Effect of gut microbiota on production traits, interaction with genetics

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Gut microbiota is a key contributor to feed use in monogastric species, in particular via the digestion dietary fibres. Molecular techniques are now available to run large studies and decipher the potential of gut microbiota to improve livestock. Studies on human and mice are more advanced: different factors have been demonstrated to influence the gut microbiota composition and functions, including maternal transmission, environment (diet composition and quantity, humidity and heat), age and physiological status. Studies also evaluated if the host controls its gut microbiota. In pigs, chicken and rabbits, microbiota differences between animals of extreme phenotypes within populations, and between lines divergently selected for specific traits, are reported. Other studies reported that some microbiota abundancies are heritable. Linear mixed models have been used to evaluate its contribution to trait variability, or microbiability, with different data (full vs 16S sequencing of gut or faecal contents) and different variance matrices. They showed significant contribution to production traits, reaching more than 30%. However, confounding effects exist, such as the maternal inheritance of the microbiota and the genetic determinism by the host: many studies show reduction of the genetic additive variance, in addition to reduction of the residual variance with microbiability. Specific datasets, testing a given genetic in different environments or using cross-fostering, are used to better understand the relative contribution of each effect (host genetics and microbiota) to the trait variance, and propose solutions to livestock. This work is part of the European Union's H2020 Feed-a-Gene Project (grant 633531).

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.