

4C-106: Impact of pig gut microbiology on pig nutrition and health

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Aims and Objectives

- Identify optimal methodology for extraction of DNA from manure samples.
- Conduct large scale next generation sequencing on 95 pigbal trial samples using the optimal extraction technique and identify linkages between microbial community characteristics, feed and other factors, and nutritional outcomes.

Key Findings

- Optimal extraction technique identified. Mismatch of sample-technique results in null rather than false outcomes.
- Gut community dominated by firmicutes (common anaerobic bacteria).
- Diet and age major predictor of gut community, with wheat diets clustering and having lower diversity.
- Community diversity decreased through age and metabolism shifted towards carbohydrate and lipid capability.
- Nutritional outcomes (weight gain) strongly correlated with microbiome, but there was no unexplained impact apart from those due to age and diet.
- Hence microbiome is an excellent predictor of nutritional state, but is not a direct factor in comparison with diet or age.
- Predictors of low weight gain included *Clostridia*
- Antibiotics cause measurable change in specific microbial populations, but does not act as overall driver.
- Pig sample size (16 pigs across 4 feeds) too small to identify correlation between microbiome and health indicators.

Application to Industry

- It is unlikely that microbiome can be directly manipulated to achieve better nutritional outcomes (due to lack of unexplained correlation).
- Microbiome markers help explain mechanism of diet on nutritional outcomes and may be better used to better design optimal feeds, particularly across pig age. An example may be using the identified markers of positive nutritional outcomes as evaluated in this study, and varying feed to enhance these measures, particularly at different ages.