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Select the Congress: PORC SHOW

Research Domain: Microbiota

Title: Association between pig fecal microbiota, performance, and host genotype.

Short Description: 60 words and indicate language

English presentation. Pig microbiota, performance and genotype of eight cohorts from Ontario and Quebec were analyzed. Two enterotypes were identified when pigs were 11 days old that were associated with distinct microbiota composition. Pigs in one enterotype had better performance during pre-weaning and growing production stages. A 2-Mb span on Chromosome 13 contains twelve SNVs associated with these enterotypes.

Description here.

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Summary:

Thousands of microorganisms colonize the gastrointestinal tract of swine forming a complex community referred to as the microbiota. Swine gut microbiota has been linked to health, growth, and meat quality. Targeting the microbiota by promoting the development of beneficial microbiota communities may be an alternative tool for improving swine health and performance. The relationship between host genotype and gut microbiota is unknown. The objective of this study was to investigate the associations between pig performance with pre-weaning porcine gut microbiota and pig genotype. Eight cohorts of 40 pigs (n = 320) from distinct farrowing sources in Ontario and Quebec were included in this study. Tissue samples collected from pigs were used to genotype for 63K single nucleotide variants (SNVs). Rectal swabs collected 11 days after birth were subjected to DNA extraction and MiSeq Illumina sequencing of the V3 - V4 regions of 16S rRNA genes to identify microbiota. Pre-weaning averaged daily gain (ADG) from within a few days of birth until one day before weaning and growing-stage heart girth daily gain from ~60 – 95 days of age were used as performance metrics.

Based on beta diversity, two distinct enterotypes including enterotype 2A (n = 211) and enterotype 2B (n = 49) were identified. Fecal microbiota classified into enterotype 2B had higher abundance of the genera *Phascolarctobacterium* and *Prevotella* ($p < 0.05$). Piglets that exhibited enterotype 2A had better

performance during both the pre-weaning and growing stages. A genome-wide association study identified 57 SNVs associated with microbiota enterotype. Notably, a 2 Mb span on Chromosome 13 contains 12 SNVs that were associated with microbiota enterotype ($p < 1.0E-5$). Two candidate genes are located near the span: LMCD1 and GRM7. These represent candidate genes associated with microbiota community.

These data show that piglet exhibit one of two enterotypes, that appear at 11 days of age. These enterotypes are compositionally distinct and associated with performance in the suckling and growing production stage. Further one position on chromosome 13 seems to be associated with microbiota enterotypes. These findings may help to understand a genetic component to microbiota and performance. Candidate genes that are associated with microbiota should be considered when practicing selective breeding within the pork industry. Further identification of external variables that can be used to manipulate microbiota variation to improve swine health and performance are necessary such as antibiotic use, sow factors, and rearing conditions. The project findings will decrease antimicrobial use, increase animal welfare, and have positive economic impacts for the swine industry in Canada.