기후변화 대응 동물 오믹스 빅데이터 활용 연구

박종은
(제주대학교)

Curriculum Vitae

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제주대학교
JEJU NATIONAL UNIVERSITY

Research on Utilizing Animal Omics Big Data for Climate Change

- 기후변화 대응 동물 오믹스 빅데이터 활용 연구

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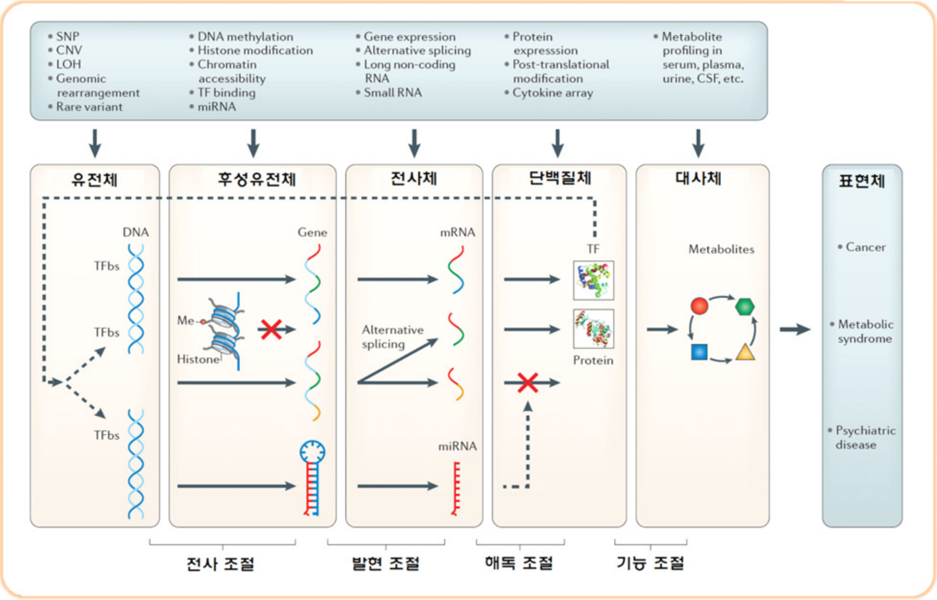
Contents

1. Past
   1) Animal Breeding
   2) Bioinformatics

2. Present

1. Past: Research Experience

Multi-Omics (다중 오믹스)



- SNP
- CNV
- LOH
- Genomic rearrangement
- Rare variant

- DNA methylation
- Histone modification
- Chromatin accessibility
- TF binding
- miRNA

- Gene expression
- Alternative splicing
- Long non-coding RNA
- Small RNA

- Protein expresssion
- Post-translational modification
- Cytokine array

- Metabolite profiling in serum, plasma, urine, CSF, etc.

유전체

후성유전체

전사체

단백질체

대사체

표현체

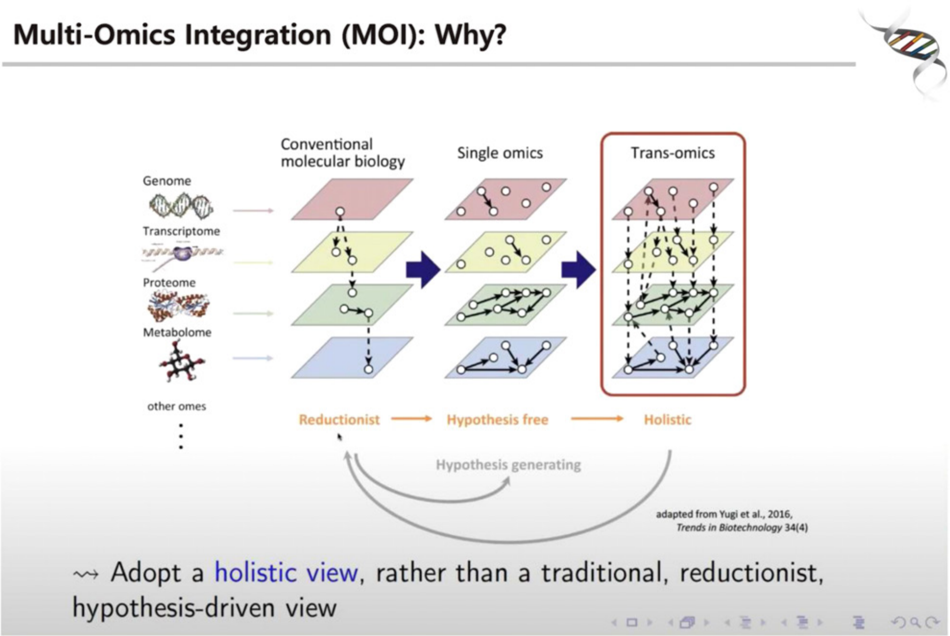
- Cancer
- Metabolic syndrome
- Psychiatric disease

전사 조절

발현 조절

해독 조절

기능 조절



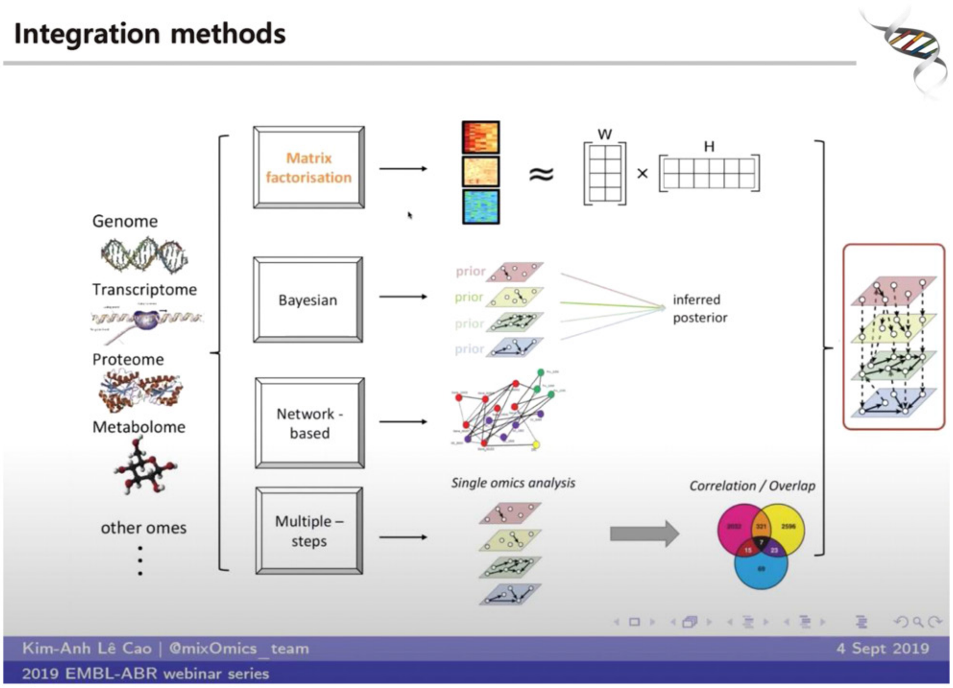
Multi-Omics Integration (MOI): Why?

adapted from Yugi et al., 2016, *Trends in Biotechnology* 34(4)

⇝ Adopt a holistic view, rather than a traditional, reductionist, hypothesis-driven view

Kim-Anh Le Cao's Webinar, Multi omics statistical integration with mixOmix (2019)

5

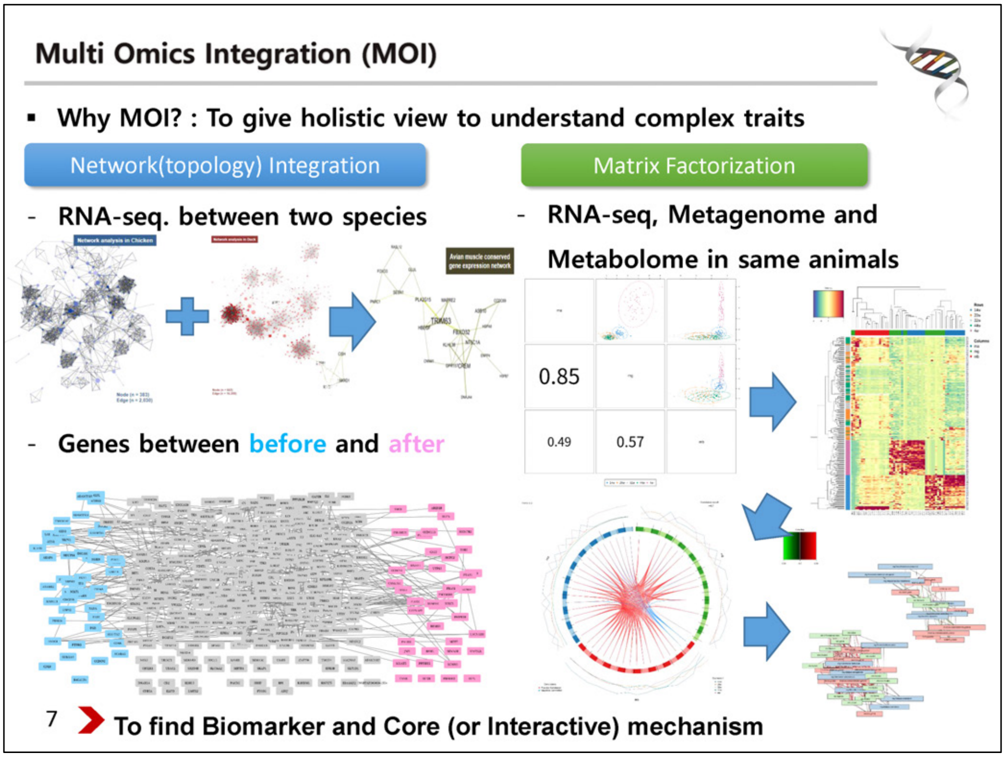


Integration methods

Kim-Anh Lê Cao | @mixOmics_team 4 Sept 2019

2019 EMBL-ABR webinar series

6 Kim-Anh Le Cao's Webinar, Multi omics statistical integration with mixOmix (2019)



Multi Omics Integration (MOI)

- Why MOI? : To give holistic view to understand complex traits

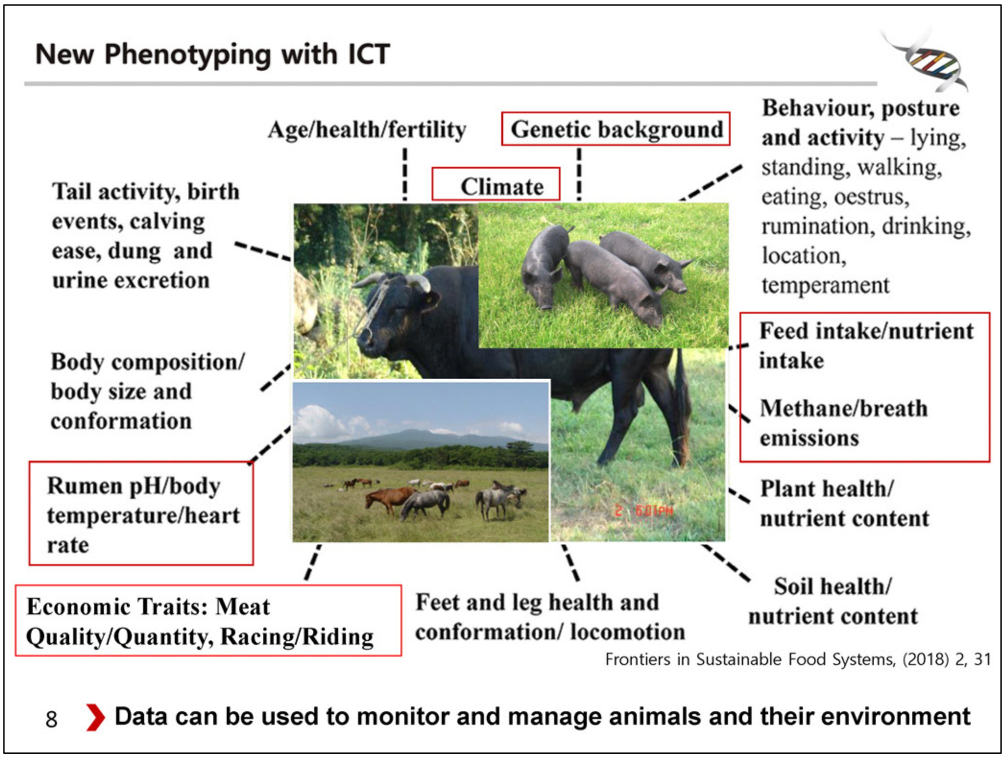
Network(topology) Integration

- RNA-seq. between two species
- Genes between before and after

Matrix Factorization

- RNA-seq, Metagenome and Metabolome in same animals

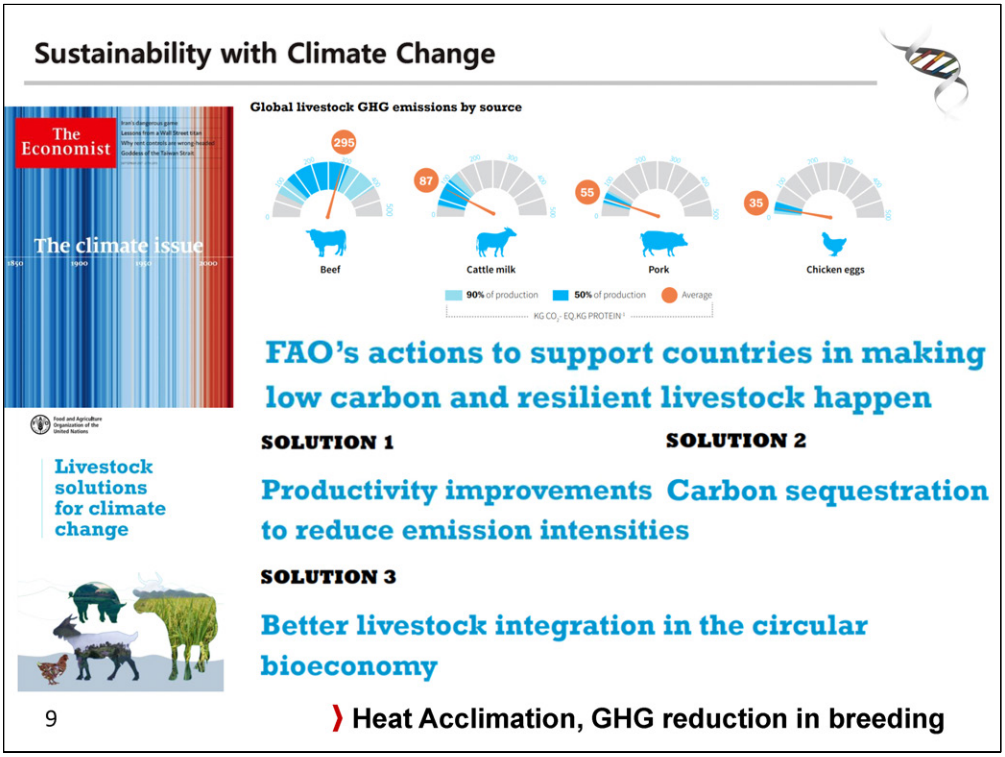
❯ To find Biomarker and Core (or Interactive) mechanism



New Phenotyping with ICT

Frontiers in Sustainable Food Systems, (2018) 2, 31

❯ Data can be used to monitor and manage animals and their environment



Sustainability with Climate Change

The Economist

The climate issue

Food and Agriculture Organization of the United Nations

Livestock solutions for climate change

Global livestock GHG emissions by source

FAO's actions to support countries in making low carbon and resilient livestock happen

SOLUTION 1

Productivity improvements to reduce emission intensities

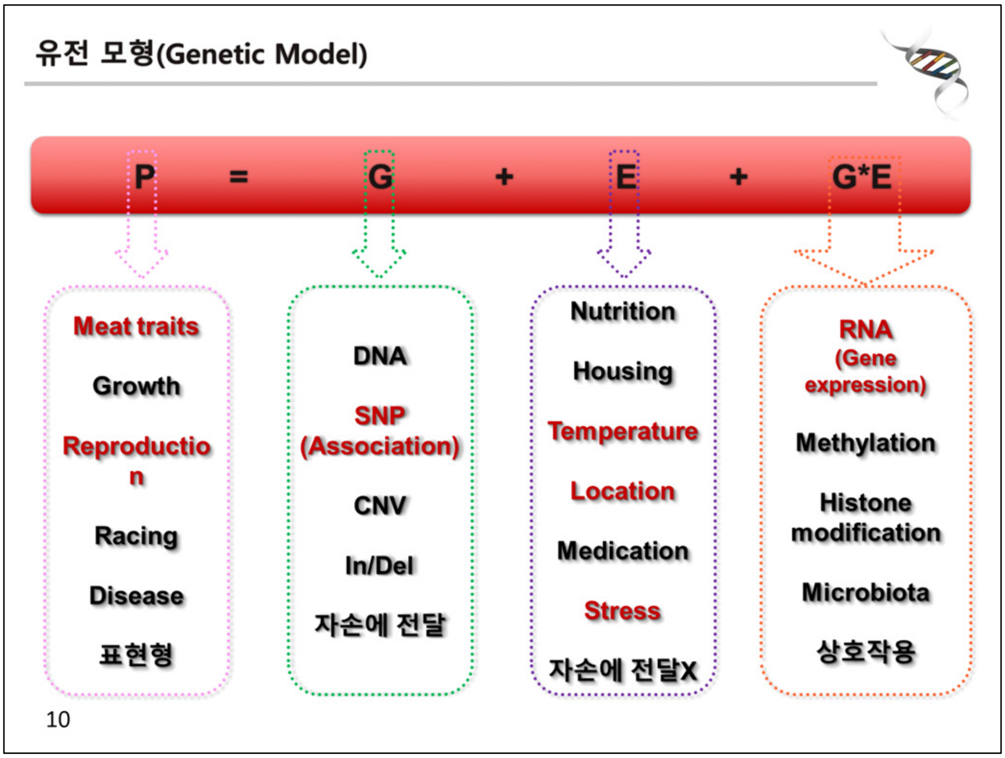
SOLUTION 2

Carbon sequestration

SOLUTION 3

Better livestock integration in the circular bioeconomy

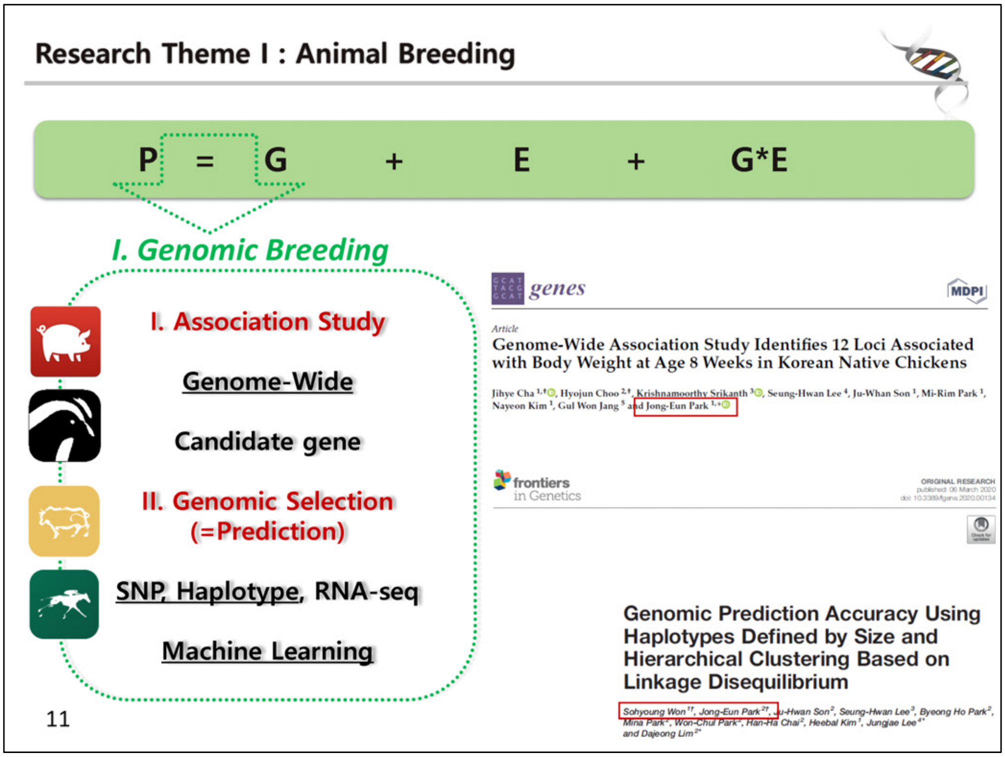
❯ **Heat Acclimation, GHG reduction in breeding**



유전 모형(Genetic Model)

P = G + E + G*E

P	G	E	G*E
Meat traits Growth Reproduction Racing Disease 표현형	DNA SNP (Association) CNV In/Del 자손에 전달	Nutrition Housing Temperature Location Medication Stress 자손에 전달X	RNA (Gene expression) Methylation Histone modification Microbiota 상호작용



Research Theme I : Animal Breeding

P = G + E + G*E

I. Genomic Breeding

I. Association Study

Genome-Wide

Candidate gene

II. Genomic Selection (=Prediction)

SNP, Haplotype, RNA-seq

Machine Learning

Article

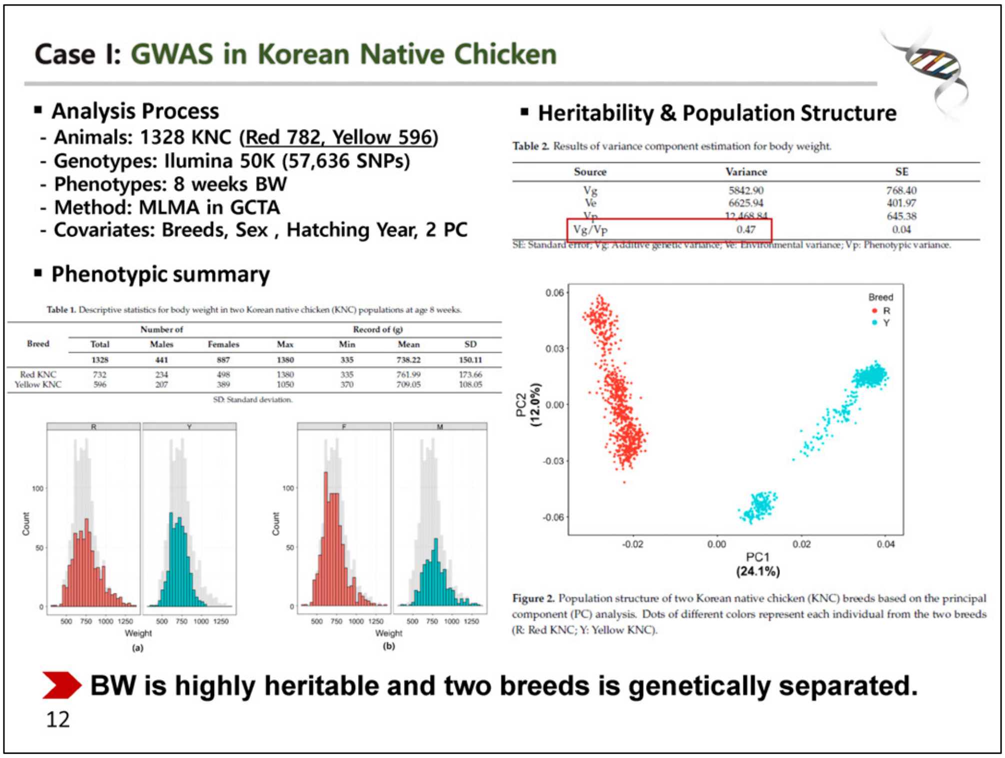
Genome-Wide Association Study Identifies 12 Loci Associated with Body Weight at Age 8 Weeks in Korean Native Chickens

Jihye Cha [1,†], Hyojun Choo [2,†], Krishnamoorthy Srikanth [3], Seung-Hwan Lee [4], Ju-Whan Son [1], Mi-Rim Park [1], Nayeon Kim [1], Gul Won Jang [5] and Jong-Eun Park [1,*]

ORIGINAL RESEARCH
published: 06 March 2020
doi: 10.3389/fgene.2020.00134

Genomic Prediction Accuracy Using Haplotypes Defined by Size and Hierarchical Clustering Based on Linkage Disequilibrium

Sohyoung Won [1†], Jong-Eun Park [2†], Ju-Hwan Son [2], Seung-Hwan Lee [3], Byeong Ho Park [2], Mina Park [2], Won-Chul Park [2], Han-Ha Chai [2], Heebal Kim [1], Jungjae Lee [4] and Dajeong Lim [2*]*



Case I: GWAS in Korean Native Chicken

- **Analysis Process**
  - Animals: 1328 KNC (Red 782, Yellow 596)
  - Genotypes: Ilumina 50K (57,636 SNPs)
  - Phenotypes: 8 weeks BW
  - Method: MLMA in GCTA
  - Covariates: Breeds, Sex , Hatching Year, 2 PC

- **Phenotypic summary**

Table 1. Descriptive statistics for body weight in two Korean native chicken (KNC) populations at age 8 weeks.

Breed	Number of			Record of (g)			
	Total	Males	Females	Max	Min	Mean	SD
	1328	**441**	**887**	**1380**	**335**	**738.22**	**150.11**
Red KNC	732	234	498	1380	335	761.99	173.66
Yellow KNC	596	207	389	1050	370	709.05	108.05

SD: Standard deviation.

- **Heritability & Population Structure**

Table 2. Results of variance component estimation for body weight.

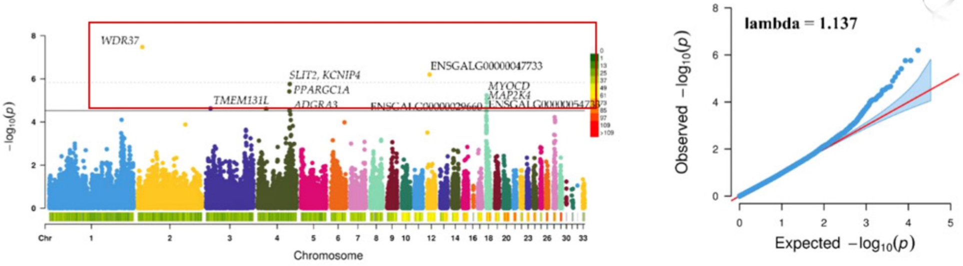
Source	Variance	SE
Vg	5842.90	768.40
Ve	6625.94	401.97
Vp	12,468.84	645.38
Vg/Vp	0.47	0.04

SE: Standard error; Vg: Additive genetic variance; Ve: Environmental variance; Vp: Phenotypic variance.

Figure 2. Population structure of two Korean native chicken (KNC) breeds based on the principal component (PC) analysis. Dots of different colors represent each individual from the two breeds (R: Red KNC; Y: Yellow KNC).

BW is highly heritable and two breeds is genetically separated.

Association Result



(a) (b)

Table 3. Top single nucleotide polymorphisms (SNPs) associated with body weight trait identified using a linear mixed model approach.

SNP ID	Chr	Position	Minor Allele	Major Allele	MAF	p-Value	SNP Effect	Gene	Location
Gga_rs15062501	2	10469206	G	A	0.28	3.37×10^{-8}	33.67	*WDR37*	Intron
GGaluGA083256	12	6388108	C	A	0.23	6.33×10^{-7}	−28.50	ENSGALG00000047733	Intron
Gga_rs14490865	4	75155441	G	A	0.21	1.73×10^{-6}	33.42	*SLIT2*	Intron
GGaluGA265847	4	74925016	G	A	0.14	1.75×10^{-6}	40.33	*KCNIP4*	Intron
GGaluGA265650	4	74010712	A	G	0.09	3.85×10^{-6}	46.22	*PPARGC1A*	Intragenic
Gga_rs14105952	18	893043	G	A	0.34	5.80×10^{-6}	27.70	*MYOCD*	Intragenic
Gga_rs13506093	18	804322	A	G	0.47	8.70×10^{-6}	−25.80	*MAP2K4*	Downstream
Gga_rs13506254	18	1185022	C	A	0.28	1.27×10^{-5}	26.63	ENSGALG00000054733	Intron
Gga_rs15809279	18	353546	G	A	0.46	2.17×10^{-5}	−22.30	ENSGALG00000029660	Intron
Gga_rs13503427	3	10517429	G	A	0.32	2.35×10^{-5}	24.12	–	Intergenic
Gga_rs15508929	4	19924807	G	A	0.05	2.48×10^{-5}	−40.57	*TMEM131L*	Upstream
GGaluGA265746	4	74486766	A	G	0.14	2.89×10^{-5}	33.16	*ADGRA3*	Downstream

Chr: Chromosome; MAF: Minor allele frequency; SNP effect: the β coefficient indicating the SNP effect size estimated for the minor allele.

12 SNP markers, Chr. 4 & 18 is possible Quantitative Trait Loci.

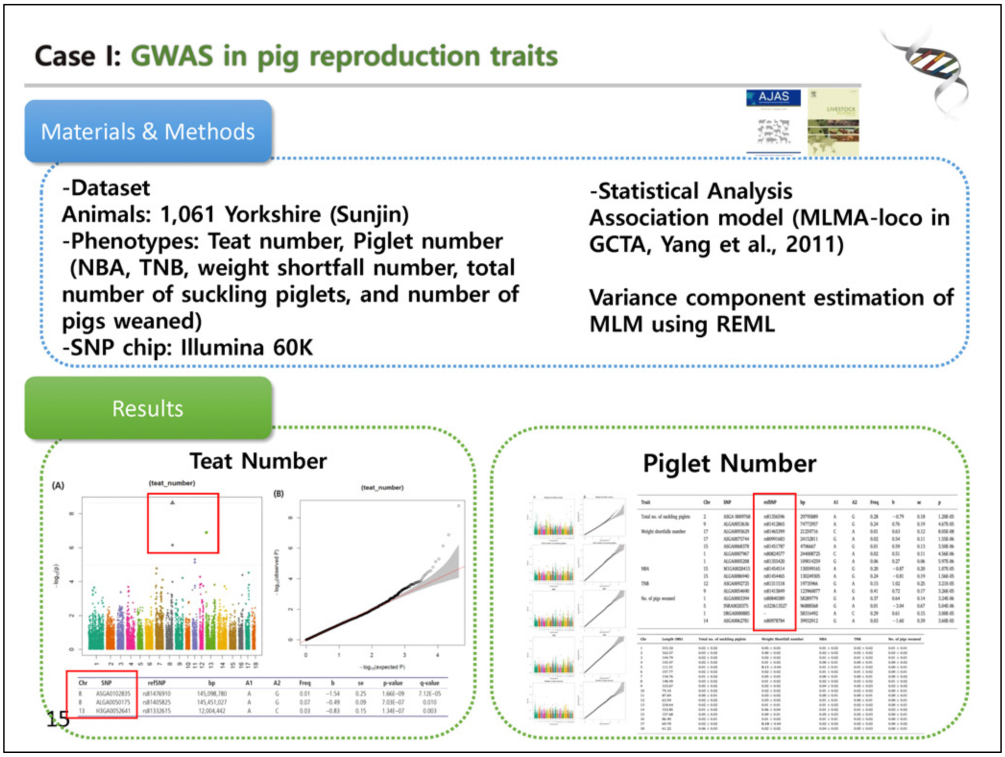
Functional Annotation (SNPs' P-value <0.05)

Table 4. Gene Ontology (GO) terms and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways significantly enriched ($p < 0.05$) for genes associated with body weight.

Category	Term_ID	Term	Count	%	p-Value	Genes
KEGG_PATHWAY	gga04010	MAPK signaling pathway	21	3.0043	0.00	*MAP2K3, MAP2K4, MAP3K3, TGFB2, IL1R1, BDNF, NFATC3, MAPK8IP3, TGFBR1, MAPK8IP1, PPP3CA, FGF7, TAOK1, GNA12, MKNK2, RAC2, MAPT, SOS1, SOS2, MAP4K3, MAP4K4*
KEGG_PATHWAY	gga04530	Tight junction	9	1.2876	0.03	*PPP2R2B, MYH1E, MYH1F, MYH1D, PPP2R2A, MYH1A, MYH1B, AMOTL1, MYH10*
GOTERM_MF_DIRECT	GO:0003774	Motor activity	6	0.8584	0.01	*MYH1E, MYH1F, MYH1A, MYH1B, MYH10, MYO1F*
GOTERM_MF_DIRECT	GO:0001077	Transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding	13	1.8598	0.02	*ARNT2, MYOCD, PLAG1, NFATC3, EBF2, NRF1, HIF1A, MEOX1, ELF1, NFIA, TBX20, TP63, ZNF750*
GOTERM_MF_DIRECT	GO:0004702	Receptor signaling protein serine/threonine kinase activity	7	1.0014	0.02	*MAP3K3, MAP2K4, TGFB2, BMPR2, TAOK1, TGFBR1, MAP4K4*
GOTERM_BP_DIRECT	GO:0045944	Positive regulation of transcription from RNA polymerase II promoter	34	4.8641	0.01	*RB1, RNASEL, BMPR2, PID1, KDM1A, TNKS, PLAG1, GATA4, TCF20, LDB2, MYSM1, HIF1A, NPAS2, ABRA, SPIC, PPP3CA, EPCAM, CREB3L1, TBX20, CYTL1, PPARGC1A, E2F7, TP63, NCOA1, XRCC6, AUTS2, LMO4, DAB2IP, ARNT, EBF2, ASH1L, BMP5, NFIA, CDH13*
GOTERM_BP_DIRECT	GO:2001235	Positive regulation of apoptotic signaling pathway	5	0.7153	0.01	*DAB2IP, PTEN, CASP2, TP63, TGFBR1*

%: the percentage of genes associated with particular annotation terms in the total input gene list; MF: Molecular function; BP: Biological process.

These pathways are involved in cell growth and development, related to BW gain.



Case I: GWAS in pig reproduction traits

Materials & Methods

-Dataset
Animals: 1,061 Yorkshire (Sunjin)
-Phenotypes: Teat number, Piglet number (NBA, TNB, weight shortfall number, total number of suckling piglets, and number of pigs weaned)
-SNP chip: Illumina 60K

-Statistical Analysis
Association model (MLMA-loco in GCTA, Yang et al., 2011)

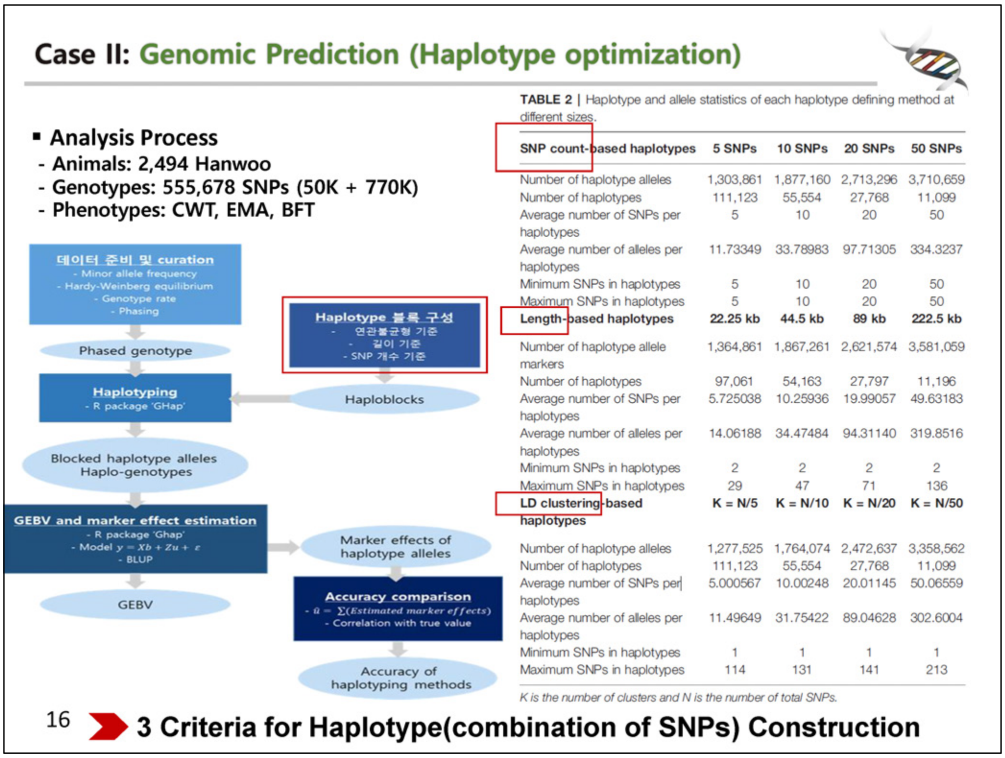
Variance component estimation of MLM using REML

Results

Teat Number

Chr	SNP	refSNP	bp	A1	A2	Freq	b	se	p-value	q-value
8	ASGA0102835	rs81476910	145,098,780	A	G	0.01	−1.54	0.25	1.66E−09	7.12E−05
8	ALGA0050175	rs81405825	145,451,027	A	G	0.07	−0.49	0.09	7.03E−07	0.010
13	H3GA0052641	rs81332615	12,004,442	A	C	0.03	−0.83	0.15	1.34E−07	0.003

Piglet Number



Case II: Genomic Prediction (Haplotype optimization)

- **Analysis Process**
  - Animals: 2,494 Hanwoo
  - Genotypes: 555,678 SNPs (50K + 770K)
  - Phenotypes: CWT, EMA, BFT

데이터 준비 및 curation
- Minor allele frequency
- Hardy-Weinberg equilibrium
- Genotype rate
- Phasing

Phased genotype

Haplotyping
- R package 'GHap'

Blocked haplotype alleles
Haplo-genotypes

GEBV and marker effect estimation
- R package 'Ghap'
- Model $y = Xb + Zu + \varepsilon$
- BLUP

GEBV

Haplotype 블록 구성
- 연관불균형 기준
- 길이 기준
- SNP 개수 기준

Haploblocks

Marker effects of haplotype alleles

Accuracy comparison
- $\hat{u} = \sum(\text{Estimated marker effects})$
- Correlation with true value

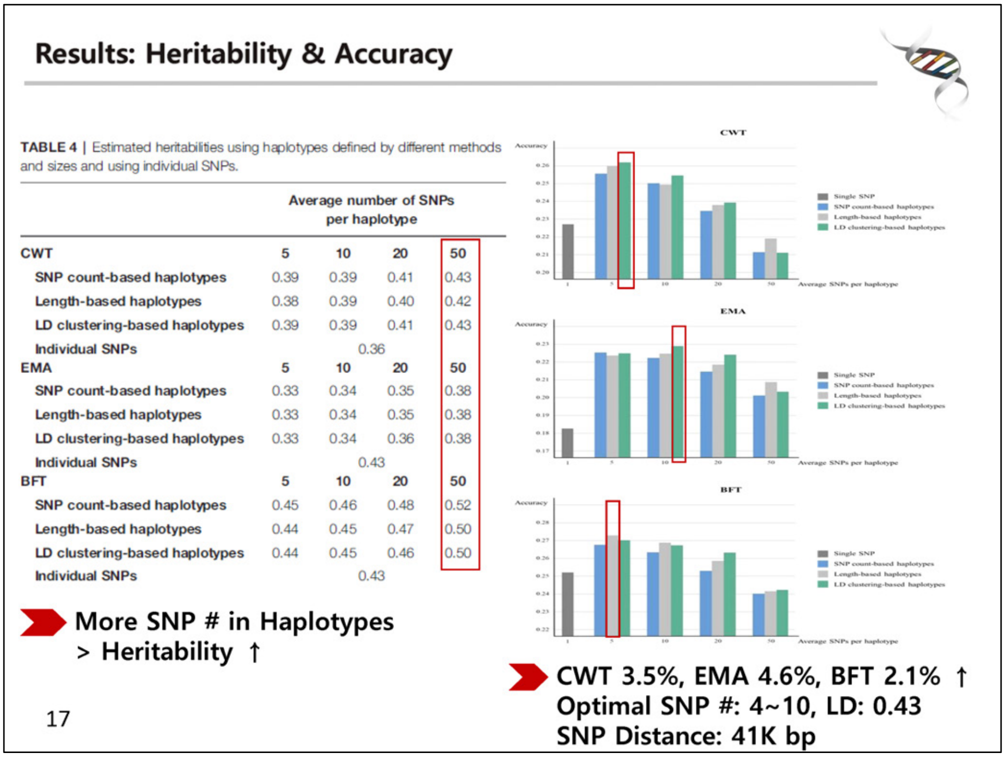
Accuracy of haplotyping methods

TABLE 2 | Haplotype and allele statistics of each haplotype defining method at different sizes.

SNP count-based haplotypes	**5 SNPs**	**10 SNPs**	**20 SNPs**	**50 SNPs**
Number of haplotype alleles	1,303,861	1,877,160	2,713,296	3,710,659
Number of haplotypes	111,123	55,554	27,768	11,099
Average number of SNPs per haplotypes	5	10	20	50
Average number of alleles per haplotypes	11.73349	33.78983	97.71305	334.3237
Minimum SNPs in haplotypes	5	10	20	50
Maximum SNPs in haplotypes	5	10	20	50
Length-based haplotypes	**22.25 kb**	**44.5 kb**	**89 kb**	**222.5 kb**
Number of haplotype allele markers	1,364,861	1,867,261	2,621,574	3,581,059
Number of haplotypes	97,061	54,163	27,797	11,196
Average number of SNPs per haplotypes	5.725038	10.25936	19.99057	49.63183
Average number of alleles per haplotypes	14.06188	34.47484	94.31140	319.8516
Minimum SNPs in haplotypes	2	2	2	2
Maximum SNPs in haplotypes	29	47	71	136
LD clustering-based haplotypes	**K = N/5**	**K = N/10**	**K = N/20**	**K = N/50**
Number of haplotype alleles	1,277,525	1,764,074	2,472,637	3,358,562
Number of haplotypes	111,123	55,554	27,768	11,099
Average number of SNPs per haplotypes	5.000567	10.00248	20.01145	50.06559
Average number of alleles per haplotypes	11.49649	31.75422	89.04628	302.6004
Minimum SNPs in haplotypes	1	1	1	1
Maximum SNPs in haplotypes	114	131	141	213

K is the number of clusters and N is the number of total SNPs.

3 Criteria for Haplotype(combination of SNPs) Construction



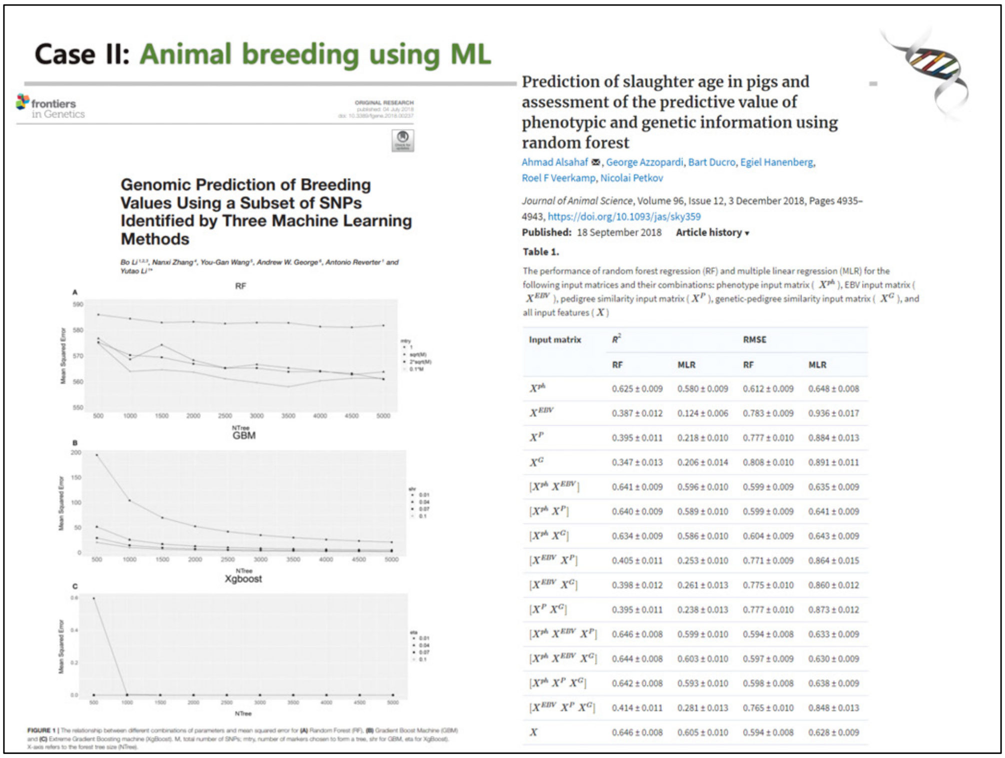
Results: Heritability & Accuracy

TABLE 4 | Estimated heritabilities using haplotypes defined by different methods and sizes and using individual SNPs.

	Average number of SNPs per haplotype			
CWT	**5**	**10**	**20**	**50**
SNP count-based haplotypes	0.39	0.39	0.41	0.43
Length-based haplotypes	0.38	0.39	0.40	0.42
LD clustering-based haplotypes	0.39	0.39	0.41	0.43
Individual SNPs		0.36		
EMA	**5**	**10**	**20**	**50**
SNP count-based haplotypes	0.33	0.34	0.35	0.38
Length-based haplotypes	0.33	0.34	0.35	0.38
LD clustering-based haplotypes	0.33	0.34	0.36	0.38
Individual SNPs		0.43		
BFT	**5**	**10**	**20**	**50**
SNP count-based haplotypes	0.45	0.46	0.48	0.52
Length-based haplotypes	0.44	0.45	0.47	0.50
LD clustering-based haplotypes	0.44	0.45	0.46	0.50
Individual SNPs		0.43		

More SNP # in Haplotypes
> Heritability ↑

CWT 3.5%, EMA 4.6%, BFT 2.1% ↑
Optimal SNP #: 4~10, LD: 0.43
SNP Distance: 41K bp



Case II: Animal breeding using ML

frontiers in Genetics

ORIGINAL RESEARCH
published: 04 July 2018
doi: 10.3389/fgene.2018.00237

Genomic Prediction of Breeding Values Using a Subset of SNPs Identified by Three Machine Learning Methods

Bo Li[1,2,3], Nanxi Zhang[4], You-Gan Wang[5], Andrew W. George[6], Antonio Reverter[1] and Yutao Li[1]*

FIGURE 1 | The relationship between different combinations of parameters and mean squared error for **(A)** Random Forest (RF), **(B)** Gradient Boost Machine (GBM) and **(C)** Extreme Gradient Boosting machine (XgBoost). M, total number of SNPs; mtry, number of markers chosen to form a tree, shr for GBM, eta for XgBoost). X-axis refers to the forest tree size (NTree).

Prediction of slaughter age in pigs and assessment of the predictive value of phenotypic and genetic information using random forest

Ahmad Alsahaf ✉, George Azzopardi, Bart Ducro, Egiel Hanenberg, Roel F Veerkamp, Nicolai Petkov

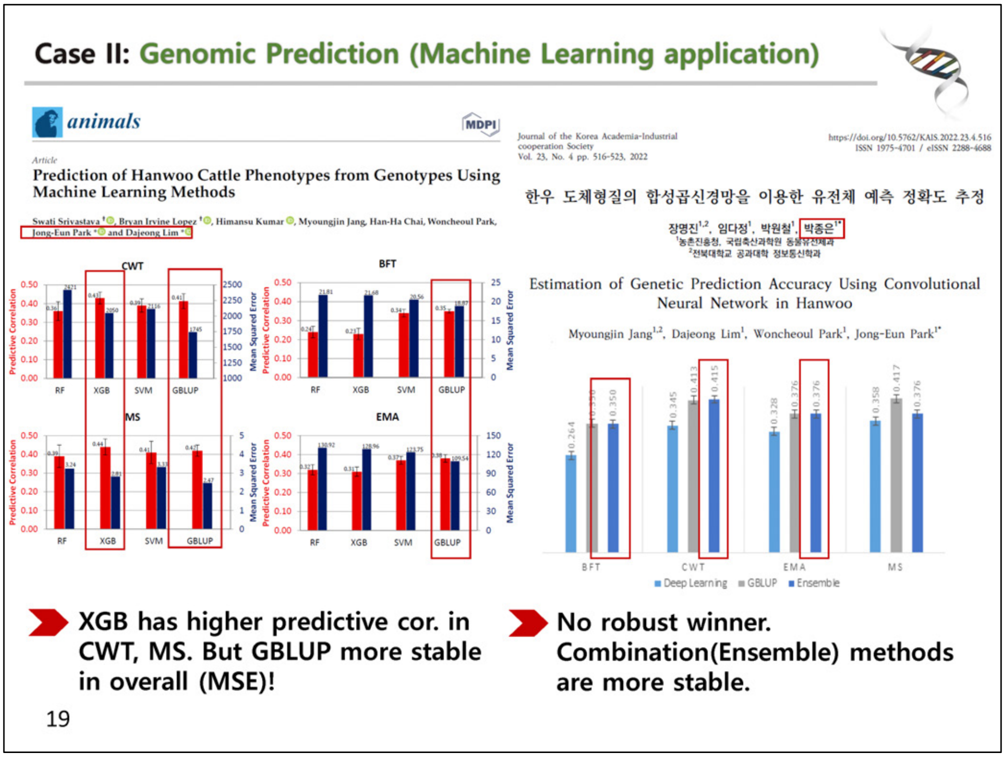
Journal of Animal Science, Volume 96, Issue 12, 3 December 2018, Pages 4935–4943, https://doi.org/10.1093/jas/sky359

Published: 18 September 2018 **Article history ▾**

Table 1.

The performance of random forest regression (RF) and multiple linear regression (MLR) for the following input matrices and their combinations: phenotype input matrix (X^{ph}), EBV input matrix (X^{EBV}), pedigree similarity input matrix (X^{P}), genetic-pedigree similarity input matrix (X^{G}), and all input features (X)

Input matrix	R^2		RMSE	
	RF	MLR	RF	MLR
X^{ph}	0.625 ± 0.009	0.580 ± 0.009	0.612 ± 0.009	0.648 ± 0.008
X^{EBV}	0.387 ± 0.012	0.124 ± 0.006	0.783 ± 0.009	0.936 ± 0.017
X^{P}	0.395 ± 0.011	0.218 ± 0.010	0.777 ± 0.010	0.884 ± 0.013
X^{G}	0.347 ± 0.013	0.206 ± 0.014	0.808 ± 0.010	0.891 ± 0.011
$[X^{ph}\ X^{EBV}]$	0.641 ± 0.009	0.596 ± 0.010	0.599 ± 0.009	0.635 ± 0.009
$[X^{ph}\ X^{P}]$	0.640 ± 0.009	0.589 ± 0.010	0.599 ± 0.009	0.641 ± 0.009
$[X^{ph}\ X^{G}]$	0.634 ± 0.009	0.586 ± 0.010	0.604 ± 0.009	0.643 ± 0.009
$[X^{EBV}\ X^{P}]$	0.405 ± 0.011	0.253 ± 0.010	0.771 ± 0.009	0.864 ± 0.015
$[X^{EBV}\ X^{G}]$	0.398 ± 0.012	0.261 ± 0.013	0.775 ± 0.010	0.860 ± 0.012
$[X^{P}\ X^{G}]$	0.395 ± 0.011	0.238 ± 0.013	0.777 ± 0.010	0.873 ± 0.012
$[X^{ph}\ X^{EBV}\ X^{P}]$	0.646 ± 0.008	0.599 ± 0.010	0.594 ± 0.008	0.633 ± 0.009
$[X^{ph}\ X^{EBV}\ X^{G}]$	0.644 ± 0.008	0.603 ± 0.010	0.597 ± 0.009	0.630 ± 0.009
$[X^{ph}\ X^{P}\ X^{G}]$	0.642 ± 0.008	0.593 ± 0.010	0.598 ± 0.008	0.638 ± 0.009
$[X^{EBV}\ X^{P}\ X^{G}]$	0.414 ± 0.011	0.281 ± 0.013	0.765 ± 0.010	0.848 ± 0.013
X	0.646 ± 0.008	0.605 ± 0.010	0.594 ± 0.008	0.628 ± 0.009



Case II: Genomic Prediction (Machine Learning application)

animals MDPI

Article

Prediction of Hanwoo Cattle Phenotypes from Genotypes Using Machine Learning Methods

Swati Srivastava †, Bryan Irvine Lopez †, Himansu Kumar, Myoungjin Jang, Han-Ha Chai, Woncheoul Park, Jong-Eun Park * and Dajeong Lim *

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Vol. 23, No. 4 pp. 516-523, 2022

https://doi.org/10.5762/KAIS.2022.23.4.516
ISSN 1975-4701 / eISSN 2288-4688

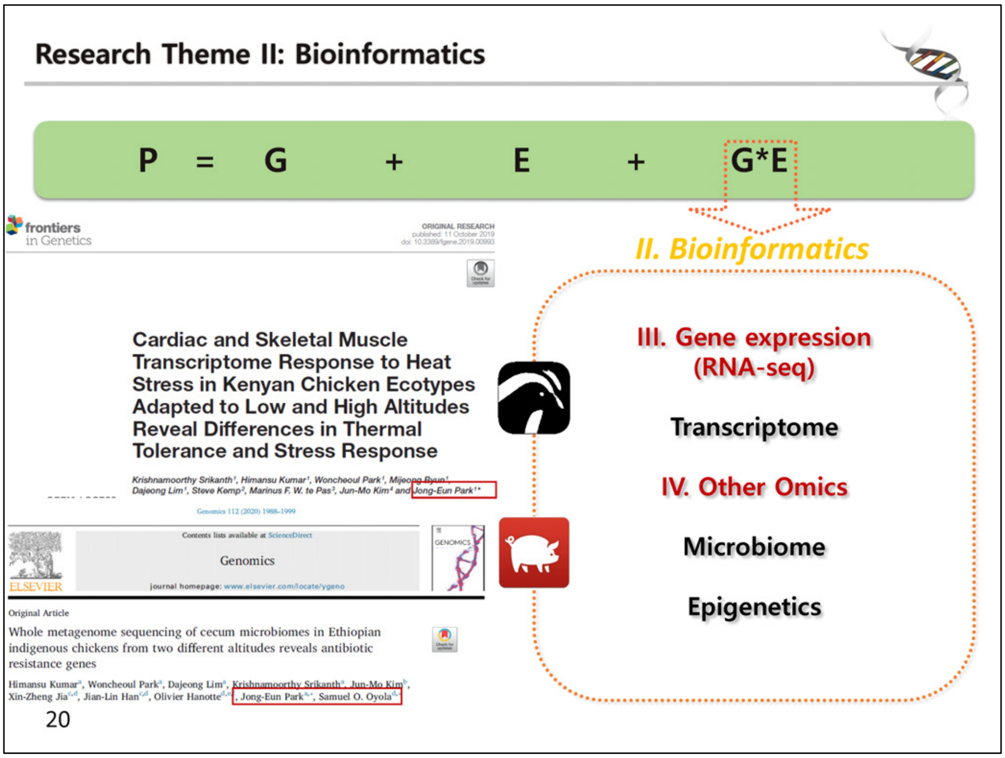
한우 도체형질의 합성곱신경망을 이용한 유전체 예측 정확도 추정

장명진[1,2], 임다정[1], 박원철[1], 박종은[1*]
[1]농촌진흥청, 국립축산과학원 동물유전체과
[2]전북대학교 공과대학 정보통신학과

Estimation of Genetic Prediction Accuracy Using Convolutional Neural Network in Hanwoo

Myoungjin Jang[1,2], Dajeong Lim[1], Woncheoul Park[1], Jong-Eun Park[1*]

- XGB has higher predictive cor. in CWT, MS. But GBLUP more stable in overall (MSE)!
- No robust winner. Combination(Ensemble) methods are more stable.



Research Theme II: Bioinformatics

P = G + E + G*E

frontiers in Genetics

ORIGINAL RESEARCH
published: 11 October 2019
doi: 10.3389/fgene.2019.00993

Cardiac and Skeletal Muscle Transcriptome Response to Heat Stress in Kenyan Chicken Ecotypes Adapted to Low and High Altitudes Reveal Differences in Thermal Tolerance and Stress Response

Krishnamoorthy Srikanth[1], Himansu Kumar[1], Woncheoul Park[1], Mijeong Byun[1], Dajeong Lim[1], Steve Kemp[2], Marinus F. W. te Pas[3], Jun-Mo Kim[4] and Jong-Eun Park[1]*

Genomics 112 (2020) 1988–1999

Contents lists available at ScienceDirect

Genomics

journal homepage: www.elsevier.com/locate/ygeno

ELSEVIER

Original Article

Whole metagenome sequencing of cecum microbiomes in Ethiopian indigenous chickens from two different altitudes reveals antibiotic resistance genes

Himansu Kumar[a], Woncheoul Park[a], Dajeong Lim[a], Krishnamoorthy Srikanth[a], Jun-Mo Kim[b], Xin-Zheng Jia[c,d], Jian-Lin Han[c,d], Olivier Hanotte[d,e], Jong-Eun Park[a,*], Samuel O. Oyola[d,*]

II. Bioinformatics

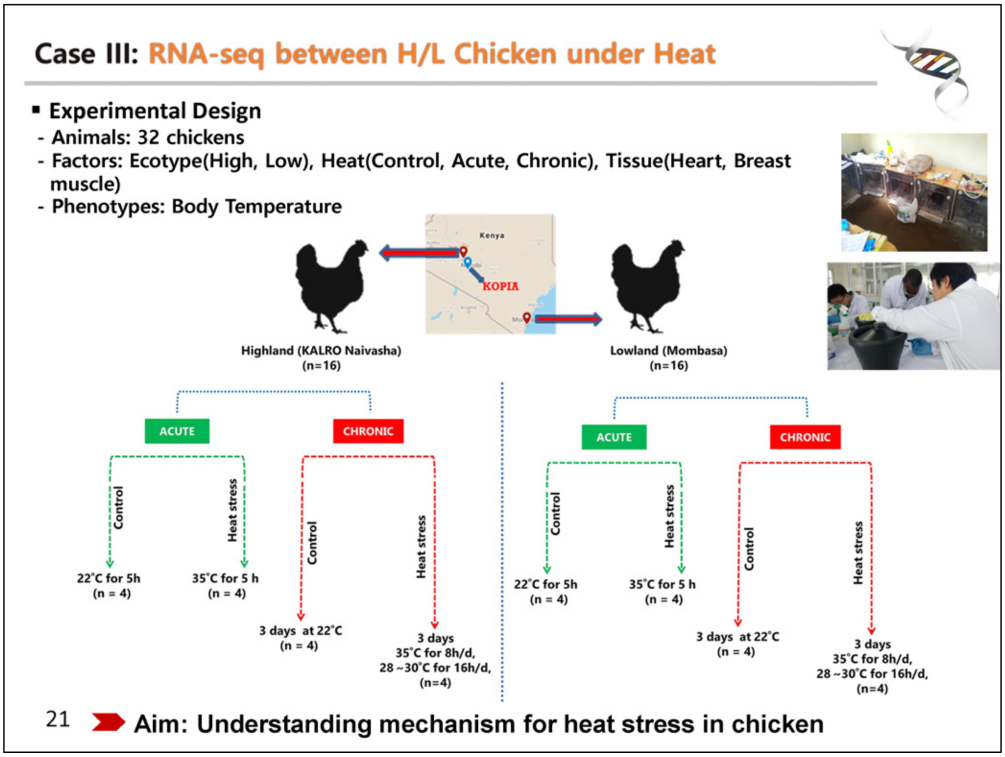
III. Gene expression (RNA-seq)

Transcriptome

IV. Other Omics

Microbiome

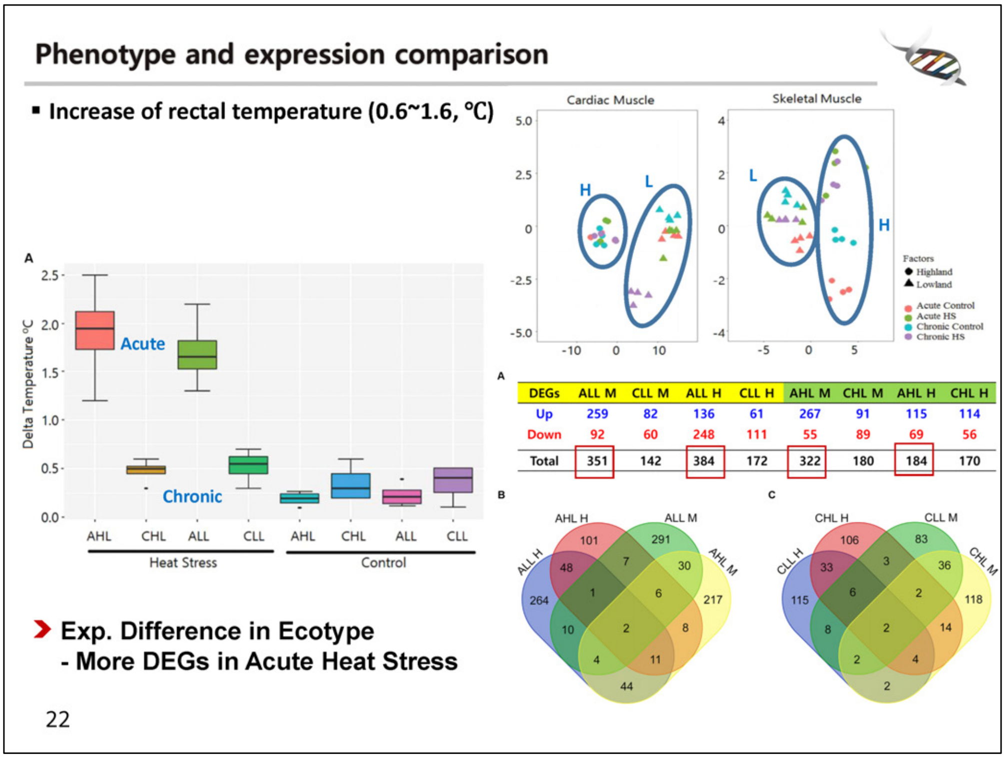
Epigenetics



Case III: RNA-seq between H/L Chicken under Heat

- **Experimental Design**
  - Animals: 32 chickens
  - Factors: Ecotype(High, Low), Heat(Control, Acute, Chronic), Tissue(Heart, Breast muscle)
  - Phenotypes: Body Temperature

Aim: Understanding mechanism for heat stress in chicken



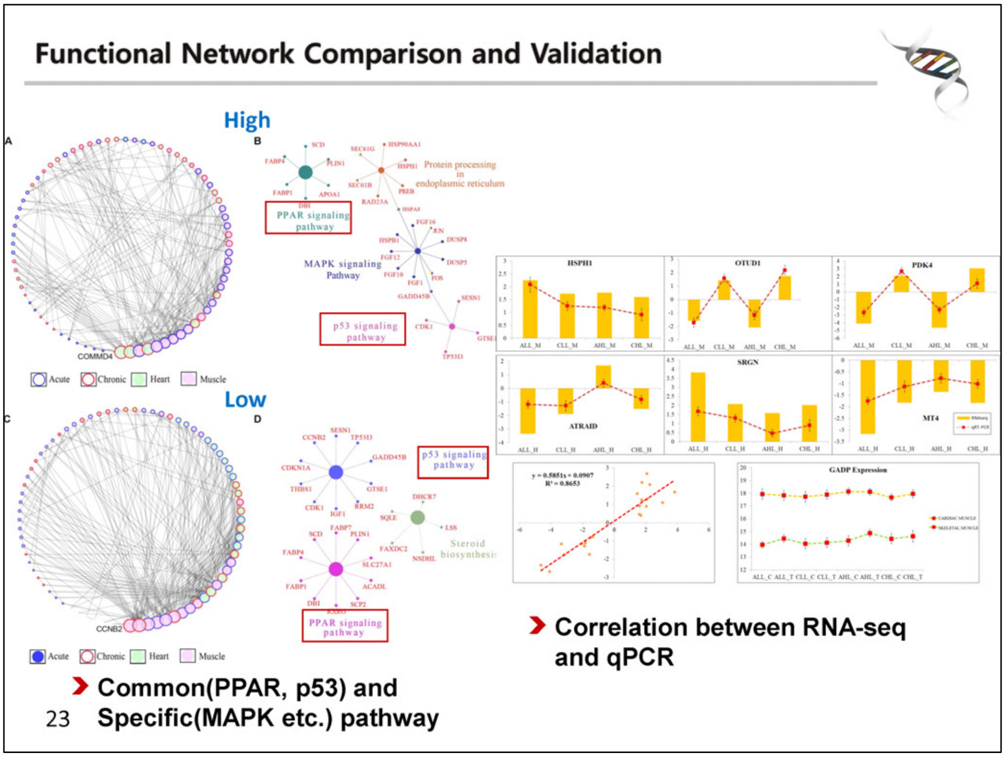
Phenotype and expression comparison

- Increase of rectal temperature (0.6~1.6, ℃)

A

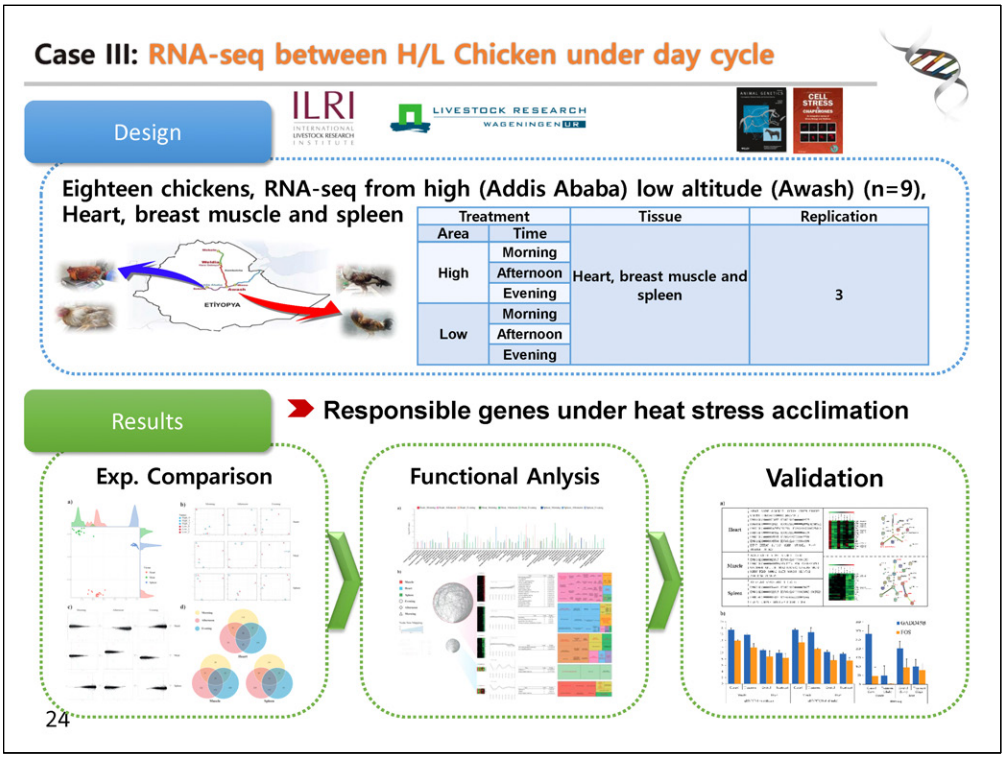
DEGs	ALL M	CLL M	ALL H	CLL H	AHL M	CHL M	AHL H	CHL H
Up	259	82	136	61	267	91	115	114
Down	92	60	248	111	55	89	69	56
Total	351	142	384	172	322	180	184	170

Exp. Difference in Ecotype
- More DEGs in Acute Heat Stress



Functional Network Comparison and Validation

- Common(PPAR, p53) and Specific(MAPK etc.) pathway
- Correlation between RNA-seq and qPCR



Case III: RNA-seq between H/L Chicken under day cycle

Design

Eighteen chickens, RNA-seq from high (Addis Ababa) low altitude (Awash) (n=9), Heart, breast muscle and spleen

Treatment		Tissue	Replication
Area	Time		
High	Morning	Heart, breast muscle and spleen	3
	Afternoon		
	Evening		
Low	Morning		
	Afternoon		
	Evening		

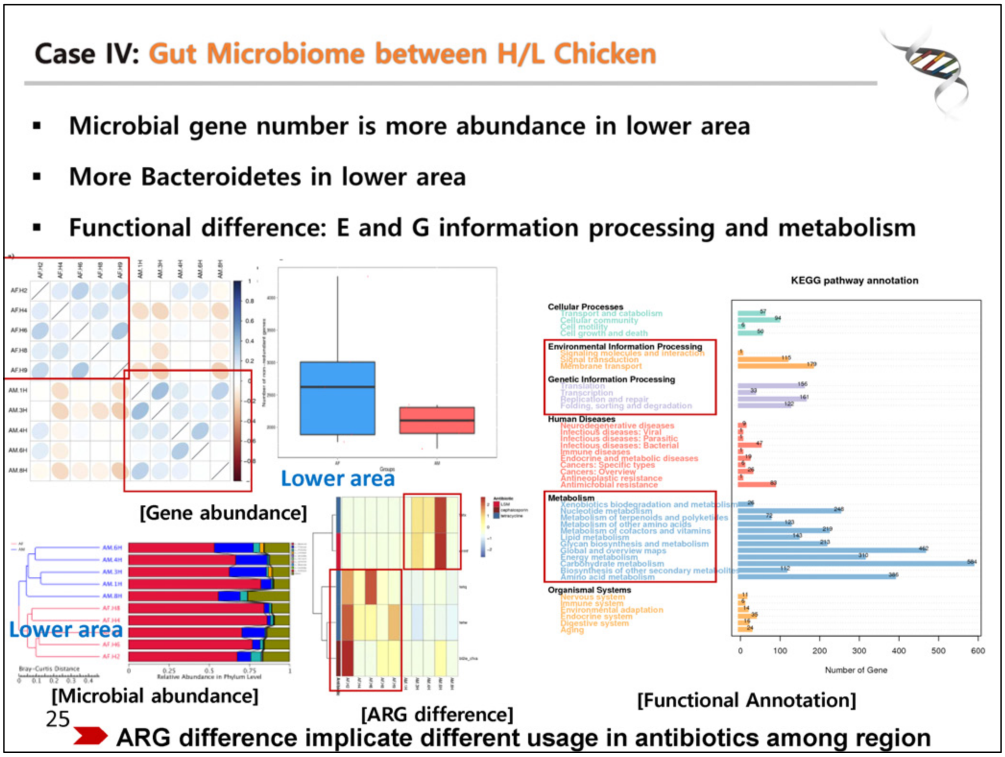
Results

- Responsible genes under heat stress acclimation

Exp. Comparison

Functional Anlysis

Validation



Case IV: Gut Microbiome between H/L Chicken

- Microbial gene number is more abundance in lower area
- More Bacteroidetes in lower area
- Functional difference: E and G information processing and metabolism

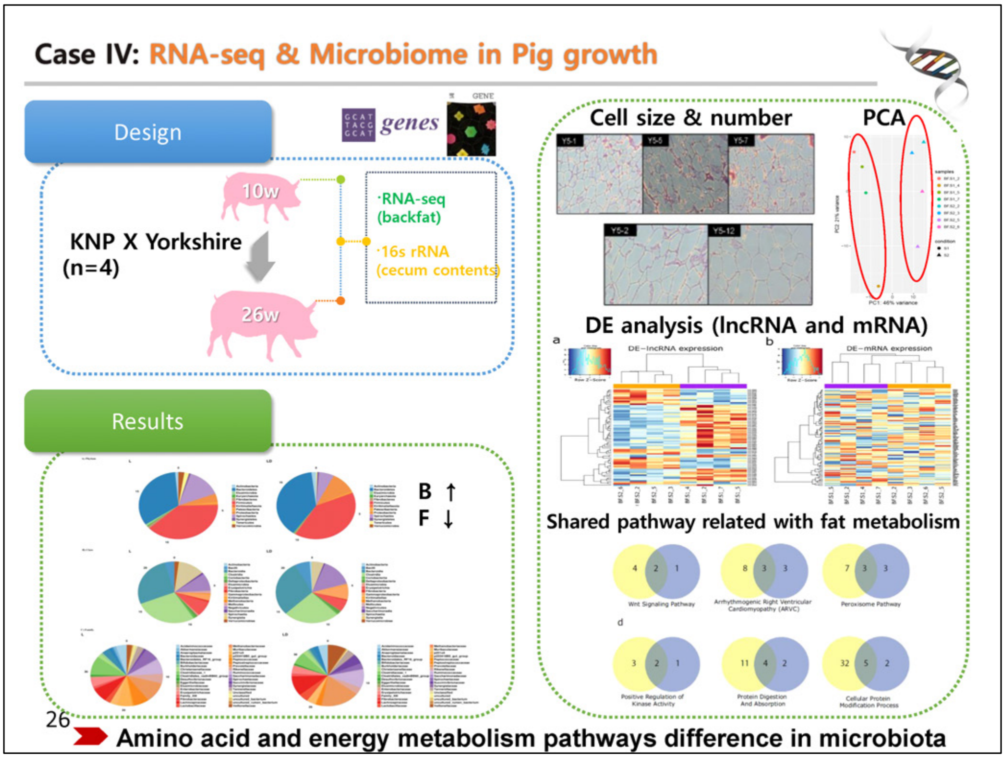
[Gene abundance]

[Microbial abundance]

[ARG difference]

[Functional Annotation]

ARG difference implicate different usage in antibiotics among region



Case IV: RNA-seq & Microbiome in Pig growth

Design

KNP X Yorkshire
(n=4)

·RNA-seq
(backfat)

·16s rRNA
(cecum contents)

Results

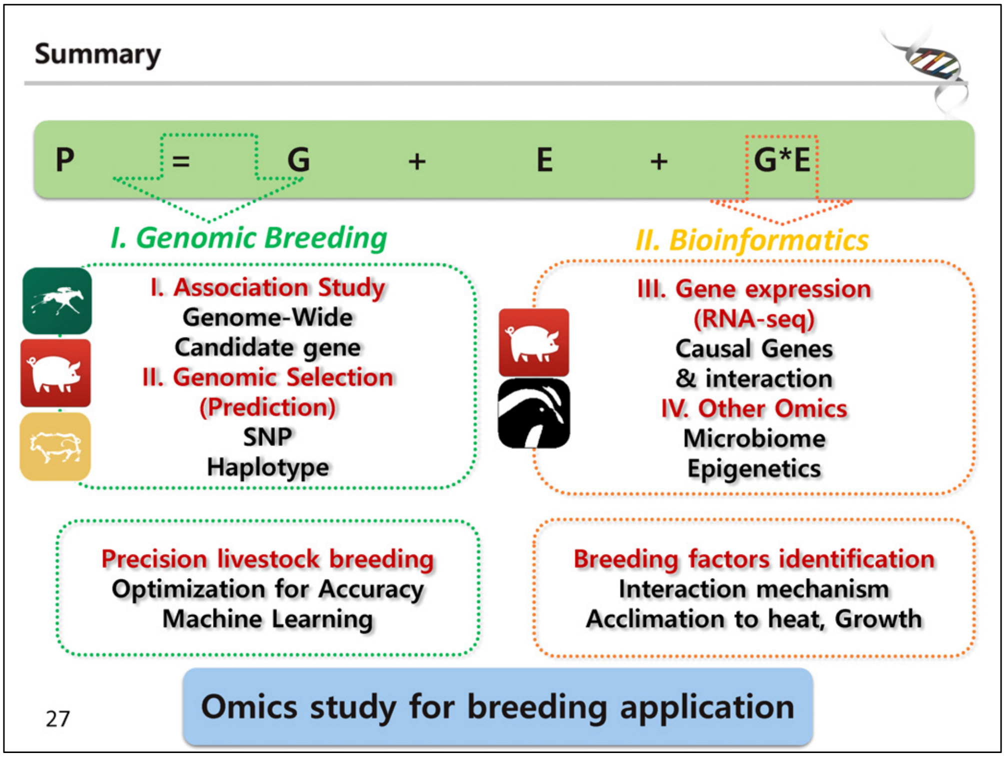
Cell size & number

PCA

DE analysis (lncRNA and mRNA)

Shared pathway related with fat metabolism

Amino acid and energy metabolism pathways difference in microbiota



Summary

P = G + E + G*E

I. Genomic Breeding

I. Association Study
Genome-Wide
Candidate gene
II. Genomic Selection
(Prediction)
SNP
Haplotype

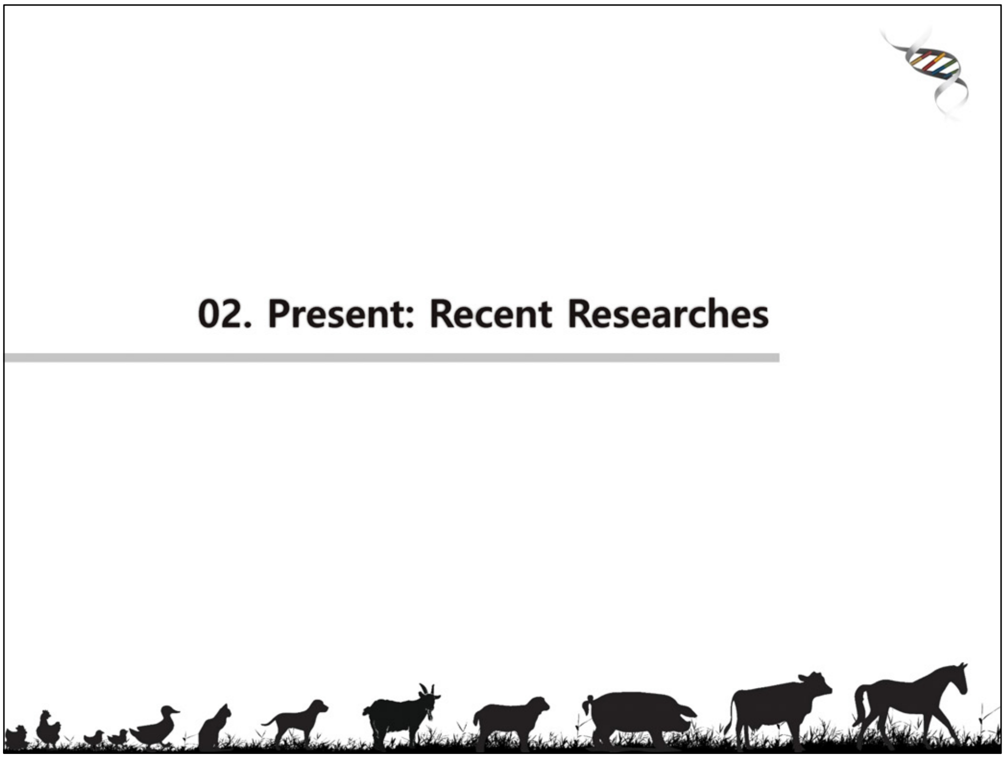
II. Bioinformatics

III. Gene expression
(RNA-seq)
Causal Genes
& interaction
IV. Other Omics
Microbiome
Epigenetics

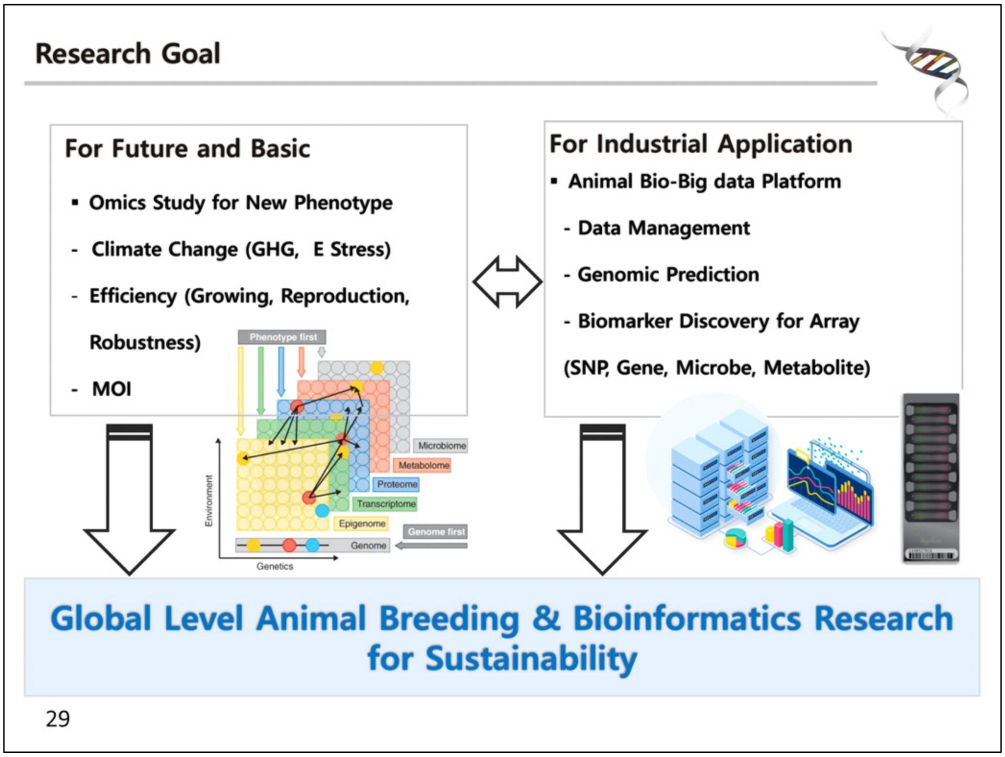
Precision livestock breeding
Optimization for Accuracy
Machine Learning

Breeding factors identification
Interaction mechanism
Acclimation to heat, Growth

Omics study for breeding application



02. Present: Recent Researches



Research Goal

For Future and Basic

- Omics Study for New Phenotype
  - Climate Change (GHG, E Stress)
  - Efficiency (Growing, Reproduction, Robustness)
  - MOI

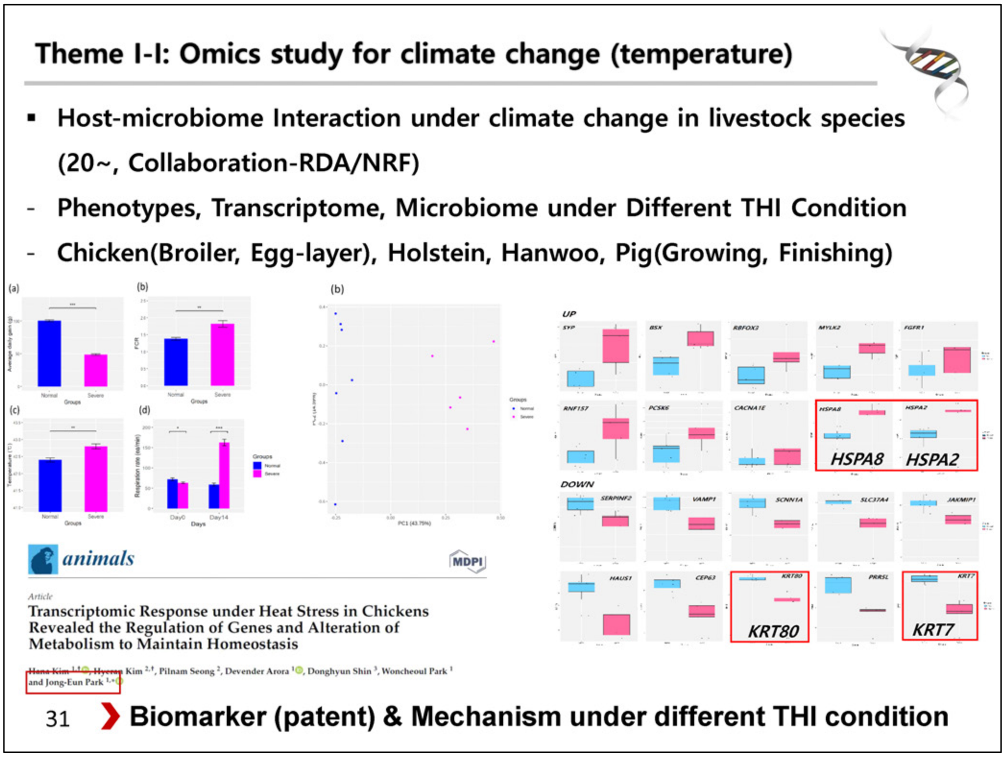
For Industrial Application

- Animal Bio-Big data Platform
  - Data Management
  - Genomic Prediction
  - Biomarker Discovery for Array (SNP, Gene, Microbe, Metabolite)

Global Level Animal Breeding & Bioinformatics Research for Sustainability

Recent projects

- Comparative transcriptomics under different biotic or abiotic conditions
  - Breeds
  - Environmental factors
- Effects of Low-methane feeding in cattle
- Basic Research Laboratory for Survival Strategy of Marine Climate-sensitive Biological Indicator Species
- Jeju Genome Project



Theme I-I: Omics study for climate change (temperature)

- Host-microbiome Interaction under climate change in livestock species (20~, Collaboration-RDA/NRF)

- Phenotypes, Transcriptome, Microbiome under Different THI Condition
- Chicken(Broiler, Egg-layer), Holstein, Hanwoo, Pig(Growing, Finishing)

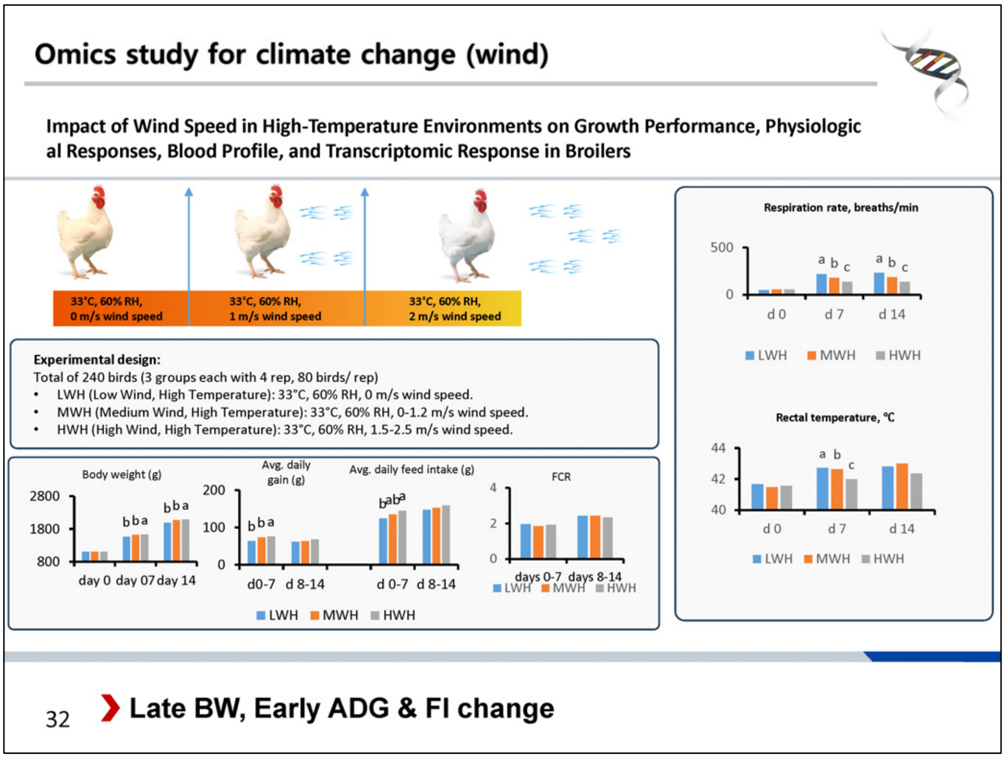
animals MDPI

Article

Transcriptomic Response under Heat Stress in Chickens Revealed the Regulation of Genes and Alteration of Metabolism to Maintain Homeostasis

Hana Kim [1,†], Hyeran Kim [2,†], Pilnam Seong [2], Devender Arora [1], Donghyun Shin [3], Woncheoul Park [1] and Jong-Eun Park [1,*]

❯ **Biomarker (patent) & Mechanism under different THI condition**



Omics study for climate change (wind)

Impact of Wind Speed in High-Temperature Environments on Growth Performance, Physiological Responses, Blood Profile, and Transcriptomic Response in Broilers

Experimental design:
Total of 240 birds (3 groups each with 4 rep, 80 birds/ rep)
- LWH (Low Wind, High Temperature): 33°C, 60% RH, 0 m/s wind speed.
- MWH (Medium Wind, High Temperature): 33°C, 60% RH, 0-1.2 m/s wind speed.
- HWH (High Wind, High Temperature): 33°C, 60% RH, 1.5-2.5 m/s wind speed.

❯ **Late BW, Early ADG & FI change**

Omics study for climate change (wind)

Impact of Wind Speed in High-Temperature Environments on Growth Performance, Physiological Responses, Blood Profile, and Transcriptomic Response in Broilers

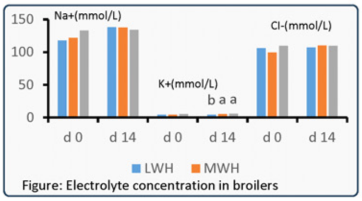
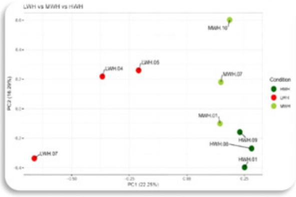
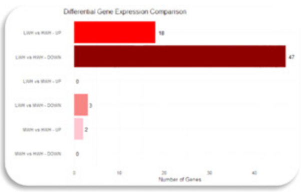
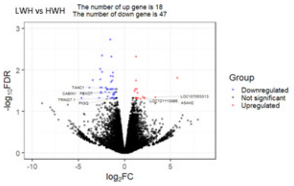
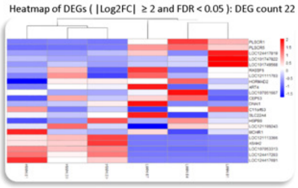


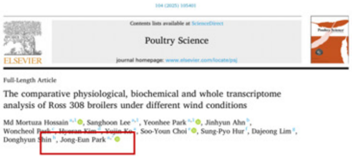
Figure: Electrolyte concentration in broilers











104 (2025) 105401

Contents lists available at ScienceDirect

Poultry Science

journal homepage: www.elsevier.com/locate/psj

Full-Length Article

The comparative physiological, biochemical and whole transcriptome analysis of Ross 308 broilers under different wind conditions

Md Mortuza Hossain[a,1], Sanghoon Lee[a,1], Yeonhee Park[a,1], Jinhyun Ahn[b], Woncheol Park[c], Hyeran Kim[d], Yujin Ko[e], Soo-Youn Choi[e], Sung-Pyo Hur[f], Dajeong Lim[g], Donghyun Shin[h], Jong-Eun Park[a,*]

❯ **Transcriptomic differences between Low and Medium pathways related to vital processes, innate immune responses, and biosynthesis**

Genomic characteristics in Jeju Breeds

- Omics based characterization in Korean Native breeds in Jeju
- Genomic Difference proved. But small within diversity (Ne < 40~50)
- For Jeju chicken and dog, genomic studies are required (with Pop. ↑)

SCIENTIFIC REPORTS
natureresearch

There are amendments to this paper

Comprehensive genome and transcriptome analyses reveal genetic relationship, selection signature, and transcriptome landscape of small-sized Korean native Jeju horse

Krishnamoorthy Srikanth[1,10], Nam-Young Kim[2,10], WonCheoul Park[1], Jae-Min Kim[3], Kwon-Do Kim[4], Kyung-Tai Lee[5], Ju-Hwan Son[1], Han-Ha Chai[1], Jung-Woo Choi[6], Gul-Won Ja… Heebal Kim[4], Youn-Chul Ryu[7], Jin-Wu Nam[8], Jong-Eun Park[1], Jun-Mo Kim[9*] & Dajeong Lim[1*]

scientific reports

OPEN **Integration of multi-omics approaches for functional characterization of muscle related selective sweep genes in Nanchukmacdon**

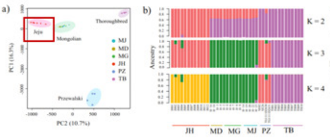
Devender Arora[1], Krishnamoorthy Srikanth[1], Jongin Lee[3], Daehwan Lee[3], Nayoung Park[3], Suyeon Wy[3], Hyeonji Kim[3], Jong-Eun Park[1], Han-Ha Chai[1], Dajeong Lim[1], In-Cheol Cho[2], Jaebum Kim[3] & Woncheoul Park[1]

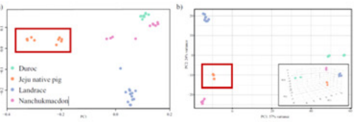
Open Access
Anim Biosci
Vol. 34, No. 5:789-800 May 2021
https://doi.org/10.5713/ajas.19.0888
pISSN 2765-0189 eISSN 2765-0235

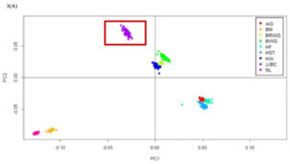
ANIMAL BIOSCIENCE

Genetic characteristics of Korean Jeju Black cattle with high density single nucleotide polymorphisms

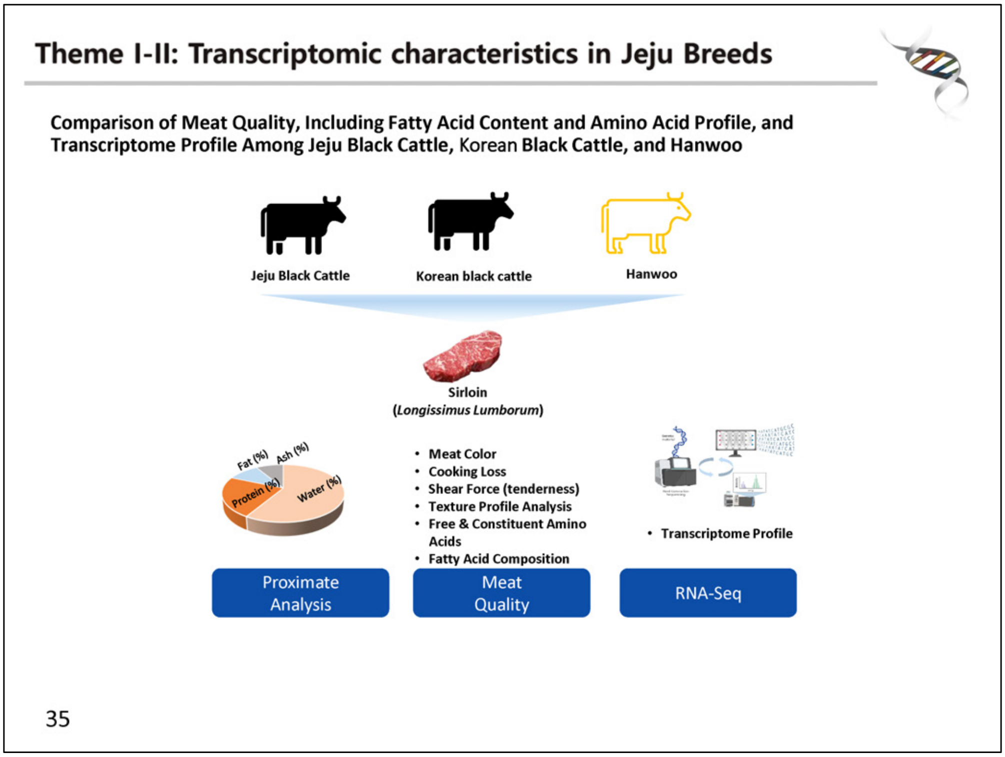
M. Zahangir Alam[1,2,a], Yun-Mi Lee[1,a], Hyo-Jung Son[1], Lauren H. Hanna[3], David G. Riley[4], Hideyuki Mannen[5], Shinji Sasazaki[5], Se Pill Park[6], and Jong-Joo Kim[1,*]







❯ **Unique Breed and Phenotype - Valuation**

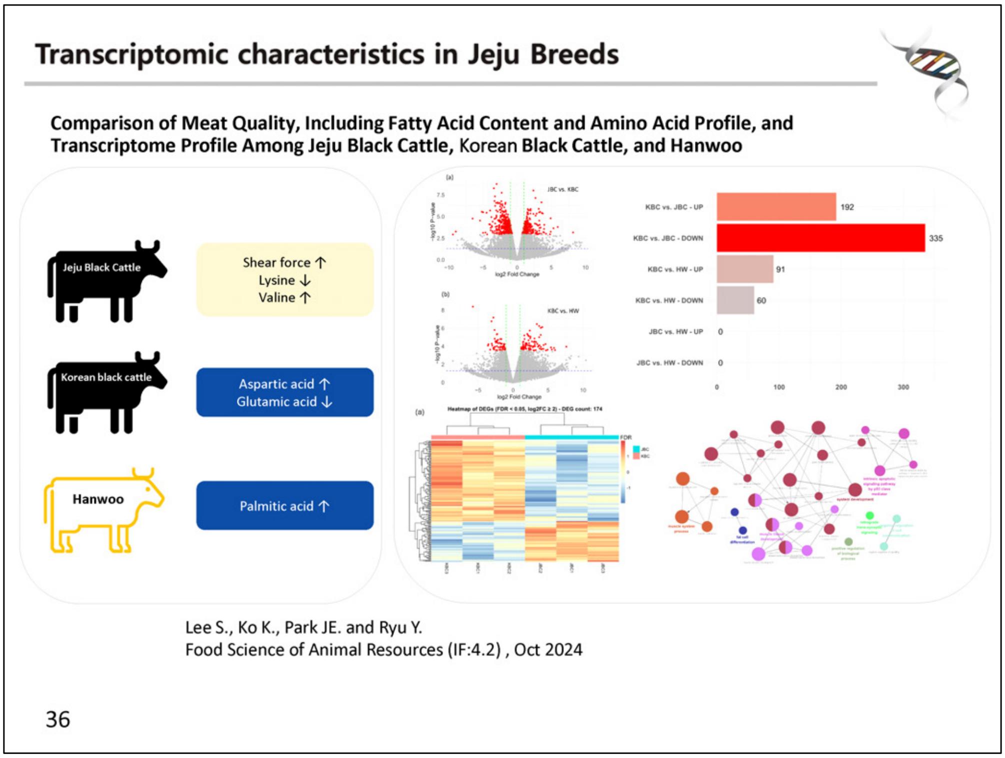


Theme I-II: Transcriptomic characteristics in Jeju Breeds

Comparison of Meat Quality, Including Fatty Acid Content and Amino Acid Profile, and Transcriptome Profile Among Jeju Black Cattle, Korean Black Cattle, and Hanwoo

- Meat Color
- Cooking Loss
- Shear Force (tenderness)
- Texture Profile Analysis
- Free & Constituent Amino Acids
- Fatty Acid Composition

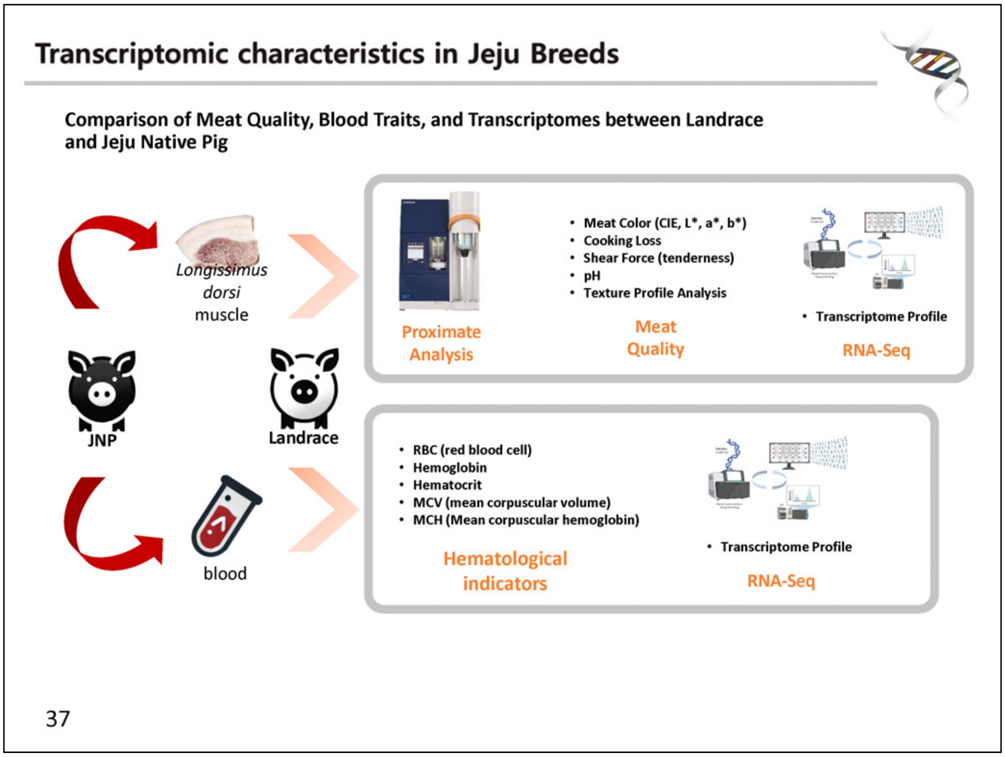
- Transcriptome Profile



Transcriptomic characteristics in Jeju Breeds

Comparison of Meat Quality, Including Fatty Acid Content and Amino Acid Profile, and Transcriptome Profile Among Jeju Black Cattle, Korean Black Cattle, and Hanwoo

Lee S., Ko K., Park JE. and Ryu Y.
Food Science of Animal Resources (IF:4.2) , Oct 2024



Transcriptomic characteristics in Jeju Breeds

Comparison of Meat Quality, Blood Traits, and Transcriptomes between Landrace and Jeju Native Pig

Longissimus dorsi muscle

JNP

Landrace

blood

- Meat Color (CIE, L*, a*, b*)
- Cooking Loss
- Shear Force (tenderness)
- pH
- Texture Profile Analysis

- Transcriptome Profile

Proximate Analysis

Meat Quality

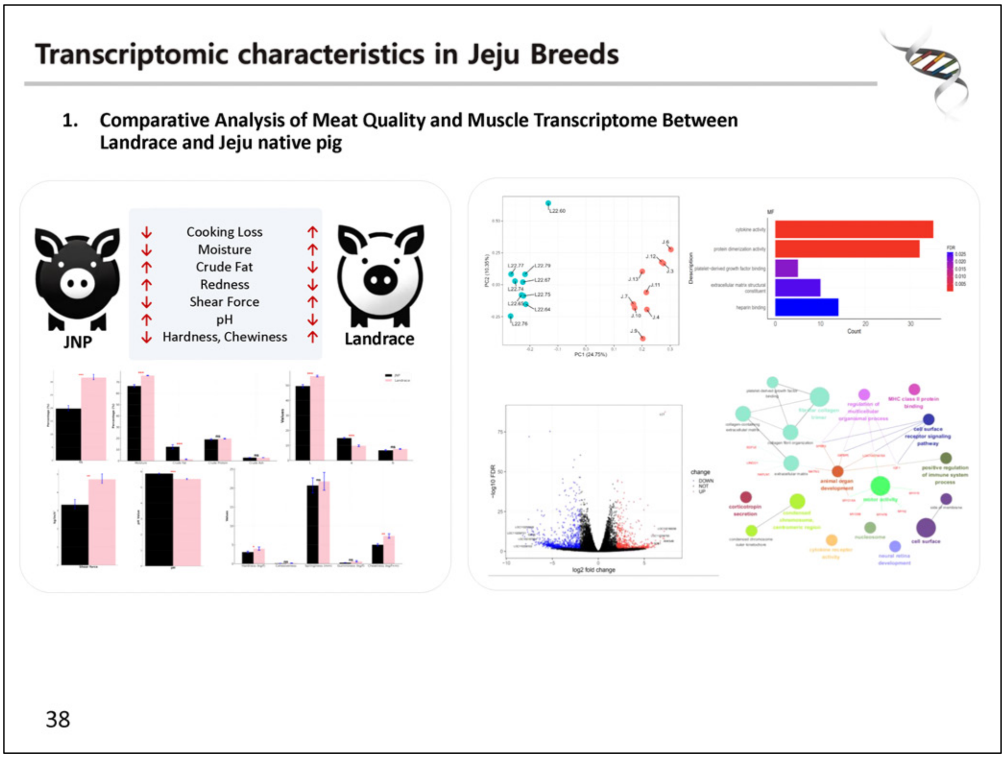
RNA-Seq

- RBC (red blood cell)
- Hemoglobin
- Hematocrit
- MCV (mean corpuscular volume)
- MCH (Mean corpuscular hemoglobin)

- Transcriptome Profile

Hematological indicators

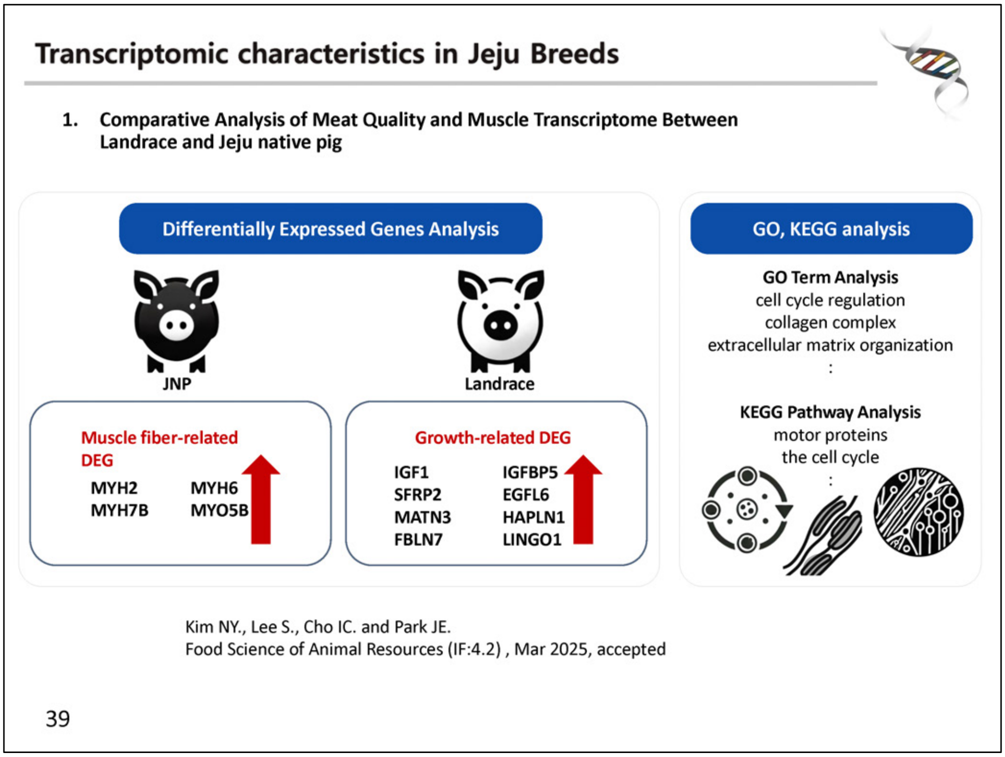
RNA-Seq



Transcriptomic characteristics in Jeju Breeds

1. **Comparative Analysis of Meat Quality and Muscle Transcriptome Between Landrace and Jeju native pig**

JNP		Landrace
↓	Cooking Loss	↑
↓	Moisture	↑
↑	Crude Fat	↓
↑	Redness	↓
↓	Shear Force	↑
↑	pH	↓
↓	Hardness, Chewiness	↑



Transcriptomic characteristics in Jeju Breeds

1. Comparative Analysis of Meat Quality and Muscle Transcriptome Between Landrace and Jeju native pig

Differentially Expressed Genes Analysis

JNP

Landrace

Muscle fiber-related DEG

MYH2 MYH6
MYH7B MYO5B

Growth-related DEG

IGF1 IGFBP5
SFRP2 EGFL6
MATN3 HAPLN1
FBLN7 LINGO1

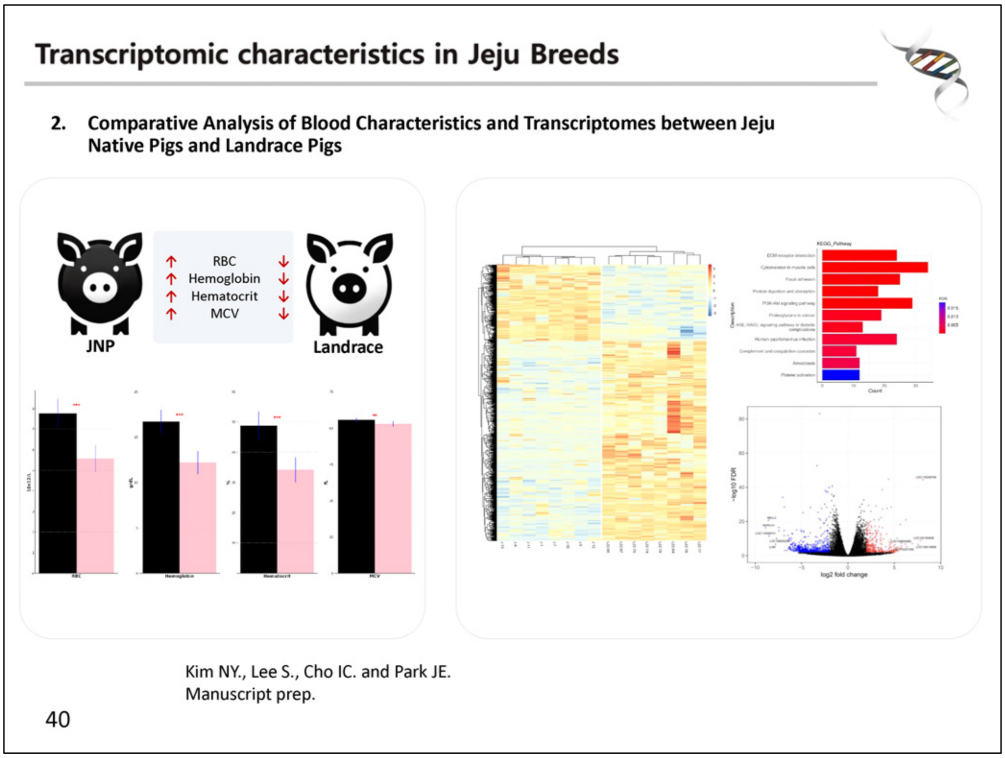
GO, KEGG analysis

GO Term Analysis
cell cycle regulation
collagen complex
extracellular matrix organization
:

KEGG Pathway Analysis
motor proteins
the cell cycle
:

Kim NY., Lee S., Cho IC. and Park JE.
Food Science of Animal Resources (IF:4.2) , Mar 2025, accepted

39



Transcriptomic characteristics in Jeju Breeds

2. Comparative Analysis of Blood Characteristics and Transcriptomes between Jeju Native Pigs and Landrace Pigs

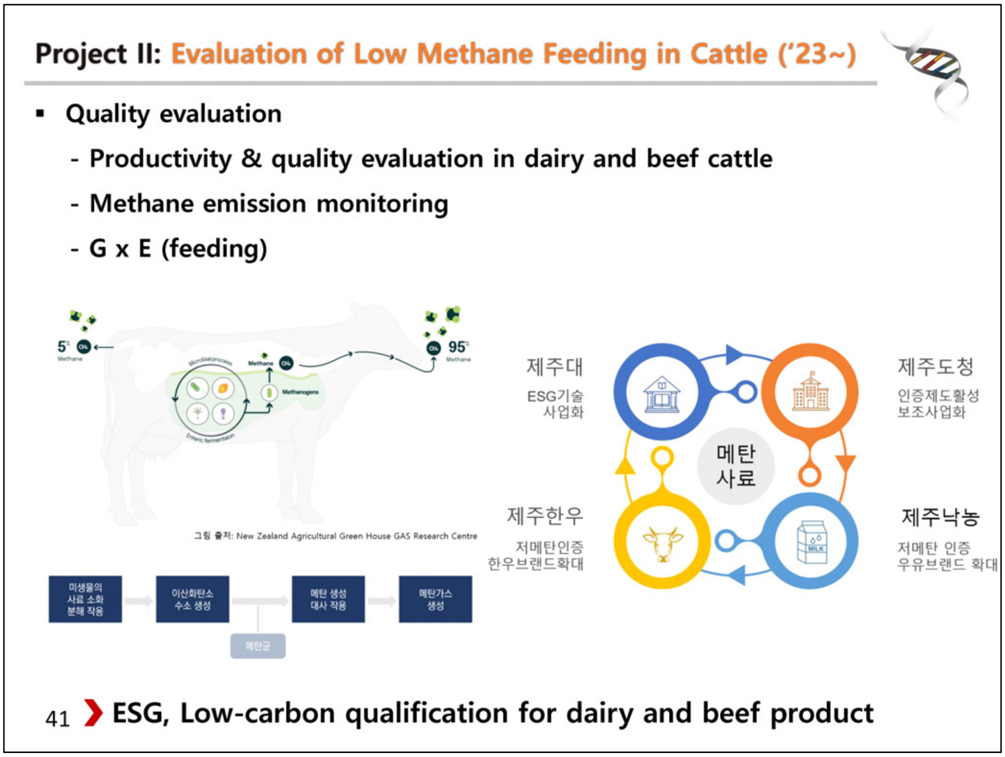
JNP

↑ RBC ↓
↑ Hemoglobin ↓
↑ Hematocrit ↓
↑ MCV ↓

Landrace

Kim NY., Lee S., Cho IC. and Park JE.
Manuscript prep.

40



Project II: Evaluation of Low Methane Feeding in Cattle ('23~)

- Quality evaluation
  - Productivity & quality evaluation in dairy and beef cattle
  - Methane emission monitoring
  - G x E (feeding)

그림 출처: New Zealand Agricultural Green House GAS Research Centre

미생물의 사료 소화 분해 작용 → 이산화탄소 수소 생성 → 메탄 생성 대사 작용 → 메탄가스 생성

메탄균

메탄 사료

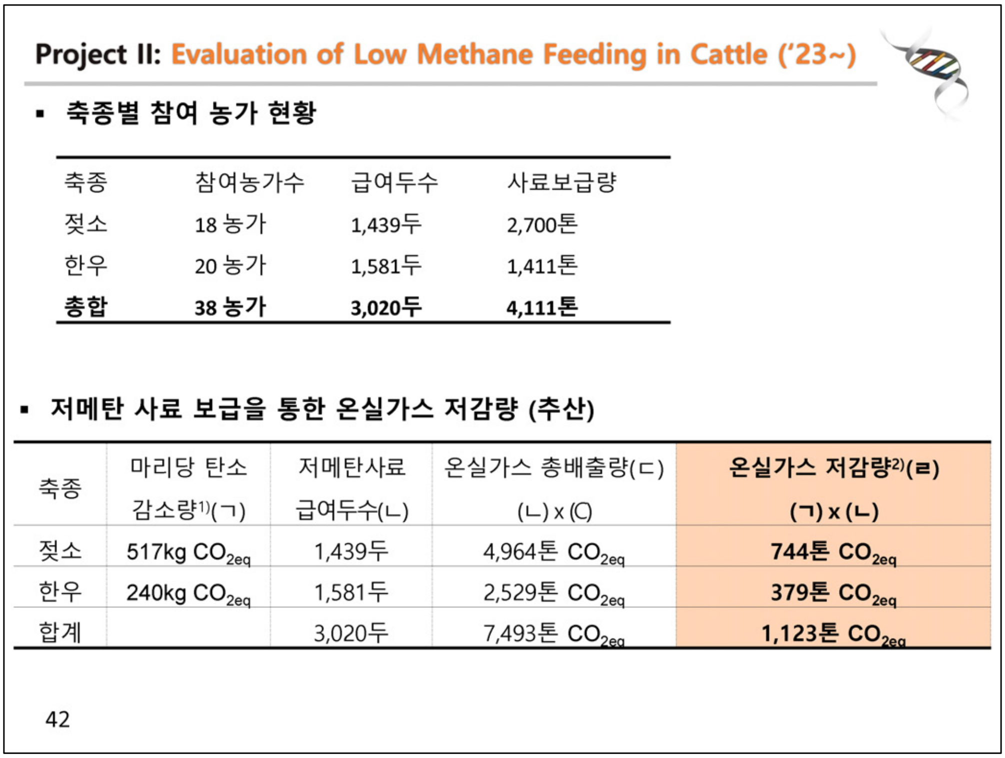
제주대
ESG기술 사업화

제주도청
인증제도활성 보조사업화

제주낙농
저메탄 인증 우유브랜드 확대

제주한우
저메탄인증 한우브랜드확대

ESG, Low-carbon qualification for dairy and beef product



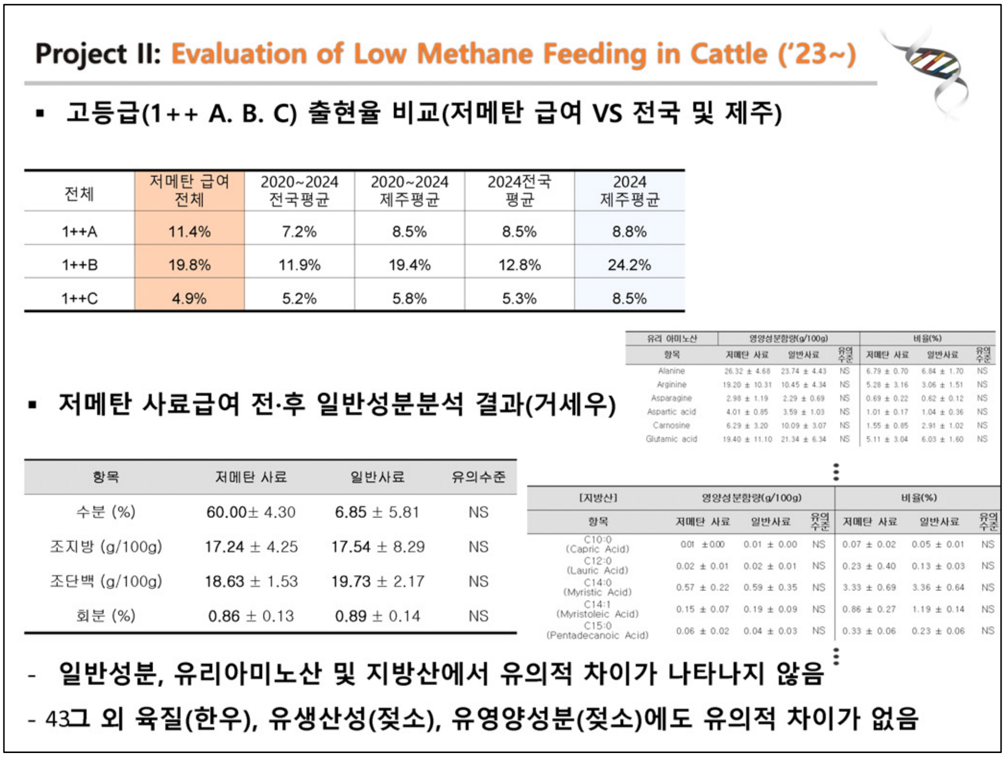
Project II: Evaluation of Low Methane Feeding in Cattle ('23~)

- 축종별 참여 농가 현황

축종	참여농가수	급여두수	사료보급량
젖소	18 농가	1,439두	2,700톤
한우	20 농가	1,581두	1,411톤
총합	**38 농가**	**3,020두**	**4,111톤**

- 저메탄 사료 보급을 통한 온실가스 저감량 (추산)

축종	마리당 탄소 감소량1)(ㄱ)	저메탄사료 급여두수(ㄴ)	온실가스 총배출량(ㄷ) (ㄴ) x (ㄷ)	**온실가스 저감량2)(ㄹ) (ㄱ) x (ㄴ)**
젖소	517kg CO_{2eq}	1,439두	4,964톤 CO_{2eq}	**744톤 CO_{2eq}**
한우	240kg CO_{2eq}	1,581두	2,529톤 CO_{2eq}	**379톤 CO_{2eq}**
합계		3,020두	7,493톤 CO_{2eq}	**1,123톤 CO_{2eq}**



Project II: Evaluation of Low Methane Feeding in Cattle ('23~)

- 고등급(1++ A. B. C) 출현율 비교(저메탄 급여 VS 전국 및 제주)

전체	저메탄 급여 전체	2020~2024 전국평균	2020~2024 제주평균	2024전국 평균	2024 제주평균
1++A	11.4%	7.2%	8.5%	8.5%	8.8%
1++B	19.8%	11.9%	19.4%	12.8%	24.2%
1++C	4.9%	5.2%	5.8%	5.3%	8.5%

- 저메탄 사료급여 전·후 일반성분분석 결과(거세우)

항목	저메탄 사료	일반사료	유의수준
수분 (%)	60.00± 4.30	6.85 ± 5.81	NS
조지방 (g/100g)	17.24 ± 4.25	17.54 ± 8.29	NS
조단백 (g/100g)	18.63 ± 1.53	19.73 ± 2.17	NS
회분 (%)	0.86 ± 0.13	0.89 ± 0.14	NS

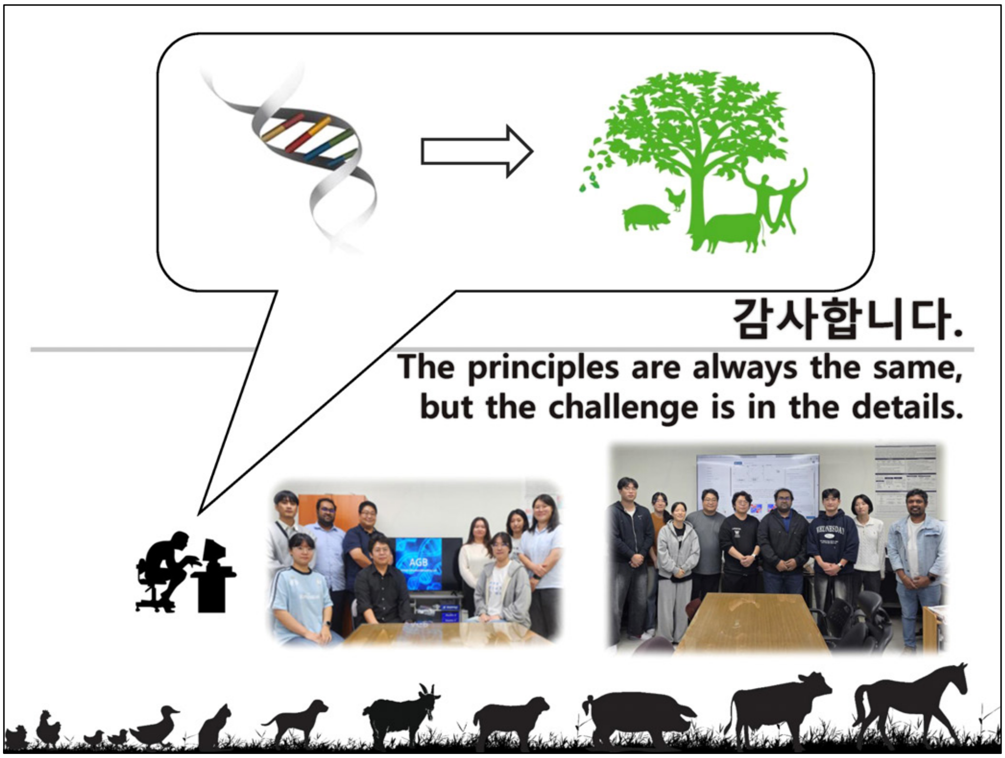
유리 아미노산	영양성분함량(g/100g)			비율(%)		
항목	저메탄 사료	일반사료	유의수준	저메탄 사료	일반사료	유의수준
Alanine	26.32 ± 4.68	23.74 ± 4.43	NS	6.79 ± 0.70	6.84 ± 1.70	NS
Arginine	19.20 ± 10.31	10.45 ± 4.34	NS	5.28 ± 3.16	3.06 ± 1.51	NS
Asparagine	2.98 ± 1.19	2.29 ± 0.69	NS	0.69 ± 0.22	0.62 ± 0.12	NS
Aspartic acid	4.01 ± 0.85	3.59 ± 1.03	NS	1.01 ± 0.17	1.04 ± 0.36	NS
Carnosine	6.29 ± 3.20	10.09 ± 3.07	NS	1.55 ± 0.85	2.91 ± 1.02	NS
Glutamic acid	19.40 ± 11.10	21.34 ± 6.34	NS	5.11 ± 3.04	6.03 ± 1.60	NS

⋮

[지방산]	영양성분함량(g/100g)			비율(%)		
항목	저메탄 사료	일반사료	유의수준	저메탄 사료	일반사료	유의수준
C10:0 (Capric Acid)	0.01 ±0.00	0.01 ± 0.00	NS	0.07 ± 0.02	0.05 ± 0.01	NS
C12:0 (Lauric Acid)	0.02 ± 0.01	0.02 ± 0.01	NS	0.23 ± 0.40	0.13 ± 0.03	NS
C14:0 (Myristic Acid)	0.57 ± 0.22	0.59 ± 0.35	NS	3.33 ± 0.69	3.36 ± 0.64	NS
C14:1 (Myristoleic Acid)	0.15 ± 0.07	0.19 ± 0.09	NS	0.86 ± 0.27	1.19 ± 0.14	NS
C15:0 (Pentadecanoic Acid)	0.06 ± 0.02	0.04 ± 0.03	NS	0.33 ± 0.06	0.23 ± 0.06	NS

⋮

- 일반성분, 유리아미노산 및 지방산에서 유의적 차이가 나타나지 않음
- 43그 외 육질(한우), 유생산성(젖소), 유영양성분(젖소)에도 유의적 차이가 없음



감사합니다.

The principles are always the same,
but the challenge is in the details.