Association between pig performance, pre-weaning fecal microbiota, and genotype

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Background

- The gut microbiota is made of thousands of organisms which colonize the gastrointestinal tract, aiding in metabolism[1].
- External factors such as diet, housing, antibiotic use, and sow attributes are associated with microbiota[2,3].
- Genotype has been linked to average daily gain and daily food intake, but the link between genotype and microbiota is largely understudied[4].

Objective

Investigate associations between pig performance, pre-weaning fecal microbiota, and genotype.

Methods

Study Population

8 cohorts of 40 pigs each from ON and QC

Sample Collection

Fecal Sample



Age = 11 days old

1. Bacterial DNA Extraction



V3/V4 region of 16S rRNA gene

2. DNA Sequencing



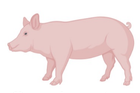
3. Microbial Community Analysis[5]

Performance Metrics



Pre-weaning average daily gain (ADG)

Birth to weaning



Growing stage heart girth daily gain (HGDG)

~60 to 97 days old

Tissue Sample



1. Host DNA Extraction



2. SNV Identification



63 K SNVs

Bioinformatics analysis to integrate sample types

Results & Discussion

Pre-weaning enterotypes

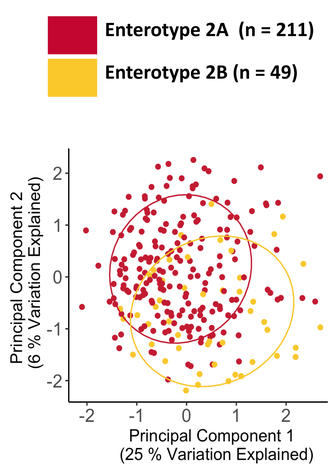


Figure 1. Biplot of Aitchison's Distance between fecal samples, identifying 2 clusters with different beta diversity ($p < 0.05$)

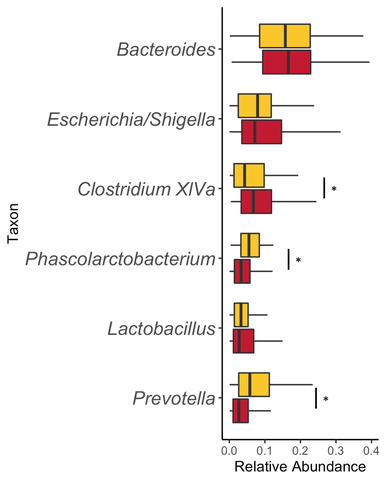


Figure 2. Relative abundance of top genera within each enterotype. (* denotes $p < 0.05$)

Enterotypes and performance

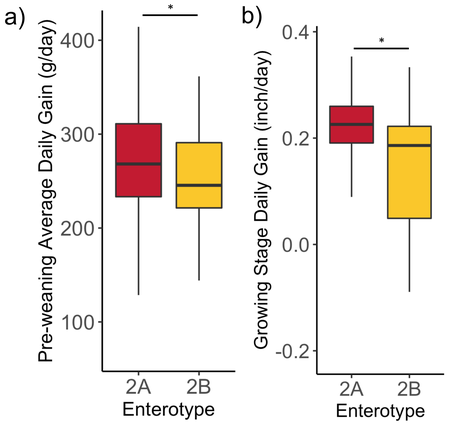


Figure 3. Comparison of pig performance using **a)** pre-weaning average daily gain, and **b)** growing stage heart girth daily gain between two enterotypes (* denotes $p < 0.05$)

Enterotypes and genotype

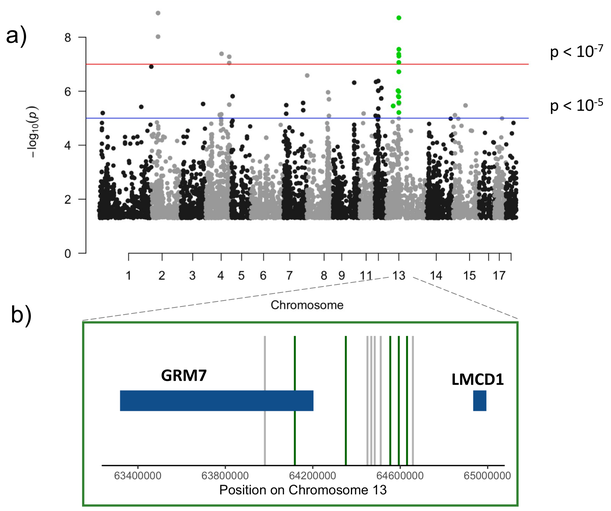


Figure 4. a) Manhattan plot of genome-wide association study with higher points indicating a stronger association, and **b)** illustration of subsection of Chromosome 13 showing 5 significant SNVs ($p < 10^{-7}$;green), 7 suggestive SNVs ($p < 10^{-5}$; grey), and nearby genes (blue rectangle)

Table 1. Pig genome locations significantly associated with enterotype and nearby genes to each SNV

Chromosome	SNP Position (Mb)	Nearest Gene	Gene Position
2	34.8	*LUZP2*	+ 53484
	34.9		+ 27126
4	81.7	*NME7*	0 intron
	121.4	Unnamed	+ 38244
	121.4		+ 58475
13	64.1		0 intron
	64.3	*GRM7*	- 147962
	64.5		- 351214
	64.5	*LMCD1*	+ 340266
	64.6		+ 302569

Gene Functional Information

LUZP2: *leucine zipper protein 2*
- Unknown function

NME7: *NME/NM23 family member 7*
- Functional component of gamma-tubulin ring complex[6].

GRM7: *glutamate metabotropic receptor 7*
- G-protein coupled-receptor signaling pathway; associated with epilepsy, microcephaly and cerebral atrophy in humans[7].

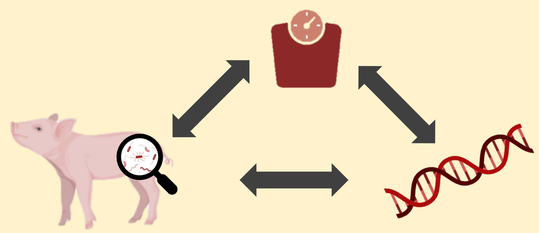
LMCD1: *LIM and cysteine rich domains 1*
- Regulates cell growth, differentiation and interaction with structural proteins; associated with muscle cell proliferation[8].

Conclusion

- Swine exhibit two compositionally distinct enterotypes in early life that are associated with growth performance pre-weaning and at a later production stage.
- Enterotype 2B exhibits lower abundance of the genus *Prevotella* which may result from increased levels of dietary fibre through creep-feed consumption during the nursery stage, leading to poorer performance[9].
- Enterotypes are associated with a region on Chromosome 13 which contained 5 significant ($p < 10^{-7}$) and 7 suggestive ($p < 10^{-5}$) SNVs.

Take Home

- Pig fecal microbiota is associated with performance and genotype, suggesting it may be a key consideration when improving pig production.
- Promoting gut colonization with beneficial microbiota in early stages is a potentially powerful tool for improving swine health, increasing growth and decreasing production costs.



References

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Acknowledgements

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