Genetic parameters of disease in growing pigs under a polymicrobial natural disease challenge

Usamah Kabuye[1,2], John C. S. Harding[3], Michael K. Dyck[4], Frederic Fortin[5], Graham S. Plastow[4], PigGen Canada[6] and Jack C. M. Dekkers[2]

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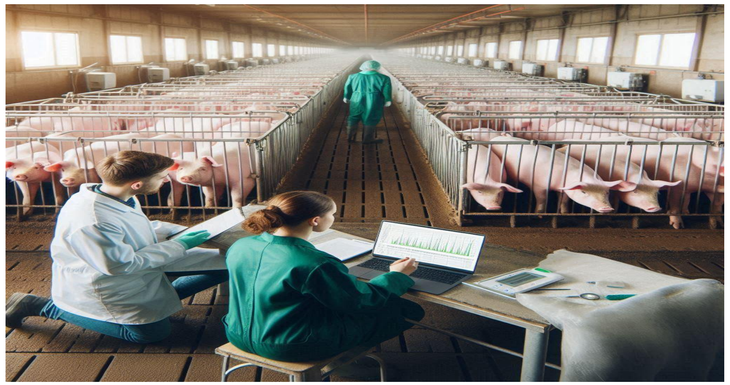
Introduction

- **Selection** in most pig breeding programs is conducted in high-health nucleus herds, but pigs typically encounter multiple pathogens in commercial herds.



- **Knowledge gap** of genetic parameters of disease related traits under a polymicrobial disease challenge still exists.
- **Genetic parameters** e.g., **heritabilities** and **genetic correlations** between traits are key to strategic animal breeding.

Objective

- Estimate genetic parameters for treatment and mortality associated with specific diseases of growing pigs under a severe natural polymicrobial disease challenge.

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Materials and methods

A three-phase natural polymicrobial disease challenge (Putz et al.,2019, Frontiers in Genetics)

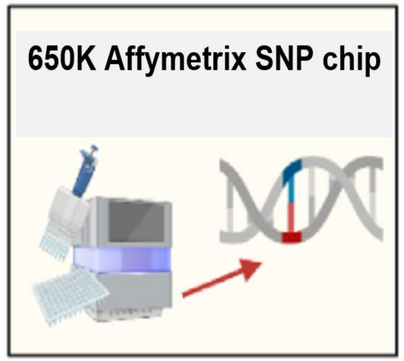
PigGen Canada	Natural challenge wean-to-finish protocol at CDPQ, Québec, Canada			
Multiplier herds	~21days old		~40 days old	~70 days old ~180 days old
Farrowing – weaning (21-day old barrows)	qNursery (~19 days)	1 km north	cNursery (~27 days)	Finisher (~100 days)
Biosecure	Biosecure		Natural polymicrobial disease challenge through continuous flow (Common pathogens in commercial pig farms)	

Birth — Weaning — Market

Disease resilience data collection

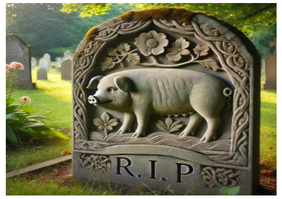
Animals and genotyping

- 4,095 Y × LR barrows
- 66 batches (each ~60 -75 pigs)



Phenotypic data - Individual health treatments and mortality records categorized as:

1. Meningitis
2. Respiratory distress
3. Scours
4. Unthriftiness
5. Other viral and/or bacterial infections



Variance Component Estimation

- Single trait and bivariate analyses using generalized and linear mixed models with genomic relationships using ASReml (4.2)

Model: $y_{ijklm} = Batch_i + EntryAge_{ijklm} + Pen_k + Sow_{ijkl} + Pig(grm)_{ijklm} + e_{ijklm}$

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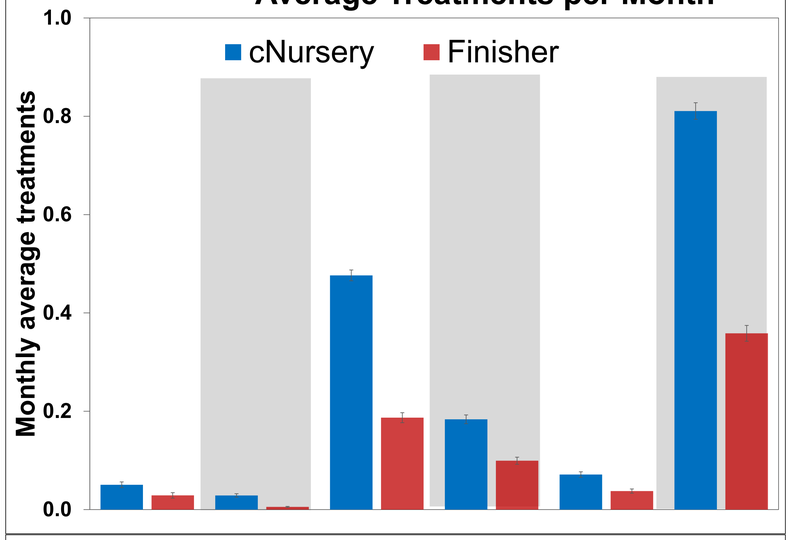
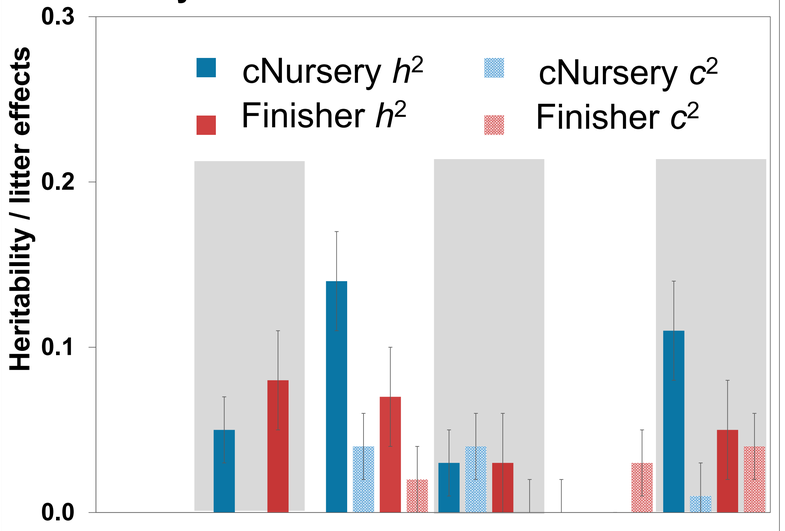
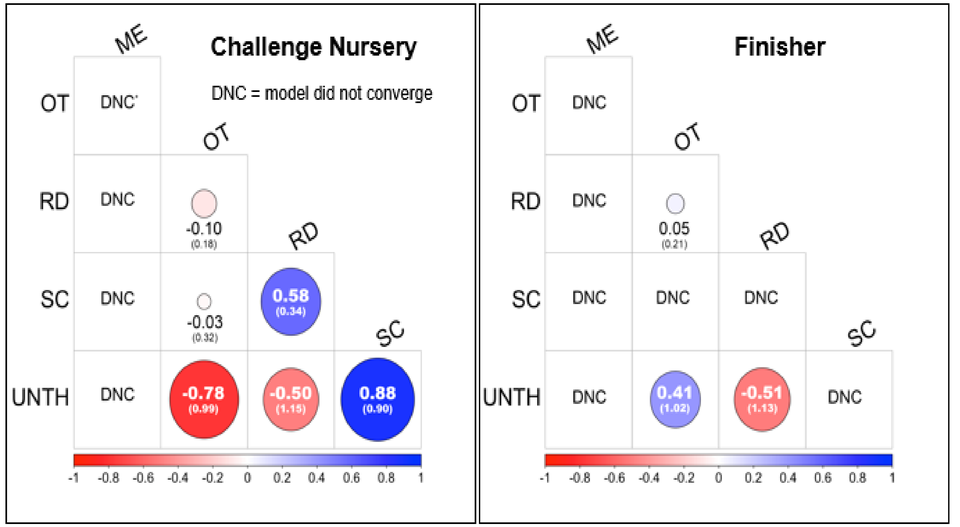
Average Treatments per Month



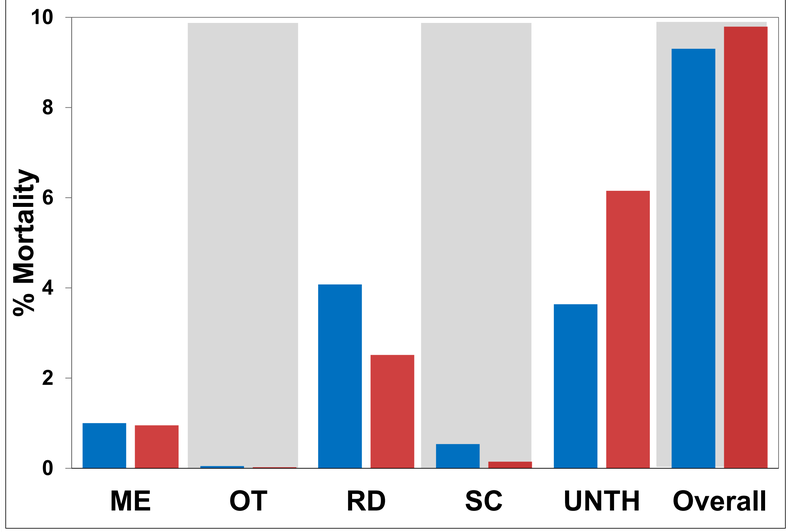
Heritability and Litter Effects for Treatment Rates



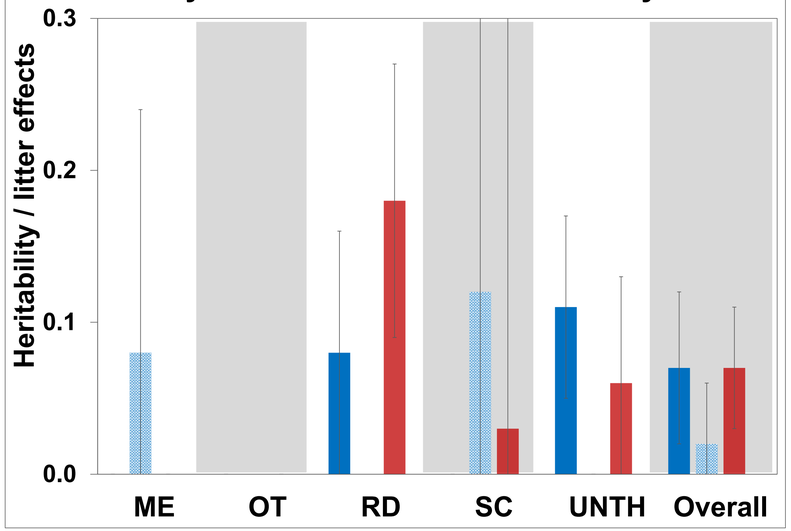
Estimates of Genetic Correlations (SE) between Treatment Rates



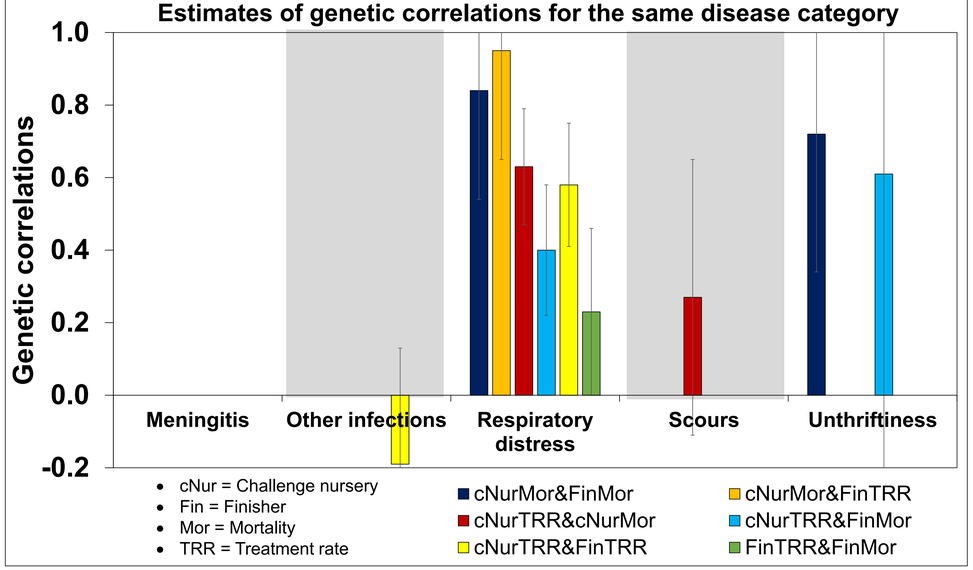
Incidence of Mortalities



Heritability and Litter Effects for Mortality Traits



Estimates of genetic correlations for the same disease category



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Discussion

- Heritability estimates for treatment rate and mortality were generally higher in the challenge nursery than in the finisher.
- Compared to other diseases, respiratory distress treatment rate and mortality tended to have higher heritability estimates both in the nursery and finisher.
- Litter effects were generally low in both in the nursery and finisher but stronger in the nursery.
- Genetic correlation estimates for respiratory distress among treatment rate and mortality in the nursery and finisher were generally positive.
- Corresponding genetic correlation estimates for other disease categories were either moderately negative, not positive definite, or the model did not converge.

Conclusions

- Respiratory distress treatment rate and mortality are substantially influenced by genetics, making it a key target for genetic selection.
- Litter effects are critical in early life stages but diminish as the pigs mature.
- Selection strategies to improve health treatment and mortality traits should be balanced to avoid unintended consequences.
- Genetic parameters provide the roadmap for breeding programs, and this study provides valuable information to breed for disease resilience.