



Pig gut microbiome project: Characterization of the core gut microbiome associated with pig health and performance: Towards fecal diagnostics and microbiome therapy

Vahab Farzan, University of Guelph

Andrew Van Kessel, University of Saskatchewan

Ben Willing, University of Alberta

Why is this project important?

There is ample evidence that the gut microbiome has a great influence on disease resistance, health and performance of humans and domestic animals, including pigs. In fact, the mechanism-of-action of many commercially available intervention strategies and products designed to promote health and performance in pigs and replace antibiotics, is associated with an ability to modify the composition of the gut microbiome.

The application of molecular tools has allowed scientists to demonstrate that the gut microbiome is abundant, complex, and highly dynamic, influenced by a combination of genetic, maternal and environmental factors. This complexity and significant variation is a major challenge in identifying core members of the gut microbial communities that are consistently associated with improved health and performance, or, alternatively, with infection and poor performance. To date, there is no clear consensus on the composition of a healthy microbiome that can guide product developers as well as those in the industry who are charged with improving pig health and performance.

What will be the benefit of this research?

.This project fulfills the swine innovation research priorities to optimize the microbiome in newborn pigs via dam and progeny and to determine the role of nutrition in optimizing the gut microbiome and immunity. To that end, researchers will characterize the role of the sow microbiome on development of the gut microbiome in pre- and post-weaning piglets, and its impact on immunity, growth performance and disease resistance. The research will also explore the impact of sow nutrition, sow management and pig genotype on piglets' gut microbiomes.

The knowledge of the core microbiome produced by this research will directly inform development of novel products consisting of a cocktail of core members. Exposing neonatal piglets to a core microbiome cocktail could help stabilize or “normalize” succession among piglets, minimizing enteric infection and diarrheal diseases during the first few weeks of a piglet’s life. This will decrease production loss and increase feed efficiency, while reducing antimicrobial use and drug resistance in swine herds. A first step in developing such an approach is the determination of the core microbiome, which will be achieved in this project.

What will be the benefit of this research?

This project addresses an industry priority to optimize the microbiome in newborn pigs via the dam and progeny and to determine the role of nutrition in optimizing the gut microbiome and immunity.

The knowledge of the core microbiome produced by this research will directly inform the development of novel products consisting of a cocktail of core members. Exposing neonatal piglets to a core microbiome cocktail could help stabilize or “normalize” succession among piglets, minimizing enteric infection and diarrheal diseases during the first few weeks of a piglet’s life. This will decrease production loss and increase feed efficiency, while reducing antimicrobial use and drug resistance in swine herds. A first step in developing such an approach is the determination of the core microbiome, which will be achieved in this project.

What was done?

The microbiota of 1140 fecal samples, collected from 360 piglets and from 90 sows were analyzed. These animals were reared under “raised without antibiotics” or conventional systems at four timepoints, from birth to post-weaning, from nine farrowing sources in Ontario and Quebec. Additionally, the microbiota of fecal and vaginal samples collected from 90 sows were analyzed. Piglets were genotyped for a panel of approximately 63,000 single nucleotide variants, and their growth performance during pre-weaning and growing stages was measured. Three successive clusters of microbiota were identified across the piglets’ early lives.

Further, sow microbes accounted for about 30% of microbes found in piglet fecal microbiota. Lastly, genome-wide association studies identified associations between pig genotype and microbiota diversity, and interactions between microbiota and genotype on pig performance. These findings may help identify factors used to manipulate gut microbiota to improve health and performance of pigs on commercial farms.

For the observational studies in swine genetics nucleus herds, researchers have agreements with Fast Genetics, Hypor and Topigs Norsvin for access, and have completed sampling for two of the three lines. An initial examination of performance results suggested these pigs represent a valuable dataset with significant variation in performance.

Collaborators

Denise Beaulieu John Harding Janet Hill Matthew Links	University of Saskatchewan
Matheus Costa	Utrecht University
Robert Friendship Brandon Lillie	University of Guelph
Martin Nyachoti Chengbo Yang	University of Manitoba

Project status

Completed in 2023.

Additional resources &
information about this project

R&D Featured Articles by Swine Innovation Porc

- [Where Does the Gut Go From Here?](#)
July 30, 2020

Farmscape interviews

- [Researchers Look to Pig Gut Microbiome to Improve Health and Performance Without Antibiotics](#)
May 25, 2023

Financial support for this project

This project is part of the Swine Cluster 3 (2018-2023) research program, made possible through financial support from Agriculture and Agri-Food Canada's Canadian Agricultural Partnership, eight provincial pork producer organizations and over 30 industry partners. [Click here to learn more about the financial partners for Swine Cluster 3.](#)