and IL-1β were below the detection limit in all samples. CBC results showed no significant group differences. At the phylum level, The SCE group was enriched in potentially pathogenic taxa such as *Pseudomonadota*, while the healthy cow (HC) group was dominated by *Bacillota* and *Bacteroidota* with greater microbial diversity. Pregnancy rates were markedly reduced in the SCE group. The integrated results support an exploratory heifer SCE assessment framework linking PMN%-based grouping, IL-6 elevation, uterine microbiota shifts, and reduced ET pregnancy outcome, with validation in larger cohorts required.

Key words : dairy heifers, subclinical endometritis, polymorphonuclear neutrophils, inflammatory cytokines, uterine microbiota

PD26019

Runs of homozygosity analysis reveals candidate genomic regions underlying spontaneous abortion in Hanwoo

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Spontaneous abortion causes significant economic losses and welfare concerns in cattle populations on a global scale. Hanwoo (*Bos taurus coreanae*) has formed a population with limited genetic diversity due to geographic isolation and breed conservation policies, including the intensive use of artificial insemination from a minority of elite sires. This is likely to elevate inbreeding levels in the population and facilitate the spread and homozygous expression of recessive lethal alleles, potentially contributing to increased rates of spontaneous abortion. To investigate the genetic mechanisms underlying abortion in Hanwoo, we performed whole-genome sequencing-based analysis on 112 aborted fetuses. We identified 37 shared ROH regions with lengths $\geq$ 1 Mb, 274 regions with lengths $\geq$ 500 kb, and 277 regions using a 500 kb sliding-window approach in more than 30% of aborted fetuses across all autosomes. Gene annotation revealed several candidate genes, including *SIL1, LRRTM2*, and *ENO1*. *LRRTM2* is expressed in neural tube during embryo development. *ENO1* primarily suppressed the growth and invasion of villous trophoblasts. The significantly shared genes identified in the genomes of aborted fetuses were associated with placental development, chorionic membrane function, and fetal neural development. To clarify the precise mechanisms underlying their potential roles in fetal viability, future analyses will leverage the sire-dam-offspring trio structure to perform *de novo* mutation detection, which may reveal additional genetic risk factors underlying spontaneous abortion in this isolated breed.

Key words : runs of homozygosity, spontaneous abortion, Hanwoo

PD26020

Associations of mating body weight and lactation feed intake with reproductive performance and piglet growth in gilts

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This study was conducted to investigate the associations of mating body weight (MBW) and total lactation feed intake (LFI) with reproductive performance and piglet growth performance in gilts. A total of 679 PIC-breed gilts were included, and data on MBW, LFI, weaning-to-estrus interval (WEI), total born, born alive, stillborn piglets, birth weight, piglet weaning weight, and average daily gain (ADG) were collected. Spearman's rank correlation analysis was used to examine associations between MBW or LFI and reproductive and piglet performance. Each variable was divided into five quintile-based groups (T1–T5), and differences among groups were assessed using one-way analysis of variance (ANOVA). Spearman's Correlation analysis showed that total born was positively correlated with MBW ($r = 0.128$, $p = 0.012$). Piglet weaning weight ($r = 0.259$, $p < 0.001$) and ADG ($r = 0.246$, $p < 0.001$) were both positively correlated with LFI. In the quintile-based group comparisons, gilts in the highest MBW group (T5, > 159 kg) had significantly higher total born. However, the number of stillborn piglets was significantly higher in the T5 group ($p < 0.05$). Gilts in the highest LFI group (T5, > 125 kg) showed significantly higher piglet weaning weight and ADG compared to the other groups ($p < 0.001$). These findings suggest that securing an optimal MBW and ensuring adequate feed intake during lactation may contribute to improved reproductive and piglet performance in gilts. However, excessively high MBW may be accompanied by increased stillbirth, highlighting the importance of managing body weight within an appropriate range.

This work was supported by Korea Institute of Planning and Evaluation for Technology in Food, Agriculture and Forestry (IPET) through Smart Farm Innovation Technology Development Program, funded by Ministry of Agriculture, Food and Rural Affairs (MAFRA) (RS-2025-02219935).

Key words : sow, body weight, feed intake, reproductive performance, piglet

PD26021

한우 생체 난소 내 난자 생검 기술 활용 분만 유래 거세우 도체 성적에 관한 연구

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본 연구는 전남지역 농가를 대상으로 우량 한우 사육기반 조성을 위해 생체 난소 내 난자 생검(OPU) 기술을 활용하였다. 수정란 생산을 위해 우수 한우 암소를 활용하여 초음파 영상장비를 활용한 OPU 기술로 채취된 난자를 활용하여 체외발달 및 체외수정 배양 등을 걸쳐 수정란을 생산하였다. 이식 가능한 수정란을 발정관찰이 확인되고, 난소 내 황체 형성이 양호한 대리모에 이식하여 송아지를 생산하였다. 이식 후 분만된 수송아지는 6~8개월령에서 거세를 실시한 다음 육성 후 비육을 실시하였고 생후 30개월령 내외에 도축을 실시하였다. 도축된 거세우 65두의 출하 성적을 조사한 결과, 육질의 경우 1++등급 34두(52.3%), 1+등급 20두(30.8%), 1등급 9두(13.8%), 2등급 2두(3.1%)로 조사되었다. 65두의 평균 도체중은 509㎏으로 한우 OPU 기술 유래 거세우의 도체중이 일반 인공수정 유래 거세우 대비 다소 높은 것으로 조사되었다. 본 연구 결과를 바탕으로 고능력 암소와 적절한 씨수소 교배조합을 통한 우량 수정란 이식을 지속적으로 추진한다면 한우 농가의 출하소득 향상과 개량 가속화에 기여가 가능할 것으로 사료된다.

Key words : 한우, OPU, 수정란, 도체중, 거세우

PD26022

Effect of recipient age in months on conception rate in Hanwoo OPU-derived embryo transfer

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In vitro cultured fertilized eggs produced by *in vivo* ovarian oocyte biopsy technology are a technology that is very useful for improving Hanwoo cattle and for preserving and propagating the genetic resources of the native livestock Chikso. Recently, the production of *in vitro* fertilized Hanwoo embryos following live oocyte biopsy using ultrasound imaging equipment is actively underway in Korea through relevant institutions, universities, and private companies. The greatest advantage of embryo transfer technology is that it can accelerate the rate of improvement through the simultaneous use of high-performance male and female cattle, and expand the scope of utilization for high-performance female cattle when using in vivo ovarian oocyte biopsy technology. To expand embryo transfer, it is necessary to improve the management techniques of recipient cows to address the disadvantage of low conception rates. Accordingly, in this study, we investigated the conception rate according to the age of the recipient cows to utilize the findings for conducting related research aimed at improving the conception rate following the transplantation of Hanwoo embryos derived from live oocyte biopsy. A total of 217 animals were tested for conception rates, and the results showed 32.1% for 12–36 months of age, 45.5% for 37–60 months of age, 31.3% for 61–84 months of age, and 42.1% for 85–108 months of age.

Key words : embryo transfer, OPU, conception rate, feeding and management

PD26023

Effects of sow-specific pheromone on body weight gain in weaned pigs

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Maternal olfactory cues are associated with reduced stress-related behaviors and improved adaptation in newly weaned pigs. This study evaluated whether a sow-specific volatile compound identified by GC-MS-TOF analysis could improve nursery growth performance when delivered as wax-based olfactory enrichment blocks under commercial conditions. Three independent room trials were conducted using sequential batch designs in which untreated control groups preceded treated groups within identical facilities. Rooms differed in target scent concentration and spatial allowance: Room 1 (low concentration; 0.130 vs 0.131 m²/head), Room 2 (medium; 0.174 vs 0.168 m²/head), and Room 3 (high; 0.129 vs 0.121 m²/head for control and treatment, respectively). Pigs were stratified by weaning body weight into weight classes ($p < 0.001$). Nursery body weight gain was analyzed separately by room using general linear models including Group, Time, Weight Class, Sex, and their interactions. Body weight increased over time in all rooms ($p < 0.001$), but no significant Group × Time interaction was detected in Room 1 (3.61 ± 0.22 vs 3.67 ± 0.10 kg, $p = 0.967$), Room 2 (4.95 ± 0.13 vs 4.89 ± 0.13 kg, $p = 0.748$), or Room 3 (5.01 ± 0.10 vs 5.24 ± 0.10 kg, $p = 0.120$). However, a significant Group × Weight Class × Time interaction was identified in Room 3 ($p = 0.004$), where treated pigs in heavier weight classes exhibited greater body weight gain despite reduced spatial allowance, including Weight Class 3 (5.33 ± 0.21 vs 5.01 ± 0.21 kg) and Weight Class 4 (6.10 ± 0.20 vs 5.09 ± 0.21 kg). These findings suggest that sow-specific olfactory enrichment may selectively improve nursery growth performance in heavier pigs under high-density conditions, indicating that initial body mass influences responsiveness to maternal scent cues.

Key words : sow-specific scent, weaned pigs, volatile exposure, body weight change, growth performance, size-dependent response

PD26024

Effectiveness of an ovarian ultrasonography centric practical training program for Hanwoo embryo transfer technicians

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With the expanding field application of Ovum Pick-Up (OPU) derived *in vitro* embryo production (IVP) and the growing need for precise selection of donor and recipient cows, securing skilled embryo transfer (ET) technicians has become increasingly important. Because ET conception rates are primarily determined by three factors—(1) the condition of the cow and farm environment, (2) embryo quality, and (3) the operator's skill and experience—targeted improvements in technician competency are essential to enhance overall reproductive outcomes. This study evaluated the efficacy of a novel training protocol that prioritizes ovarian and ultrasonographic examinations, diverging from the conventional pedagogical sequence that typically begins with artificial insemination (AI). Four undergraduate students participated in an intensive, two?month training program at the Jeonnam National University Naju Experimental Farm using six dairy cows. Trainees first prioritized ovarian examination and ultrasonography, followed by pregnancy diagnosis, AI, and OPU. Ovarian and cervical palpation were practiced daily. OPU sessions were performed every two weeks during a subsequent one-year follow-up period. Technical competency was quantitatively assessed by measuring diagnostic accuracy and procedural success rates at each stage (reported as Mean ± SD). Upon completion of the program and the one-year follow-up OPU practice, all trainees demonstrated high proficiency in ovarian ultrasonography, with a mean interpretation accuracy of 85.0 ± 2.9%. Pregnancy diagnosis accuracy reached 75.0 ± 2.9%. The procedural success rate for ET and AI attempts was 82.5 ± 4.8%. Through OPU practice conducted every two weeks over the following year, all trainees achieved an oocyte recovery rate of 51.3 ± 8.3%, consistent with field-ready proficiency. In resource-limited training environments, prioritizing ovarian examination and ultrasonographic training—followed by sustained, periodic OPU practice—can effectively shorten the time required to achieve technical proficiency. Early intensive training utilizing ultrasound systems equipped with vaginal probes, combined with regular OPU practice every two weeks for one year, represents an efficient model for cultivating specialists in large animal reproduction.

Key words : embryo transfer, training protocol, ovarian ultrasonography, ovum pick-up, Hanwoo

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PE26001

Emergence and genomic characterization of carbapenem-resistant *Morganella morganii* carrying bla_{NDM-1} isolated from a Korean commercial livestock farm

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Morganella morganii is a Gram-negative opportunistic pathogen widely distributed in humans, animals, and environmental sources. Its intrinsic multidrug resistance is particularly concerning, as the acquisition of carbapenemase genes may further limit therapeutic options and facilitate the dissemination of antimicrobial resistance genes (ARGs). Here, we report the first NDM-1-producing *M. morganii* isolate identified in the Korean livestock farm. The isolate GCUSY-1A was recovered from a farm-related environmental sample during routine surveillance at a local farm in 2024. Antimicrobial susceptibility testing confirmed a pan-drug-resistant (PDR) phenotype, with resistance to all tested agents, including carbapenems, aminoglycosides, and fluoroquinolones. Hybrid Illumina/PacBio sequencing revealed a 3,927,038-bp chromosome and a 265,008-bp plasmid. Comparative ARG profiling against 1,365 *M. morganii* genomes showed that GCUSY-`1A harbored 32 ARGs, the highest number reported to date. Of these, 21 ARGs, including bla_{OXA-1} and bla_{DHA-10}, were chromosomal, whereas 11 ARGs, including bla_{NDM-1}, bla_{OXA-10}, and *cfrA*, were plasmid-borne. Replicon typing identified the plasmid as an $Inc_{pCHS4.1-3}$ lineage, a replicon frequently related to the NDM dissemination in Morganellaceae. Core-genome SNP analysis further showed a close clustering between GCUSY-1A and clinical/environmental strains, suggesting ARG circulation across human, animal, and environmental sectors. These findings highlight the potential role of livestock-associated *M. morganii* as a reservoir of ARGs and underscore the need for systematic genomic surveillance within a One Health framework.

Key words : *Morganella morganii*, antibiotic resistance, swine farm, carbapenemase, bla_{NDM-1}

PE26002

Isolation and characterization of a novel bacteriophage vB_SenP-GCUTh1 infecting *Salmonella enterica* serovar Thompson

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Salmonella enterica serovar Thompson (*S.* Thompson) is a major cause of foodborne gastroenteritis associated with contaminated poultry and dairy products. In this study, a novel lytic phage, vB_SenP-GCUTh1 (GCUTh1), was isolated and characterized. GCUTh1 was isolated from a wastewater treatment facility using *Salmonella* Thompson as the host. The phage showed strong lytic activity against *S.* Thompson, *S.* Montevideo, and *S.* Infantis, with moderate-to-high efficiency of plating (EOP) values, and interestingly, also efficiently infected carbapenem-resistant *S.* Thompson. The phage exhibited a short latent period, large burst size, and high stability across a wide range of pH and temperature conditions. Whole genome sequencing revealed that GCUTh1 possessed 39,528 bp dsDNA with 48.7% G+C content, and no virulence or antibiotic resistance genes were detected. A total of 45 ORFs were predicted, and no tRNA genes were identified, supporting its lytic lifestyle. Phylogenetic analysis classified the phage within the genus *Berlinvirus*, and comparative genome analysis indicated the uniqueness of the phage. Moreover, the phage showed efficient inhibitory ability against *S.* Thompson in the food matrix, thus highlighting its potential in food safety. These findings suggest that the newly isolated phage will have strong potential as an alternative biocontrol agent against *S.* Thompson in the livestock industry.

Key words : *Salmonella* Thompson, bacteriophage, lytic phage, food safety, egg liquid

PE26003

Effects of fattening starting age and slaughter age on carcass traits and meat quality of Hanwoo steers

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Determining the optimal slaughter age in Hanwoo beef production requires balancing market demand, carcass quality, production efficiency, feed utilization, and greenhouse gas emissions associated with prolonged fattening. This study examined the effects of fattening starting age (10, 13 months) and slaughter age (26, 28, 30 months) on carcass traits and meat quality using a 2 × 3 factorial design with 48 Hanwoo steers under standardized conditions. Live weight, carcass weight, dressing percentage, and meat yield showed no significant differences ($p > 0.05$), though performance increased numerically with slaughter age. Significant effects ($p < 0.05$) occurred in inedible portion and loin weights, peaking at 28 months. Meat quality improved significantly with age: water-holding capacity increased, and cooking loss decreased ($p < 0.05$), indicating better moisture retention. Muscle pH, lightness, ash content, and oxidative stability remained unaffected ($p > 0.05$). Slaughter age exerted a stronger influence than fattening starting age on both carcass characteristics and meat quality. The intermediate slaughter age optimized valuable cut development, processing yield, and premium-quality grade achievement while avoiding the diminishing returns observed at 30 months. Under this study, these findings suggest slaughtering Hanwoo steers at approximately 28 months may provide an optimal balance between carcass performance, meat quality, and production efficiency.

Key words : Hanwoo steers, fattening starting age, slaughter age, optimal slaughter, carcass characteristics, meat quality, production efficiency

PE26004

Quality and volatile changes of Korean native black goat meat by refrigerated storage and cooking

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Korean native black goat meat is recognized as a high-quality protein source with nutritional advantages, and its popularity has been expanding in Korea. However, the unique odor and toughness of black goat meat are the main hurdles for getting consumer's choice. Nonetheless, studies on quality and volatile changes during storage and cooking remain limited. Therefore, this study evaluated the changes in the quality characteristics of vacuum-packaged black goat longissimus muscle, including pH, color, shear force, texture, on days 0 and 4 of refrigerated storage. Additionally, volatile organic compounds (VOCs) of raw and cooked meat were compared. The results showed that pH significantly increased under vacuum packaging during storage ($p < 0.001$), while no significant changes were observed in color, shear force, or texture. A total of 22 VOCs were identified and quantified, 18 of which significantly increased in the raw meat after storage. However, after cooking, eight VOCs were significantly lower in meat on day 4 than that on day 0. Especially, four aldehydes, heptanal, hexanal, nonanal, and pentanal, significantly decreased when the meat was vacuum-packaged for 4 days, followed by cooking. These findings suggest that short-term storage and cooking could significantly change the pH and VOCs of black goat meat, which may be important in determining overall meat quality.

Key words : Korean native black goat meat, refrigerated storage, cooking, quality characteristics, volatile organic compounds

PE26005

Development and validation of a refined automated muscle fiber analysis algorithm for immunohistochemistry images

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Muscle fiber characteristics (MFC) reflect skeletal muscle properties and are closely associated with meat quality. However, immunohistochemistry (IHC) image analysis is time-consuming and prone to inter-analyst variability. Although a few automated MFC analysis algorithms have been reported, IHC images remain affected by color crosstalk and segmentation noise, causing misclassification and false detection. In this study, we refined a prototype-based automated analysis algorithm (PA) to improve noise reduction and classification stability. Moreover, we validated the refined algorithm (RA) against manual analysis as the reference standard using identical IHC images. Relative fiber number (RFN), mean cross-sectional area (CSA), composition error, and agreement metrics (MAE, bias, RMSE, concordance correlation coefficient [CCC], and intraclass correlation coefficient [ICC]) were evaluated. Error reduction was assessed using the Wilcoxon signed-rank test. The RA demonstrated improved agreement with manual analysis compared to the PA, particularly for Type I (CCC: 0.956 to 0.985; MAE: 2.36 to 1.52) and Type IIX fibers (CCC: 0.908 to 0.950; MAE: 3.21 to 2.42). Composition error was significantly reduced (4.02 to 3.07), while total fiber count, mean CSA, and CSA distribution were not significantly affected. These results indicate that targeted PA refinement enhances classification accuracy and robustness to noise without distorting the fiber size distribution, supporting its applicability in fluorescence image-based MFC analysis.

Key words : muscle fiber characteristics, muscle fiber analysis, immunohistochemistry, automated image analysis

PE26006

The effect of intramuscular fat content in beef on the bioaccessibility of protein and lipids

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This study analyzed the protein and lipid digestion behaviors of beef loin muscle with different intramuscular fat levels through *in vitro* digestion. Six loin muscle samples were acquired from Hanwoo steers 72 h after slaughter. Based on the results of the general composition analysis, the treatment classified the group with a crude fat content of 25% or more as the high fat (HF) group and the group with 18% or less as the low fat (LF) group. HF group showed significantly lower hardness and cohesiveness compared to the LF group ($p < 0.05$). After *in vitro* digestion, the content of α-amino groups in the beef was significantly higher in the HF group than in the LF group in both gastric and intestinal digesta ($p < 0.05$). The content of the low molecular weight proteins (< 3 kDa) in the *in vitro* digesta was significantly higher in the HF group than in the LF group ($p < 0.05$). In contrast, during *in vitro* intestinal digestion, free fatty acid release occurred more rapidly and to a greater extent in the LF group than in the HF group. Accordingly, the intestinal digesta of the LF group contained significantly higher levels of free fatty acids than that of the HF group ($p < 0.05$). Therefore, these results suggest that the intramuscular fat content of beef may influence the digestibility of proteins and lipids *in vitro*.

Key words : beef, bioaccessibility, protein digestibility, lipid digestibility, *in vitro* digestion

PE26007

Identification of proteins associated with quality changes in beef during aging

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Increasing consumer demand for premium meat has led to increased production of aged beef to enhance flavor and tenderness. Aging improves tenderness through the proteolytic degradation of muscle proteins and enhances flavor via the release of free amino acids. However, the specific proteins that are degraded and the underlying mechanisms remain unclear. Therefore, in this study, we evaluated proteolysis during beef aging using a peptidomics-based approach. Strip loin and tenderloin samples acquired from 10 Hanwoo steers (30.5 months, 438 ± 0.34 kg carcass weight) were aged as 3-cm-thick steaks for 1, 2, and 3 weeks. Meat quality traits (color, pH, purge loss, drip loss, cooking loss, and Warner–Bratzler shear force) and peptides were analyzed. We used one-way ANOVA to analyze meat quality data, and protein alterations were assessed based on significantly different unique peptides ($p < 0.05$). pH, purge loss, or cooking loss did not significantly differ ($p > 0.05$), whereas shear force and lightness decreased and redness and yellowness increased ($p < 0.05$). Seventeen proteins exhibited significant changes during aging, with 12 proteins exhibiting consistent increasing or decreasing trends. Among these, four core proteins were associated with carbohydrate catabolic and methylglyoxal metabolic processes, and 11 proteins were distributed in the cytoplasm. These results suggest that protein degradation patterns contribute to variations in aged meat quality, and highlight their potential as predictive markers for meat quality.

Key words : beef, aging, meat quality, protein, peptidomics

PE26008

Comparison of peptide profile similarity between fresh and spoiled pork cuts

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Muscle constitutes a major part of meat. During storage and spoilage, muscle proteins are degraded into peptides and amino acids. Meat peptide profiles differ depending on factors such as animal species, breed, cuts, and storage conditions. In the present study, we compared the similarity of peptide profiles among pork cuts in fresh and spoiled meat and evaluated whether cuts with similar peptide profiles in the fresh state have similar patterns of peptide changes during spoilages. Pork cuts (n = 3, each) of loin (L), skirt (S), belly (B), and jowl (J) were used. Samples were classified as fresh meat (FR; ≤ 2log CFU/g, 1 day) or spoiled meat (SP; > 7log CFU/g, 14 days, aerobic packing). In FR, B and J showed the highest peptide profile similarity (0.43), whereas S showed a relatively low similarity to the other cuts. In SP, B and L showed the highest similarity (0.66), whereas L and J showed the lowest similarity (0.40). In addition, paired delta analysis of peptide changes between FR and SP showed B and L to have the most similar change patterns (0.68), whereas L and J had the lowest similarity (0.53). When only the newly identified peptides in SP were compared, B and J showed the highest similarity. Principal coordinate analysis (PCoA) and PERMANOVA results showed that peptide profiles differed significantly between FR and SP, regardless of pork cut, whereas no significant difference was observed among cuts. The similarity in peptide profiles among pork cuts differed between FR and SP, indicating that cuts with similar peptide profiles in the fresh state did not exhibit similar peptide change patterns during spoilage. Thus, peptide degradation and changes differed among pork cuts during spoilage, suggesting that the intrinsic characteristics of each muscle cut may influence changes in the peptide profile.

Key words : muscle cut, spoilage, peptide profile

PE26009

From pig feces to functional feed additives: Development of multi-strain probiotics for gut health in pigs

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This study was conducted to develop a solid-state fermented probiotic feed additive for improving intestinal robustness in growing and finishing pigs. Probiotic candidate strains were isolated from healthy sow and piglet feces, kimchi, and other biological samples. Based on acid tolerance, bile tolerance, and intestinal adhesion ability, four strains with high overall scores were selected: *Limosilactobacillus fermentum, Lactiplantibacillus plantarum, Lactilactobacillus sakei*, and *Enterococcus faecium*. The selected strains passed safety evaluations including hemolysis, antibiotic resistance, biogenic amine production, and bile salt hydrolase activity. In addition, the strains showed anti-inflammatory and antioxidant activities under LPS-induced inflammatory conditions, suggesting their potential to improve intestinal health. Based on these strains, a solid-state fermented probiotic product was developed using wheat bran, soybean meal, corn, and molasses. Fermentation conditions including substrate composition, moisture content, and fermentation time were optimized by comparing viable cell counts. The optimized fermented product showed high viable cell counts and increased beneficial metabolites such as organic acids. These results suggest that the developed multi-strain solid-state fermented probiotic product could be used as a functional feed additive for improving gut health in growing and finishing pigs.

Key words : pig, multi-strain probiotics, feed additive, gut health

PE26010

Association of postmortem metabolic characteristics and ultimate pH in *longissimus dorsi* of Korean native black goat

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Despite the association between post-mortem metabolites and the ultimate pH of meat, relevant studies on the Korean native black goat (KNBG) are limited. Hence, this study was conducted to investigate the nucleotides during post-mortem time on KNBG *Longissimus dorsi*. KNBG (n = 30, BW = 46.60 ± 4.93 kg, ≧ 35% genetic composition as KNBG) were slaughtered, and chilled at 5°C/h. The data were collected for pH, adenosine triphosphate (ATP), adenosine diphosphate (ADP), adenosine monophosphate (AMP), and inosine monophosphate (IMP) contents, which were measured (1–48 h). Data were analyzed using SAS 9.4 PROC GLIMMIX (Tukey-Kramer, $p < 0.05$) and PROC REG to evaluate relationships between metabolites and pH. As a result, the ultimate pH was 5.81. ATP and ADP contents significantly declined within the 1–2 h post-mortem, while AMP and IMP contents increased from 4h onwards (< .0001). Regression analysis showed that pH was positively correlated with ATP ($\beta = 0.42$, $R^2 = 0.21$) and ADP ($\beta = 0.42$, $R^2 = 0.24$), but negatively correlated with IMP ($\beta = -0.03$, $R^2 = 0.29$). Rapid initial ATP and ADP degradation (1–2 h) and conversion to IMP induce (after 4 h) a high ultimate pH by terminating the ATP resynthesis process. The results indicate that the initial 2 h nucleotide turnover is closely linked to the ultimate pH of KNBG, suggesting that managing early post-mortem metabolism could be enhance meat quality.

Key words : Korean native black goat, postmortem, meat quality

PE26011

Effects of initial chilling rate on the oxidative stability and volatile compound profiles of Korean native black goat loin under different storage conditions

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Korean native black goats are highly sensitive to temperature changes due to their relatively small carcass size and thin subcutaneous fat layer, making the initial chilling rate critical for meat quality. This study investigated the effects of delayed (10°C) versus rapid (0°C) initial chilling on black goat loins during refrigerated (4°C for 10 days) and frozen (60 days) storage. Carcasses were exposed to treatment temperatures for 6 hours, then chilled at 4°C until 48 hours post-slaughter; frozen samples were thawed after 60 days and analyzed following the same protocol as the refrigerated group. The samples were analyzed for pH, lipid oxidation (TBARS), protein oxidation (carbonyl content), and volatile organic compounds (VOCs). While pH values showed no significant difference ($p > 0.05$), lipid oxidation was significantly higher in the rapid chilling group for frozen storage ($p < 0.01$). Protein oxidation was also higher in the rapid chilling group for refrigerated meat ($p < 0.05$). Peak areas of aldehyde-based volatile compounds (nonanal and hexanal), which serve as oxidative indicators in meat, were significantly larger in the rapid chilling group for refrigerated meat ($p < 0.05$). In conclusion, delayed chilling is considered a more suitable initial chilling method for Korean native black goats, as it provides better oxidative stability compared to rapid chilling.

Key words : Korean native black goat, chilling rate, storage characteristic

PE26012

Effect of initial carcass chilling conditions on oxidative stability of *Longissimus dorsi* in Korean native black goats

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The carcass chilling rate determines meat quality and shelf-life through post-mortem muscle temperature changes. This is particularly critical in Korean native black goats (KNBG), whose smaller carcass size makes them more susceptible to chilling rates than larger livestock. This study evaluated the impact of different chilling rates on the oxidative stability and volatile compounds of KNBG loins during storage. Twenty 12-month-old KNBGs raised under identical conditions were randomly assigned to slow (3°C/h decrease) or fast (6°C/h decrease) chilling treatments. Once the carcass core temperature reached 10°C, carcasses were chilled at 5 ± 1°C for 48 h, then loins were separated and stored at 4°C for 1, 5, 10, or 15 days. The ultimate pH was significantly higher in the fast group than in the slow group ($p < 0.01$). TBARS and carbonyl contents, indicators of lipid and protein oxidation, increased significantly during storage and were higher in the fast treatment, with the most notable differences on days 10 and 15 ($p < 0.01$). Regarding volatile compounds, the fast group showed higher peak intensities of representative aldehydes, including hexanal, heptanal, octanal, and nonanal. In conclusion, the initial chilling rate could influence the oxidative stability of KNBG loins. Given the specific carcass characteristics of KNBGs, slow chilling may be considered more suitable than fast chilling for ensuring meat quality and safety.

Key words : black goat, chilling condition, shelf-life

PE26013

Impact of dietary betaine supplementation on the quality characteristics of refrigerated and frozen-thawed pork loin

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This study investigated the effects of dietary supplementation with 0.5% betaine on the quality characteristics and storage stability of pork loin under refrigerated and frozen–thawed conditions. Three-way crossbred pigs were used, and the treatment group was fed a betaine-supplemented diet for five months after weaning, whereas the control group received a normal commercial diet. Pork loin samples were analyzed for proximate composition, physicochemical properties, texture profile, lipid oxidation, volatile compounds, and sensory characteristics. The treatment group showed higher moisture and protein contents with relatively lower fat content compared with the control group. Dietary betaine supplementation significantly reduced cooking loss, shear force, hardness, and yellowness values of pork loin during refrigerated storage ($p < 0.05$). Lower aldehyde formation was observed in the treatment group at 14 d of storage, indicating improved oxidative stability and storage quality. Under frozen–thawed conditions, pork loin from the betaine-fed group showed lower thawing loss and higher sensory acceptability, suggesting that dietary betaine can effectively improve pork loin quality and stability during storage.

Key words : betaine, pork loin, oxidative stability, meat quality, water-holding capacity

PE26014

Detection of foreign materials in chicken meat using SWIR hyperspectral imaging

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Chicken meat is one of the most widely consumed animal protein sources worldwide, and its demand continues to increase according to FAO and OECD reports. However, foreign material contamination remains a critical food safety concern in poultry processing, where contaminants from gloves, masks, machine parts, plastics, wood, glass, and metals may be introduced. This study investigated the feasibility of hyperspectral imaging in the 1,000–2,200 nm range for detecting foreign materials (FMs) on chicken meat surfaces using a binary partial least squares discriminant analysis (PLS-DA) model. Fifty fresh broiler samples, including 19 breasts and 31 drumsticks, were purchased and used without freezing. Thirty types of FMs, including plastics, rubber, wood, metal, glass, textiles, and grease, were cut to approximately 5 × 5 mm^2 based on FDA and USDA criteria for hard and sharp contaminants. Chicken samples were first scanned without FMs to obtain reference spectra and then scanned with FMs on the surface. A total of 32 hyperspectral images were acquired and processed to extract chicken and FM spectra. Various preprocessing methods were evaluated, and the binary PLS-DA model achieved a validation accuracy of approximately 98.9%–99.0%. These results indicate that hyperspectral imaging combined with PLS-DA can effectively distinguish FMs from chicken meat. Future work will expand this binary model into hierarchical detection logic for segmenting FM pixels, grouping object-level regions, and classifying specific material categories.

Key words : hyperspectral imaging, chicken meat, foreign material detection, binary classification, PLS-DA

PE26015

Handheld NIR spectrometer for beef carcass composition and oleic acid prediction

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This study developed a reflection-mode handheld near-infrared (NIR) spectrometer for real-time prediction of proximate composition and oleic acid content in Hanwoo beef carcasses. The system covered the 1,000–1,700 nm range and used a 40 mm illumination window to improve measurement reliability on heterogeneous carcass surfaces. Reflectance spectra were collected from 243 chilled carcasses with beef marbling scores from 1 to 9, and reference values for moisture, crude protein, crude fat, and oleic acid were obtained using standard laboratory analyses. Partial least squares regression and Random Forest models were developed using preprocessed spectra. As marbling score increased, moisture and crude protein decreased, while crude fat and oleic acid increased. Random Forest outperformed PLSR, achieving prediction R^2 values of 0.89, 0.90, 0.91, and 0.86 for moisture, crude protein, crude fat, and oleic acid, respectively. These results indicate that the developed handheld NIR system can rapidly and non-destructively assess key nutritional and quality traits of beef carcasses under slaughterhouse conditions.

Key words : handheld NIR spectrometer, beef carcass, proximate composition, oleic acid, random forest

PE26016

Anaerobic isolation and identification of *Propionibacterium freudenreichii* and lactic acid bacteria from commercial emmental cheese and their potential cross-feeding interactions

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The development of next-generation probiotics increasingly demands a shift from single-strain selection toward the design of functionally complementary multi-strain consortia capable of cross-feeding interactions. In this study, two commercial Emmental cheese products, EntreMont (EM) and Paysan Breton (PB), were used as isolation sources for anaerobic candidate probiotic bacteria. Inner portions of each cheese sample, minimally exposed to oxygen, were inoculated into yeast extract medium using Hungate tubes and incubated anaerobically at 30°C for up to 48 h. Following sequential subculturing, anaerobic plating, and colony isolation, eight representative isolates were selected based on colony morphology and growth characteristics. Bacterial identification was performed via DNA extraction, PCR amplification of the 16S rRNA gene using universal primers 27F and 1492R, supplementary internal sequencing for near full-length 16S rRNA gene coverage, and NCBI BLAST analysis. Species-specific PCR targeting *P. freudenreichii* was additionally conducted for confirmation. Sequencing results identified EM1 and PB5 as *Lactiplantibacillus plantarum* (99.93% and 99.72% sequence similarity, respectively), EM12 as *Levilactobacillus brevis* (99.93%), and PB13 as *Pediococcus pentosaceus* (98.13%). Four isolates — EM5, EM6, PB11, and PB16 — were identified as *Propionibacterium freudenreichii* subsp. *shermanii*, with sequence similarities ranging from 98.37% to 99.91%. Under the tested culture conditions, *P. freudenreichii* isolates exhibited comparatively faster growth than the isolated lactic acid bacteria. Collectively, these findings indicate that commercial Emmental cheese represents a valuable reservoir for propionate-producing and lactic acid–producing candidate strains suited for cross-feeding-based multi-strain probiotic development. Further investigation into metabolic compatibility, cross-feeding potential, and functional stability among the isolated strains is warranted to advance their application in next-generation probiotic formulations.

Key words : probiotics, cross-feeding, emmental cheese, propionate, lactic acid bacteria, 16S rRNA gene

PE26017

Microbial succession and proteolytic activity during high-temperature fermentation of traditional wheat-based nuruk

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Efficient protein bioconversion and amino acid metabolism are critical determinants of productivity in livestock-related fermentation systems, including feed fermentation and silage processing. Traditional nuruk is a solid-state fermentation system operating under high-temperature and low-moisture conditions that selectively enriches stress-tolerant microorganisms with strong proteolytic potential, making it a compelling model for identifying functionally relevant microbial resources in livestock applications. In this study, metagenomic analysis and amino acid profiling were conducted to investigate microbial succession and protease-associated metabolic changes during the traditional manufacturing process of wheat-based nuruk. Fermentation at 45℃ substantially reshaped both bacterial and fungal communities, driving the dominance of thermotolerant fungi, particularly *Saccharomycopsis* and *Lichtheimia*. Concurrently, protease activity increased sharply, accompanied by marked accumulation of total free amino acids and proline. Correlation analysis revealed strong positive associations between dominant microbial taxa and protease-related biochemical parameters, indicating active proteolytic metabolism under thermal stress. Progressive decline in fungal diversity further reflected the selective enrichment of functionally adapted microbiomes. These findings suggest that traditional nuruk serves as a valuable reservoir of stress-tolerant, protease-producing microbiomes. The thermotolerant taxa identified here may offer practical utility as microbial resources for improving protein degradation efficiency and amino acid availability in livestock feed fermentation systems.

Key words : wheat-based nuruk, solid-state fermentation, thermotolerant microbiome, protease activity, amino acid metabolism, livestock feed fermentation

PE26018

Impact of different black soldier fly powder supplementation levels on broiler chicken breast meat quality

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This study was conducted to evaluate the feed value by analyzing the effects of black soldier fly powder (BSFP) feeding levels on the physicochemical properties and storage stability of broiler breast meat. Chicken breast meat treated with BSFP at different feeding levels (a basal diet supplemented with 0 [control], 0.1 [T1], 0.5 [T2], or 1.0% BSFP [T3]) was used as the test material, and meat color, pH, shear force, cooking loss, lipid oxidation, and DPPH radical scavenging activity were measured before and after storage. Proximate composition showed no significant differences in moisture, protein, fat, and ash content following the feeding of BSFP ($p > 0.05$). Lightness (CIE L^*) was significantly higher in all treatment groups compared to the control group ($p < 0.05$). There was no significant difference in cooking loss due to BSFP treatment ($p > 0.05$). The shear force of T3 was the highest than other treatments ($p < 0.05$). After 7 days of storage, lipid oxidation in T2 and T3 was significantly lower than in the control ($p < 0.05$). It is determined that the feeding of BSFP does not have a negative effect on meat color and water-holding capacity in broiler chicken breast. In particular, it is expected to improve storage stability by effectively inhibiting lipid oxidation during storage. Therefore, BSFP is considered to have high potential as a feed resource for improving meat quality and ensuring shelf-life.

Key words : black soldier fly powder, broiler chicken breast, meat quality, shelf-life

PE26019

Effect of packaging method on physicochemical quality traits in goat meat during storage

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This study examined the influence of packaging methods on the physicochemical quality of goat meat during refrigerated storage (1 ± 0.5℃). Samples were stored under aerobic (AP) or vacuum packaging (VP) for 0, 3, and 7 days. Quality traits including pH, TBARS, drip loss, moisture, water activity, and color were analyzed. The pH decreased initially and increased later, with the lowest value observed in AP on day 3 ($p < 0.001$). TBARS values rose over time but were lower in VP on day 7 ($p < 0.001$). Drip loss increased progressively, while a* and chroma values declined, indicating color deterioration. VP samples maintained lower lipid oxidation and better moisture retention than AP. Overall, VP effectively preserved goat meat quality during storage, suggesting a shelf life of up to 7 days under refrigeration.

Key words : goat meat, vacuum packaging, aerobic packaging, storage period, physicochemical properties

유전 및 육종

PF26001

Comparison of genomic prediction methods for carcass traits in Hanwoo (Korean Brown Cattle) using genomic best linear unbiased prediction and machine learning approaches

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Genomic selection has become an essential tool for accelerating genetic improvement in livestock breeding. This study aimed to compare the predictive ability of single-trait GBLUP (ST-GBLUP), multi-trait GBLUP (MT-GBLUP), Random Forest (RF), Extreme Gradient Boosting (XGBoost), and Support Vector Regression (SVR) for four carcass traits in Hanwoo cattle: carcass weight (CWT), eye muscle area (EMA), backfat thickness (BFT), and marbling score (MS). A total of 10,170 Hanwoo steers were used, partitioned into a reference population (n = 9,170) and a validation population (n = 1,000). Genotyping was performed using the Illumina Bovine SNP50K BeadChip. ST-GBLUP and MT-GBLUP were implemented using the BLUPF90 software package, while RF, XGBoost, and SVR were applied as machine learning alternatives. Predictive ability was assessed as the Pearson correlation between predicted and observed values in the validation population. ST-GBLUP yielded predictive abilities of 0.487, 0.451, 0.429, and 0.453 for CWT, EMA, BFT, and MS, respectively, while MT-GBLUP produced comparable results at 0.487, 0.449, 0.431, and 0.451. Among machine learning models, SVR achieved the highest predictive ability at 0.411, 0.429, 0.414, and 0.447, followed by XGBoost at 0.425, 0.387, 0.316, and 0.384, and RF at 0.386, 0.359, 0.299, and 0.346. Although GBLUP-based methods generally outperformed ML models, SVR demonstrated competitive predictive ability, particularly for BFT and MS, suggesting that kernel-based approaches may partially capture nonlinear genomic effects in Hanwoo carcass traits.

Key words : Hanwoo, single nucleotide polymorphism (SNP), genomic best linear unbiased prediction (GBLUP), machine learning (ML), predictive ability

PF26002

Genomic characterization of Korean native chickens compared with Kyrgyz populations using genome-wide SNPs

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Indigenous chicken breeds represent important genetic resources due to their adaptability and unique genetic characteristics. However, intensive selection and commercialization have raised concerns about the loss of genetic diversity in native populations. This study aimed to investigate the population structure, genetic diversity, and effective population size (*Ne*) of Korean native chickens (KNC) in comparison with Kyrgyz chicken populations using genome-wide SNP data. Whole-genome sequencing data were obtained from five Korean native chicken lines (GWR, GWY, CNW, GWB, and GWL) and two Kyrgyz populations (18_KYG and 21_KYG). Population structure was analyzed using principal component analysis (PCA), phylogenetic tree construction, and admixture analysis. Linkage disequilibrium (LD) decay patterns were used to estimate the effective population size. The results showed clear genetic differentiation between the Korean and Kyrgyz populations. Within the Korean native chickens, four distinct genetic clusters were identified, indicating lineage differentiation. Admixture analysis (K=6) revealed well-defined ancestry components with limited gene flow among lines. LD decay analysis indicated that Kyrgyz populations exhibited faster decay rates, suggesting higher genetic diversity compared to that of Korean native chickens. Estimated *Ne* values varied among populations, with some Korean lines showing relatively low effective population sizes. These findings suggest that while Korean native chickens possess distinct genetic characteristics, they may face reduced genetic diversity in certain lines. Therefore, genomic-based conservation and management strategies are required to maintain genetic diversity and ensure the sustainable utilization of these valuable genetic resources.

Key words : Korean native chicken, genomic analysis, SNP, population structure, genetic diversity, effective population size

PF26003

Genetic evaluation of milk yield and heat tolerance in Korean Holstein cattle using a random regression model

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This study aimed to evaluate genetic parameters of milk yield and heat stress responses in Korean Holstein dairy cattle using a random regression model (RRM). A total of 5,620,888 test-day records from 380,940 animals across 3,326 herds were analyzed, incorporating temperature-humidity index (THI) as an environmental indicator of heat stress.

Heritability of milk yield varied across lactation stages, showing the lowest values in early lactation and gradually increasing toward mid- and late lactation. Among parities, second-parity cows exhibited the highest heritability and estimated breeding value (EBV) reliability, indicating optimal conditions for genetic evaluation.

Reaction norm analysis revealed clear genetic variation in heat tolerance. Heat-tolerant individuals maintained or increased EBVs under high THI conditions, whereas heat-sensitive individuals showed declining trends. Additionally, incorporating THI into the model resulted in substantial re-ranking of individuals, suggesting that genetic evaluation without environmental factors may misrepresent true performance.

These findings highlight the importance of integrating environmental factors such as THI into genetic evaluation systems and provide a foundation for improving heat tolerance in dairy cattle breeding programs.

Key words : random regresion model, temperature-humidity index, days in milk, heterogeneous residual variance

PF26004

Comparison of growth curve models for Hanwoo cattle: a simulation analysis of sample size and measurement interval

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This study evaluated the effects of sample size and measurement interval on the goodness of fit of growth curve models in Hanwoo steers using simulated body weight data. A simulated population of 2,000 animals was generated from the 2024 monthly reference body weights for Hanwoo steers, and sample sizes of 10, 30, 50, and 100 animals were tested under three measurement interval schemes: monthly, every 2 months, and every 3 months. Each sampling condition was repeated 10 times. The Gompertz, Logistic, and von Bertalanffy models were fitted under each condition, and model performance was assessed using the coefficient of determination (R^2) and root mean square error (RMSE). The von Bertalanffy model consistently showed the best fit across all sample sizes and measurement intervals, followed by the Gompertz model, whereas the Logistic model showed the poorest fit. Model fit improved as sample size increased, but the improvement became limited beyond 50 animals. In contrast, differences among measurement intervals were relatively small. Under the monthly measurement condition with 100 animals, the von Bertalanffy model showed the highest fit ($R^2 = 0.99995$, RMSE = 1.935 kg), followed by the Gompertz model ($R^2 = 0.99937$, RMSE = 6.723 kg), whereas the Logistic model showed the lowest fit ($R^2 = 0.99473$, RMSE = 19.479 kg). These results suggest that the von Bertalanffy model is the most suitable for describing average growth patterns in Hanwoo steers and that practical growth curve analysis may be possible with moderate sample sizes and less frequent measurements.

Key words : Hanwoo, growth curve, Gompertz, Logistic, von Bertalanffy, R^2, RMSE

PF26005

Meta-GWAS reveals hidden shared genetic signals for meat quality traits across the Korean chicken populations

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Meat quality traits in chicken are genetically complex and often difficult to resolve within individual populations due to limited sample sizes and population-specific signals. This study applied a meta-genome-wide association study (meta-GWAS) framework to detect shared genetic variants associated with meat quality traits across three Korean chicken populations. Population-specific GWAS results were generated for multiple phenotypes and integrated through meta-analysis. Because of the limited sample size in each population, most traits did not reach significance in either single-population GWAS or meta-GWAS. Nevertheless, meta-GWAS identified a significant shared locus for inosine monophosphate (IMP), a representative nucleotide contributing to umami taste, on chromosome 5. Two significant SNPs showed consistent effect directions across populations with low heterogeneity, indicating a stable common association signal. Functional enrichment analysis of genes within the ± 1 Mb windows of these SNPs highlighted muscle structure-related components: troponin complex, striated muscle thin filament, myofilament, and insulin receptor recycling pathway. These findings suggest that the identified region may influence flavor-related variation through its effects on muscle structure and metabolic regulation. Overall, this study demonstrates the utility of meta-GWAS for identifying shared loci underlying complex meat quality traits in chickens under limited statistical power.

Key words : meta-GWAS, meat quality, flavor-related traits, Korean chicken populations

PF26006

Microsatellite markers for parentage testing in Korean native black goats: a review

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The domestic goat meat industry in South Korea has grown rapidly in recent years, raising concerns about mislabeled imported meat and the loss of purebred genetic characteristics through indiscriminate crossbreeding. To preserve the genetic integrity of Korean Native Black Goats (KNBG) and support traceability, a reliable microsatellite marker (MS) set is needed for parentage testing. This study reviewed articles on MS marker sets for parentage testing in goat. Literature screening was conducted using the databases PubMed, Web of Science, Scopus, and KCI with the terms “goat,” “microsatellite,” and “parentage,” along with their corresponding Korean keywords. As a result, 10 relevant articles were identified, collectively evaluating 430 candidate MS markers and ultimately recommending 125 final markers for goat parentage testing. The analysis showed that marker effectiveness varied across goat breeds, likely due to differences in genetic diversity, allele frequency distributions, and breed-specific mutations. Furthermore, only three of the 10 MS marker sets were validated in KNBG. Of these, the two earlier studies employed dinucleotide markers, which demonstrated high discriminatory power. A more recent study developed tri- and tetranucleotide markers, which reduced genotyping errors. However, these markers showed lower polymorphism than dinucleotide loci. Overall, the variable performance of existing marker sets highlights the need for a robust MS marker set with reliable performance across goat breeds in South Korea.

Key words : Korean native black goat, parentage testing, MS marker

PF26007

First haplotype-resolved assembly of Korean Jeju Black cattle using a trio-binning approach with nanopore sequencing

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Korean Jeju Black cattle are an important native genetic resource in Korea, yet a high-quality reference assembly is still needed to support future conservation and breed-specific genomic studies. In this study, we generated haplotype-resolved genome assemblies for both Hanwoo and Jeju Black cattle using a parent-offspring trio composed of a Hanwoo sire, a Jeju Black cattle dam, and their F1 hybrid fetus. Illumina short-read data from the parental individuals were generated at approximately 22.7× and 23.3× coverage, respectively, whereas the F1 offspring was sequenced using Oxford Nanopore Technologies (ONT) long-read sequencing at 75.8× coverage. To improve read accuracy prior to assembly, raw ONT reads were error-corrected using HERRO, and the corrected reads were assembled with Verkko using parental haplotype-specific k-mers. The Jeju Black cattle-derived haplotype assembly had a total length of 3,004,838,613 bp, which was close to the expected Hanwoo genome size (3.1 Gb). The longest haplotype-resolved scaffold length was 107.61 Mb and a scaffold N50 was 34.38 Mb. However, the assembly comprises 11,313 contigs, indicating limited contiguity and a fragmented state. The assembly achieved a BUSCO completeness of 95.36%, with 87.12% single-copy and 8.24% duplicated orthologs. Phasing accuracy showed switch and hamming error rates of 1.36% and 1.00%, respectively. This is the first *de novo* genome assembly of Korean Jeju Black cattle and provides a valuable resource for investigating breed-specific genomic research.

Key words : *de novo* assembly, Jeju Black cattle, long-read sequencing, phasing, trio-binning

PF26008

Genomic characterization of Holstein-Jersey crossbred cattle in Korea using genome-wide SNP data

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This study was conducted to establish a genomic reference for the Jersey population in Korea and to evaluate changes in breed composition across F1–F6 crossbred generations produced by repeated backcrossing of Jersey to Holstein. Genotype data were obtained using the Illumina BovineSNP50 V3 chip, and after quality control, 26,931 common SNPs from 742 Holstein, 494 Jersey, and 98 crossbred animals were used for analysis. Genetic structure was assessed using principal component analysis (PCA), and breed composition was estimated using supervised ADMIXTURE analysis. PCA clearly separated Holstein and Jersey into distinct genetic clusters, indicating strong genetic differentiation between the two breeds. ADMIXTURE analysis showed a progressive increase in Jersey ancestry across generations, with mean Jersey proportions of 55.2% in F1, 74.1% in F2, 87.0% in F3, and 99.7% in F4. The F5 and F6 generations also maintained more than 99% Jersey ancestry, and PCA showed that individuals from F4 onward nearly overlapped with the Jersey reference population. These results indicate that crossbred animals from the F4 generation onward are genetically almost indistinguishable from pure Jersey cattle. This study provides fundamental genomic information for establishing Jersey reference populations, determining breed composition in crossbred cattle, and developing registration criteria for Holstein–Jersey backcross progeny in Korea.

Key words : Jersey, Holstein, crossbred cattle, SNP, ADMIXTURE

PF26009

Blood transcriptome-based cell deconvolution for dissecting intrinsic gene expression changes in pigs

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Blood transcriptomes reflect both intrinsic gene expression and the composition of cell populations. Cell heterogeneity can substantially influence observed gene expression, potentially confounding conventional differential expression analyses. Therefore, this study aimed to integratively investigate the effects of cell composition and intrinsic gene expression changes in pigs. Blood transcriptome data were obtained from weaning (n = 3) and growing pigs (n = 3), and cell composition enrichment was estimated using the xCell method. Principal component analysis (PCA) was applied to cell enrichment profiles to capture the major variation in cellular composition, revealing that pigs were clearly separated by developmental stage. This indicated that the cell composition differed substantially between groups. Differentially expressed genes (DEGs) were identified using edgeR under two models: a baseline model without adjustment (WO) and an adjusted model account for cell type enrichment (WI). In the WO model, multiple DEGs were identified between groups; however, after adjusting for cell composition (WI), the number of significant DEGs was reduced. These results demonstrate that most gene expression differences in porcine blood are strongly influenced by cell composition. Our findings highlight the importance of accounting for cellular heterogeneity in blood transcriptome studies and provide a framework for disentangling cell composition effects from intrinsic gene expression changes.

Key words : pig, blood, transcriptome, cell deconvolution, intrinsic gene expression

PF26010

Glycobiology-based engineering of O-linked glycans in monkey FSH

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Follicle-stimulating hormone (FSH) is a glycoprotein hormone composed of α- and β-subunits and plays essential roles in reproductive physiology. Because glycosylation is closely associated with hormone stability and biological activity, this study aimed to develop recombinant monkey FSH analogs with prolonged biological activity by introducing non-native O-linked glycosylation sites into single-chain monkey FSH. Two C-terminal peptide motifs, a 35-amino-acid equine CTP and a 31-amino-acid human CTP, were inserted between the β- and α -subunits to generate O-linked glycan-enriched recombinant constructs. Recombinant proteins expressed in mammalian cells exhibited an increased molecular weight of approximately 50 kDa compared with native single-chain monkey FSH, which is generally 35–40 kDa. Enzymatic deglycosylation analysis using N-linked, O-linked, and sialic acid–cleaving enzymes partially confirmed that O-linked glycosylation contributed approximately 10–15 kDa to the observed molecular weight increase. These findings indicate that CTP-mediated O-linked glycosylation was efficiently incorporated into recombinant monkey single-chain FSH. In addition, receptor-mediated intracellular signaling, including pERK1/2 activation, is currently being investigated using FSH receptor-expressing cells and β-arrestin/GRK knockout systems. These results suggest that O-linked glycan engineering may provide a useful strategy for improving the molecular stability and sustained bioactivity of recombinant FSH.

Key words : recombinant monkey single-chain FSH, O-linked glycosylation, C-terminal peptide, pERK1/2 signaling

PF26011

Validation of an in-house SNP quality control pipeline using pedigree- and genomic-based relationship matrices

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This study validated an in-house SNP quality control (QC) pipeline for genomic estimated breeding value (GEBV) prediction in livestock using a pedigree of 7,498 individuals derived from 4,628 genotyped animals and genomic data from 4,032 individuals that passed batch- and population-level QC. Pipeline performance was evaluated by comparing the pedigree-based relationship matrix (***A***) with the genomic relationship matrix (***G***). Among the total 8,126,496 pairwise comparisons generated from 4,032 QC-passed individuals, 7,959,032 pairs with non-zero coefficients in ***A*** showed high concordance between ***A*** and ***G*** (r = 0.82, $RMSE$ = 0.068). Linear regression analysis showed that the relationship between the two matrices was expressed as $\boldsymbol{G} = 0.9650\boldsymbol{A} - 0.0569$, indicating slight underestimation of ***G*** relative to ***A***. The mean inbreeding coefficient was 3.55 ± 1.74% in ***A*** and 0.50 ± 4.94% in ***G***, suggesting that genomic information more effectively captured Mendelian sampling variation. In addition, genomic relationship analysis identified 30,986 highly related pairs ($\boldsymbol{G} \geq 0.25$) among 4,028 pedigree-unrelated individuals. The number of related pairs per individual showed a median of 12 (IQR, 7–19), indicating that related pairs were concentrated within a subset of individuals. These findings suggest potential cryptic relatedness or undocumented pedigree relationships.

Key words : SNP quality control; in-house pipeline; validation; genomic relationship matrix; pedigree based relationship matrix

PF26012

Evaluation of single-step genomic best linear unbiased prediction integrating transformer embeddings in a closed nucleus herd

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To leverage complex genomic interactions in livestock evaluation, we incorporated deep feature representations from a Transformer architecture into single-step genomic best linear unbiased prediction (ssGBLUP). The simulated population, modeled as a closed nucleus herd to reflect the high levels of relatedness and linkage disequilibrium characteristic of intensive breeding programs, consisted of 20,000 individuals: 16,000 for training, 2,000 for validation, and 2,000 for testing. Transformer embeddings were utilized as a feature matrix to define an additional random effect, which was jointly predicted alongside the additive genetic effect in the single-step mixed model equations. Compared with baseline ssGBLUP, the integration of transformer embeddings improved the correlation between true breeding values and estimated breeding values from 0.3215 to 0.3418 for the validation set and from 0.2616 to 0.2994 for the test set. Similarly, the root mean square error (RMSE) decreased from 0.1604 to 0.1573 and from 0.1629 to 0.1586, respectively. These results indicate that Transformer embeddings can provide complementary information to standalone ssGBLUP. Further experiments using additional simulation replicates, hyperparameter tuning, and large observed datasets are required to assess robustness and practical utility.

Key words : genomic prediction, transformer, ssGBLUP, closed nucleus herd, stochastic simulation

PF26013

Single-cell transcriptomic atlas of Hanwoo *longissimus dorsi* muscle reveals marbling-associated cellular and molecular features

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Marbling is an important meat quality trait in Hanwoo cattle, but the cellular and molecular characteristics of skeletal muscle according to marbling grade remain unclear at single-cell resolution. In this study, we performed pilot single-cell RNA sequencing of Hanwoo *longissimus dorsi* muscle from high- and low-marbling samples to investigate marbling-associated cellular and transcriptional features. Single-cell transcriptomic data were processed and analyzed using standard bioinformatic pipelines, including quality control, doublet removal, integration, clustering, and marker-based cell type annotation. After filtering, 5,997 singlets from the high-marbling sample and 3,691 singlets from the low-marbling sample were analyzed. Integrated clustering identified 17 cell populations, including fibroblasts, myofibers, endothelial cells, pericytes, immune cells, satellite cells, and stromal populations. Marker gene analysis confirmed cell type-specific expression patterns related to muscle fibers, extracellular matrix, angiogenesis, immune cells, satellite cells, and metabolism. Differential expression analysis between high- and low-marbling samples revealed distinct transcriptional differences, including enrichment of muscle structural and contractile genes in the high-marbling sample. These findings provide a preliminary single-cell transcriptomic atlas of Hanwoo loin muscle and suggest potential cellular and molecular features associated with marbling grade. Further validation with additional biological replicates is required.

Key words : Hanwoo, biomarkers, marbling-associated cellular

PF26014

Wnt signaling pathway associated *cis*-lncRNA-mRNA crosstalk in Ogye breast muscle

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The Ogye, a unique Korean indigenous chicken breed with distinct black phenotypes, was compared to the Cornish breed to explore the molecular characteristics underlying the development of Ogye breast muscle. RNA-sequencing was performed on breast muscle tissues from 10-week-old Ogye and Cornish breeds to identify differentially expressed mRNAs and lncRNAs ($|\log_2(FC)| \geq 1$, $P\ adj < 0.05$). Functional enrichment was conducted through GSEA-based GO and KEGG analyses, and cis-acting targets of lncRNAs were predicted within a ± 100 kb window, followed by Spearman correlation and qRT-PCR validation. We identified 192 DEGs (61 up, 131 down). Down-regulated DEGs were primarily enriched in melanogenesis (e.g., *PMEL*, *TYRP1*, *MLANA*), while GSEA revealed that the Wnt signaling pathway and cell cycle regulation were significantly enriched in Ogye breast muscle tissues. Notably, the Wnt ligands *WNT16* and *WNT9A*, and the transcription factor *TCF7L2*, were up-regulated, alongside down-regulation of inhibitors such as *DKK2*. Furthermore, *cis*-acting analysis identified a strong positive correlation ($|\rho| \geq 0.8$) between the DE lncRNA *MSTRG.4144* and its target *WNT9A* in both breeds, which was validated by qRT-PCR. These findings suggest that *MSTRG.4144*-mediated regulation of WNT9A may constitute a conserved mechanism, and its differential activation may contribute to the distinct developmental and functional characteristics of Ogye breast muscle. This research was supported by the Regional Innovation System & Education(RISE) program through the Jeonbuk RISE Center, funded by the Ministry of Education(MOE) and the Jeonbuk State, Republic of Korea.(2025-RISE-13-JBU)

Key words : Ogye, LncRNA, Wnt signaling pathway, *WNT9A*, *MSTRG.4144*

PF26015

Visualization of GEBV-phenotype relationships in Hanwoo steers for precision feeding

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This study aims to develop an AI-based precision feeding decision-making system that automatically recommends individualized feeding strategies for Hanwoo steers based on genomic information. The system is designed to maximize farm profit by applying enhanced feeding and extended rearing to top-GEBV (genomic estimated breeding value) animals and early slaughter to lower-GEBV ones. As a foundational module of this system, this study developed a visualization framework for the relationship between GEBV and carcass phenotypes using large-scale slaughter data. Phenotypic measurements and GEBV for carcass weight (CWT), eye muscle area (EMA), backfat thickness (BFT), and marbling score (MAR) were collected from 18,140 Hanwoo steers. CWT-GEBV and MAR-GEBV served as the X- and Y-axes of a 3 × 3 matrix (top 30%, middle 40%, bottom 30%), on which phenotypic distributions (count, mean, variance) and individual-level patterns were overlaid. EMA phenotype responded positively to both axes, revealing genetic correlations among traits, while BFT phenotype responded only to CWT-GEBV. Within each GEBV region, phenotypic expression varied across individuals, enabling identification of animals that underperformed, matched, or exceeded their genetic potential. Future work will expand the matrix to 6 × 6 or finer grids and integrate slaughter age, feeding stage, and ration data, advancing this framework into an AI-based decision-making system that automatically recommends differentiated feeding strategies by GEBV interval.

Key words : Hanwoo, genomic estimated breeding value (GEBV), carcass traits, visualization

PF26016

Genome-wide association study of coat color traits in Korean brindled cattle using genotype

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The Chikso is a Korean native cattle breed distinguished by its brindle coat color. This study aimed to elucidate the genetic signals affecting variation in brindle in Chikso cattle. The expression of brindle coat color was classified into four ordered scores, where higher scores indicate more extensive brindle expression (0 = non-brindle; 1 = sparse brindle; 2 = light whole-body brindle; 3 = clear whole-body brindle). A total of 9,370 phenotypic records and 4,100 genotyped animals were used in this study. A genome-wide association study (GWAS) was performed with sex and principal components included as covariates to account for potential false-positive associations. Estimated marginal mean brindle expression scores were lower in females than males (1.03 vs. 1.20). The heritabilitys of brindle coat color was estimated at 0.52 using a Bayesian threshold animal model. In the GWAS, 18 SNPs reached genome-wide significance ($p < 5 \times 10^{-8}$). Among these association signals, some were located near the previously reported ASIP and MC1R genes on BTA13 and BTA18, respectively. We also identified a novel locus on BTA6 harboring the CORIN gene, which is known to regulate ASIP signaling and therefore may act as a modifier of brindle expression in Chikso cattle. This study provides biologically plausible evidence for the variation in brindle expression and may contribute to breeding improvement of brindle expression in the Chikso population.

Key words : Korea Brindled Cattle (Chikso), coat color, GWAS, heritability, ASIP, CORIN, MC1R

PF26017

Evaluation of oleic acid and physicochemical meat quality in Hanwoo cattle

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This study investigated the potential of using oleic acid to enhance marbing score and tenderness in Hanwoo cattle. Using 2,852 progeny-test steers from the Korean Proven Bull program, genetic parameters for major fatty acid traits were estimated, and sires were classified into low-oleic, high-oleic, and intermediate groups based on estimated breeding values (EBVs) through clustering analysis. The progeny-test steers from the high-oleic sire group indicated a significantly higher ratio of monounsaturated to saturated fatty acids (MUFA/SFA) (mean = 1.290 vs. 1.184) than the low-oleic group, while maintaining comparable or slightly higher marbling scores (mean = 4.179 vs. 4.164). Multiple regression analysis showed that increased oleic acid proportion was significantly associated with reduced shear force, an indicator of meat tenderness (standardized coefficient = –0.435), and increased marbling score (standardized coefficient = 0.249). In particular, the genetic correlation between oleic acid and marbling score EBVs was estimated to be low (–0.028), indicating that oleic acid and marbling score may be regulated by relatively independent genetic mechanisms. Logistic regression analysis showed that progeny-test steers from the high-oleic sire group were significantly more likely than those from the low-oleic sire group to simultaneously rank within the top 25% for MUFA/SFA ratio and the bottom 25% for shear force (odds ratio = 3.04). Overall, incorporating oleic acid EBVs into breeding programs may provide an effective strategy for improving beef palatability and nutritional quality in Hanwoo cattle without adversely affecting current marbling levels.

Key words : Hanwoo, oleic acid, MUFA/SFA ratio, EBV, meat quality

PF26018

젖소 산유능력 평가를 위한 신규 305일 보정계수 개발 및 정확도 검증

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젖소의 산유능력 평가를 위해 전 세계적으로 305일 보정유량을 개량 형질로 유전능력평가에 활용하고 있다. 우리나라는 2009년 개발된 보정계수(adjustment factor, AF)를 현재까지 사용하고 있으나, 개량 및 사육환경 변화로 기존 보정계수의 개선 필요성이 제기되고 있다. 본 연구는 유량, 유지방량, 유단백량 및 무지고형분량에 대한 신규 305일 보정계수(AF25)를 개발하고, 기존 보정계수(AF09)와 예측 정확도를 평가하였다. 분석에는 2019~2024년 유우군능력검정자료를 활용하였으며, 산차별로 이상치 제거와 검정일 범위, 군-분만년도, 검정횟수 및 비유기간 조건을 적용하여 자료를 정제하였다. 정제된 자료(1,728,258건)를 이용하여 최소자승평균을 추정하였으며, 이를 통해 형질·산차·그룹별 305일 보정계수를 산출하고, 보정계수 비선형 모델을 개발하였다. 정확도 검증은 두 단계로 수행하였다. 첫째, 검정 완료 개체 자료(46,080건)의 305일 누적 생산량을 실측값으로 설정하고, 305일부터 이전 검정기록을 단계적으로 삭제하여 AF09·AF25의 검증값과 실측값 간 RMSE(Root Mean Square Error)를 비교하였다. 그 결과, 유량, 유지방량, 유단백량 및 무지고형분량 모두에서 AF25의 RMSE가 AF09 대비 약 10%~20% 감소하였다. 둘째, 전자 유량계 자료(18,573건)의 실제 누적 유량을 실측값으로 설정하고, 10개의 가상 검정일 집단을 설정하여 검증값과 실측값 간 상관계수 및 RMSE를 비교하였다. AF25는 모든 집단에서 AF09 대비 높은 상관계수와 낮은 RMSE를 나타냈다. 결론적으로, AF25는 AF09보다 국내 젖소 산유능력 예측 정확도를 개선할 수 있으며, 향후 산유능력 평가에 활용할 수 있을 것으로 판단된다.

Key words : 젖소, 산유능력, 305일 유량, 보정계수

PF26019

Comparison of genetic evaluation models for meat quality pH traits in a Korean Duroc pigs

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This study was conducted to identify the optimal genetic evaluation model for the 24-h field pH trait in pigs, which is a critical indicator of pork meat quality. A total of 1,272 Duroc pigs, slaughtered between 2012 and 2025, were recorded for the phenotype. The herd-year-season (HYS) effect was fitted as fixed and random in two models, and termed as model-F and model-R, respectively. Slaughter year-season and slaughter age group were included as additional fixed effects in both models. Variance components were estimated using an animal model through REML in BLUPF90+ software. The estimated heritability (h^2) was lower using model-R (0.087) than the h^2 value using model-F (0.117). This difference in h^2 could be attributable to the fit of HYS as a random effect. The AIC and –2logL values from the model-R were –922.91 and –928.91, respectively, which were lower than those of model-F (–912.76 and –916.76). The mean accuracy of estimated breeding values was 1.5%p higher in model-R (0.45 ± 0.04) than in model-F (0.44 ± 0.04). Despite the model-R yielded a lower h^2 than the model-F, the former demonstrated higher breeding value accuracy and lower model fit indices (AIC and –2logL), suggesting that model-R could be more appropriate genetic evaluation model for 24-h field pH in Korean Duroc pigs.

Key words : Duroc, pH, genetic evaluation, model comparison, accuracy

PF26020

Engineering of O-linked glycan modification in recombinant bovine FSH

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Follicle-stimulating hormone (FSH) and luteinizing hormone (LH) are essential glycoproteins that regulate mammalian gonadal function via GPCR-mediated signaling. In this study, we engineered long-acting bovine FSH (bFSH) analogues by designing single-chain constructs that link the a-subunit to the C-terminus of the b-subunit using overlapping PCR. To enhance biological activity and metabolic half-life, we incorporated O-glycosylated peptide sequences: the human CG b-subunit carboxyl-terminal peptide (hCTP) and the equine CTP (eCTP), featuring four and twelve O-linked glycosylation sites, respectively. These recombinant proteins (rec-bFSH), containing C-terminal Strep tags, were expressed in CHO-K1 and CHO-S cells. Western blot analysis identified broad bands at 44–52 kDa, which shifted to approximately 35 kDa upon deglycosylation, confirming the successful attachment of N- and O-linked oligosaccharides. Functional characterization is currently evaluating signal transduction through the FSH receptor, specifically examining b-arrestin and GRK pathways using knockout cell models. Our results suggest that strategic glyco-structure manipulation provides a powerful framework for developing next-generation, long-acting FSH analogues with enhanced therapeutic potential.

Key words : rec-bovine FSH, CHO cells, O-linked modification, knock out cell

PF26021

Genomic selection and metabolite profiling for quality differentiation of Goheung Hanwoo

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This study established a precision breeding system and brand strategy for Goheung Hanwoo by integrating genomic selection with scientific quality characterization. Based on a pedigree analysis of 41,616 cattle and MS marker-based paternity testing of 809 samples, a core foundation group was established by selecting superior individuals from 128 genomically analyzed cows. This selection maximized genetic reliability, securing vital resources for independent proven bull production. Simultaneously, quality assessments revealed superior water-holding capacity and juiciness, while metabolite profiling identified unique amino acid and fatty acid patterns contributing to the flavor profile of Goheung Hanwoo. By linking genomically verified resources with metabolic data, this study provides a scientific foundation for a self-reliant breeding model and premium branding.
This paper was supported by Sunchon National University Glocal University Project Fund in 2025.

Key words : Hanwoo, genomic selection, foundation cow, metabolite profiling, quality differentiation

PF26022

Genetic analysis of stage-specific survivability traits in Korean Holstein cattle

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Survivability is critical to dairy farm efficiency, reducing involuntary culling and replacement costs. This study evaluated the genetic potential of stage-specific survivability across the first three lactations in Korean Holsteins. Data from 92,591 cows calving between 2002 and 2024 were analyzed. Survivability was defined across three lactation stages (0–90, 91–299, and 300 days to next parity) within each lactation for three consecutive parities, and each stage was treated as a separate trait (T1–T9). Phenotypes were coded as binary (1 = survived, 0 = culled/dead). Both censored and uncensored records were included. Variance components were estimated with a 9-trait animal model in REMLF90, with calving herd-year, calving season, and age at first calving as fixed effects. Heritability estimates ranged from 0.012–0.013 (parity 1), 0.009–0.016 (parity 2), and 0.017–0.031 (parity 3), with slightly higher values in late lactation. Genetic correlations were generally low within parity, though T3, T6, and T9 showed the strongest associations. Early (0.22–0.38) and late (0.31–0.50) stage traits were more strongly correlated than intermediate stages. These results suggest that survivability is lowly heritable but genetically structured, supporting stage-specific selection to improve longevity and herd profitability in Korean Holstein.

Key words : survivability, lactation stage, multiple-trait, animal model, Korean Holstein

PF26023

Microsatellite Marker 기반 국내 소형견 품종의 개체식별 및 유전적 다양성 분석

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국내 가구 구조의 변화(1인 가구, 고령 가구 등)에 따라 반려동물 양육 가구 수는 지속적으로 증가하는 추세이다. 이에 따라 국가에서는 반려동물의 유실과 유기 방지 및 보호자 책임 강화를 위해 반려견 등록제를 시행하고 있으나, 기존 등록 방식은 장치의 분실·훼손 및 삽입 시술에 대한 부담 등의 한계를 가지고 있다. 이러한 문제를 보완하기 위한 방안으로 개체별 유전정보를 활용한 유전자 등록제가 주목받고 있다. 따라서 본 연구에서는 국내 반려견 양육 환경을 고려하여 소형견을 대상으로 Microsatellite Marker를 활용한 개체식별 및 유전적 다양성 분석을 수행하였다. 분석에는 국내에서 양육된 소형견 5품종, 총 189두의 샘플을 이용하였다. 분석에 활용된 17개 MS marker의 전체 대립유전자 수는 167개로 확인되었고, 푸들에서 132개로 가장 많은 대립유전자가 확인되었다. MS marker별 PIC값은 PEZ6에서 0.880으로 가장 높게 나타났고, REN197E16에서 0.458로 가장 낮게 나타났다. 집단의 유전적 균일도를 분석한 결과 K=2에서 시츄가 다른 품종과 차이를 보였고, K=5에서 품종별로 구분이 되었다. PCoA 및 유전거리 분석 결과 몰티즈와 시츄가 가장 먼 유전적 거리(0.244)를 나타냈으며, 비숑프리제와 푸들이 가장 가까운 유전적 거리(0.124)를 나타냈다. 본 연구 결과 품종 간 유전적 차이가 뚜렷하게 확인되었으며, 이를 활용한 개체식별 가능성을 확인할 수 있었다. 또한 본 연구 결과는 향후 반려견 유전자 등록제 구축 및 품종 관리 체계를 마련하기 위한 기초자료로 활용될 수 있을 것으로 사료된다.

Key words : 반려견, 유전적 거리, 유전적 다양성, Microsatellite, 개체식별

PF26024

Estimation of genetic parameters for carbon emission intensity in dairy cattle based on milk production performance in Korea

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In September 2021, the Korean government enacted the 'Framework Act on Carbon Neutrality and Green Growth' to transition toward a carbon-neutral society. Furthermore, the '2030 Nationally Determined Contributions (NDC)' target was established, aiming for a 40% reduction in total greenhouse gas (GHG) emissions compared to 2018 levels. The agricultural, livestock, and fisheries sectors are required to reduce emissions by 27.1% (targeting 18 million tons of CO_2eq by 2030). As of 2020, the agricultural sector accounted for 3.2% (21.1 million tons CO_2eq) of the national total, with the livestock sub-sector—specifically enteric fermentation (4.7 million tons CO_2eq) and manure management (5.0 million tons CO_2eq)—representing approximately 46% of agricultural emissions. This study calculated GHG emission intensity per 1 kg of milk produced by participating farms. The calculation formula for carbon emission intensity was derived by estimating the annual milk yield per cow, utilizing FAO data indices spanning from 1961 to 2020.Using herd examination and performance data provided by the Dairy Cattle Improvement Center, this study calculated the nationwide carbon emission intensity of milk. Furthermore, genetic parameters were estimated to evaluate the potential of using emission intensity as a selection trait.

Key words : carbon neutrality, greenhouse gas (GHG), dairy cattle, milk carbon intensity, genetic parameter estimation

PF26025

Genome-wide association analysis of insulin function phenotypes reveals distinct genetic architecture in Koreans

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Insulin regulates glucose homeostasis and broader metabolic processes, and its dysfunction is implicated in type 2 diabetes, cardiometabolic and hepatic diseases. Because insulin dysfunction in Koreans involve different contributions of secretion defects, insulin resistance, and β-cell compensation failure, these components should be analyzed separately. Therefore, this study aimed to dissect the genetic architecture of insulin secretion, insulin sensitivity, and β-cell compensation and identify related genetic signals in Koreans. Using oral glucose tolerance test data from 6,736 KoGES Ansan-Anseong participants, we calculated insulin indices and performed genome-wide association analyses. Independent signals were identified by LD clumping of variants using a suggestive significance threshold ($p < 1 \times 10^{-5}$). We identified 15, 14, and 17 independent variants associated with insulin secretion, insulin sensitivity, and β-cell compensation, respectively. Candidate genes included *CDKAL1*, *KCNQ1*, and *HNF4A* for insulin secretion and β-cell compensation, and *RYR1*, *PTPRG*, and *SCARB2* for insulin sensitivity, suggesting involvement of β-cell function, insulin signaling, calcium regulation, and lipid metabolism. These findings suggest that insulin function associated genetic architecture in Koreans can be characterized according to distinct insulin phenotypes and provide insight into the pathophysiological basis of insulin-related diseases.

Key words : glucose homeostasis, insulin secretion, insulin sensitivity, β-cell compensation, genome-wide association study

PF26026

Integrative network propagation analysis of GWAS candidate genes for carcass traits in Hanwoo

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Carcass weight, eye muscle area, backfat thickness, and marbling score are economically important carcass traits in Hanwoo cattle. Although previous GWAS studies have identified multiple candidate genes associated with these traits, their biological interpretation remains challenging due to polygenic architecture and linkage disequilibrium. This study aimed to reinterpret GWAS-derived candidate genes for Hanwoo carcass traits at the functional network level. Candidate genes reported in three Hanwoo GWAS studies were used as seed genes, and protein–protein interaction networks were constructed using the STRING database in Cytoscape with Bos taurus as the reference species. Network propagation analysis was performed using Cytoscape Diffusion, and genes were prioritized based on diffusion heat scores. The PLAG1–CHCHD7 axis was repeatedly prioritized for carcass weight and eye muscle area, suggesting shared mechanisms related to growth and muscle development. For backfat thickness, BECN1 and ENPP1 were identified as candidates related to autophagy, insulin signaling, and metabolic homeostasis. For marbling score, GPAT4 and lipid-related genes such as ACACA, BMP4, TWIST2, and MITF were highlighted. These results provide a network-based interpretation of GWAS findings and useful candidates for functional validation and genomic improvement of Hanwoo carcass traits.

Key words : Hanwoo, carcass traits, GWAS, network propagation

PF26027

Accuracy of genomic estimated breeding values for carcass traits in Hanwoo cattle

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Carcass weight (CWT), eye muscle area (EMA), backfat thickness (BF), and marbling score (MS) are major economically important carcass traits in Korean Hanwoo cattle. This study evaluated the accuracy of genomic estimated breeding values (GEBVs) for these traits using the GBLUP and Bayes B methods. Genotype and phenotype data from 9,303 Hanwoo cattle were analyzed using the Illumina 50K bovine SNP chip. Prediction accuracy was evaluated using genomic estimated breeding values (GEBV) and deregressed genomic estimated breeding value (DGEBV) by applying five-fold cross-validation. In each validation round, 80% of animals were used as the reference population, while the remaining 20% were treated as the validation group with masked phenotypes. Heritability estimates under the GBLUP model were 0.42, 0.36, 0.36, and 0.47 for CWT, EMA, BF, and MS, respectively. Corresponding estimates under the Bayes B model were 0.47, 0.37, 0.36, and 0.42. The accuracies under the GBLUP model for the four traits ranged from 0.69–0.74 using complete data set. GBLUP model accuracies for CWT, EMA, BF and MS were 0.72, 0.70, 0.69 and 0.74 respectively while Bayes B model accuracies were 0.80, 0.72, 0.73 and 0.72 respectively. On the other hand, the realized accuracy estimates using cross validation data set were 0.66, 0.60, 0.55 and 0.54 respectively for the CWT, EMA, BF and MS traits whereas model accuracy were 0.62, 0.59, 0.59 and 0.63 respectively under GBLUP method. The difference between model and realized accuracy under GBLUP method was ~3%. Whereas Bayesian B method demonstrated ~30% difference between model and realized accuracy. The accuracies of model versus realized under Bayes B model was estimated in CWT (0.53 vs 0.66), EMA (0.40 vs 0.61), BF (0.41 vs 0.57) and MS (0.37 vs 0.58) respectively using cross validation procedure. Therefore, both GBLUP and Bayes B method could be used to estimate the GEBV in Hanwoo genomic selection.

Key words : genomic selection, GEBV accuracies, GBLUP, carcass traits, Hanwoo

PF26028

제주마의 혈통 분석 및 유효집단크기 추정

장찬우, 고유진, 송지연, 박연희, 이상훈, 박종은

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제주마는 제주의 고유의 품종으로서 제주도의 거친 자연환경에 적응하며 살아온 체구가 작고 강인한 체력을 가진 대한민국 천연기념물 제347호 고유 품종이다. 본 연구는 지속 가능한 번식 및 개량 전략을 개발하고 제주마 집단의 유전적 편향 문제를 진단하기 위해 수행되었다. 이를 위해 1968년부터 2025년 사이에 태어난 9,684마리의 혈통 데이터를 사용하여 집단의 유전적 구조를 분석하였다. 제주마의 혈통 구성 및 유효집단 크기(Ne)를 추정하기 위해 POPREP 소프트웨어를 사용하였으며, Gutierrez 등(2009)이 제안한 계산 방법을 활용하였다. 제주마의 평균 근친교배 계수는 세대가 거듭됨에 따라 2004년 이후 증가 추세를 보였다. 또한, 세대 당 근친교배율을 기반으로 계산한 유효집단 크기는 40으로 추정되었다. 이러한 결과는 보전유전학적 임계치인 50을 하회하는 수준으로, 제주마 집단의 유전적 다양성 소실 위험이 높음을 시사한다. 이에 따라 특정 가계 중심의 번식이 경주성능에 미치는 영향을 규명하기 위한 후속 연구의 필요성 제기된다. 향후 이러한 분석 결과를 토대로 유전적 편중을 방지하고 다양성을 유지할 수 있는 체계적인 개량 전략 수립이 병행되어야 할 것이다.

Key words : 제주마, 혈통정보, 근교계수, 혈연계수, 유효집단크기

PF26029

Assessment of genetic structure, diversity, and inbreeding in a conserved line-breeding Hanwoo population

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This study evaluated the genetic structure, genetic diversity, and inbreeding level of a line-breeding Hanwoo population (LB), which has been conserved without the introduction of Korean proven bulls, and compared it with a general Hanwoo population (GH). A total of 2,599 animals, including LB and GH, with Bovine 50K SNP data and pedigree records were analyzed. Principal component analysis (PCA) and ADMIXTURE analysis were performed using quality-controlled SNP data to assess population structure. Genomic inbreeding was evaluated using runs of homozygosity (ROH) analysis in PLINK, and individual ROH-based inbreeding coefficients (FROH) were calculated from ROH segments $\geq$ 5 Mb. ROH segments were classified into four length categories to characterize genomic inbreeding patterns. Observed and expected heterozygosity were calculated using PLINK, and pedigree-based inbreeding coefficients and pedigree depth were also examined in relation to FROH. All results were visualized using R. These analyses provided an integrated assessment of the genetic structure and inbreeding status of the Hanwoo line-breeding population and may provide useful baseline information for maintaining genetic diversity and establishing sustainable conservation and breeding strategies in small and closed populations.

Key words : genetic diversity, genomic inbreeding, Hanwoo, line-breeding, runs of homozygosity (ROH)

PF26030

Blood type diagnostic method using the GGTA1 gene structure differences in pigs

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Pig are known to two-types of blood type, A and O. We developed a method to analyze precisely and rapidly pig blood types by utilizing gene structural differences in the causative gene, GGTA1. Pig blood type A has eight normal exons of the GGTA1 gene, whereas blood type O has an incomplete gene structure due to nucleotide large deletions after exon 7. Specifically, nucleotide deletions (731 bp, 260 bp, and 43 bp) were observed at three different locations within the intron 7 region of blood type O. In this study, we designed primers capable of distinguishing 43 bp sequence insertions/deletions (INDELs) within intron 7 region. As a result, we were able to detect the three genotypes of GGTA1 (AA, AO and OO) by electrophoresis after simple PCR amplification. PCR product sizes for each genotype were 272 bp (A-type) and 229 bp (O-type) on a 2% agarose gel. Using this method, it is possible to accurately identify the GGTA1 genotype and select pigs with specific blood types. When organs from pigs with blood type O are transplanted into humans, it may help alleviate immune responses caused by differences in ABO antigens.

Key words : AO blood types, gene structure, GGTA1, INDEL, pigs

PF26031

Evaluation of single-step genomic BLUP for milk production traits in Korean Holstein cattle

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Korean Holstein is the predominant dairy breed in South Korea and contributes most of the national milk production. This study aimed to estimate the accuracy of estimated breeding values (EBVs) for 305-day milk production traits, including milk yield (Milk305), fat yield (Fat305), and protein yield (Prot305), using pedigree-based best linear unbiased prediction (PBLUP) in Korean Holstein cows. A single-trait and multi-trait repeatability model was applied for five parities using the BLUPF90 software package. The phenotypic records were collected from a total of 11,036 Korean Holstein cows for the studied traits, while the pedigree information was covered up to the 5th generation, with a total of 21,553 individuals. In single-trait analysis, the estimated heritability across the five parities was 0.17, 0.16, and 0.16 for Milk305, Fat305, and Prot305, respectively. Similarly, in multi-trait analysis, the estimated heritability across the five parities was 0.17, 0.16, and 0.15 for Milk305, Fat305, and Prot305, respectively. The accuracies of EBVs for the single trait model were 0.47, 0.45, 0.45; while the accuracies of EBVs in the multi-trait was 0.48, 0.47, 0.46 for Milk305, Fat305, and Prot305, respectively. The repeatability value for both the single-trait and multi-trait models was similar such as 0.37, 0.35, and 0.37 for Milk305, Fat305, and Prot305, respectively. The results showed that multi-trait analysis slightly outperformed the single-trait model, providing higher EBV accuracies, while heritability and repeatability estimates were similar between the two approaches. Therefore, multi-trait pedigree-based BLUP may provide more reliable selection information than single-trait pedigree-based BLUP for improving milk production traits in Korean Holstein cattle.

Key words : Holstein, milk production traits, PBLUP, repeatability, accuracy

PF26032

Pedigree-based genetic evaluation of milk production traits in Korean Holstein cattle across different parities

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Key words : Holstein, PBLUP, milk production traits, prediction accuracy

PF26033

유전체 통계 분석 툴킷(PLINK)과 새로운 SNP 품질관리 검증 프로그램(popQC)의 성능 비교 분석

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유전체 품질관리(QC)는 GWAS 및 가축의 유전체 선발 분석의 정확성을 높이기 위한 필수 전처리 과정이다. 현재 널리 사용되는 PLINK는 인간 유전체 데이터를 위해 개발되어 가축 집단에 적용 시 친자 확인, 정밀한 HWE 검정, 중복 개체 관리 등 한계를 보인다. 본 연구에서는 가축의 유전체 QC 파이프라인인 popQC를 개발하고, 4,628두의 요크셔 돼지 및 76,756개 SNP 데이터를 이용해 PLINK v1.9와의 성능을 비교하였다. popQC는 분석 전 단계에서 중복 SNP 142개를 자동 감지 및 제거하여 76,614개의 고유 마커를 확보하였다. QC 수행 결과, popQC는 53,208개, PLINK는 46,977개의 SNP를 최종 통과시켜, popQC가 13.3% 더 많은 유효 마커를 확보하였다. popQC는 Bonferroni 보정 HWE 정확 검정 (임계값: 1.31×10^{-7})으로 10,033개의 SNP를 제거하였으며, 이는 PLINK의 일괄 제거 방식보다 정밀하다. 또한 popQC는 2-pass Mendelian 불일치 검증, 156두에 대한 자동 부모 재탐색, X염색체 기반 성별 불일치 탐지, 그리고 유전자 일치도를 통한 중복 개체 자동 병합 기능을 수행하였다. 이는 단순 필터링 위주인 PLINK의 기능을 넘어, 가축 집단의 계통 정보를 유기적으로 통합 관리하는 고도화된 처리 공정이다. 메모리 사용량 측면에서도 popQC는 해시테이블 기반 Architecture를 통해 경량 구동이 가능한 반면, PLINK는 동일 데이터셋에 대해 128,706 MB의 RAM을 차지하는 것으로 나타났다. 이상의 결과는 popQC가 돼지 유전체 QC에 있어 보다 포괄적이고 정확하며 효율적인 솔루션을 제공함을 입증하며, 타 가축 종에도 폭넓게 적용 가능한 파이프라인임을 시사한다.

Key words : popQC, PLINK, hardy-weinberg, mendelian inconsistency

초지 및 환경

PG26001

착유우의 물리적, 감각적 환경 풍부화의 유형과 효과에 대한 고찰

이우도, 김찬호, 문예진, 김수미, 방한태, 양가영, 차지혜

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유제품에 대한 소비자의 인식은 안전성과 품질을 넘어 착유우의 사육 환경과 관리 방식으로 확대되면서 동물복지에 대한 관심이 증가하고 있다. 동물복지는 신체적 건강과 생리적 기능을 유지하고, 부정적 정서를 최소화하며 자연행동을 표현할 수 있는 상태를 의미한다. 이러한 복지 향상을 위해 환경적 스트레스 완화와 행동 욕구 충족, 긍정적 정서 유도를 목표로 하는 환경 풍부화(environmental enrichment)가 주목받고 있다. 본 연구는 착유우에 적용되는 물리적 및 감각적 환경 풍부화의 유형과 특성을 고찰하고, 생산성, 행동, 청결도 및 복지 측면에서의 효과를 분석하였다. 브러시, 사슬, 장난감 및 젖꼭지형 장치와 같은 물리적 풍부화와 시각, 청각 및 후각 자극을 포함한 감각적 풍부화를 구분하여 총 32편의 문헌을 분석하였다. 물리적 환경 풍부화는 털고르기 행동 증가, 활동성 향상 및 스트레스 감소와 관련이 있었으며, 일부에서는 유량 증가 등 생산성 개선 효과도 보고되었다. 감각적 환경 풍부화는 거울, 사진, 비디오 등의 시각적 자극과 음악의 종류, 템포 및 데시벨을 활용한 청각적 자극을 중심으로 연구되었으며, 청각 자극의 경우 적정 자극 수준이 제안된 바 있다. 그러나 감각 기반 풍부화 연구는 제한적이며, 효과의 일관성이 부족하거나 유의한 결과가 나타나지 않는 한계도 확인되었다. 따라서 환경 풍부화의 효과를 명확히 규명하기 위해서는 자극의 강도와 특성, 제공 기간 및 사육 환경을 고려한 체계적인 연구가 필요하다. 본 고찰은 착유우의 환경 풍부화 전략 수립과 향후 연구 방향 설정에 기초 자료를 제공할 것으로 기대된다.

Key words : dairy cattle, animal welfare, environmental enrichment, physical enrichment, sensory enrichment

PG26002

Effect of negative pressure on exhaust fan performance and determination of critical ventilation rate in pig housing

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This study aimed to analyze the effects of negative pressure conditions on the performance of exhaust fans in pig housing facilities and to propose criteria for stable ventilation system design. In mechanically ventilated windowless pig houses, temperature, humidity, and harmful gases are controlled using air inlets and exhaust fans. The negative pressure environment formed during operation can cause the actual performance of exhaust fans to deviate from their rated conditions. To investigate this, a modified container-based chamber was used to establish static pressure conditions ranging from −5 to −30 Pa. The performance of a 50 cm exhaust fan was evaluated under ventilation rates from 10% to 60%. The results showed that, as static pressure increased, backflow occurred or airflow decreased. In particular, at a negative pressure of −20 Pa, backflow was observed even at a ventilation rate of 40%. Additionally, a nonlinear behavior was identified in which the fan’s ability to overcome static pressure increased sharply between ventilation rates of 50% and 55%. Based on these findings, the Critical Ventilation Rate (CVR) and Safe Operating Range were defined. These results highlight the importance of considering negative pressure conditions when establishing operational criteria for the design of pig housing ventilation systems.

Key words : negative pressure, exhaust fan performance, ventilation rate, mechanical ventilation, critical ventilation rate

PG26003

제주 지역에서 한·난지형 목초 및 사료작물 혼파에 따른 초지 식생 구성 및 생산성 비교

정진우, 고하늘, 박형수, 우제훈, 양승학, 정종성

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본 연구는 제주 지역을 대상으로, 한지형과 난지형 목초 및 사료작물의 혼파를 통해 초지 식생을 유지하고 연중 생산성을 극대화할 수 있는 최적의 조합을 구명하고자 수행되었다. 제주 난지축산연구센터 시험포장에서 한지형(이탈리안 라이그라스, 톨페스큐)과 난지형(바랭이, 사료피) 목초 및 사료작물을 이용해 단파 및 혼파 처리구 6개를 난괴법 3반복으로 조성하였다. 2025년 4월부터 9월까지 총 6차에 걸쳐 예취를 진행하였으며, 각 수확 시기별로 식생비율, 초장, 건물생산성 및 사료가치를 조사하였다. 식생 비율의 경우, 1차 수확 시 모든 처리구에서 한지형 목초 및 사료작물이 우점하였으나, 한지형 목초 및 사료작물 단파구는 3차 수확 이후부터 점차 식생비율이 감소하여 상대적으로 잡초 비율이 증가하였다. 반면 혼파구인 T3(이탈리안 라이그라스+바랭이)는 6차 수확 시 난지형인 바랭이가 90%를 점유하며 잡초 발생을 10%로 억제해 하절기에도 안정적인 식생을 유지하였다. 건물생산성의 경우, 혼파구인 T3(이탈리안 라이그라스+바랭이, 21,833 kg/ha)가 단파구인 T2(이탈리안 라이그라스, 14,588 kg/ha) 대비 약 49.7% 높았다. 결론적으로 제주 지역에서는 이탈리안 라이그라스에 바랭이를 혼파하는 것이 식생 유지와 건물생산성 극대화에 가장 효과적인 조합으로 확인되었다. 단, 본 연구는 제주 지역에 국한된 결과이므로, 기후 조건이 상이한 타 지역에서도 동일한 식생 유지 및 생산성 향상 결과가 도출되는지를 확인하는 후속 연구가 요구된다.

Key words : botanical composition, cool-season grass, productivity, seed mixture, warm-season grass

PG26004

이유자돈 환경풍부화물 선택을 위한 문헌 기반 효과 분석

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이유자돈 시기는 어미로부터 분리된 직후 체온 조절, 모유에서 사료의 급격한 사료 전환, 환경 변화 및 개체 혼합 등 복합적인 스트레스 요인에 노출되면서 이유 스트레스를 경험한다. 이러한 급격한 환경변화는 면역 기능 저하, 공격 행동 및 이상행동의 증가로 이어질 수 있어 적절한 관리가 요구된다. 환경풍부화물은 사육 환경에서 돼지의 종 특이적 행동을 표현할 수 있도록 하는 관리 요소로 스트레스 완화 및 행동 안정화를 위한 관리 요소 중 하나이다. 본 고찰은 총 37편의 문헌을 수집하여 이유자돈의 환경풍부화물 유형을 체계적으로 검토하고 그 효과를 분석함으로써, 향후 환경풍부화물 선택을 위한 근거 마련에 기초자료로 활용하고자 한다. 최근 환경풍부화물 연구는 단일 제공에서 복합 제공으로 확장되며, 환경풍부화물 이용의 지속성과 행동 유도 유지에 초점을 두는 방향으로 발전하고 있다. 환경풍부화물의 행동학적 특성이 저작, 조작 및 탐색 행동을 유도하는 물질의 경우 탐색 행동 증가와 함께 공격 및 이상행동이 유의하게 감소하는 것으로 나타났으며, 생산성과 관련된 지표에서는 전반적으로 유의한 변화가 확인되지 않았다. 한편, 행동 및 생산성 지표에 대한 변화 분석은 활발히 이루어진 반면, 코티졸과 같은 스트레스 지표를 활용한 생리학적 측정은 상대적으로 제한적인 수준에 머물렀다. 결론적으로 본 고찰을 통해 환경풍부화물 효과 평가는 행동뿐 아니라 생리 및 생산성 지표를 포함한 다중지표 기반의 통합적 해석이 필요하며, 향후에는 돼지의 기능적 행동 유도와 환경풍부화물 이용 지속성을 함께 고려한 연구 설계가 필요할 것으로 판단된다.

Key words : weaning piglets, environmental enrichment, animal welfare

PG26005

Adaptive ventilation control strategy based on heat balance modeling for improved microclimate management in broiler housing

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The rapid intensification of broiler production systems has increased the importance of precise indoor climate control. Insufficient ventilation management can lead to thermal stress, accumulation of harmful gases, and consequent declines in productivity. Despite this, many commercial broiler facilities continue to rely on manual operation or simplified rule-based control approaches, with limited availability of rigorously validated control algorithms. In this study, an adaptive ventilation control strategy grounded in heat and energy balance modeling was developed to provide a more accurate estimation of ventilation requirements. A year-long dataset obtained from an experimental broiler facility was used to evaluate performance. The conventional control approach maintained target thermal conditions for 74% of the production cycle, whereas the proposed strategy improved this to 92%. Field validation was conducted in two commercial-scale broiler houses during the finisher phase (20–34 days of age). The proposed system reduced indoor daytime temperatures by 1.5℃–2.0℃, thereby mitigating heat stress conditions. While the operation frequency of evaporative cooling pads increased substantially, the use of tunnel ventilation fans decreased by 52%, leading to an overall improvement in energy efficiency. Additionally, mortality rates were reduced by 16.5%, indicating enhanced animal welfare and production outcomes.

Key words : energy-efficient ventilation, field-scale validation, heat–energy balance analysis, poultry housing environment, thermal stress mitigation

PG26006

A comprehensive framework for monitoring and enhancing animal welfare and environmental safety in livestock transport systems

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The transportation of livestock represents a vital link in Korea's agri-food supply chain, involving the daily movement of thousands of cattle, tens of thousands of pigs, and millions of poultry. During transit, animals are often subjected to challenging conditions, including thermal stress, inadequate ventilation, degraded air quality, vehicle-induced vibration, and physical injury, all of which can adversely affect welfare and production efficiency. This study proposes an integrated assessment framework designed to simultaneously evaluate animal welfare and environmental risks during livestock transportation. The framework combines a physics-based microclimate prediction model, incorporating animal heat exchange and airflow dynamics, with computational fluid dynamics simulations to characterize in-vehicle environmental conditions. Validation is conducted through field measurements using sensor-equipped commercial transport vehicles operating under a range of climatic and driving conditions. The proposed framework offers a scientifically grounded and practically applicable solution for improving transport management, enhancing animal welfare during transit, and mitigating environmental and economic risks associated with livestock transportation.

Key words : livestock transportation, animal welfare, transport microclimate, heat stress

PG26007

Estimation annual nitrogen excretion from gestating and lactating sow

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The objective of the present study was to estimate the annual nitrogen (N) excretion from gestatining and lactating sows in Korea. Eighteen diets (9 gestation diets and 9 lactation diets) collected from 9 commercial farms were analyzed for dry matter and crude protein. Crude protein contents in gestation and lactation diets were 13.1% and 17.7%, respectively. Daily N intake of gestatining and lactating sows was calculated using daily feed intake from the literature and dietary crude protein content. The N retention of sows was calculated using the models in the literature. Daily N excretion inclusive fecal and urinary N was calculated as the difference between daily N intake and daily N retention. Annual N excretion from a sow was calculated as a weighted mean based on the duration of gestation and lactation. The daily N intake of gestatining and lactating sows was 44.5 and 151.1 g/day, respectively. Daily N excretion of gestatining and lactating sows was 35.9 and 89.9 g/day, respectively. The annual N excretion from a sow was 16.2 kg/year which was less ($p < 0.001$) than 26.35 kg/year suggested by the Intergovernmental Panel on Climate Change (2019). In conclusion, the annual N excretion from a sow in Korea estimated to be 16.2 kg/year.

Key words : gestating sow, Intergovernmental Panel on Climate Change, lactating sow, nitrogen excretion

PG26008

저전력 엣지 환경에 최적화된 비육염소 행동 분류 Transformer-CNN 모델 개발

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가축의 반추 및 사료섭취와 같은 개체유지행동의 자동 분류는 건강 및 생산성 관리의 핵심 지표이다. 본 연구는 6축 IMU 신호 기반 Transformer-CNN 행동 분류 모델을 개발하고, 저샘플링 및 저연산 엣지 환경에서의 적용 가능성을 평가하고자 수행되었다. 경기도 소재 농장의 축사 사육(housing system) 환경에서 사육 중인 5–6개월령 거세 흑염소 19두를 공시하였으며, 2025년 9월 18일부터 26일까지 9일간 CCTV 영상과 목 부착형 6축 IMU 센서(Farmer's Hands, Bodit Inc., South Korea)를 이용하여 행동 데이터를 수집하였다. 수집된 가속도 3축 및 각속도 3축 신호를 10초 단위 윈도우로 분할하여 총 132,887개 표본을 구축하였고, Transformer Encoder와 1D CNN을 결합한 End-to-End 모델을 적용하여 사료섭취, 반추 및 기타행동에 대한 3-class 분류를 수행하였다. 모델은 5–25 Hz 조건에서 학습 및 평가되었으며 일반화 성능은 Leave-One-Subject-Out(LOSO, n = 15) 및 Stratified 5-Fold 교차검증으로 분석하였다. 그 결과 25 Hz에서 매크로 평균 F1 점수는 LOSO 82.3%, 5-Fold 86.7%를 기록하였으며, 5 Hz에서도 각각 78.6%, 84.2%로 4%p 이내의 성능 저하만 나타났다. 또한 CPU 기반 추론 지연 시간은 25 Hz에서 1.55 ms, 5 Hz에서 0.68 ms로 모든 주파수 조건에서 실시간 처리 성능을 만족하였다. 이상의 결과는 제안한 Transformer-CNN 모델이 저샘플링 및 저전력 엣지 환경에서도 안정적인 행동 분류 성능을 제공함을 시사하며, 축산 IoT 기반 실시간 모니터링 시스템에 효과적으로 활용될 수 있음을 보여준다.

Key words : artificial intelligence, deep learning, six-axis IMU, goat behavior classification, inference latency

PG26009

IMU 센서 기반 젖소 헐떡임 탐지를 통한 고온 스트레스 모니터링 기술 개발

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고온 스트레스는 젖소의 생산성과 복지를 저해하는 주요 요인이며 기후변화에 따라 그 심각성이 증가하고 있다. 본 연구는 젖소의 헐떡임(panting)을 자동 탐지하여 고온 스트레스를 정량적으로 모니터링하기 위한 기술을 개발하고자 수행되었다. 2024년 8월부터 11월까지 경기도 소재 젖소 농장에서 착유우 20두를 대상으로 목걸이형 IMU 센서(Farmer's Hands, Bodit Inc., South Korea)를 부착하고 CCTV 기반 행동 라벨링을 수행하였다. 이를 토대로 가속도 신호의 정적성, 호흡 주파수 대역 에너지, 호흡 규칙성 및 스펙트럼 피크 강도를 결합한 rule-based 헐떡임 탐지 알고리즘을 설계하였다. 개발된 알고리즘은 2024–2025년 동안 총 119두의 젖소에 적용되어 헐떡임 시간을 수집하였으며, 온습도지수(THI)와의 관계를 분석하였다. 또한 헐떡임 데이터를 바탕으로 추정 호흡수(BPM)를 산출하여 THI 변화와 비교하였다. 헐떡임 탐지 성능은 개체 단위 5-fold GroupKFold 교차검증에서 F1 score 0.763을 나타냈다. 헐떡임 시간은 THI와 유의한 양의 상관관계를 보였으며(THI ≥ 70, Pearson r = 0.671), 추정 호흡수는 THI 82 이상에서 급격히 증가하여 THI 88에서 최대 94 BPM에 도달하는 비선형 임계 반응을 나타냈다. 이러한 결과는 행동 센서 기반 헐떡임 탐지가 젖소의 고온 스트레스를 실시간으로 모니터링할 수 있는 효과적인 기술임을 시사한다.

Key words : heat stress, dairy cattle, IMU sensor, panting detection, respiration rate, temperature-humidity index

PG26010

Evaluation of methane reduction effects in swine farm slurry by application of a methane reducing agent

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Methane (CH_4) emissions from the livestock sector have recently gained increasing attention in relation to carbon neutrality and low-carbon livestock production, leading to the demand for various technologies to reduce methane generated during animal husbandry. Following the 2015 Paris Agreement and the 2019 UN Climate Action Summit, carbon neutrality by 2050 emerged as a global paradigm, and South Korea also declared its goal of achieving carbon neutrality by 2050 in October 2020. Accordingly, the Korean government revised its 2030 Nationally Determined Contribution (NDC) targets upward in October 2021 and established a 2050 carbon neutrality scenario. This study was conducted to evaluate the methane reduction effect of applying a methane-reducing agent to swine farm slurry. The experiment was carried out using slurry collected from a manure storage tank at a finishing pig farm with a capacity of 3,000 pigs located in Boseong, Jeollanam-do, Republic of Korea. *Methanotrophs* sp. were inoculated into 500 mL of slurry and incubated at 30°C in a constant-temperature water bath. Methane (CH_4) concentrations were analyzed using gas chromatography (GC; 7890A GC system, Agilent Technologies, Germany) equipped with a flame ionization detector (FID). The methane emission data obtained in this experiment were analyzed using the SAS (Statistical Analysis System) statistical package (2003). Differences among treatment means were evaluated using Duncan's multiple range test at a significance level of $p < 0.05$. The results showed that the treatment with 0.2% *Methanotrophs* sp. supplementation produced the lowest methane emissions at both 12 and 48 hours of incubation. Compared with the control group, methane emissions were reduced by 13% after 12 hours and by 23% after 48 hours of incubation.

Key words : swine, methane reduction, slurry, odor reduction

PG26011

Evaluation of odor reduction effects of microorganisms isolated from swine feces, slurry, and wastewater

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This study aimed to evaluate the odor-reducing activities of microorganisms isolated from swine feces, slurry, and wastewater against ammonia, amines, and hydrogen sulfide, and to select potential microbial strains for livestock odor. Among 43 isolates, 19 strains showing proteolytic activity were selected, and *Bacillus subtilis* CACC885 was used as a positive control. Each strain was inoculated at 1% (v/v) into diluted swine slurry samples and incubated for 24 h. Based on hydrogen sulfide reduction activity, nine *Bacillus* strains and one lactic acid bacterium were selected for further evaluation of ammonia and amine reduction. Among the evaluated strains, slurry-derived *Limosilactobacillus reuteri* CACC1861 showed hydrogen sulfide and amine reduction efficiencies of 25.00% and 35.45%, respectively. Slurry-derived Bacillus velezensis CACC1854 exhibited the highest ammonia and amine reduction efficiencies at 85.00% and 80.00%, respectively. *Bacillus velezensis* CACC1819 also showed stable reductions against hydrogen sulfide, ammonia, and amines, with efficiencies of 18.92%, 24.48%, and 26.53%, respectively. Additionally, wastewater-derived *Bacillus subtilis* CACC1833 showed high ammonia reduction efficiency (35.68%), while swine feces-derived Bacillus subtilis CACC1846 exhibited broad odor-reducing activity across the tested odor compounds. Based on the overall odor reduction profiles, the slurry-derived strains *Bacillus velezensis* CACC1854, *Limosilactobacillus reuteri* CACC1861, and *Bacillus velezensis* CACC1819 were selected as promising candidates. These results suggest that the selected strains may serve as functional microbial resources for reducing livestock-derived odor.

Key words : swine slurry, livestock odor mitigation, ammonia reduction, hydrogen sulfide, *Bacillus velezensis, Limosilactobacillus reuteri*

PG26012

한우사 내부 및 부지경계에서 악취물질 발생 조사 연구

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한우사에서 발생하는 주요 악취물질의 농도 특성을 파악하고, 축사 내부와 부지경계에서의 악취 발생 양상을 비교하여 한우 사육시설의 악취관리 기초자료를 제시하고자 수행하였다. 현장 조사는 12개소의 한우사 내부와 부지경계를 측정지점으로 설정하여 수행하였으며, 자연환기식 개방형 바닥깔개 우사 시설을 대상으로 총 11종의 악취물질을 분석하였다. 분석 결과, 한우사 내부에서는 암모니아, 황화수소, 아민류 및 일부 지방산류가 주요 악취물질로 확인되었으며, 부지경계에서는 복합악취와 암모니아가 주요 관리지표로 활용될 수 있을 것으로 판단되었다. 한우사는 개방형 구조로 인하여 밀폐형 축사(돈사 및 계사)에 비해 악취농도는 낮은 편이나, 깔짚 상태, 분뇨 체류시간, 환기 조건, 기상조건에 따라 부지경계에서 악취 영향이 달라질 수 있다. 따라서 축산시설별 악취물질 농도뿐만 아니라 최소감지농도와 악취활동도 평가를 고려한 저감관리 기준 마련이 필요할 것으로 판단된다.

Key words : 한우사, 악취물질, 지방산, 아민류, 부지경계, 복합악취

PG26013

Phylogenomic analysis of the Korean *Mycobacterium bovis* JW-1 isolate using pacbio-illumina hybrid assembly

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Bovine tuberculosis caused by *Mycobacterium bovis* remains an important infectious disease affecting livestock and public health. In this study, the Korean JW-1 isolate was assembled using PacBio long-read and Illumina short-read hybrid sequencing to generate a high-quality genome assembly. Comparative phylogenomic analysis was performed using publicly available international *M. bovis* genomes, including Chinese isolates. Core genome SNP-based phylogenetic analysis showed that JW-1 clustered closely with several East Asian isolates, suggesting possible regional evolutionary relationships. Pairwise SNP distance analysis further supported the genomic relatedness between JW-1 and selected Asian isolates. These findings provide preliminary insights into the evolutionary characteristics and molecular epidemiology of Korean *M. bovis* strains. In addition, this study demonstrates the usefulness of hybrid genome assembly and SNP-based phylogenomic analysis for high-resolution surveillance of bovine tuberculosis.

Key words : *Mycobacterium bovis*, bovine tuberculosis, hybrid assembly, phylogenomics, SNP analysis

PG26014

Spatial characteristics of heat stress risk in Hanwoo cattle based on the temperature-humidity index

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Recent climate change has intensified the frequency and severity of heat waves, thereby increasing thermal stress vulnerability in the livestock industry. In particular, hot and humid summer conditions negatively affect the productivity and welfare of Hanwoo cattle. This study investigated regional patterns of heat stress risk in Hanwoo cattle across South Korea using the Temperature–Humidity Index (THI). Weather data from 167 cities and counties collected during the summer of 2024 (June–September) were used to calculate the proportions of days exceeding the warning threshold (THI ≥ 79) and danger threshold (THI ≥ 90).

The results revealed that warning-level exceedance rates were particularly high in the inland plains of the Honam and Chungcheong regions, where average exceedance rates exceeded 90% in several areas. In contrast, lower exceedance rates were observed in the mountainous regions of Gangwon Province and coastal areas influenced by marine climates. These findings suggest that topographic and regional climatic conditions substantially influence the thermal vulnerability of Hanwoo cattle. This study provides fundamental information for establishing climate change adaptation strategies and region-specific heatwave mitigation policies in livestock management.

Key words : heat stress, Hanwoo, temperature-humidity index

PG26015

한우 거세우의 생애주기 열스트레스 노출 수준이 도축성적에 미치는 영향

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본 연구는 개체별 한우의 축산물이력제 이동정보를 기반으로 일별 기상 데이터를 연계하여 한우 거세우의 생애주기 열스트레스 누적 노출이 도체형질에 미치는 영향을 분석하였다. 공공데이터 API를 활용해 아비 및 외조부의 씨수소가 동일한 29~32개월령 한우 거세우 865마리의 축산물이력제 및 품질 데이터를 수집하였으며 개체별 이동 이력에 따라 카카오맵 API를 활용해 농장 주소지의 위도 및 경도를 매칭하고 이를 ASOS 최근접 기상관측소에 매칭하여 생애주기 전체의 기상 데이터를 획득하였다. THI 72 초과 노출일수·비율·평균 등을 산출하였으며 도체중, 근내지방도 등 9개 도체 형질과의 분석을 수행한 결과, 열스트레스 지표와 도체형질 간 유의한 연관성은 확인되지 않았다(R = 0.02–0.10). 차후 사료공급, 사육단계별 노출, 출하계절 등 교란변수를 통제한 혼합모형을 적용함으로써 열스트레스 노출과 도체형질 간 인과관계를 보다 정밀하게 규명할 필요가 있을 것으로 보인다.

Key words : 한우, 열스트레스, THI, 생애주기, 공공데이터

PG26016

Analysis of greenhouse gas emission trends in the livestock sector based on the 2023 National GHG Inventory

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To establish effective GHG reduction policies and monitor their implementation in the livestock sector, an accurate analysis of emission trends from the annual national GHG inventory is essential. This study utilized livestock category data from the '2023 National GHG Inventory Statistics' to analyze emissions from enteric fermentation and manure management in 2023. In 2023, total GHG emissions from the livestock sector were calculated at 12.7 million tons CO_2eq, accounting for approximately 56% of the agricultural sector. By specific source, emissions from enteric fermentation were 6.7 million tons CO_2eq, representing about 29.9% of agricultural emissions. In terms of emission contributions, cattle accounted for the highest proportion at 94.2%, followed by pigs (4.5%) and poultry (1.3%). Emissions from the manure management sector were estimated at 6.0 million tons CO_2eq, representing 26.5% of the agricultural sector. Direct CH_4 and N_2O emissions amounted to 4,895 thousand tons CO_2eq, with pig manure management facilities accounting for 60.4% and cattle facilities for 33.8%. Indirect N_2O emissions were 1,087 thousand tons CO_2eq, making up 18.2% of the manure management sector's emissions. Achieving NDC targets requires the active adoption of site-specific reduction technologies. These findings provide a vital foundation for advancing carbon neutrality implementation plans in the livestock sector.

Key words : livestock, greenhouse gas, methane, nitrous oxide, national inventory report

PG26017

Farm-level treatment-associated odor and fecal microbiota changes in pig farms

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This study investigated farm-level treatment-associated changes in odor-related indicators, slurry physicochemical properties, short-chain fatty acid profiles, and fecal microbiota before and after treatment in pig farms. Treatment A, *Bacillus licheniformis*; Treatment B, a three-strain microbial consortium consisting of *Lactiplantibacillus plantarum*, *Pediococcus pentosaceus*, and *Saccharomyces cerevisiae*; and Treatment C, curcumin, were applied to independent pig farms. Odor-related responses differed among treatments. Treatments A and C significantly reduced major odor indicators, including ammonia, amine, hydrogen sulfide, volatile organic compounds, and complex odors, whereas Treatment B showed non-significant decreasing trends in odor gases. For short-chain fatty acid and fecal microbiota analyses, fecal samples were collected from 10 pigs per farm. Acetic, propionic, and 2-methylbutyric acids significantly decreased in Treatment A, while valeric acid significantly increased in Treatment C. Slurry physicochemical parameters, including total solids, volatile solids, suspended solids, total phosphorus, and total nitrogen, were significantly reduced in Treatment A and mostly reduced except total nitrogen in Treatment B, whereas total nitrogen increased in Treatment C. Fecal microbiota analysis showed treatment-associated shifts in gut microbial community structure, suggesting distinct farm-level environmental and microbial responses.

Key words : swine, feed additives, odor mitigation, slurry characteristics, short-chain fatty acids, fecal microbiota, farm-level variation

PG26018

액티브 시니어 대상 말교감치유 융복합 프로그램 개발 및 효과 연구

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초고령사회 진입과 함께 은퇴 후 삶을 살아가는 액티브 시니어의 심리적·신체적 건강 증진에 대한 관심이 높아지고 있으며, 이러한 맥락에서 말 교감활동은 긍정적인 치유 효과를 제공하는 대안으로 주목받고 있다. 따라서 본 연구에서는 말 교감활동과 원예치유를 결합한 융복합 치유프로그램을 설계하고, 해당 프로그램이 액티브 시니어의 생리적·심리적 건강에 미치는 효과를 검증하고자 하였다. 전주시 거주 61~74세 성인 30명을 대상으로 실험군(n = 15)과 대조군(n = 15)으로 나누어 실험을 진행하였다. 실험군은 비기승 말교감치유 중심의 융복합 프로그램(주 1회, 회기당 120분, 총 8회기)에 참여하였으며, 각 회기는 말교감활동(80분)과 원예치유활동(40분)으로 구성되었다. 원예치유활동은 말교감활동 후 정서 이완 및 마무리를 목적으로 구성되었다. 대조군은 복지관의 일상 프로그램에 참여하였다. 집단 간 차이와 시계열 변화 양상을 확인하기 위해 반복측정 분산분석(Repeated Measures ANOVA)을 실시하였다. 실험군은 프로그램 참여 후 우울감과 불안감 점수가 유의적으로 감소하였으며($p < 0.05$), 긍정정서 점수는 증가하는 경향을 나타내었다. 또한 심박수는 프로그램 참여 전 대비 평균 6.3 bpm 감소한 것으로 나타났으며($p < 0.05$), 대조군에서는 유의적인 변화가 나타나지 않았다. 반복측정분산분석 결과, 집단과 시점 간 상호작용 효과가 확인되어($p < 0.05$), 말교감치유 중심 융복합 프로그램이 액티브 시니어의 스트레스 완화 및 심리적 안정 증진에 긍정적인 영향을 미치는 것으로 나타났다. 본 연구는 말교감치유 융복합 프로그램이 액티브 시니어의 심리·생리적 건강 증진을 위한 효과적인 중재 방안으로 활용될 수 있음을 시사한다.

본 연구는 농촌진흥청 국립축산과학원 축산시험연구의 노인 대상 농촌자원 융복합 치유활동 콘텐츠 개발(4_축산원, PJ01747701) 과제의 지원사업에 의해 이루어진 것임. 본 연구는 2026년도 농촌진흥청 국립축산과학원 전문연구원 과정 지원사업에 의해 이루어진 것임.

Key words : 동물교감치유, 말, 액티브 시니어, 스트레스, 융복합 치유프로그램

PG26019

Evaluation of heat stress in adult Korean native black goats during summer

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This study was conducted to evaluate heat stress responses in adult Korean native black goats under hot summer conditions, to develop a respiration rate (RR) prediction model using major environmental factors, and to determine the upper critical temperature. A total of 12 clinically healthy adult goats (6 males and 6 females) were used. Temperature (T, ℃), relative humidity (RH, %), radiant energy (RE, W/m^2), skin temperature (ST, ℃), and respiration rate (RR, breaths/min) were measured under field conditions. Pearson correlation analysis showed that T, ST, and RH were positively correlated with RR ($p < 0.001$), whereas RE was not significantly correlated with RR ($p = 0.232$). Contribution analysis indicated that T had the greatest effect on RR variation (48.5%), followed by ST (40.2%) and RH (11.3%). The regression model was derived as $RR = 8.35 - 10.05T + 0.24T^2 + 4.20ST + 0.26RH$, and the model was statistically significant ($p < 0.001$) with high explanatory power ($R^2 = 0.893$). The upper critical temperature at which RR reached 60 breaths/min in adult goats was estimated to be 27.4℃. These results indicate that heat stress responses in adult Korean native black goats are mainly influenced by temperature and surface thermal load, suggesting that preventive heat stress management should be initiated before animals reach this upper critical temperature.

Key words : Korean native black goat, heat stress, respiration rate, upper critical temepratura

PG26020

융복합 자원 기반 반려견 교감 치유프로그램의 효과: 활동적 은퇴자 대상 우울감 및 자기효능감 개선

양가영[1,*], 김찬호[1], 이우도[1], 차지혜[1], 방한태[1], 장명진[1], 김경희[2], 김소현[3], 장경아[4], 문지원[5]

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초고령사회 진입에 따라 활동적 은퇴자의 정신건강 관리 필요성이 증대되고 있다. 본 연구는 동물교감(산책·행동관찰)에 원예(허브볼), 식량자원(모시브러시), 농촌환경(라탄바구니) 등 융복합 자원을 결합한 치유프로그램(6회기, 주 1회)을 전주시 거주 61~74세 활동적 은퇴자 15명(N = 15)에게 적용하여 생리·심리적 효과를 검증하였다. 사전·사후 측정 결과, 타액 코르티솔이 32.43%($p < 0.01$) 감소하였고, 자기효능감 52.36%($p < 0.01$) 향상, 우울 37.97%($p < 0.01$) 감소, 주관적 활력 2.79%($p < 0.01$) 향상이 확인되었다. 전반적 만족도는 4.69/5점으로 높게 나타났다. 본 연구는 동물자원 융복합 치유프로그램이 활동적 은퇴자의 생리·심리적 건강 증진에 효과적임을 실증하며, 초고령사회 정신건강 정책의 기초자료로 활용될 수 있음을 시사한다.

본 연구는 농촌진흥청 국립축산과학원 축산시험연구의 노인 대상 농촌자원 융복합 치유활동 콘텐츠 개발(4_축산원, PJ017477)과제의 지원사업에 의해 이루어진 것임.

Key words : 동물교감치유, 융복합 치유프로그램, 활동적 은퇴자, 자기효능감, 타액 코르티솔

PG26021

반려견 휴식방법에 따른 심박수 및 QBA 행동 변화 분석

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본 연구는 동물교감치유 환경에서 반려견의 적정 휴식방법을 탐색하기 위한 파일럿 테스트로, 휴식 형태에 따른 생리적 및 행동적 반응을 예비적으로 비교·분석하였다. 반려견 4마리를 대상으로 △보호자와 함께 켄넬에서 휴식(보호자+켄넬) △켄넬 내 단독 휴식(켄넬) △장난감 제공 휴식(장난감) △간식 제공 휴식(간식)의 네 가지 조건을 설정하고, 각 조건을 2회 반복 적용하였다. 생리적 반응은 심박수(heart rate, HR), 행동적 반응은 QBA (qualitative behaviour assessment) 14개 항목을 활용하여 평가하였다. 분석 결과, 휴식 조건에 따라 심박수 (F(3,20) = 5.67, $p = 0.006$)와 QBA 다수 항목에서 유의한 차이가 나타났다. 특히 보호자+켄넬 조건에서 심박수는 92.4 ± 8.2 bpm으로 가장 낮았으며, 긍정 정서 항목인 content(8.31 ± 1.88)와 relaxed(8.06 ± 1.54)는 가장 높고, 부정 정서 항목인 anxious(1.75 ± 1.53)와 nervous(1.25 ± 1.68)는 가장 낮게 나타났다. 종합 웰빙 지표(ΔQBA) 또한 보호자+켄넬 조건에서 가장 높은 값을 보였다(+6.56 ± 1.23, $p < 0.001$).

이상의 결과는 보호자 동반 켄넬 휴식이 다른 조건에 비해 반려견의 생리적 안정과 긍정적 행동 반응에 보다 유리할 가능성을 시사한다. 다만 본 연구는 소규모 파일럿 테스트라는 한계가 있으므로, 향후 더 많은 개체를 대상으로 코르티솔 등 추가 생리 지표를 포함한 후속 검증이 필요하다. 이러한 결과는 동물교감치유 프로그램에서 반려견의 복지 친화적 휴식 가이드라인 마련을 위한 기초자료로 활용될 수 있다.

본 연구는 농촌진흥청 반려동물 전주기 사업의 반려동물 행동특성 평가 방법 및 시스템 개발(RS-2023-00232319)의 지원사업에 의해 이루어진 것임.

Key words : dog, behavior, QBA, HR, stress

PG26022

Advances in audio classification and artificial intelligence for respiratory health and welfare monitoring in swine

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Respiratory diseases are a major challenge in pig farming and can cause serious economic losses if not detected early. Traditional diagnosis relies on visual inspection and laboratory testing, which are time-consuming and often identify problems only after disease has spread. In recent years, artificial intelligence (AI)-based sound analysis has emerged as a promising, non-invasive approach for monitoring pig health by automatically detecting changes in vocalizations such as coughing. This review summarizes recent advances in audio-based monitoring systems for respiratory disease detection and behavior monitoring in pigs, covering microphone technologies, signal processing techniques, machine learning and deep learning models, and on-farm deployment using edge and embedded devices. The strengths, limitations, and practical challenges of current systems are discussed, along with future opportunities for improving accuracy, robustness, and real-time application. AI-driven acoustic monitoring has strong potential to support early disease detection, improve animal welfare, and enhance decision making in modern pig production.

Key words : pig vocalization, respiratory disease, cough detection, audio classification, deep learning

PG26023

Comparison of popular YOLO's (YOLOv5 & YOLOv8) for the detection of postures, feeding and drinking behaviors of pig

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This study comparatively evaluated two lightweight object detection architectures, YOLOv5s and YOLOv8s, for detecting pig postural (Lateral Lying, Sternal Lying, Standing, and Sitting) and nutritive (Feeding, Drinking, and Not Feeding/Drinking) behaviors. Three detection models were developed: posture detection, feeding and drinking detection, and a combined model integrating both behavior types. Grad-CAM was applied to visualize and compare the key visual features underlying model predictions. For both architectures, task formulation affected performance more strongly than model version. The nutritive model produced the best results (mAP50: 96.0%–96.9%), followed by the posture model (95.7%–96.3%), whereas the combined 10-class model was the most challenging because of greater class overlap and imbalance (78.5%–79.3%). YOLOv8 generally achieved slightly better recall and localization, including the highest average mAP50 in the posture and combined tasks, while YOLOv5 remained highly competitive and even outperformed YOLOv8 for some classes. Grad-CAM analysis confirmed that both detectors relied on biologically meaningful cues that combined global posture with localized head-resource interactions. Overall, this focused comparison shows that upgrading from YOLOv5 to YOLOv8 yields only modest gains unless dataset balance and class design are improved, especially for the integrated multi-behavior setting.

Key words : deep learning, object detection, computer vision, artificial intelligence, precision farming

PG26024

Farm-scale pig posture and behavior monitoring: a critical review of vision-based technologies

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Monitoring pig behavior and posture is important for animal welfare assessment, early warning of 29 health problems, and productivity optimization in intensive farming systems. This review critically synthesizes recent advances in pig 32 posture detection and behavior analysis, with particular emphasis on digital image processing, machine 33 learning, and deep learning approaches. Current evidence shows a clear transition from conventional 34 feature-based methods to deep-learning-based detection, segmentation, tracking, and temporal analysis 35 frameworks, including CNNs, Faster R-CNN, YOLO variants, Mask R-CNN, and Deep SORT. Deep 36 learning generally provides stronger robustness in complex farm scenes, while RGB cameras remain 37 the most practical sensing option for commercial deployment. However, practical performance remains 38 strongly influenced by dataset design, environmental variability, occlusion, annotation burden, 39 computational constraints, and weak cross-farm generalization. Welfare and activity monitoring appear 40 more mature than disease-specific diagnosis and fully integrated decision-support systems. Emerging 41 directions such as multimodal sensor fusion, explainable artificial intelligence, edge AI, and digital 42 twin–based decision support are also reviewed. The review identifies key research gaps and outlines 43 future directions for scalable, reliable, and welfare-oriented monitoring in pig.

Key words : pig behavior, posture detection, precision livestock farming, computer vision, deep learning

PG26025

A systematic literature review on the uses, benefits, challenges and prospects of digital twins in livestock farm management

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To facilitate the adoption and integration of Digital twin (DT) technologies in livestock farming systems, this study aims to discern and appraise the most recent advancements by assessing scientific and technological progressions. The objective of this study is to conduct a comprehensive review of the literature to determine the status of DT application in livestock farm management with its benefits, challenges, and prospects. Scientific databases, PRISMA guidelines, and systematic bibliometric methodologies were used for searching and sorting the most fit articles. This study found that DT technology is new to the livestock industry and mainly used for environmental control, feed management, farm planning, greenhouse gas reduction, and behavior monitoring. Key barriers to DT deployment include high establishment costs, risk of market monopolization, and technical knowledge gaps. The application of DT is limited in monitoring animal behavior and farm environment. However, DT technology has the potential for broader use, such as predicting growth, feed consumption, and improving the supply chain. Although these new areas are yet to be explored in real farm conditions. Along with expanding the new area of using DT in livestock farm management, future collaborative research should concentrate on creating new machine learning and/or deep learning models.

Key words : digital twin, animal behavior monitoring, environmental control, farm operation, livestock supply chain

PG26026

Limitations of combined posture and nutritive behaviors for a comprehensive detection model in group-housed pigs using YOLO architectures

Eddiemar B. Lagua[1,2], Hong-Seok Mun[1], Md Sharifuzzaman[1], Md Kamrul Hasan[1], Ahsan Mehtab[1],
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This study systematically evaluated four lightweight object detection architectures—YOLOv5, YOLOv8, YOLOv9, and YOLOv10—for detecting pig postural and nutritive behaviors. Three models were developed for posture, feeding/drinking, and combined behavior detection. Task formulation influenced performance more than architectural differences. Nutritive models achieved the highest accuracy (mAP50 = 94.1%–95.4%), followed by posture models (90.6%–90.8%), while combined models showed lower performance (80.0%–80.5%) due to increased classification complexity and class imbalance. Standing, Feeding, and Not Feeding/Drinking were detected most reliably, whereas Sitting, Drinking, Sitting Drinking, and Sternal Lying Feeding remained challenging. Grad-CAM analysis confirmed that predictions relied on biologically meaningful visual features. Among the architectures, YOLOv9 achieved the highest overall accuracy, whereas YOLOv5 and YOLOv8 provided superior computational efficiency (> 130 FPS). This study establishes a benchmark for lightweight YOLO-based detectors and provides practical insights for developing reliable, real-time, and comprehensive behavioral monitoring systems in precision livestock farming.

Key words : deep learning, object detection, computer vision, artificial intelligence, precision farming

PG26027

Computer vision-based detection of agonistic behaviors in pigs: advances and applications for precision livestock farming

Md Kamrul Hasan[1], Hong-Seok Mun[1], Ahasan Mehtab[1], Jin-Gu Kang[1,2], Md Sharifuzzaman[1],
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Agonistic behaviors remain major challenges for pig welfare, particularly during the weaning and growing periods. Computer vision (CV) technologies are emerging as scalable tools for non-invasive monitoring of agonistic behaviors. This review summarizes recent advances in CV-based detection of agonistic behaviors in pigs and identifies factors influencing their reliability and commercial adoption. Following the preferred reporting items for systematic reviews and meta-analyses (PRISMA) guidelines, a structured search identified 42 eligible studies. Most studies employ deep learning approaches, including you only look once (YOLO)-based detectors and spatio-temporal models, achieving detection accuracy of up to 97% for behaviors such as head knocking, head-to-body pushing, and tail biting, typically evaluated under controlled conditions using mAP@0.5. Three key findings emerged: rapid progress in deep learning-based detection; methodological heterogeneity in behavioral definitions, validation strategies, and annotation protocols; and a gap between high detection accuracy and demonstrated improvements in welfare or productivity. Progress is limited by scarce cross-farm validation, inconsistent bout definitions, reliance on manual annotations, and weak integration with physiological and production indicators. Future research should prioritize multimodal integration, predictive modeling, and rigorous external validation.

Key words : agonistic behaviors, computer vision, precision livestock farming, pig welfare, deep learning

PG26028

Effects of construction noise stress on growth performance and behavior in growing pigs

Jin-Gu Kang[1,2], Hong-Seok Mun[1], Eddiemar Lagua[1,2], Shariffuzzaman MD[1], Md Kamrul Hasan[1],
Ahsan Mehtab[1], Young-Hwa Kim[3], Hae-Rang Park[1], Tae-Eun Go[1], Chul-Ju Yang[1,2,*]

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Construction noise is a major environmental stressor around pig farms and may impair pig productivity and welfare. Growing pigs are particularly vulnerable to environmental disturbance because of rapid growth and high physiological demand. This study evaluated the effects of construction noise on growth performance and behavior in growing pigs under practical farm conditions. Growing pigs exposed to construction noise showed significantly reduced growth performance compared with the control group. Final body weight decreased by 5.93 kg (9.98%), average daily gain decreased by 23.08%, and feed conversion ratio worsened by 36.10% ($p < 0.05$). Behavioral analysis also indicated increased instability under noise exposure, with changes in posture, feeding activity, and aggressive behavior patterns during the noise application period. These findings indicate that construction noise can act as a substantial environmental disturbance during the growing phase, impairing both growth efficiency and behavioral stability. Therefore, construction-related noise should be carefully managed in pig production systems, particularly during the growing period when animals are more susceptible to environmental stress.

Key words : construction noise, growing pigs, noise stress, growth performance, behavior

2026 한국축산학회 종합심포지엄 및 학술발표회 Vol. Ⅲ

Proceedings of 2026 Annual Congress of KSAST Vol. III

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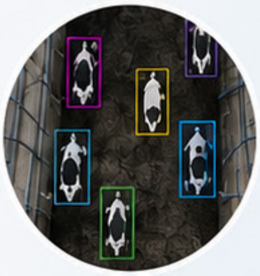

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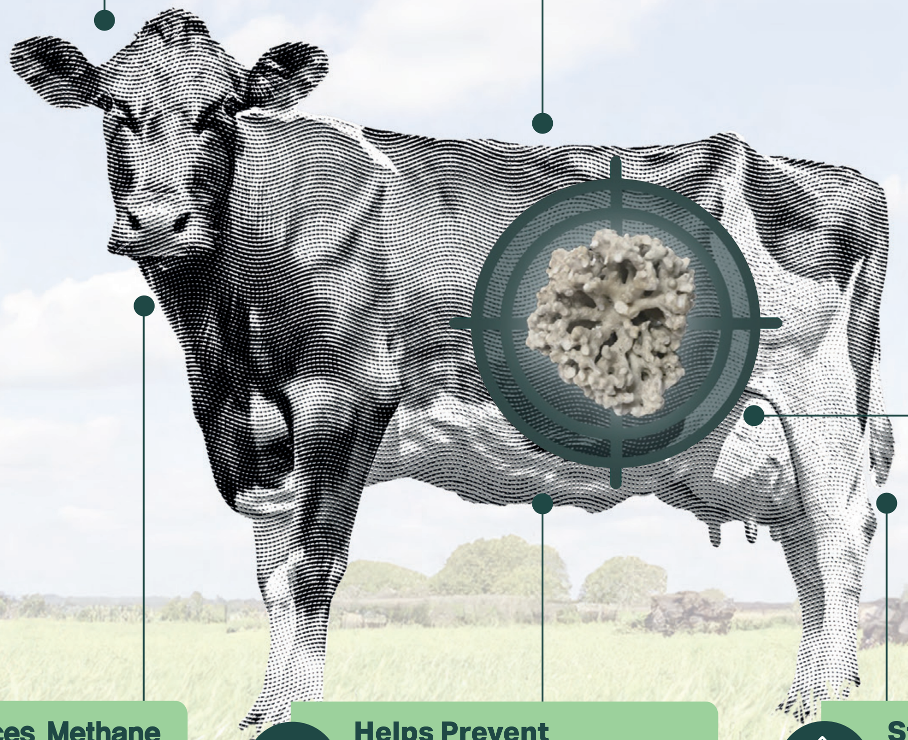

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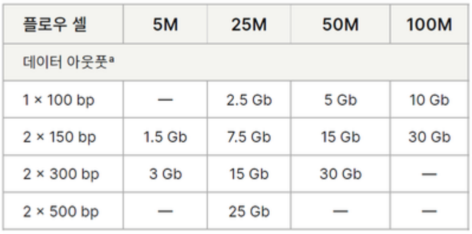

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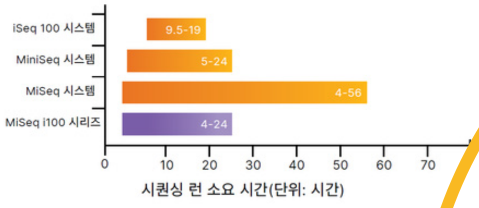

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- 미생물 비료
- 사료 첨가제(생균제)
- 동물용 의약품
- 축산환경 개선제
- 기능성 펫푸드

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❷ 농축산용 및 관련 미생물산업 육성 거점 구축 및 활성화

▸ 주요기능 ❶ 농축산미생물산업의 육성을 통한 관련 산업 고도화
❷ 농축산 분야 전문 CRO 지원기관으로서 역할 확대
❸ 산업화 지원을 통한 국제 경쟁력 확보 및 대표적 스타 기업 발굴·육성
❹ GMP 등급 농축산용 미생물제품의 고부가가치화 및 수출기반 확대

R&D

효능평가 지원사업

▸ 효능검증 공통: 미생물 동정, 효소활성 검증, 생균수 측정
작물 미생물: 항균활성, 식물생장촉진능
축산 미생물: 항균활성, 장내생존능, 축산분뇨악취저감
식물재배: 농약(약효·약해), 비료(비효·비해)

▸ 안전성 평가 항생제내성, 바이오제닉 아민, 유해미생물 정성분석, PED 진단, 용혈 반응, 곰팡이독소, 중금속, 잔류농약

에코프로바이오틱스 이용활성화 사업

▸ 목표 ❶ 축산용 생균제산업 활성화를 위한 지역 단위 보급, 과학적 효과 실증 분석, 현장 컨설팅 및 최적 활용모델 정립 등 지원
❷ 에코프로바이오틱스 이용활성화를 통한 건강한 미생물산업 생태계 구축 및 축산 현안해결 실증모델 구축으로 지속가능한 축산기반 마련

▸ 사업현황

클러스터 시범운영 농장 현황	
2018년(총 5개)	정읍-양돈농가 **5**개
2019년(총 16개)	정읍-양돈농가 **13** 개 젖소농가 **3**개
2020년(총 10개)	정읍-**6**개(양돈, 한우) 부안-**4**개(양돈)
지역확산 클러스터시범운영(컨소시엄)	
2020년 경기도 및 전라남도: **20**개(양돈, 한우)	
2021년 전북 김제, 익산 등 시범사업 확대	

에코프로바이오틱스 이용활성화 사업 현황
장수: '21~'22년 **640** 개 농가(양돈, 한우)
함평: '22년 **21** 개 농가(양돈, 한우, 젖소, 양계)
제천: '23~'24년 **29** 개 농가(양돈, 한우, 양계)
영광: '23년~'24년 **18** 개 농가(양돈)
안동: '25~'26년 **9** 개 농가(양돈)
괴산: '25~'26년 **45** 개 농가(양돈, 한우)
남원: '26년 **15** 개 농가(양돈)
정읍: '26년 **10** 개 농가(양돈)

(재)농축산용미생물산업육성지원센터 | www.cialm.or.kr | 063-536-6001

낙농진흥회
KOREA DAIRY COMMITTEE

한국낙농의 희망을 키웁니다

공정하고 합리적인 낙농시장 관리를 통해
지속가능한 한국형 낙농산업을 열어 나가겠습니다


농협사료
축산농가에게 희망을,
드림파트너 농협사료
자연을 조화롭게, 축산을 풍요롭게, 국민을 건강하게
농협사료는 언제나 축산농가 곁에 있습니다.


9단
목우촌
MOGUCHON
건강하고 맛있는 정통 비엔나
엔나소시지
원료육 100% 국산 돼지고기


목우촌
MOGUCHON
뚝심
Original
100%
국산


우유
우유자조금관리위원회
K·MILK
국산우유사용인증
우리우유엔
신선함이
살아있다
우유는
신선식품입니다
신선함이 살아있다
생산부터 유통까지 단 3일 이내
영양이 살아있다
세계가 인정한 체세포수 1등급
맛이 살아있다
엄격한 기준으로 만든 고품질 원유니까


서울우유
서울우유
A2
전용목장
100%
A2우유
플러스1.
체세포수1등급
세균수1A
플러스2.
EFL공법
"Make the world healthy with milk."
서울우유
• FOR BETTER MILK •
A2+
A2 PLUS MILK
A2 플러스 우유
A2 전용목장
100% A2우유
체세포수1등급
세균수1A
EFL공법
냉장제품 우유 710 mL(500 kcal)
서울우유답게
A2우유에 플러스까지

지구를 지키는 한우의 약속

한우산업 탄소중립

지속가능한 축산, 한우산업이 실천합니다.

✓ 부산물 업사이클링

의약품·화장품·
건강보조식품 원료
등으로 활용

✓ 자연순환 농업 실현

가축분뇨 자원화와
유기농축산물 생산으로
지속가능한 농업 실현

✓ 한우농가의 노력

저메탄 사료 공급,
분뇨처리 고도화,
한우 사육 효율 개선

✓ 농업부산물 사료자원화

식품 생산과정에서
발생되는 부산물의 사료화
※약 3조 5천억원의 경제효과

✓ 국내 축산업 온실가스 배출량

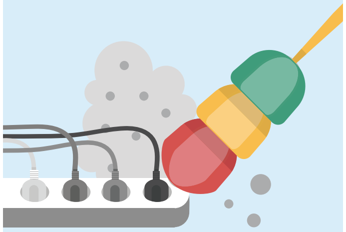
1.3%

출처 : 국가 온실가스 인벤토리 보고서

전국한우협회 한우자조금관리위원회

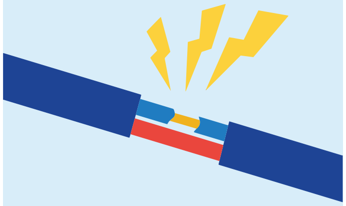
화재 예방은 내 손으로!

축사 화재 예방 위한 전기안전 점검요령



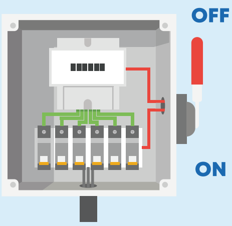
화재 원인인 먼지와 이물질 제거

콘센트, 분전반, 환풍기 모터 등에 쌓인 먼지를 깨끗하게 털어줍니다.



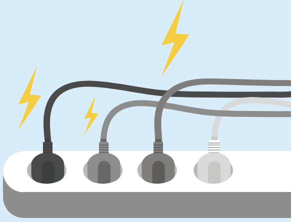
손상된 전선 유무 확인

손상된 전선이 없는지 확인해 누전과 전기 화재를 예방합니다.



축사가 물에 잠기면 축사 전기 차단부터

축사가 침수되면 전기를 먼저 차단하고, 전문가의 점검을 받은 후 사용합니다.



올바른 콘센트 사용법 지키기

용량을 초과하는 문어발식 콘센트 사용과 느슨하게 연결된 플러그는 화재의 원인이 됩니다.

이것만은 꼭 확인하자! □

축사 화재 점검 체크리스트

안전진단항목

1 전기배선의 노후, 파손, 훼손 여부 □

2 환풍기 모니터 주변에 먼지 등 기타 이물질 여부 □

3 콘센트에 분진, 먼지, 습기 등 기타 이물질 여부 □

4 분전반 내부, 플러그, 개폐기, 차단기 등 기타 이물질 여부 □

5 전기시설 용량의 적정 여부 □
한개의 콘센트에 여러개의 전열기구 꽂지 않기

6 정기적인 안전 점검 여부 □
전기 보호함, 누전 차단기 등 전기 시설은 전문가에게 의뢰해 점검

7 축사 주변에서의 쓰레기 소각과 인화성 물질 보관 금지 □

8 축사 내 소화기 구비 및 사용법 숙지와 정기적 점검 □
압력게이지 녹색 확인 및 사용기한 확인(10년)

9 축사 내 화재 진압을 위한 소화 설비 점검 □
소화기, 스프링쿨러, 호스릴 소화전 또는 고압용 펌프 점검

10 화재에 대비한 경보형 감지기 설치 · 점검 □

11 전기기계기구의 접지 여부와 접지형 콘센트 사용 여부 □

12 물기가 있는 곳에서 방수형(방적형) 배선기구 사용 여부 □

화기 주변에 가연성 물질 두지 않기

축사 시설 주변에서의 쓰레기 소각과 가연성 물질 보관을 금지합니다.

전기 안전 사전 점검 실시

축사 내 전기 안전 점검을 주기적으로 실시합니다.
*소화기 배치 및 사용 요령 숙지

내 농장은 내가 지킨다!

출처. 농협경제지주 · 농협손해보험 · 한국전기안전공사

한돈자조금 사단법인 대한한돈협회