## Differences in the microbiome and metabolome of Duroc x KHAPS black pigs with heavier and lighter bodyweight

Yu-Chun Lin<sup>1</sup>, Chien-Hsun Huang<sup>2</sup>, Jong-Shian Liou<sup>2</sup>, Bing-Sian Lin<sup>1</sup>, Shen-Chang Chang<sup>3</sup>, Lin-Liang Peng<sup>3</sup>, Chia-Hsuan Chen<sup>1</sup>

<sup>1</sup>Taiwan Livestock Research Institute, Tainan, Taiwan

<sup>2</sup>Bioresource Collection and Research Center, Food Industry Research and Development Institute,

Hsinchu, Taiwan

<sup>3</sup>Kaohsiung Animal Propagation Station, Taiwan Livestock Research Institute, Pingtung, Taiwan.

Duroc x KHAPS black pigs (DK) is a new cross-bred black pig with high meat quality. However, animal phenotypes needed to identify the connection with genomic research. Omic approaches have emerged as powerful tools for better understanding of physiological mechanisms in organisms with different phenotype. The aim of this study is to establish growth-promoting related bio-information of Duroc x KHAPS Black pigs via omic approaches, such as metagenomics, culturomics and metabolomics. To characterize differences in the composition of the fecal microbiota and serum metabolome of DK, fecal and blood samples of 70-day-old piglets with lighter body weight (LBW) and heavier body weight (HBW) were collected from approximately one hundred individuals based on their body weights. The 16S rRNA gene amplicon-based metagenomics and culturomics analyses of fecal samples were conducted. The metabolite analysis was performed using ultra performance liquid chromatography and comparative metabolomics to identify specific metabolites. The results showed the microbiota of the HBW group had significantly higher Firmicutes-to-Bacteroidetes ratio and higher levels of Dorea, Lactobacillus, Roseburia and Solobacterium. The isolates include facultative and strict anaerobes that were isolated from black pig feces samples under different culture conditions. Nearly 400 isolated colonies were identified using MALDI-TOF MS combined with 16S rRNA sequencing, and successfully cultured 22 different bacterial species. In serum metabolomic analysis, 78 peaks showed significant differences between pigs with high and low weight grouping. Among them, 10-17 high-reliability compounds can be identified by mass spectrometry, most of which are related to energy and amino acid metabolism. In this study, we characterized differences in the composition of the fecal microbiota and serum metabolome on different growth rate of DK swine. These data can be used as a reference for evaluating the growth prediction of black pigs. In the future, the isolated strains associated with the body weight of DK, were be evaluated through the pig growth model.

Key words: KHAPS black pig, omics, microbiome, metabolome, culturomics