

# Novel resilience phenotypes from a natural disease challenge model in wean-to-finish pigs

A. M. Putz<sup>1\*</sup>, J. C. S. Harding<sup>2</sup>, M. K. Dyck<sup>3</sup>, PigGen Canada<sup>4</sup>, F. Fortin<sup>5</sup>, G. S. Plastow<sup>6</sup>, and

J. C. M. Dekkers<sup>1</sup>

<sup>1</sup> Iowa State University, Department of Animal Science, 50011, Ames, IA, United States  
aputz@iastate.edu (Corresponding Author)

<sup>2</sup> University of Saskatchewan, Large Animal Clinical Sciences, SK S7N 5B4, Saskatoon, Canada

<sup>3</sup> University of Alberta, Department of Agricultural, Life, and Environmental Sciences, AB T6G 2R3, Alberta, Canada

<sup>4</sup> PigGen Canada, Guelph, Ontario, Canada

<sup>5</sup> Centre de développement du porc du Québec inc. (CDPQ), QC G1V 4M6, Quebec, Canada

<sup>6</sup> Livestock Gentec Centre, University of Alberta, Department of Agricultural, Food, and Nutritional Science, AB T6G 2C8, Edmonton, Alberta, Canada

## Summary

Selection for resilience is a practical alternative to selection for resistance and tolerance to disease, which would require collection of pathogen load and performance. If resilience is to be used in the breeding goal, resilience phenotypes are needed. Individual feed intake in a disease challenged environment is attractive as it is sensitive to illness due to physiological responses (such as IL-6 and TNF- $\alpha$ ). Pigs in this study were exposed to multiple diseases in a natural challenge environment. Phenotypes extracted from individual daily feed intake during finishing were the root mean square error (RMSE) of the individual regression of feed intake or duration at the feeder on age. These measures were heritable, moderately genetically correlated with each other ( $0.47 \pm 0.26$ ), and favorably correlated with mortality and number of treatments (0.54 to 0.65). Neither RMSE trait showed strong genetic correlations to other production traits. This research suggests that an individual's variation in feed intake and feeding duration can be used to characterize and select for resilience in finishing pigs.

*Keywords: mean square error, resilience, feed intake, disease resistance, wean-to-finish*

## Introduction

Resilience can be defined as the productivity of an animal in the face of infection (Bishop and Woolliams, 2014). This is a practical alternative to measuring and selecting for a combination of resistance and tolerance. Although selecting on estimates of resistance and tolerance derived from measurements of pathogen load over time would result in greater genetic gains compared to selection for resilience, collecting pathogen burden data is impractical in a large-scale breeding program (Mulder and Rashidi, 2017). Some have also questioned the difficulties and assumptions behind tolerance (Bishop and Woolliams, 2014). If selection for resilience is a practical breeding objective for industry, phenotypes will need to be collected in health challenged environments.

Feed intake variation has potential as an indicator of resilience due to the physiological effects of cytokines that are released during an infection, namely interleukin-6 (IL-6) and tumor necrosis factor- $\alpha$  (TNF- $\alpha$ ), (Webel et al., 1997). Feeding behavior has been used before to study relationships with feed intake and efficiency (Young et al., 2011; Lu et al., 2017), however these studies were typically under non-challenged environments. Knap (2009) suggested that within animal day-to-day variation in feed intake and behavior may be useful to study environmental sensitivity in swine.

The objective of this research was to (1) develop and evaluate measures of resilience from feed intake and behavior data of grow-finish pigs under disease challenge and (2) determine these resilience measures genetic parameters (heritability) and relationships (genetic correlations) with fitness (mortality and treatment data) and other economically relevant traits.

## Material and methods

### Data and traits

Data was collected at a test station in Quebec, Canada, by the Centre de développement du porc du Québec inc. (CDPQ). Every three weeks, batches of 56 to 77 weaned Yorkshire x Landrace barrows were entered into a healthy quarantine nursery from multipliers in Canada. In the quarantine, samples and phenotypes were collected on young healthy pigs for future biomarker research. This early nursery phase typically lasts 19 days before being sent to the challenge facility nearby. In total, this research represents data from the first 21 batches, for a total of 1341 animals from this on-going project. Each batch was provided by one of seven breeding organizations that are part of PigGen Canada (<https://piggencanada.org/>). Batches consisted of 2-4 barrows per litter, which were full or half sibs depending on whether or not pooled semen was used. A total of 1215 pigs were genotyped with the 650k Affymetrix Axiom Porcine Genotyping Array.

The challenge facility consisted of a 4-week nursery period that was seeded with multiple diseases using infected commercial pigs and a finishing period until slaughter. Disease pressure was maintained by using continuous flow system with careful veterinary oversight and provided treatments as needed. Pigs entered the finishing unit on average at 67 days of age and were slaughtered on average at 181 days of age. Individual daily feed intake was recorded during the finishing phase using electronic feeders and RFID tags. Individual feeder visits were aggregated to daily sums. Missing daily values were imputed with a five-day rolling average within individual. Preliminary analyses (visual appraisal) showed that daily duration (or time at the feeder) closely followed drops in feed intake due to illness (see Figure 1).

Analyzed traits included mortality (binary), total number of treatments (TRT), number of treatments per 180 days (TRT180), finishing average daily gain (ADG), average daily feed intake (ADFI), feed conversion ratio (FCR), residual feed intake (RFI), carcass weight (CWT), dressing proportion (DRS), lean yield (LYLD), carcass backfat (CBF), and carcass loin depth (CLD). TRT180 was calculated as the number of treatments per day times 180 (e.g. a pig died at age 79 with 1 treatment,  $(1/79)*180=2.28$ ). All pigs that made it through the nursery phase received a phenotype. This adjusted trait was found to be more predictive of resilience compared to TRT, as the TRT phenotype included only pigs that made it to slaughter. For ADG, ADFI, and RFI, pigs had to reach slaughter to receive a phenotype.

Figure 1 depicts two traits designed to extract a resilience phenotype. The root mean square error (RMSE) of feed intake (FI; Figure 1A) and duration (DUR; Figure 1B) were

calculated from the individual simple linear regression of feed intake or duration on age within each individual pig. Only animals that had at least 60 days of feed intake received a RMSE phenotype.

## Variance components and models

Variance components were estimated using BLUPF90 (renumf90 version 1.123, Misztal et al., 2002). Basic animal models were used for all traits, with additive genetic (using the **H** matrix) and residual terms as random effects. Fixed effects for mortality and treatments included batch (i.e. contemporary group) and entry age. Fixed effects for all other traits included batch, finisher entry age, and pen. Litter was initially included as another random term, but explained a limited amount of variation and was subsequently removed for these finishing and carcass traits. The **H** matrix was calculated using defaults from preGSf90. Only the sow was known and utilized in the creation of the **A** matrix (sire was unknown due to pooled semen usage). The **H** matrix contained 1767 individuals (1341 individuals and 426 parents), 1215 were genotyped and utilized to create the **G** matrix.

## Results

Table 1 shows estimates of heritability along with genetic correlations between production traits and the two resilience traits ( $RMSE_{FI}$  and  $RMSE_{DUR}$ ). Both RMSE measures were moderately heritable ( $0.22 \pm 0.07$  and  $0.25 \pm 0.08$ ) and favorably correlated with mortality and TRT180 (0.52 to 0.65). Because TRT was defined only for animals that made it to slaughter, it was not as strongly associated with either RMSE measure, especially with  $RMSE_{DUR}$ .  $RMSE_{FI}$  and  $RMSE_{DUR}$  were genetically correlated  $0.47 \pm 0.26$  and tended to not be strongly associated with production traits (less than 0.5 in absolute value).

## Discussion

Daily feed intake records on pigs in a health challenged environment were used to extract a resilience phenotype for selection. Utilizing the root mean square error (RMSE) of the individual simple linear regression of daily feed intake or duration at the feeder on age resulted in measures that were heritable. They showed favorable genetic correlations with mortality and number of treatments without being strongly associated with other economically important production traits. In the future, the use of duration may be utilized over the entire wean-to-finish period with retrofit feeders to quantify resilience.

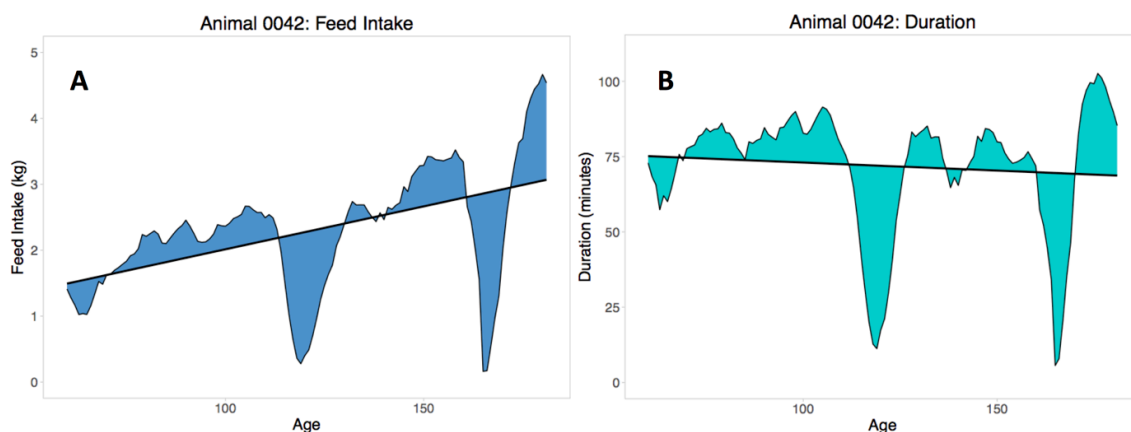


Figure 1. Example of root mean square error (RMSE) of feed intake (A) and feeding duration (B) as measures of resilience.

Table 1. Estimates of heritability ( $h^2$ ) for analysed traits and genetic correlations ( $r_g$ ) with RMSE resilience measures (SE in brackets).

Trait	$h^2$	$r_g$ RMSE <sub>FI</sub>	$r_g$ RMSE <sub>DUR</sub>
RMSE <sub>FI</sub> , kg	0.22 (0.07)	-	0.47 (0.26)
RMSE <sub>DUR</sub> , min	0.25 (0.08)	0.47 (0.26)	-
Mortality	0.13 (0.05)	0.54 (0.36)	0.65 (0.35)
TRT	0.14 (0.07)	0.52 (0.48)	0.12 (0.76)
TRT180	0.29 (0.07)	0.56 (0.20)	0.64 (0.14)
ADG, kg/day	0.26 (0.07)	-0.31 (0.26)	-0.19 (0.26)
ADFI, kg/day	0.33 (0.07)	0.03 (0.26)	-0.24 (0.21)
FCR, kg feed/ kg gain	0.35 (0.07)	0.39 (0.21)	-0.17 (0.25)
RFI, kg	0.43 (0.07)	0.35 (0.21)	-0.05 (0.22)
CWT, kg	0.32 (0.07)	-0.04 (0.28)	-0.13 (0.24)
DRS	0.12 (0.06)	-0.23 (0.07)	-0.49 (0.49)
LYLD, %	0.48 (0.08)	0.13 (0.24)	0.00 (0.23)
CBF, mm	0.45 (0.08)	-0.14 (0.26)	0.03 (0.23)
CLD, mm	0.40 (0.08)	-0.20 (0.27)	-0.05 (0.24)

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