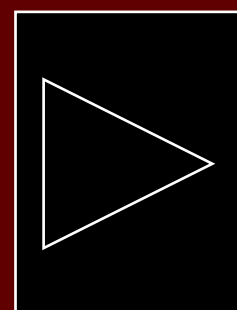




# Genetic parameters of disease in growing pigs under a polymicrobial natural disease challenge



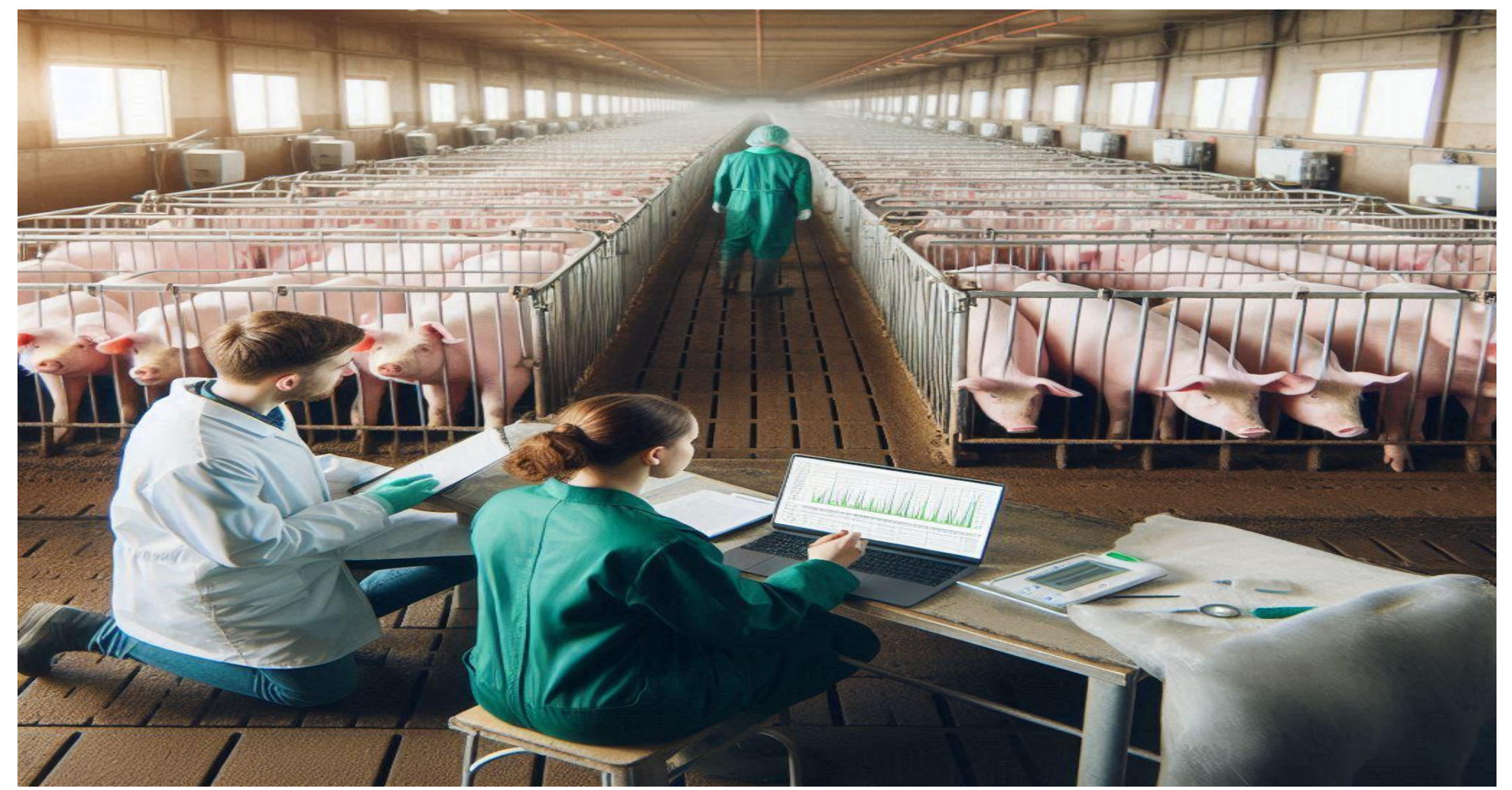
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Usamah Kabuye<sup>1,2</sup>, John C. S. Harding<sup>3</sup>, Michael K. Dyck<sup>4</sup>, Frederic Fortin<sup>5</sup>, Graham S. Plastow<sup>4</sup>, PigGen Canada<sup>6</sup> and Jack C. M. Dekkers<sup>2</sup>

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

## Introduction

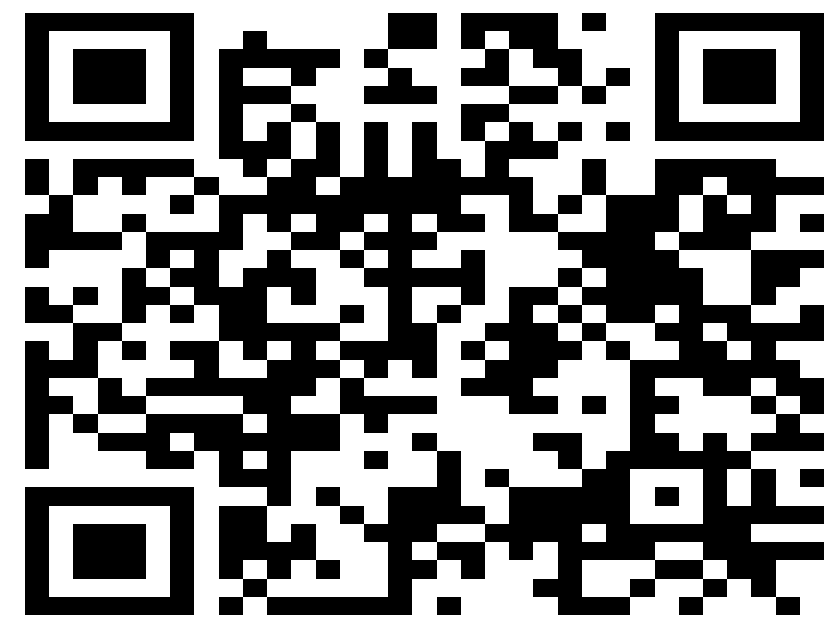
- **Selection** in most pig breeding programs is conducted in high-health nucleus herds, but pigs typically encounter multiple pathogens in commercial herds.



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

## Objective

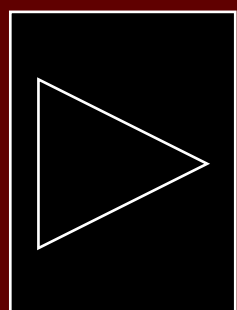
- Estimate genetic parameters for treatment and mortality associated with specific diseases of growing pigs under a severe natural polymicrobial disease challenge







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

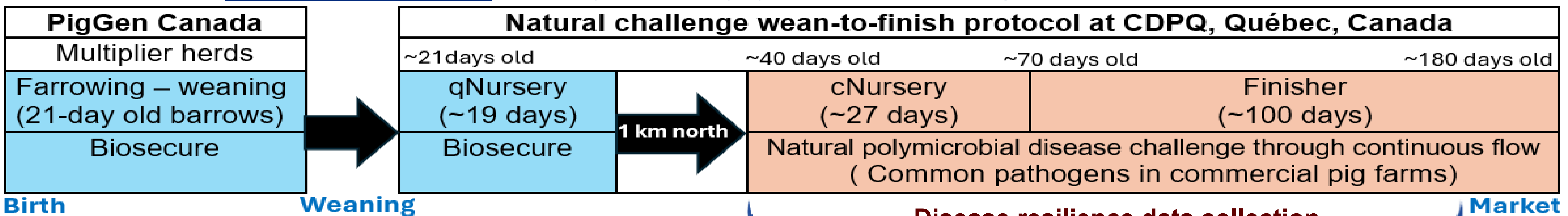


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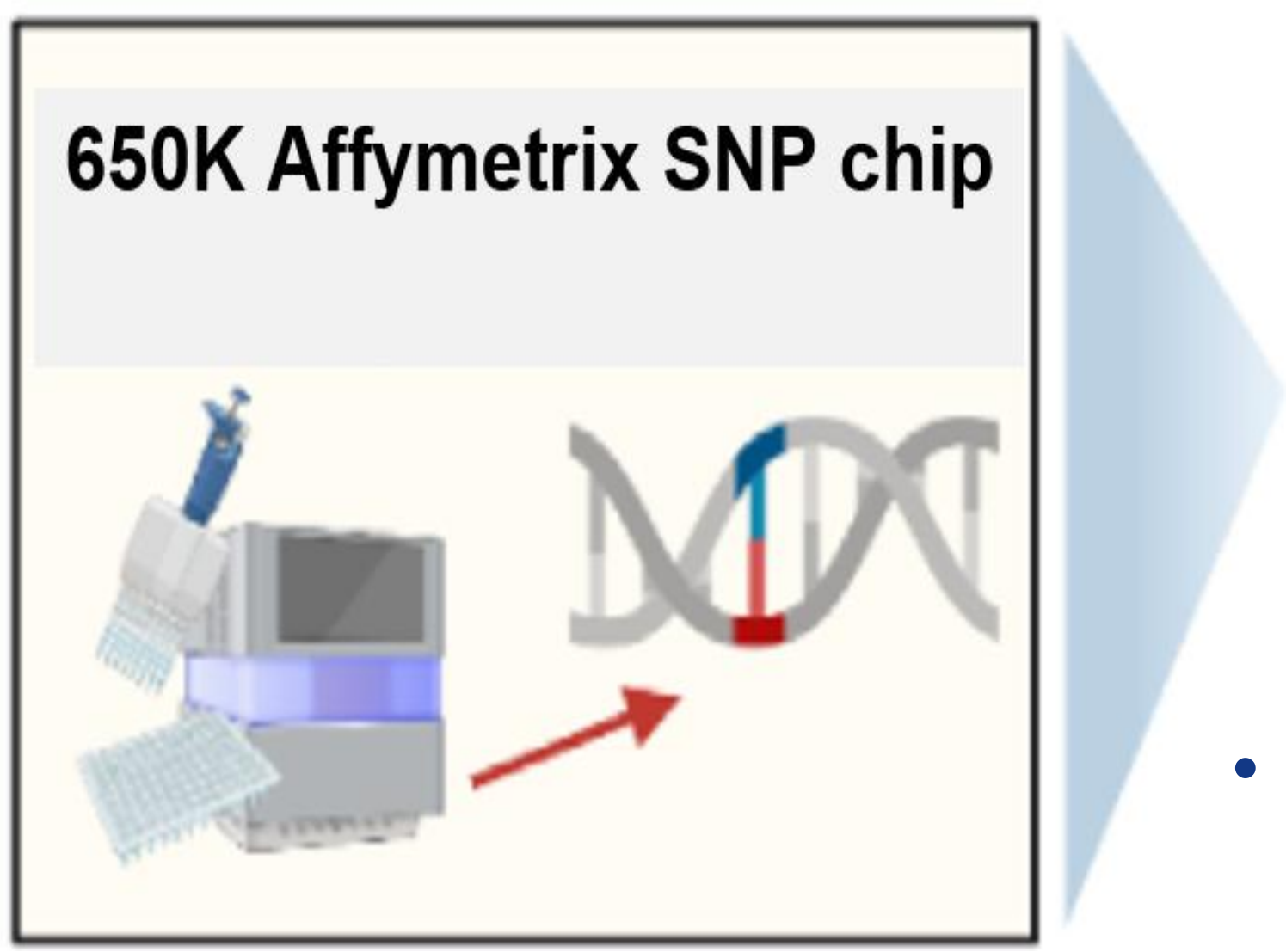
<sup>1</sup>Interdepartmental Genetics and Genomics, Iowa State University, <sup>2</sup>Department of Animal Science, Iowa State University, <sup>3</sup>Department of Large Animal Clinical Science, University of Saskatchewan, <sup>4</sup>Department of Agricultural, Food and Nutritional Science, University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

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



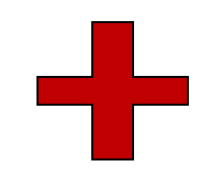
### Animals and genotyping

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



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

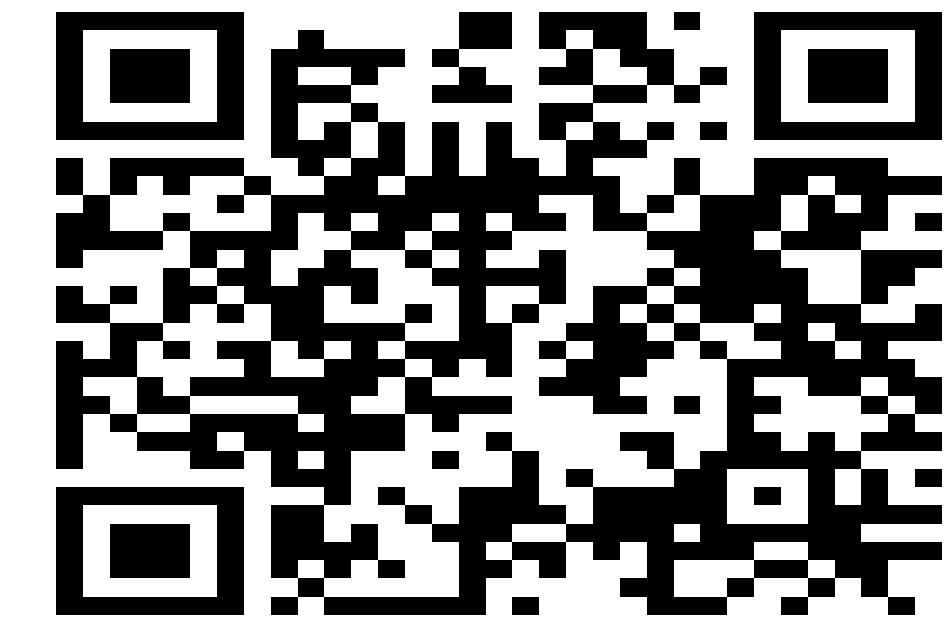
- 1.Meningitis
- 2.Respiratory distress
- 3.Scours
- 4.Unthriftiness
- 5.Other viral and/or bacterial infections



### Variance Component Estimation

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

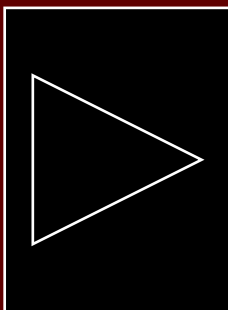
**Model:**  $y_{ijklm} = \text{Batch}_i + \text{EntryAge}_{ijklm} + \text{Pen}_k + \text{Sow}_{ijkl} + \text{Pig}(\text{grm})_{ijklm} + e_{ijklm}$







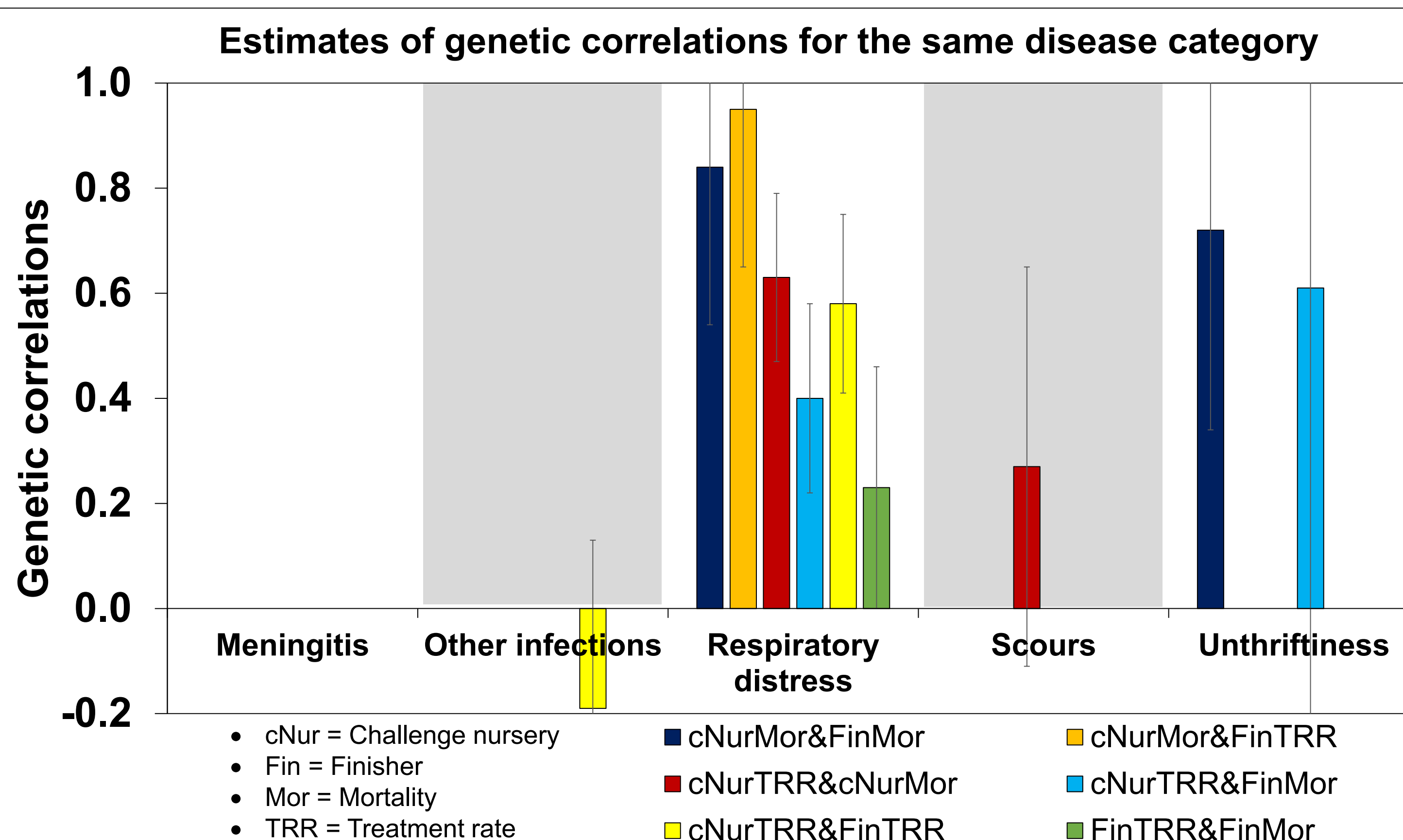
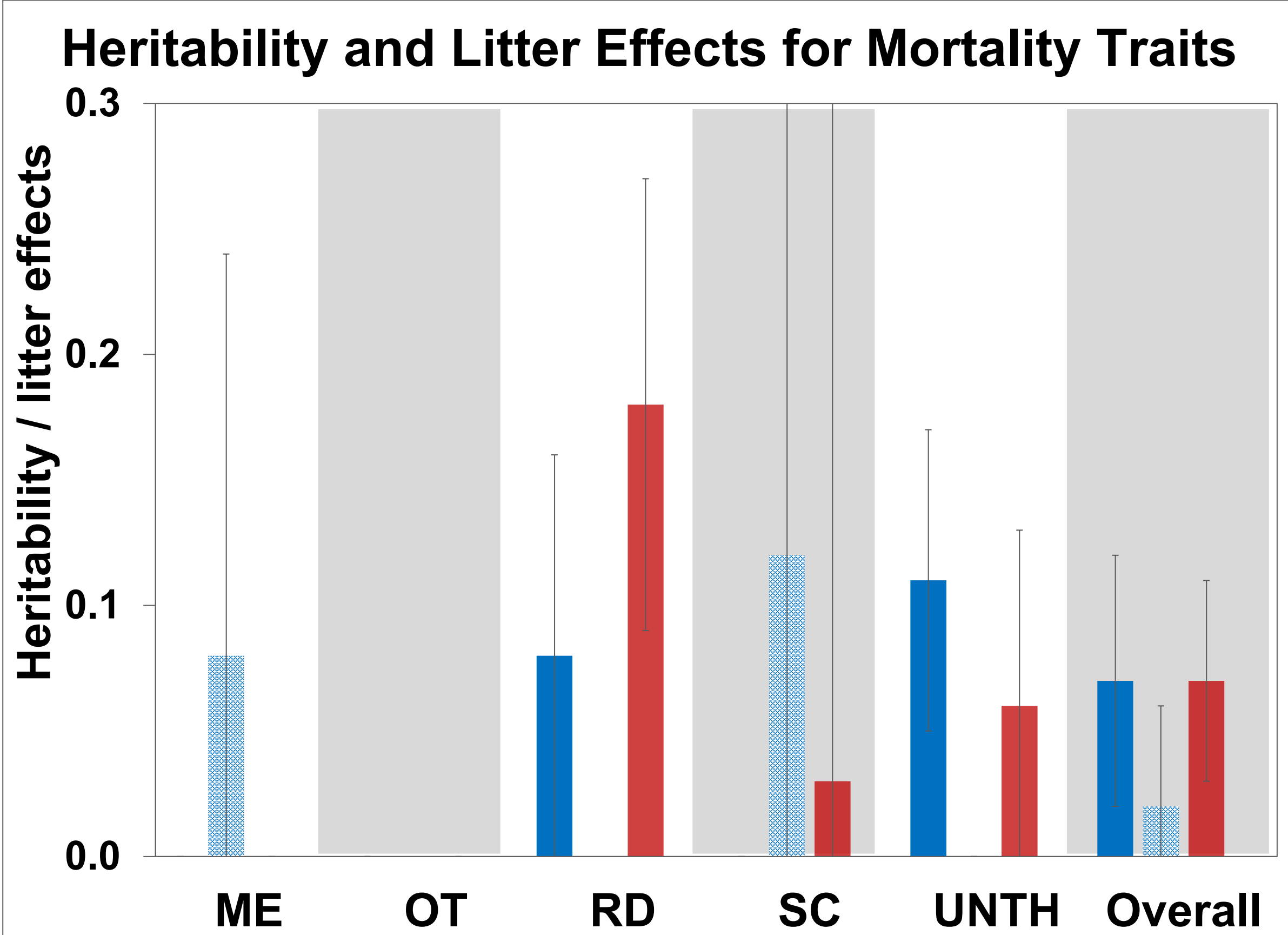
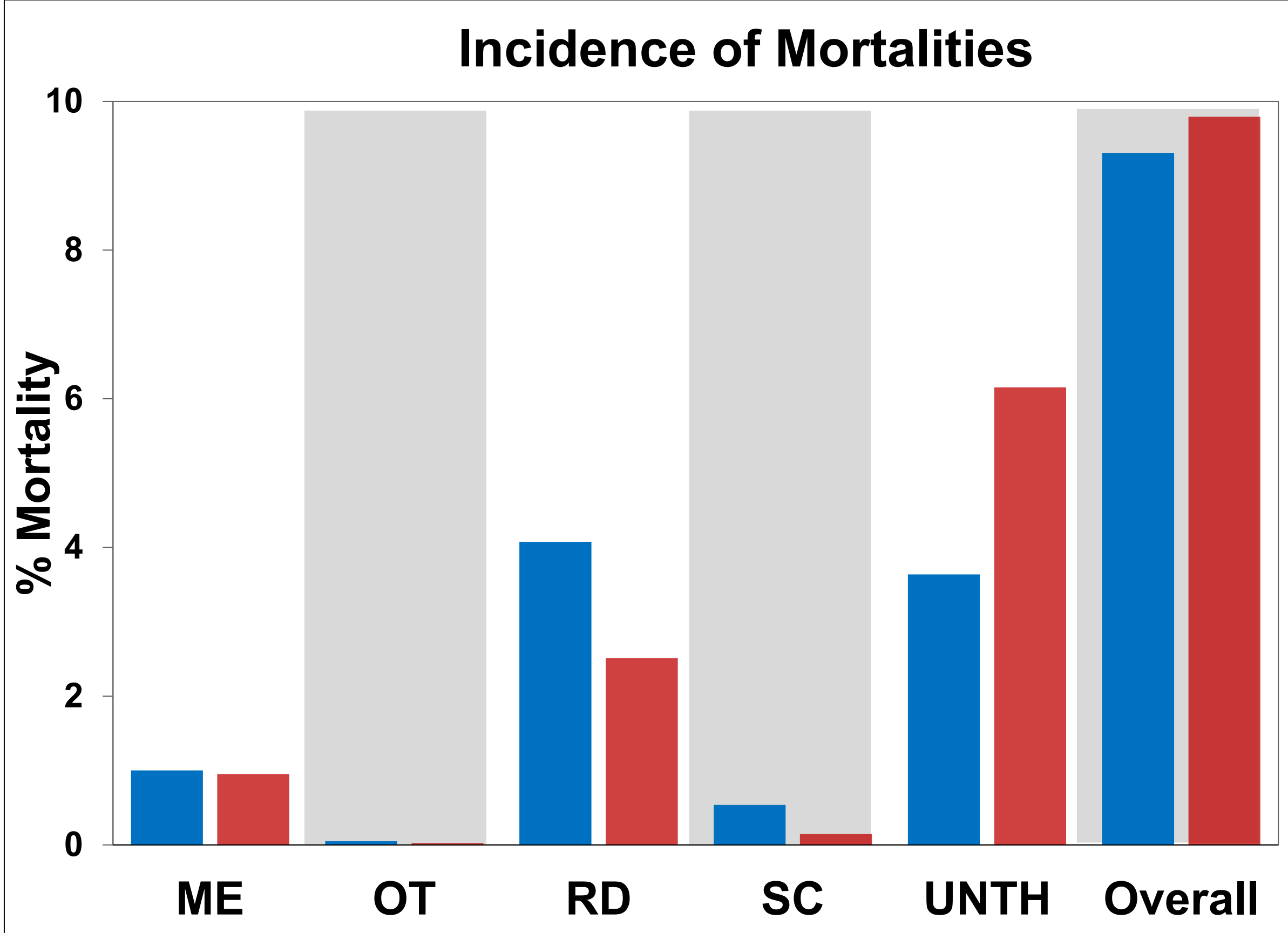
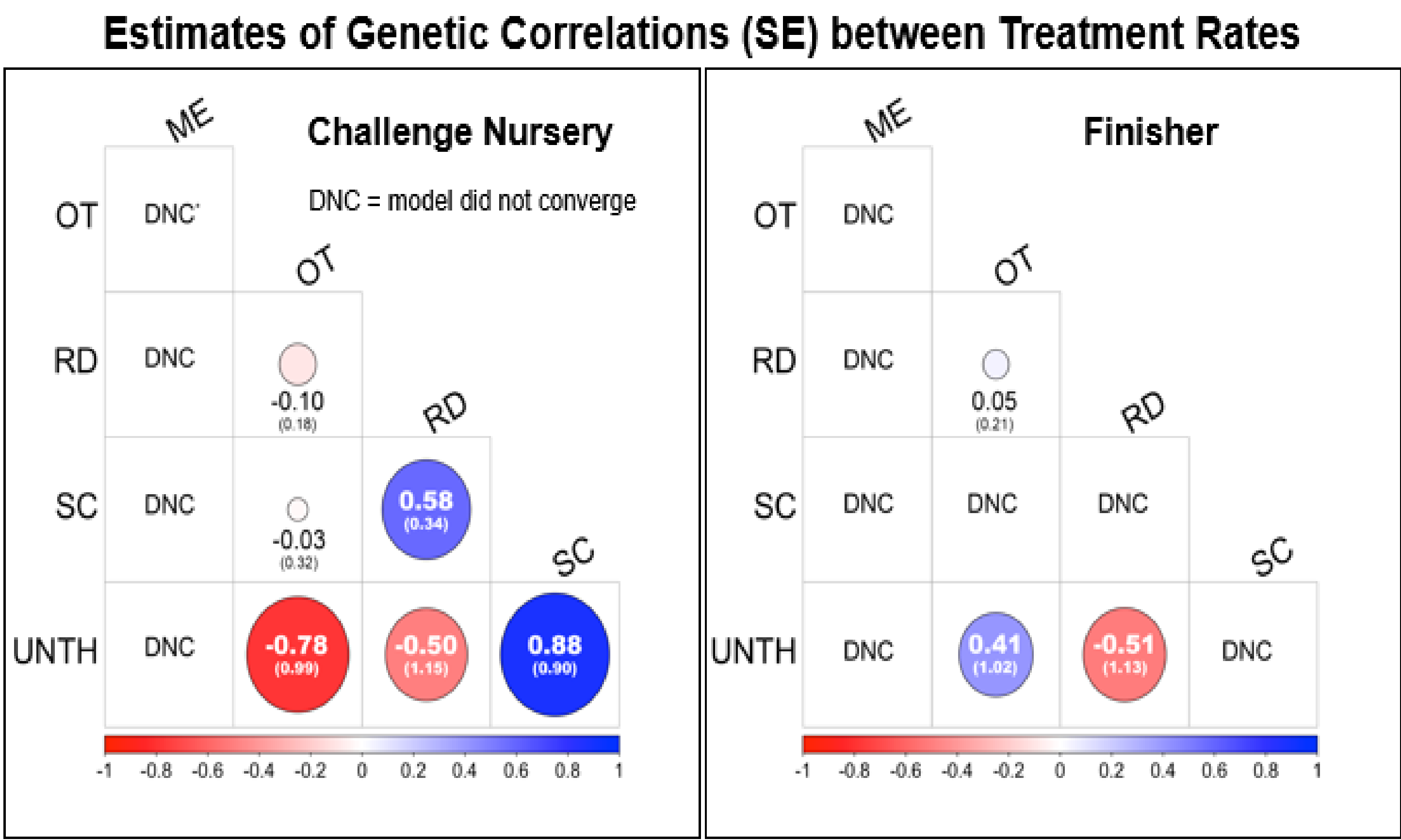
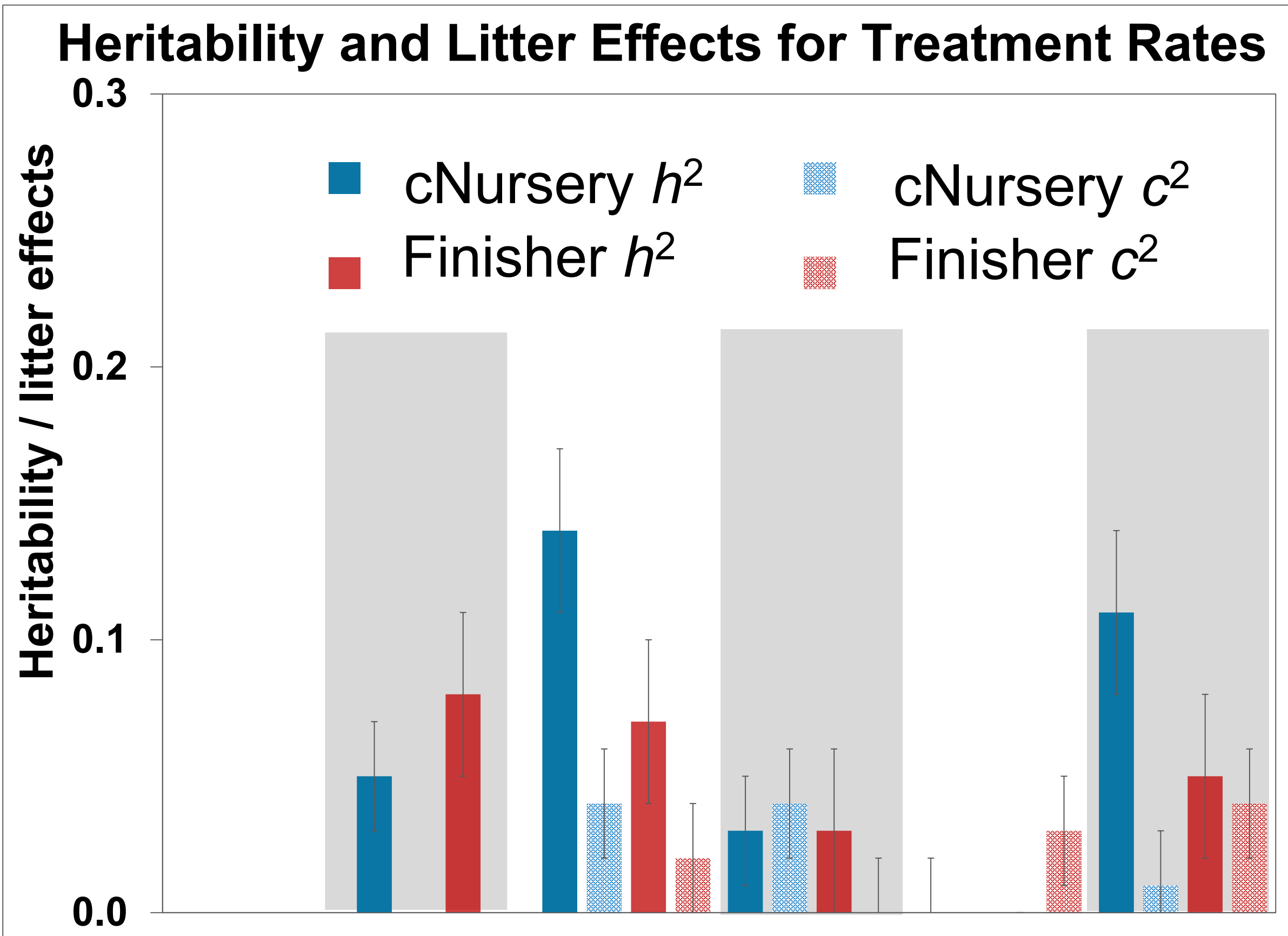
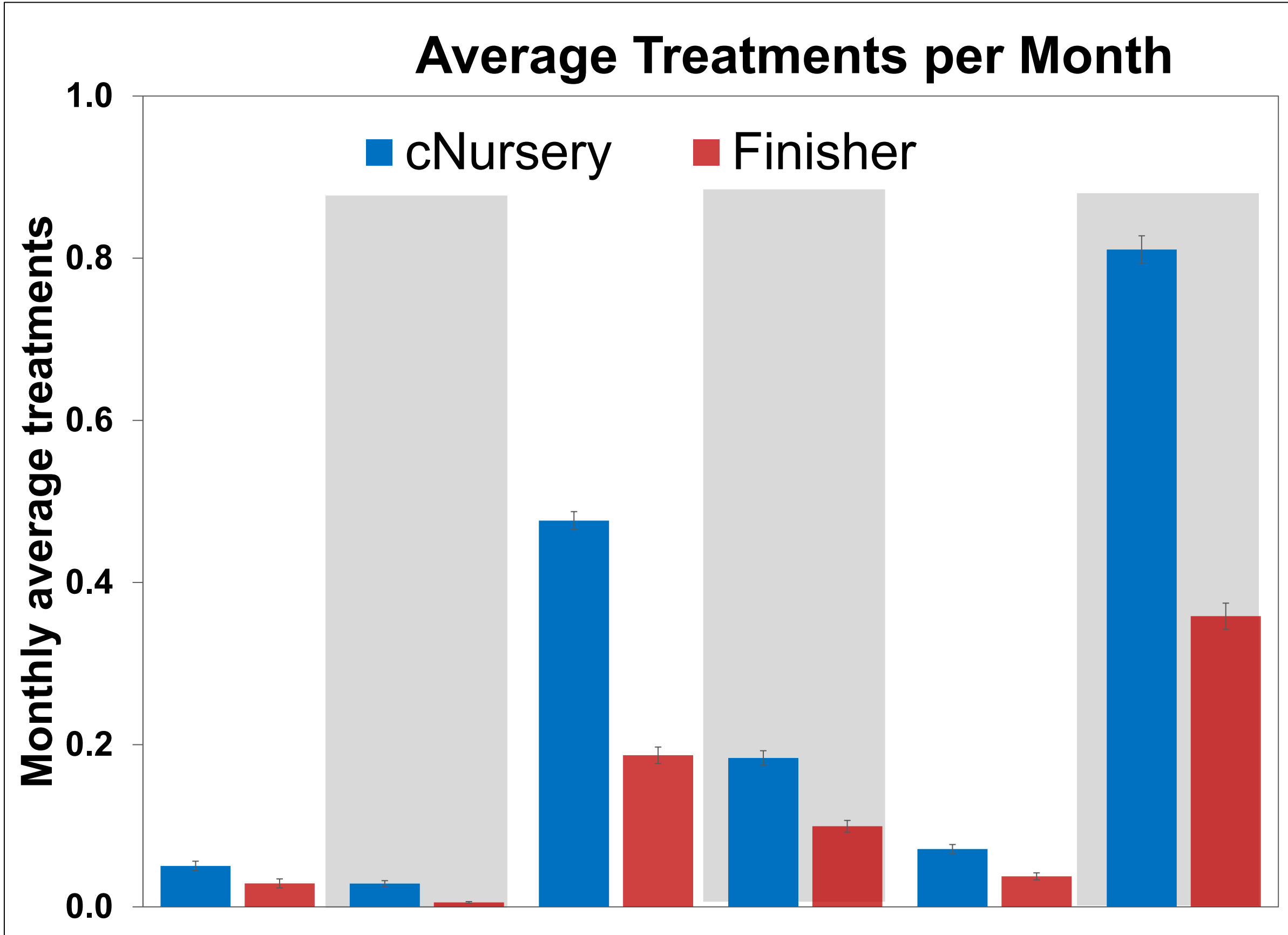
# Genetic parameters of disease in growing pigs under a polymicrobial natural disease challenge



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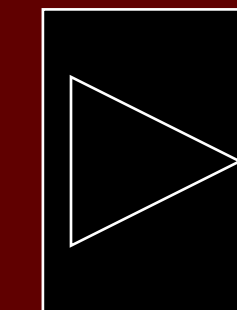




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## Key points

- 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.



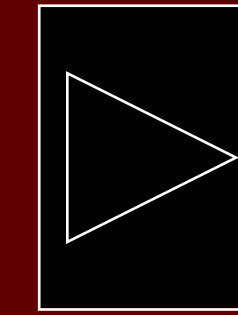




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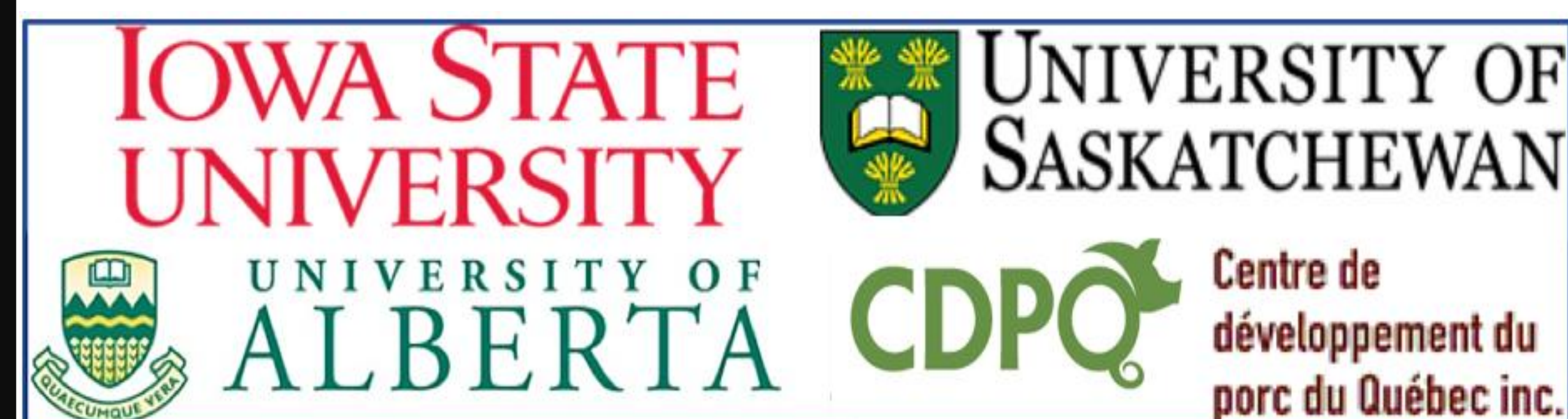
<sup>1</sup>Interdepartmental Genetics and Genomics, Iowa State University, <sup>2</sup>Department of Animal Science, Iowa State University, <sup>3</sup>Department of Large Animal Clinical Science, University of Saskatchewan, <sup>4</sup>Department of Agricultural, Food and Nutritional Science, University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



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## Next steps

- Genome Wide Association Studies
- Gene Set Enrichment Analysis
- Identifying candidate genes
- Manuscript preparation



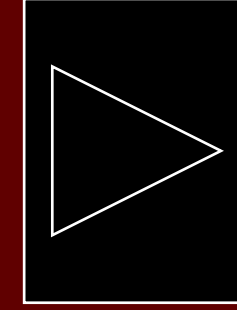




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## Acknowledgements

### ■ Major Professor & PI

- Dr. Jack Dekkers

### ■ POSC:

- Dr. Jack Dekkers
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- Dr. Daniel Linhares
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### ■ Co-authors:

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

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