Effect of gut microbiota on production traits, interaction with genetics

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Gut microbiome provides a new source of information to improve growth efficiency in swine
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Gut microbiome has been proven to affect pork production via nutritional, physiological, and immunological processes. We studied gut bacteria of the pig from host genetics gut microbiome perspectives, seeking to incorporate such relationship in genetic improvement of pigs. There were 1,205, 1,295, and 1,283 rectal samples collected from pigs at weaning (18.6±1.09 d), 15 weeks post weaning (118.2±1.18 d), and end of feeding trial (196.4±7.86 d). Of these 1,039 animals had samples collected at all 3 time points. The microbiome data was analysed at operational taxonomic unit (OTU) level, including 1,755 OTUs. The animals were also genotyped with the Illumina PorcineSNP60 Beadchip. From our association analyses, 131 OTUs were identified as large contributors to the variance of backfat thickness (BF), live weight (WT), and loin depth (LD), at 3 time points, week 14, 18, and 22, for each phenotypic record. Three OTUs, including OTU17, OTU758, and OTU1163, had the largest contribution to the total variance of the traits. Heritabilities of the 3 OTUs varied between 0.13±0.05 and 0.40±0.06 for OTU17, 0.02±0.03 and 0.20±0.06 for OTU758, 0.02±0.03 and 0.21±0.06 for OTU1163 for the 3 time points. Single nucleotide polymorphisms (SNP) that had consistently large effects on OTU17 and OTU758, at week 15 and end of the test, were also identified on chromosomes 3, 6, and 7. We further included microbiome data in estimating breeding values (BV) for BF and average daily weight gain (ADG) at 22 weeks post-weaning. We found that providing microbiome information, under the form of relatedness among individuals based on similarity of microbial communities, significantly improved the model fit for both BF and ADG, as well as reduced standard error of predictions for BF and ADG breeding values. This analysis was a preliminary attempt to effectively include gut microbiome data to improve the accuracy of BVs in the pork industry. We have plans to incorporate the results from our association analyses in forming microbiome-based and genotype-based relationship matrices to be used in estimating BVs. We have proven interaction between host genetics and its gut microbiome in regulating the host phenotypic records. Such interaction can be used to improve the accuracy of genetic evaluation of the pig.