Genetic parameters of disease in growing pigs under a polymicrobial natural disease challenge
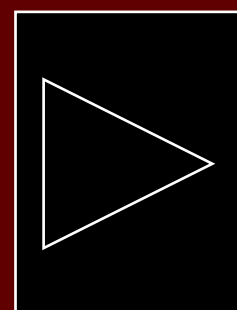
Usamah Kabuye[1,2], John C. S. Harding[3], Michael K. Dyck[4], Frederic Fortin[5], Graham S. Plastow[4], PigGen Canada[6] and Jack C. M. Dekkers[2]

[1]Interdepartmental Genetics and Genomics, Iowa State University, [2]Department of Animal Science, Iowa State University, [3]Department of Large Animal Clinical Science, University of Saskatchewan, [4]Department of Agricultural, Food and Nutritional Science, University of Alberta, [5]Centre de développement du porc du Québec, [6]PigGen Canada Industry Consortium
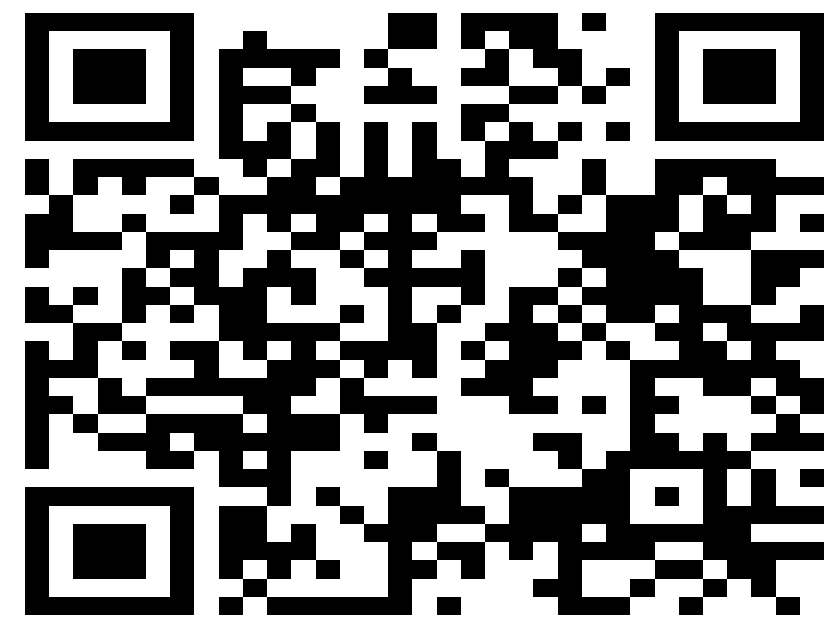
Introduction

- **Selection** in most pig breeding programs is conducted in high-health nucleus herds, but pigs typically encounter multiple pathogens in commercial herds.
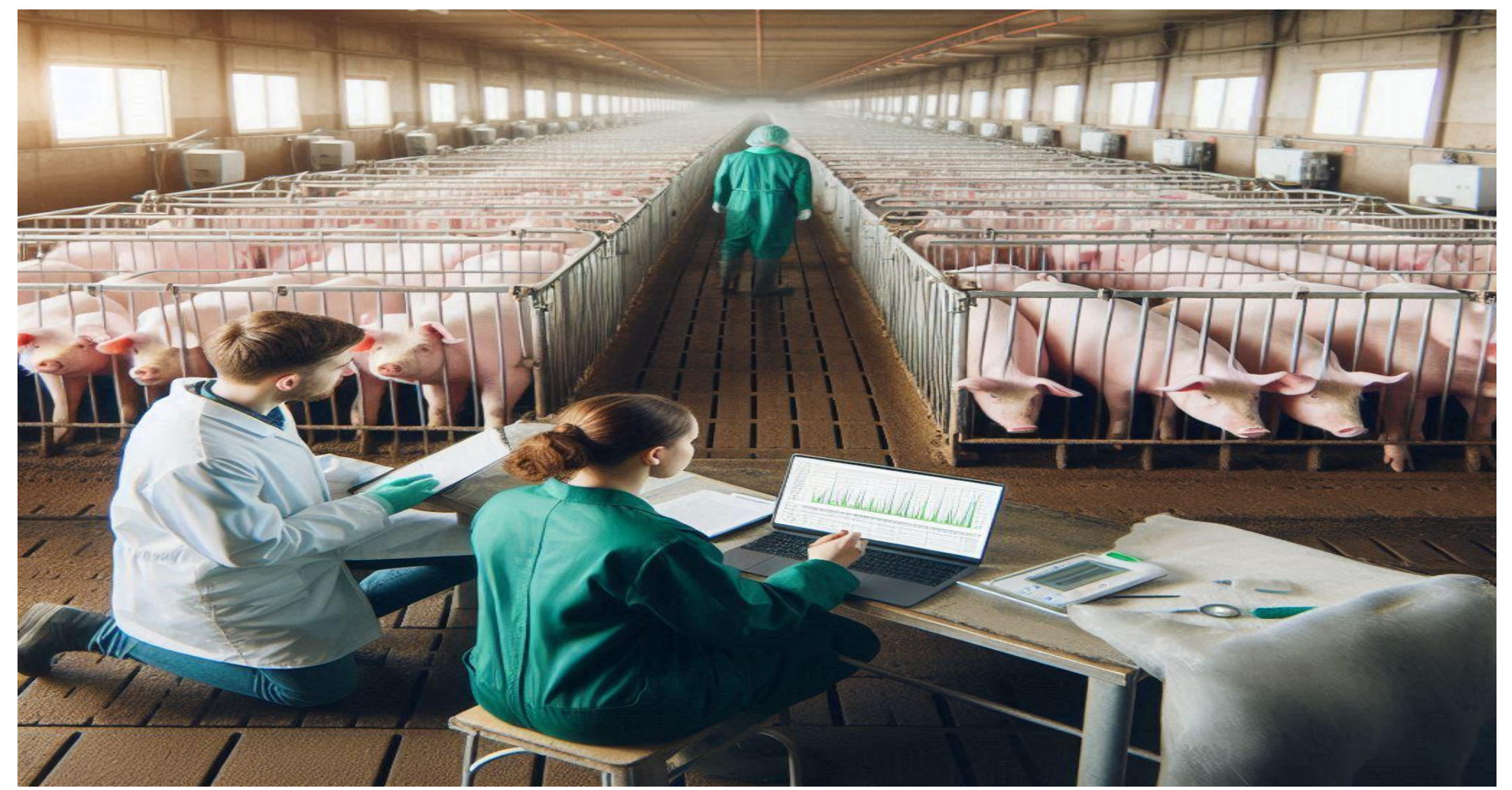
- **Knowledge gap** of genetic parameters of disease related traits under a polymicrobial disease challenge still exists
- **Genetic parameters** e.g., **heritability, genetic correlation** between traits are key to strategic animal breeding.
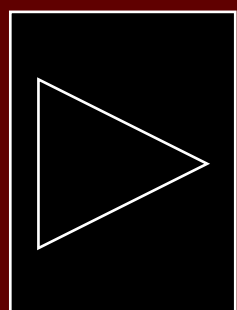
Objective

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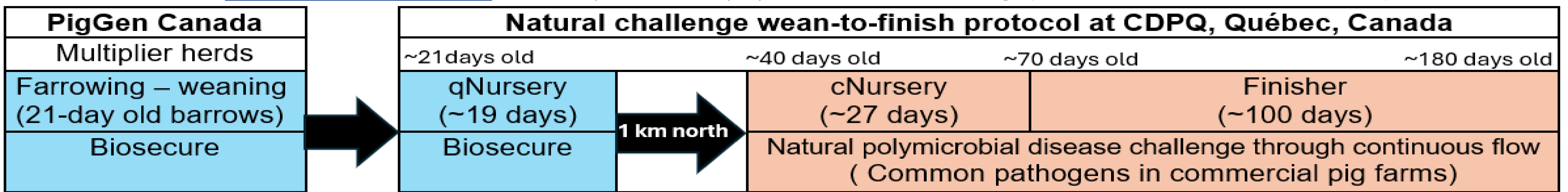
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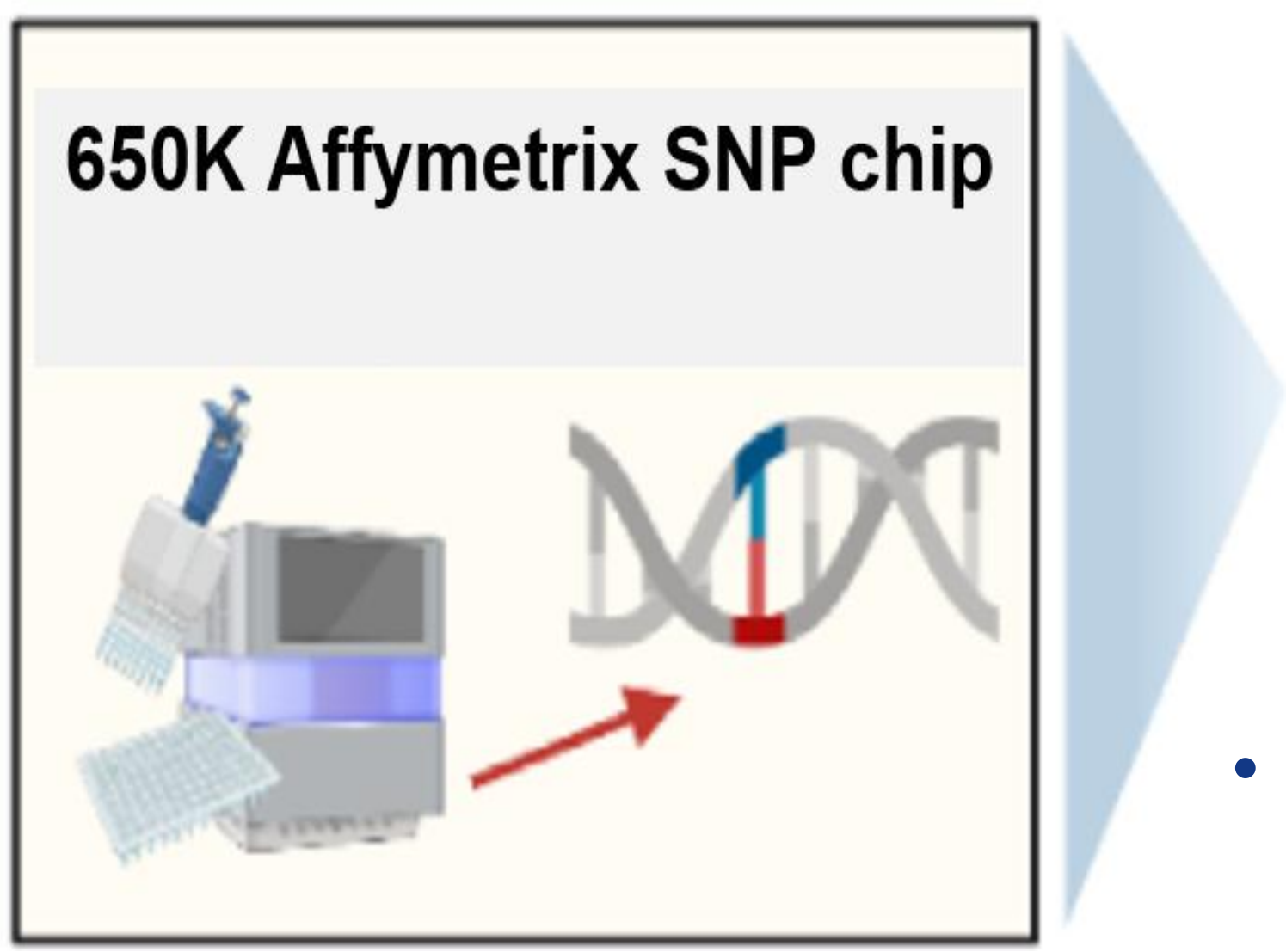
Materials and methods   A three-phase natural polymicrobial disease challenge (Putz et al.,2019, Frontiers in Genetics)

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)	cNursery (~27 days)	Finisher (~100 days)
Biosecure	Biosecure 1 km north	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)

650K Affymetrix SNP chip

Phenotypic data - Individual health treatments and mortality records categorized as:
1. Meningitis
2. Respiratory distress
3. Scours
4. Unthriftiness
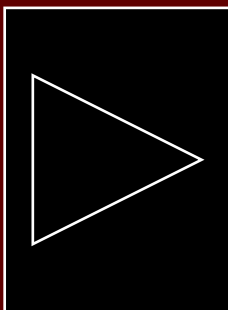5. Other viral and/or bacterial infections

Variance Component Estimation

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

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

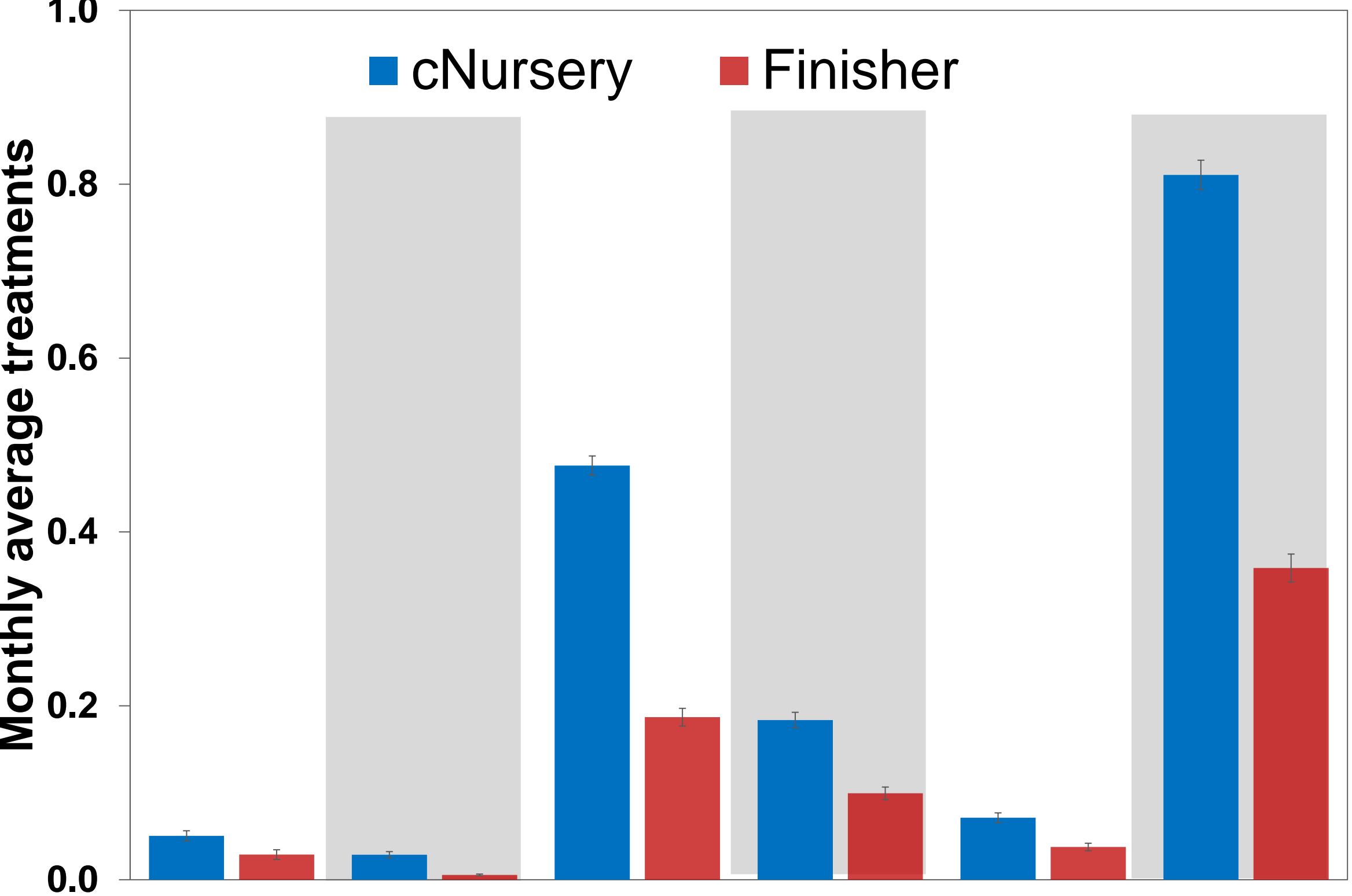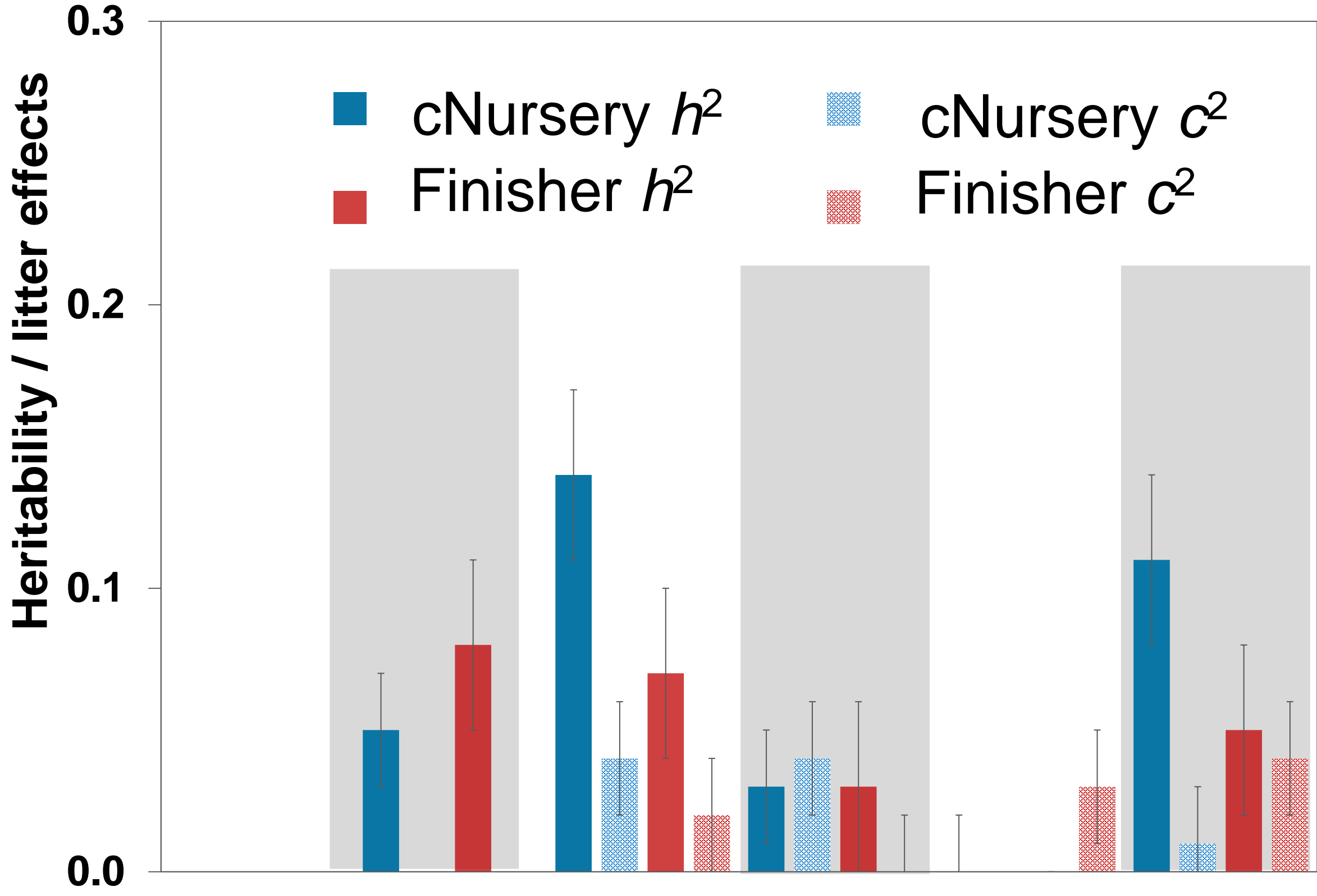# Genetic parameters of disease in growing pigs under a polymicrobial natural disease challenge

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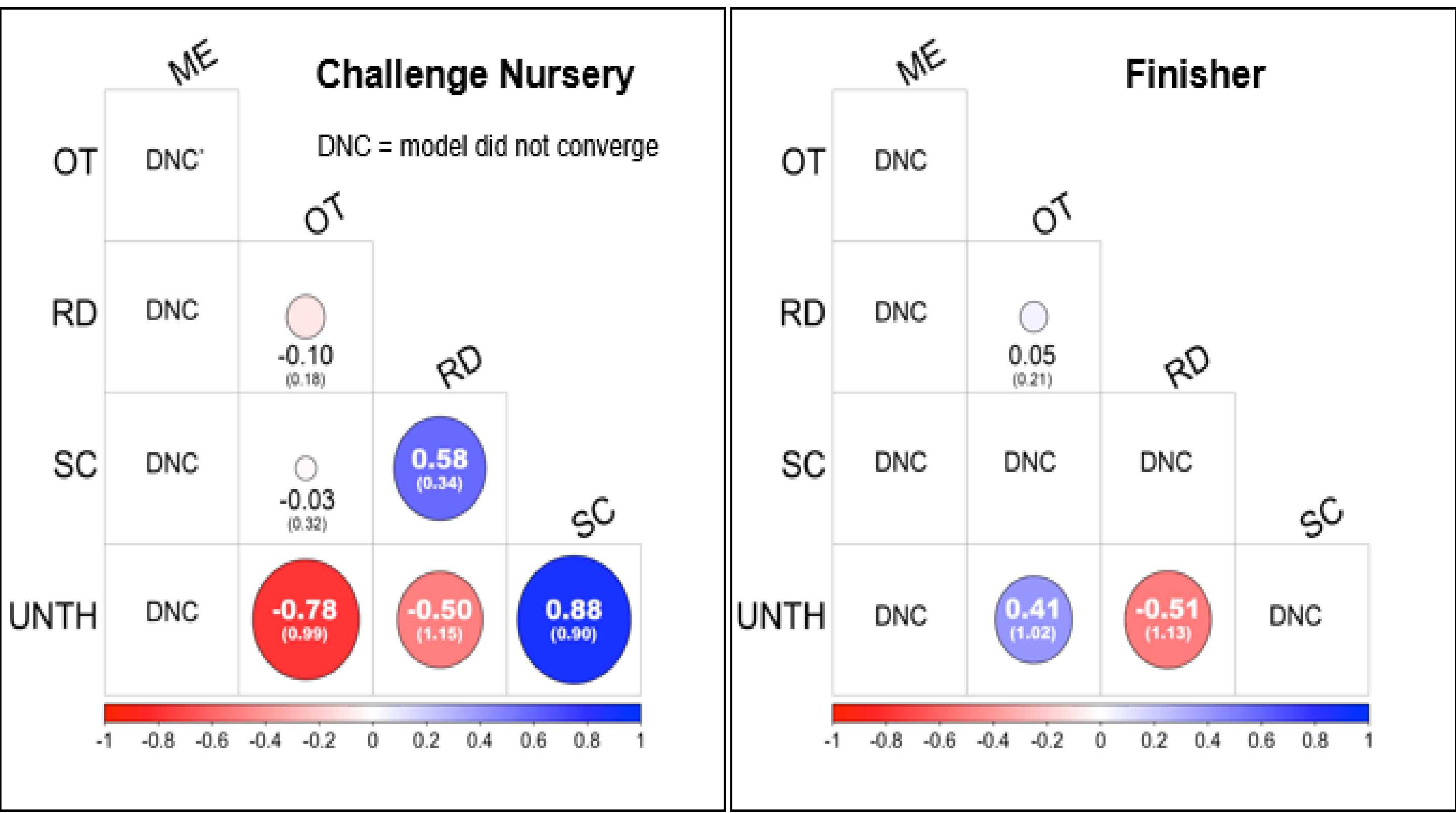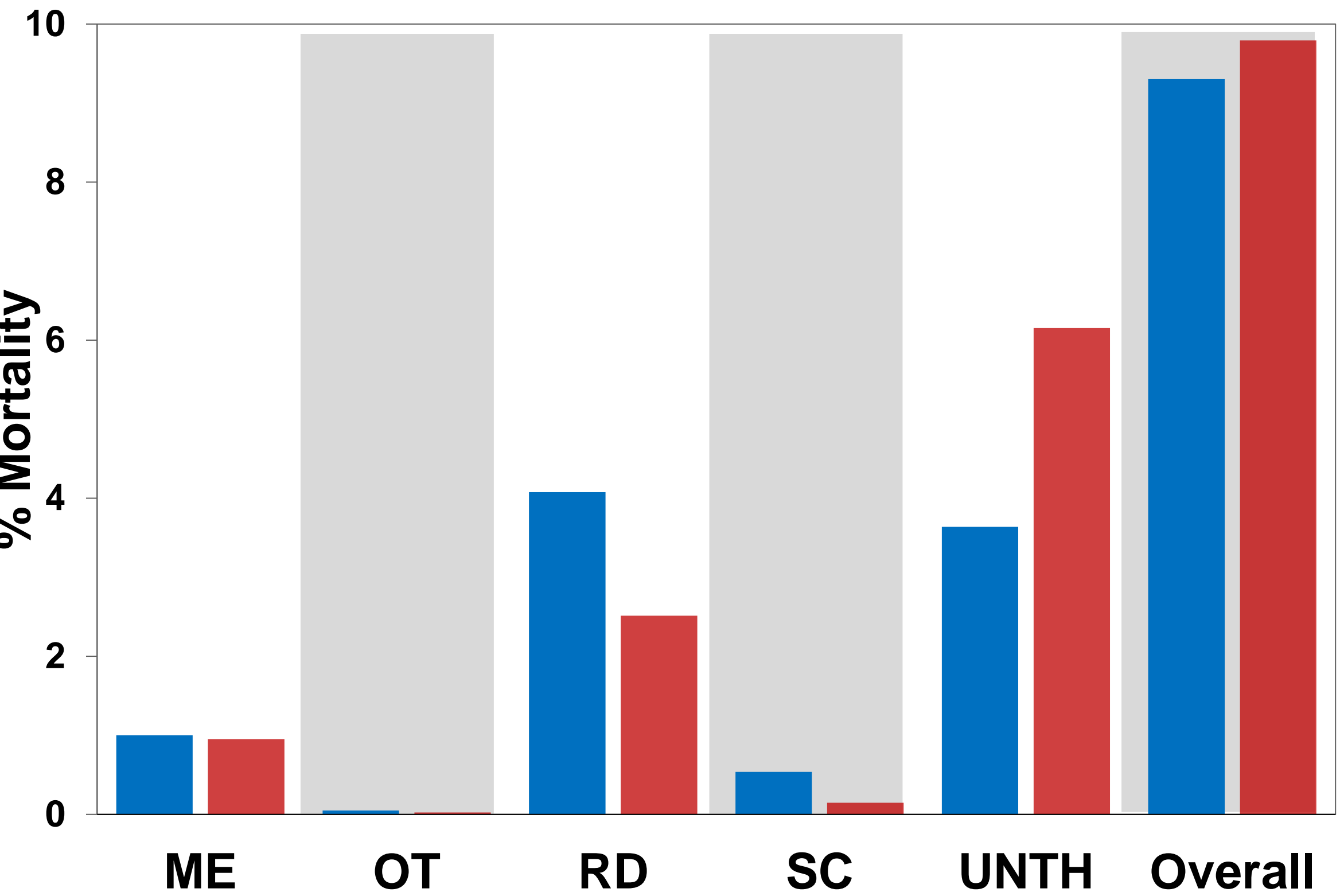
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Key points

- 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.
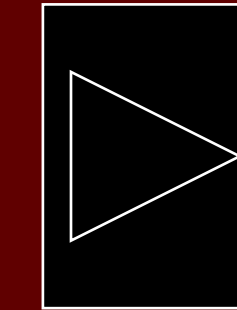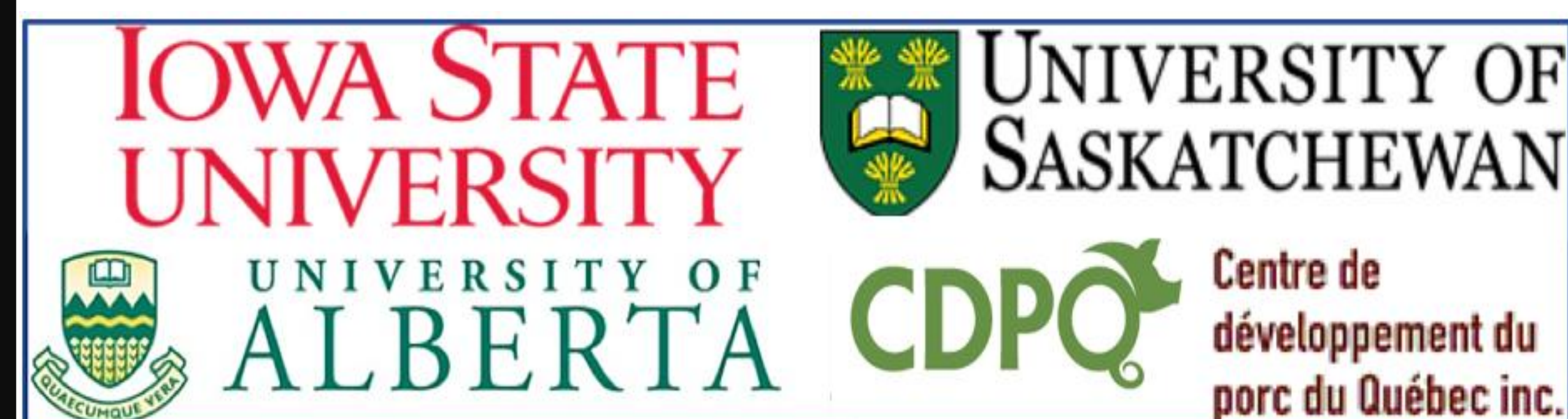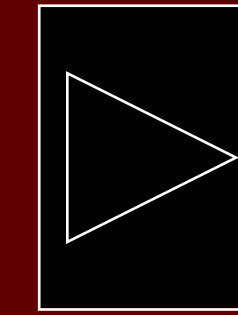
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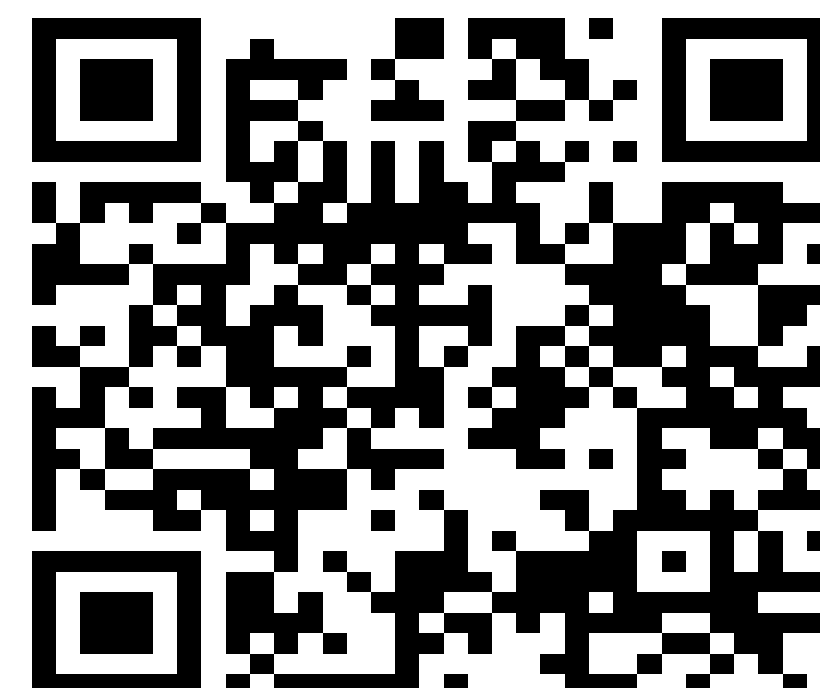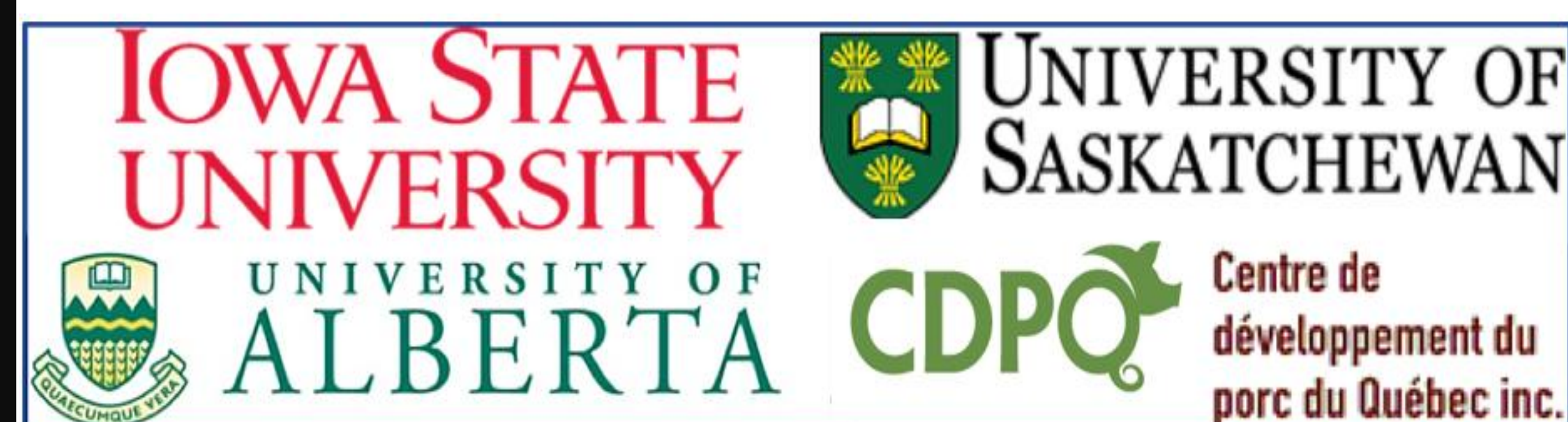
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Next steps

- Genome Wide Association Studies

- Gene Set Enrichment Analysis

- Identifying candidate genes
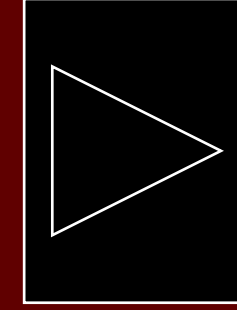
- Manuscript preparation

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Acknowledgements

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- Dr. Jack Dekkers

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- Dr. Jack Dekkers
- Dr. Juan Pedro Steibel
- Dr. Austin Putz
- Dr. Daniel Linhares
- Dr. Chong Wang

Co-authors:
- John Harding
- Michael Dyck
- Frederic Fortin
- Graham Plastow
- PigGen Canada
- Jack Dekkers