

## **Modeling microbiome information in the genetic evaluation of finishing traits in pigs**

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The pig gut microbiome consists of a diverse community of microorganisms, including bacteria, viruses, and fungi, that can influence several traits such as growth and feed efficiency. Given its potential impact, incorporating microbiome data into genetic models may increase the accuracy of breeding value estimation for finishing traits. In this study, we aimed to: (1) estimate the proportion of phenotypic variance explained by the microbiome and (2) assess whether including microbiome information improves the prediction accuracy of breeding values for five finishing traits. A total of 1,391 pigs were analyzed, each with microbiome and genomic data from a 50K SNP panel. Phenotypic records were available for backfat carcass (BF), feed intake (FI), average daily gain from birth to slaughter (ADG\_Bir), loin depth (LD), and average daily gain during the finishing period (ADG\_Fin). After quality control, 48.4K SNPs and 4.6K operational taxonomic units (OTUs) were kept. A mixed model was applied to each trait, modeling the animal effect using a genomic relationship matrix (G). Additionally, models either included or excluded a microbial relationship matrix (M), resulting in two models per trait: G\_wM and G\_woM. For validation, data from the last generation (~20%) was masked, and prediction accuracies were estimated using the linear regression method. Except for loin depth (LD), incorporating microbiome data reduced heritability estimates, suggesting a confounding effect between host genetics and microbiome influence on the traits. Furthermore, for most traits, microbiability explained approximately 30% of the phenotypic variance, often equaling or surpassing heritability estimates. For validation analyses, except backfat carcass (BF), including microbiome information improved prediction accuracy for all traits. Compared to G\_woM, relative increases in prediction accuracy ranged from 14% for ADG\_Fin to 21% for ADG\_Bir. In conclusion, this study highlights the important contribution of microbiome information in explaining the phenotypic variance of finishing traits and its potential to improve the accuracy of breeding value estimation. In the presentation, we will explore how these results can be applied in the breeding program and the challenges involved.