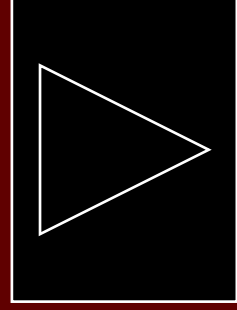# Genetic parameters of disease in growing pigs under a polymicrobial natural disease challenge

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

[1]Department of Animal Science, Iowa State University, [2]Department of Large Animal Clinical Science, University of Saskatchewan, [3]Department of Agricultural, Food and Nutritional Science, University of Alberta, [4]Centre de développement du porc du Québec, [5]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
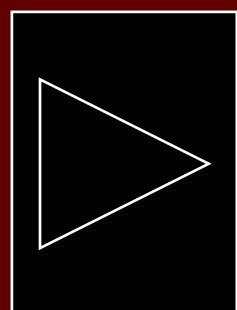
Objective

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

Genetic parameters of disease in growing pigs under a polymicrobial natural disease challenge
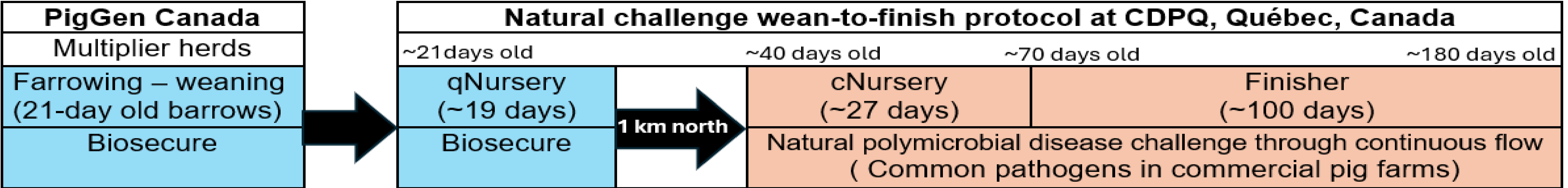
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Materials and methods
A three-phase natural polymicrobial disease challenge (Putz et al.,2019, Frontiers in Genetics)
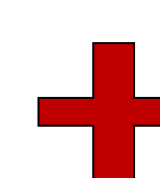
PigGen Canada	Natural challenge wean-to-finish protocol at CDPQ, Québec, Canada		
Multiplier herds	~21days old	~40 days old	~70 days old ~180 days old
Farrowing – weaning (21-day old barrows)	qNursery (~19 days)	cNursery (~27 days)	Finisher (~100 days)
Biosecure	Biosecure 1 km north	Natural polymicrobial 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
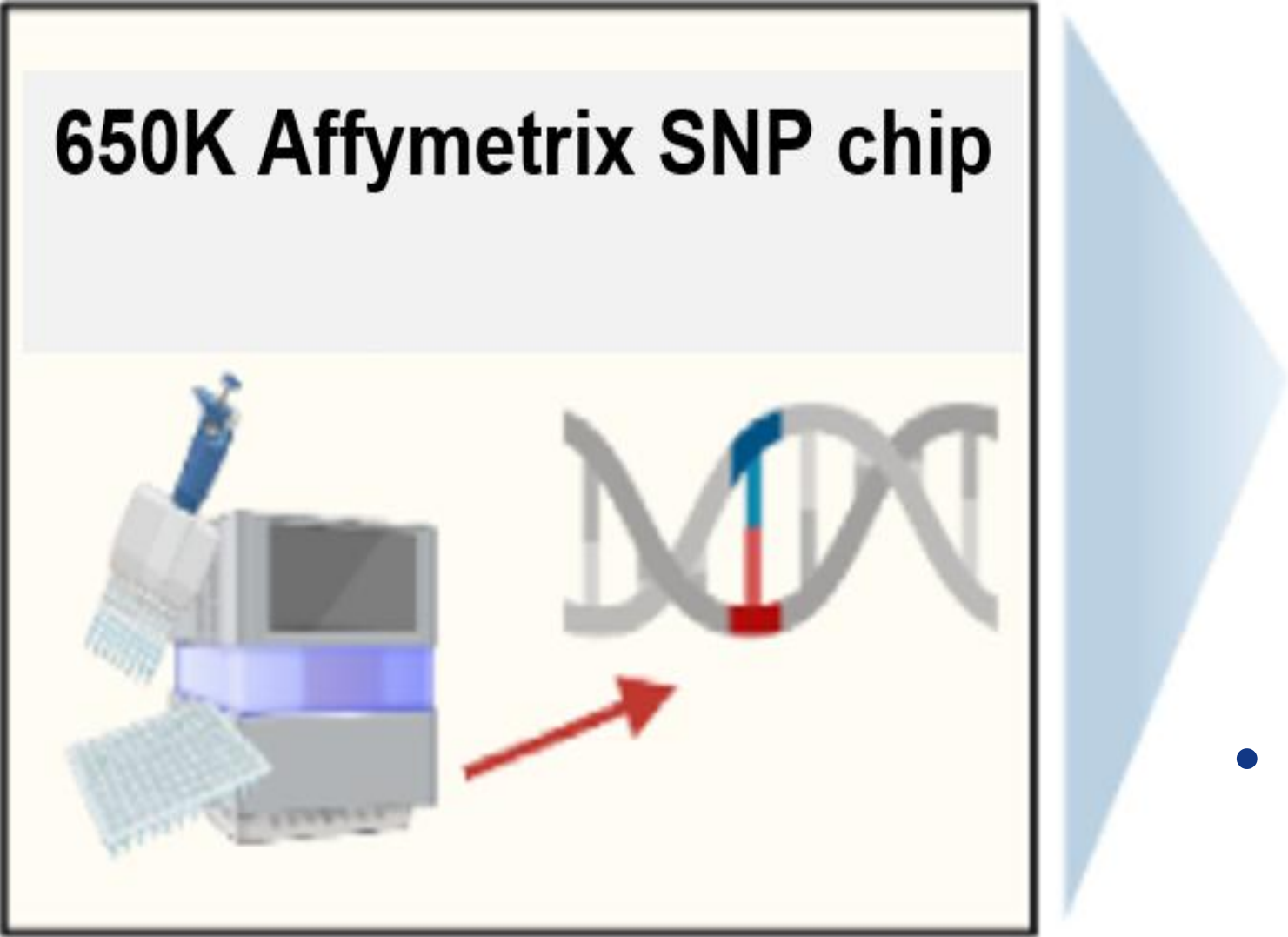
Phenotypic data - Individual health treatments and mortality records categorized as:
1. Meningitis
2. Respiratory distress
3. Scours
4. Unthriftiness
5. Other viral and/or bacterial infections

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

Model: $y_{ijklm} = Batch_i + EntryAge_{ijklm} + Pen_k + Sow_{ijkl} + Pig(grm)_{ijklm} + e_{ijklm}$
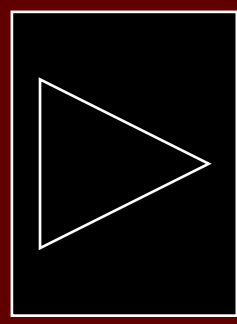
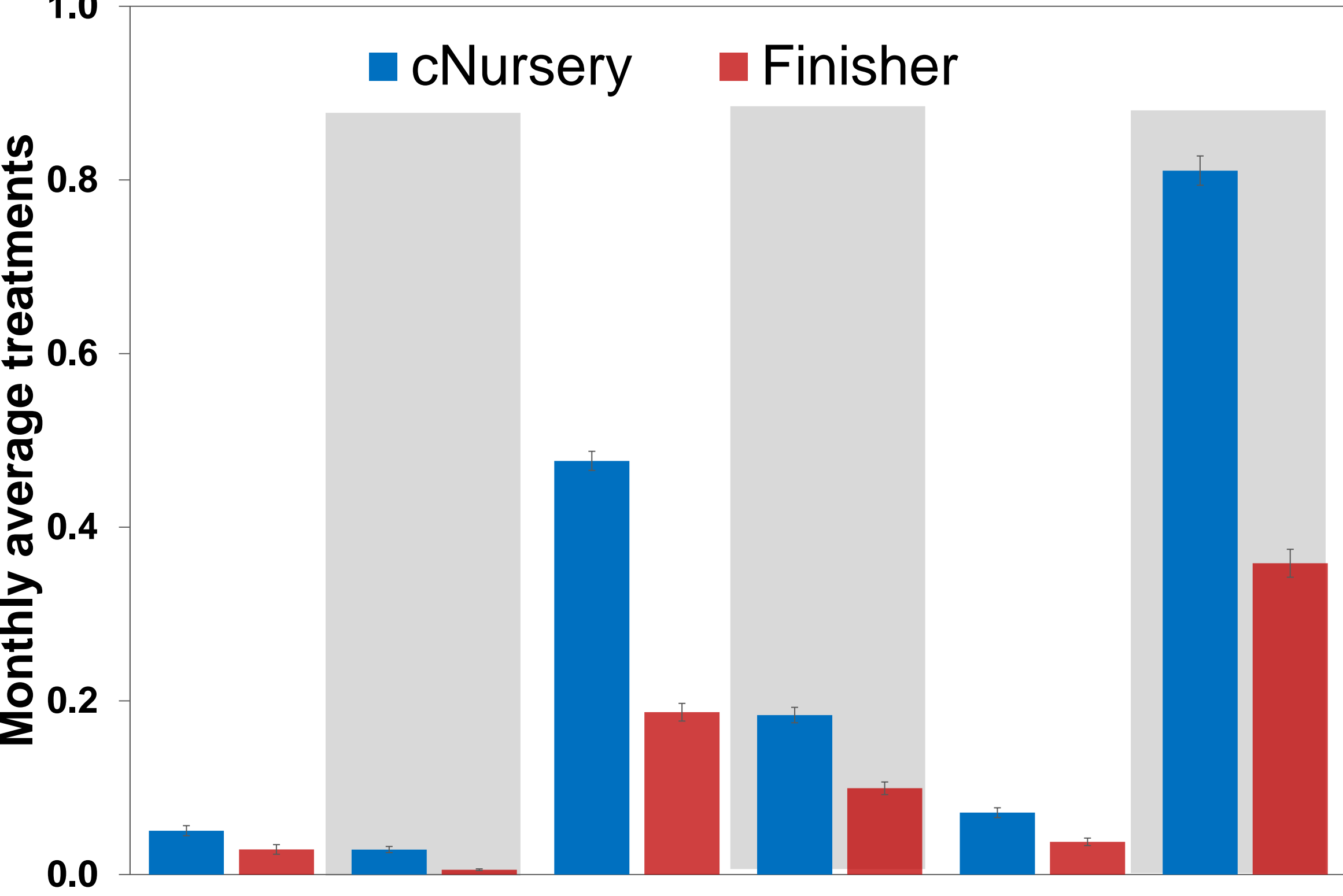# Genetic parameters of disease in growing pigs under a polymicrobial natural disease challenge

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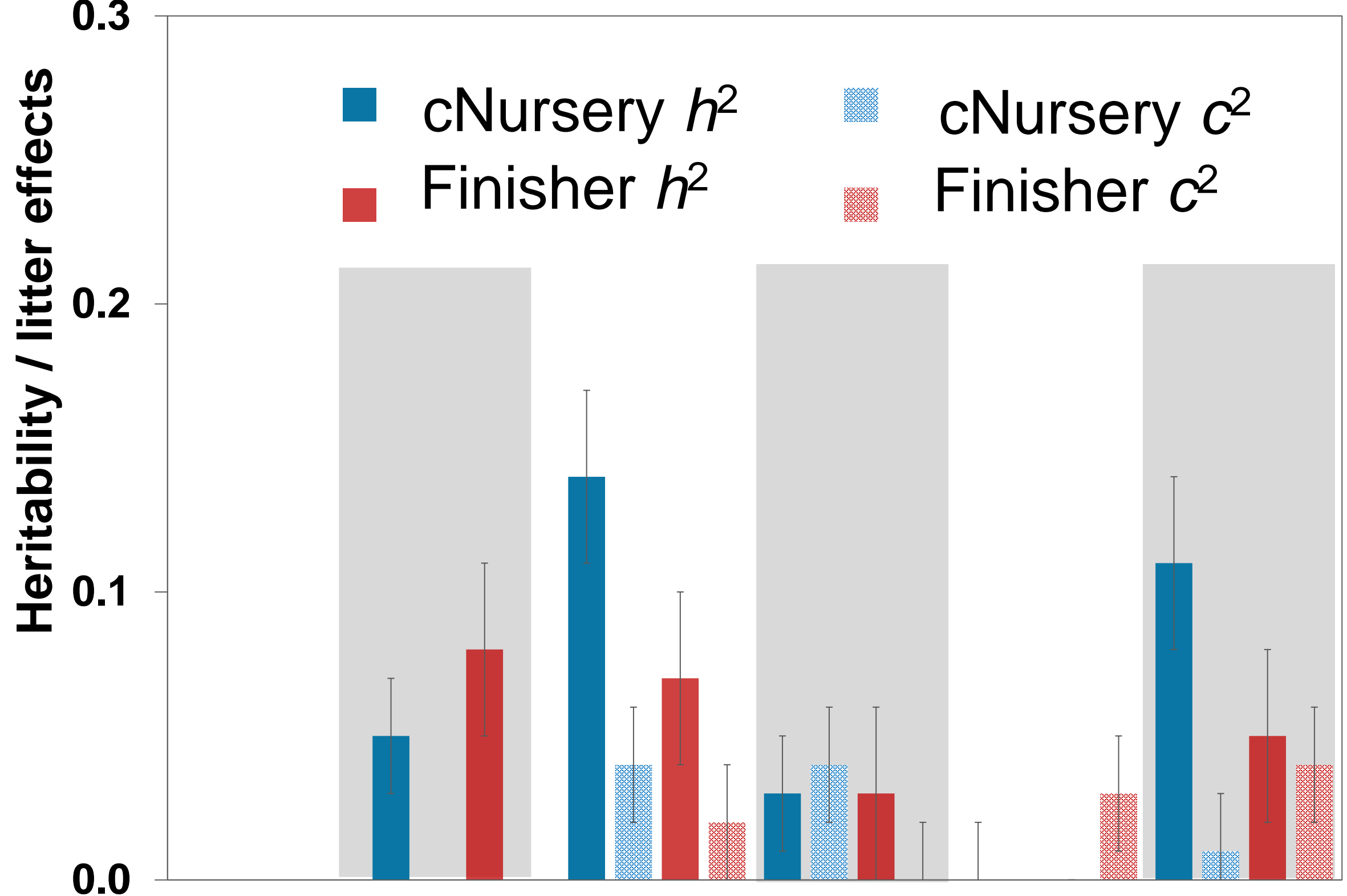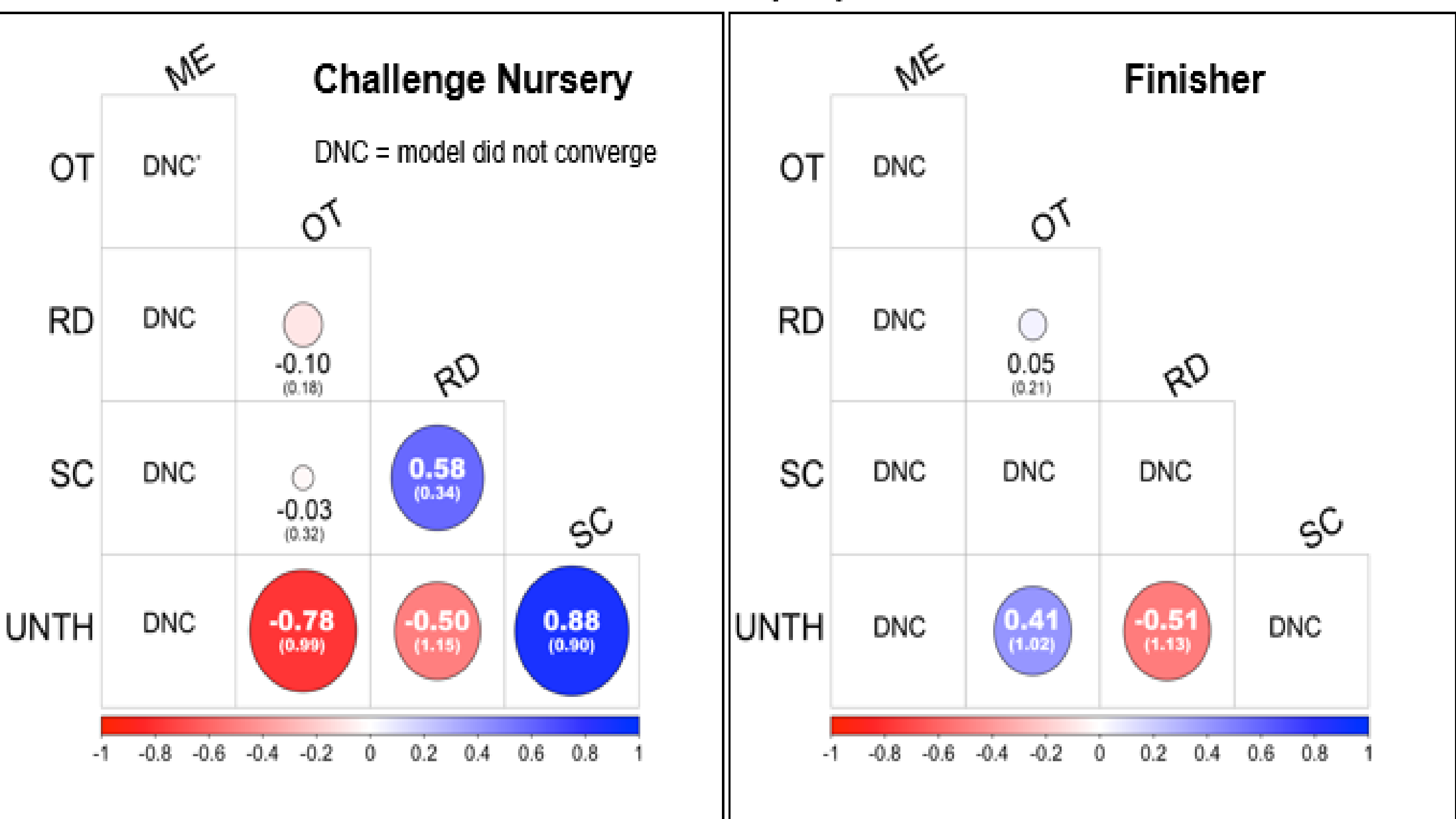

Average Treatments per Month

Incidence of Mortalities

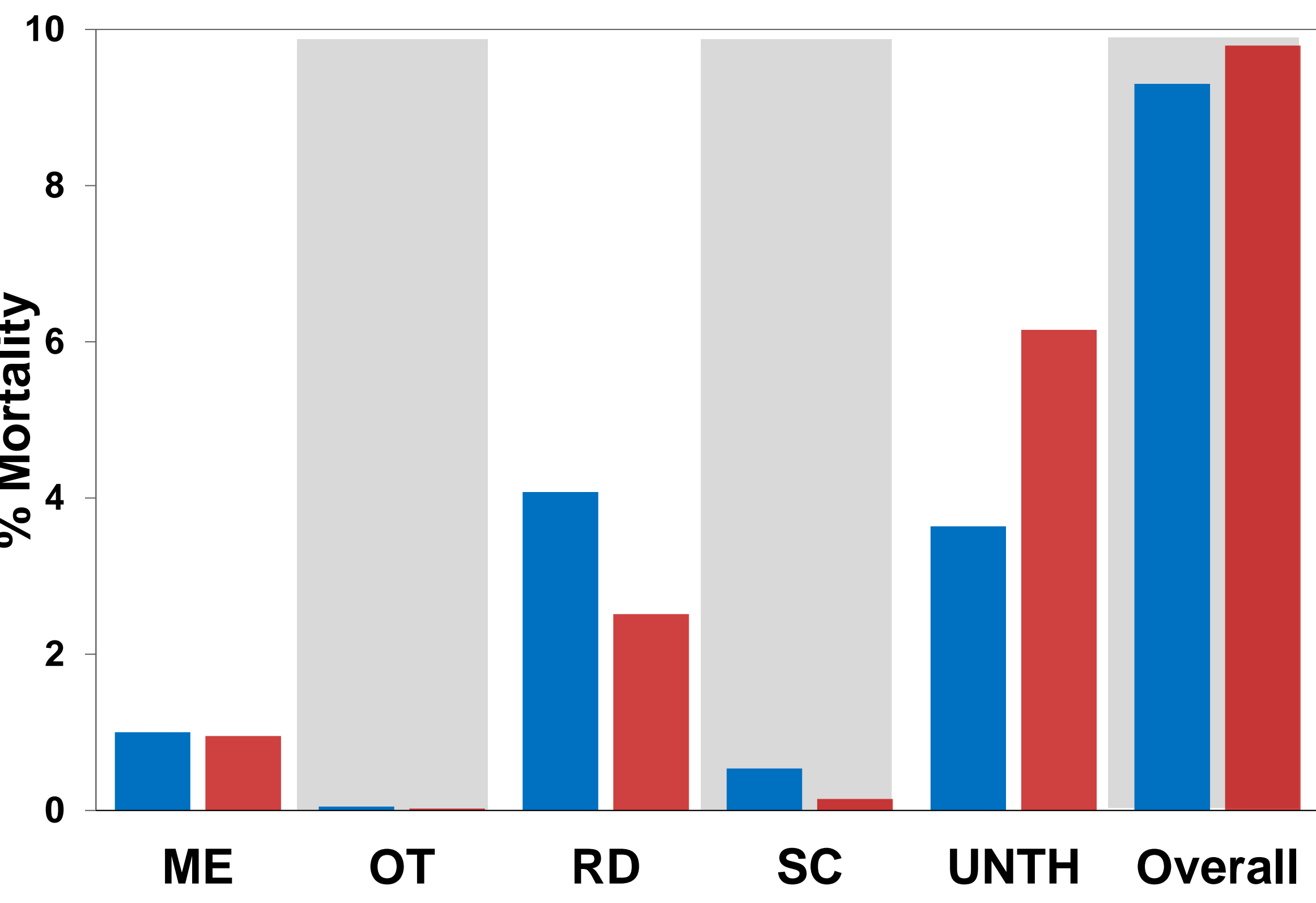Heritability and Litter Effects for Treatment Rates

Heritability and Litter Effects for Mortality Traits

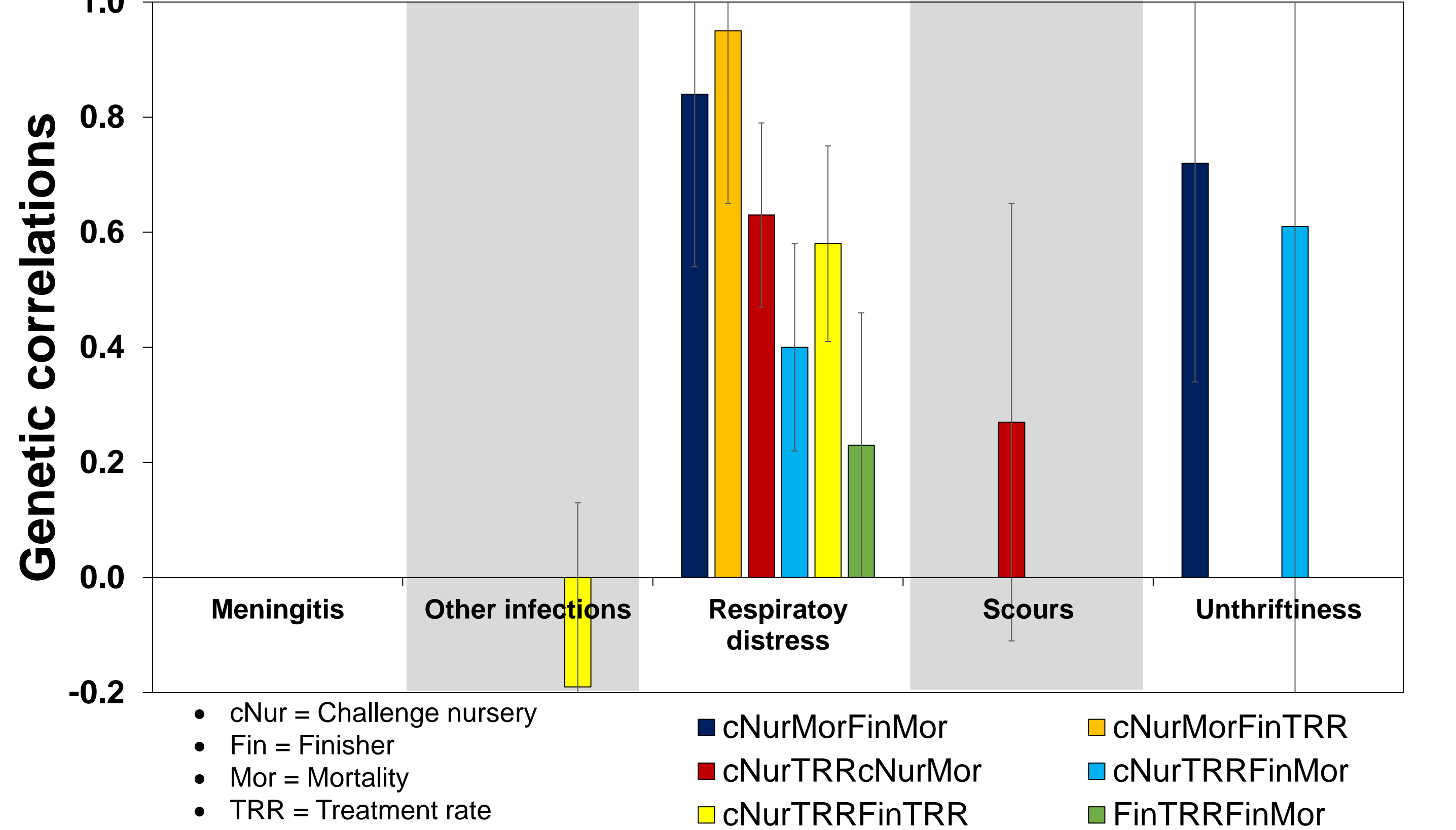Estimates of Genetic Correlations (SE) between Treatment Rates
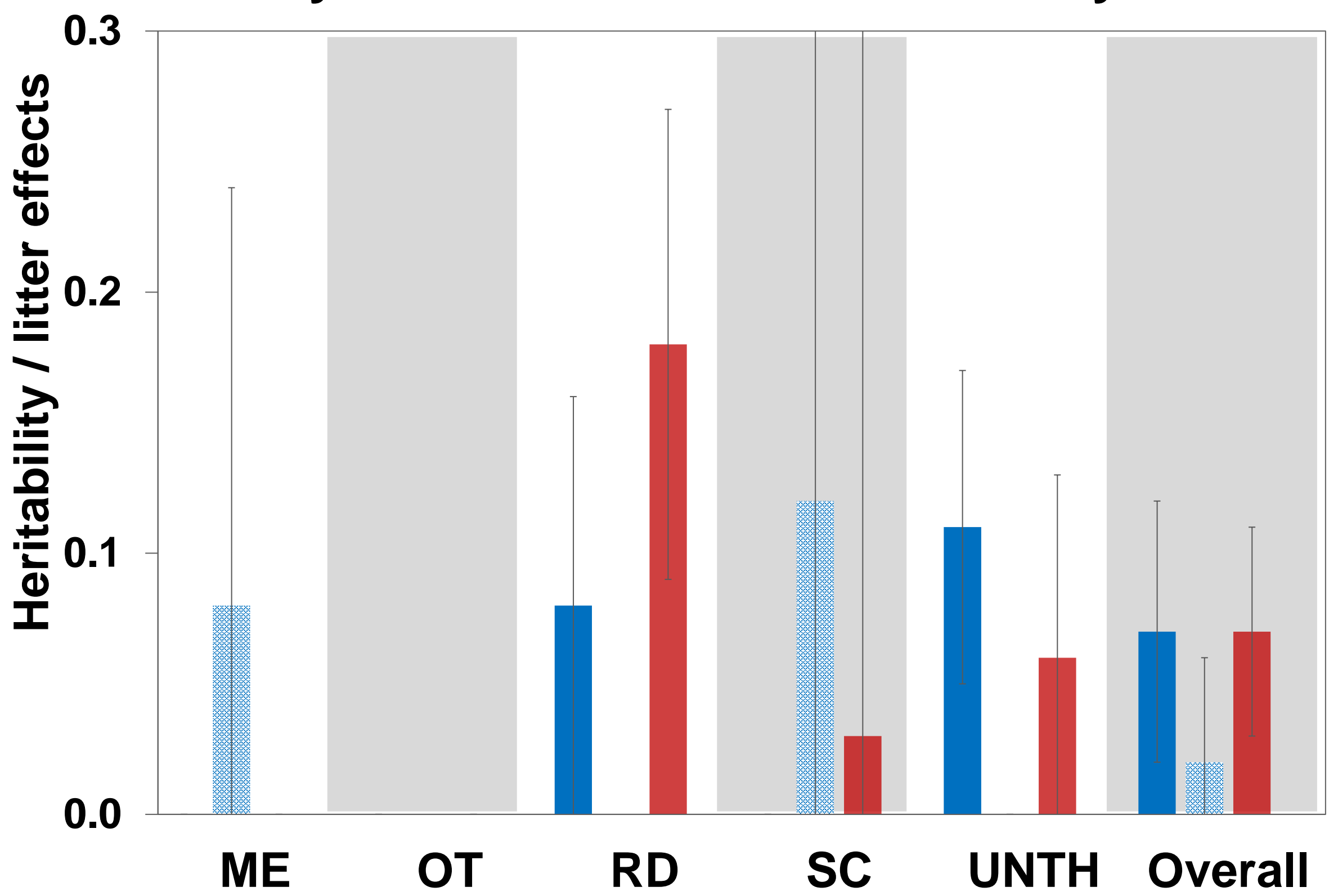
Estimates of genetic correlations for the same disease category

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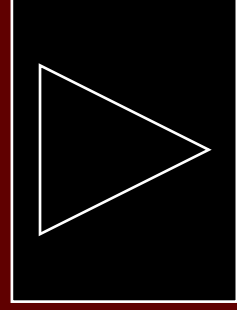
Discussion

- 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 improving 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.