

Development of intelligent ventilation control for second-generation smart poultry farms using computational fluid dynamics

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Weaning is a vulnerable stage for piglets, often accompanied by stress induced diarrhea and impaired growth due to maternal separation and dietary transition. Although antibiotics have been used to alleviate these issues, concerns over antimicrobial resistance and microbiota disruption have led to interest in alternatives. *Lactobacillus plantarum*, a well-known probiotic, shows promise in modulating gut immunity and microbial composition, but most studies rely on single-omics approaches, limiting mechanistic insights. Here, a multi-omics approach integrating transcriptomics (ileal RNA-seq), metabolomics, and microbiomics (fecal 16S rRNA) was applied to assess the effects of *L. plantarum* supplementation in weaned piglets. Six piglets were divided into control and treatment groups, with the latter receiving a diet containing 0.02% *L. plantarum* for two weeks. Analyses included gene expression profiling, microbial composition and function prediction, metabolite enrichment, and joint pathway analysis. Supplementation increased gut alpha diversity, reduced diarrhea associated pathogens, and activated immune related pathways including NOD-like receptor signaling, B cell receptor signaling, intestinal IgA production, and NF- κ B signaling. These findings suggest *L. plantarum* enhances gut immunity and growth performance by modulating host, microbiome, metabolite interactions.

Key words : multi-omics, transcriptome, metabolome, microbiome, weaning, *Lactobacillus*, bioinformatics