Quantifying the health challenges in an Australian piggery using medication records for the definition of disease resilience¹

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ABSTRACT: Disease resilience is the ability to maintain performance and health, despite infection challenges in the environment. The evaluation of disease resilience requires measures of environment infection challenges, along with other environmental challenges. The overall objective of this study was to define disease resilience using pedigree, production, and medication records from an Australian herd of Large White pigs. The extent to which the infection challenges were captured by environmental descriptors based on contemporary group (CG) estimates of growth was assessed ($n = 8,835$). There were moderately negative linear relationships ($r = -0.29$, $p = 0.08$) between CG estimates (39 CGs) of growth and the frequency of medicated pigs ($n = 812$ medicated pigs). This suggests that CG estimates of growth partly capture health challenges. However, because the health challenges were not of the pathogenic nature for this herd, these environmental descriptors may not be appropriate for the evaluation of disease resilience. Subsequently, an alternative approach to select for health was provided, where health was defined as a binary outcome of medication status, fitted in a generalized linear mixed sire model.

Two health-trait definitions were explored, which differed in the number of control (nonmedicated) pigs per litter. The ‘reduced-control’ health trait had a representative sample of littermates with available performance records, and the ‘full-control’ health trait included all piglets weaned per litter (i.e., performance-tested and non-performance-tested pigs). All 812 medicated pigs had performance records available. The remaining 8,023 pigs in the reduced-control and 21,352 pigs in the full-control health traits were assumed to have not been medicated (controls). Male pigs from litters with a higher number of postweaning deaths were more likely to be medicated for both health traits. Heritability was consistent for both trait definitions, at 0.06 ± 0.04 ($\pm$ SE) (reduced-control) and 0.04 ± 0.03 (full-control). While results may be specific for individual herds depending on health status, these estimates align with those presented in literature for other health traits. Together, these results demonstrate that routinely collected medication records may be useful for pig breeding programs and their economic importance and genetic background should be explored further.

Key words: environmental descriptor, genotype by environment interaction, health, time series

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INTRODUCTION

A robust animal has the ability to cope with and be resilient to external stressors, which can allow for unproblematic expression of high

production potential in a wide variety of conditions (Knap, 2005). Robustness against the specific challenge of infectious agents is disease resilience, which can be defined as the ability to maintain performance and health despite infection challenges in the environment. This is achieved by the animal mounting the appropriate response to directly combat the pathogen through disease resistance, and also indirectly through disease tolerance (Bishop, 2012; Doeschl-Wilson and Lough, 2014; Hermes, 2014). Genetic variation in disease resilience can be evaluated using a genotype by environment interaction ($G \times E$) approach, where E is the trajectory of environmental infection challenges. This trajectory should take into account the other environmental challenges that pigs may also be experiencing for a multi-dimensional approach so as to reflect the disease space of an infection challenge (Guy et al., 2012).

The overall quality of, and therefore challenges in an environment can be quantified through the mean performance of a contemporary group (CG). Estimates of CG effects (CG estimates), which have been adjusted for systematic and genetic effects, are assumed to simultaneously capture any known and unknown challenges that exist in the environment, which include infection challenges. Guy et al. (2017a) argued that accounting for some known challenges provides a finer definition of the unknown challenges in the pig environment, which may include infection challenges. Attempts have been made to separate the challenges that are simultaneously captured in CG estimates. Guy et al. (2017a) adjusted CG estimates of growth rate for climatic variables using splines. For this herd of interest, monthly averages of minimum air temperatures (MinT) accounted for the most known environmental variation captured in CG estimates based on growth rate. Additional seasonal effects were partitioned from the CG estimates adjusted for MinT using seasonal decomposition by Guy et al. (2017b), indicating that seasonal decomposition may be a more appropriate method to account for the regular and known fluctuations in performance due to climatic effects. However, the infection challenges captured by these descriptors need to be verified.

Producer-recorded medication records are a source of information that can provide insight into the health status of a herd and the types of challenges experienced. These medication records, which include treatment of medications and vaccinations, are routinely collected on most Australian piggeries as they are required for quality assurance programs

to minimize the risk of chemical residuals entering the food supply chain (APIQ Management, 2018). Therefore, the overall objective of this study was to define disease resilience using routinely collected pedigree, production, and medication records. This was achieved firstly by describing the health challenges experienced by a pig herd. Secondly, the extent to which the infection challenges were captured in CG estimates of growth was assessed. If the adjusted CG estimates reflect infection challenges, these definitions of the environment may provide a means to analyze variation in response to infection challenges for the routine genetic evaluation of disease resilience. Finally, an alternative approach to select for health was provided, where health was defined as a binary outcome of medication status. The health traits defined in this study provide practical approaches to incorporating health in pig breeding programs.

MATERIALS AND METHODS

This section is partitioned into three subsections relating to the three steps described above. Firstly, *Analysis I* describes the characterization of the health challenges of a pig herd using medication records. *Analysis II* assesses the alignment of environmental descriptors based on CG estimates with the health challenges described by medication records. *Analysis III* describes an alternative approach to select for health, where health was defined as a binary outcome of medication status.

Data

Analysis I. Characterization of health challenges using medication records. Pedigree, production, and medication records were obtained from the University of Queensland piggery in Gatton, Queensland Australia. This herd operated as a commercial unit and consisted of purebred Large White pigs (~300 breeding sows). Pigs in this herd were tail docked and males were not castrated. Piglets were weaned at an average age of 25.4 ± 4.9 d (mean $\pm$ SD). Pedigree and production records were exported from the genetic evaluation and herd database systems, with records available from March 1997 to December 2016. While pedigree was available for the entire time period, performance records were only available until December 2013. Medication records were available from January 2011 to the beginning of April 2015 (total number of treatment records $n = 2,854$), which included information on the date of medication, pig unit, pig

identification (ID), approximate weight (kg), medication(s) used, doses, and reason(s) for treatment. The unit from which medication records were taken from included weaner, porker (25–55 kg), grower (>55 kg), gilt (first parity), dry sow (in between litters), farrowing, and detection mating area (DMA) units. The piglets that were medicated while still on the sow in the farrowing unit before weaning were reclassified as being in the ‘piglet’ unit.

Medication records from the weaner, porker, and growing units were used to investigate the monthly prevalence of medication for the growing pigs ($n = 1,012$). Since medication records were only available from between 2011 and 2016, the pedigree records from the same time period were used in this part of the analysis. Not all pigs with medication records were aligned with pedigree records. This was because an average of 3.3 pigs per litter were recorded for performance and also hence in the pedigree. The pigs chosen to be performance tested were a representative sample of each litter. The medicated pig IDs that could not be matched up with pedigree pig IDs due to data entry errors were not included in the genetic analysis. Nevertheless, the other pigs in the pedigree that did not have a medication record and that were born in the same month as the medicated pigs were assumed to have not been medicated.

Two ways of deriving the number of control (nonmedicated) pigs were explored, which differed on the number of untreated pigs per litter. The ‘reduced-control’ numbers had a representative sample of littermates with available performance records. The reduced-controls had total of 8,835 pigs, which were all performance tested. These pigs were born between October 2010 and March 2016 inclusive. Birth-month CGs ranged in size, from 15 to 247 pigs, with an average of 134 pigs. A ‘full-control’ numbers included all piglets weaned per litter (i.e., performance-tested and non-performance-tested pigs). This was derived using additional information on the number of pigs weaned in each litter, so that all siblings in the litter were included in the pedigree via dummy IDs. Because this study is focusing on health of the growing pig, piglets that did not survive to weaning were not included in the full-control numbers because pre-weaning survival can be seen as trait of the sow. This resulted in a total of 22,164 pigs, with an average birth-month CG size of 339 pigs.

Analysis II. Validation of infection challenges captured by the environmental descriptors based on contemporary group estimates. Five definitions of

the environment were examined, which were derived by Guy et al. (2017a, b). Briefly, records from between 1999 and 2013 were used to derive CG estimates for growth. There were 31,230 individual pigs that were used to derive CG estimates. The definition of a CG was month and year of birth, and any CGs with <50 members were excluded from analysis. This resulted in 167 CGs, ranging in size from 56 to 489 pigs with an average of 187 pigs. The average body weight on test date was 90.9 ± 9.9 kg, measured at an average age of 127.9 ± 5.1 d.

Analysis III. An alternative definition of health using medication status. An alternative approach to select for health was provided, where health was defined as a binary outcome of medication status. Two health trait definitions were explored, which differed in the number of control (non-medicated) pigs per litter. The data used were the same data used in *Analysis I*, where there were 812 medicated pigs (cases), with 8,023 (controls) in the reduced-control health trait (resulting in a total of 8,835 pigs analyzed), and 21,352 nonmedicated pigs in the full-control health trait (total of 22,164 pigs).

Statistical Analysis

Analysis I. Characterization of health challenges using medication records. The reasons for medication across all units were re-coded for consistency, and further categorized into the health challenges related to ‘farrowing issues’, ‘tail bite’, ‘lameness’, ‘generally unwell’, ‘diarrhea’, ‘skin’ and ‘other’ (outlined in Table 1). These categories were decided depending on the frequency of medication records. The category of ‘other’, which included reasons that were deemed a trivial health issue for the herd, comprised <50 individual incidents recorded across all units and groups of animals (growing pigs and breeding females) over the 5.5 yr. These health challenges included ear infections ($n = 31$), mastitis ($n = 25$), urinary infection ($n = 21$), arthritis ($n = 18$), and ulcers ($n = 17$).

The monthly prevalence of medication was calculated as the percentage of pigs born each month which were medicated at any point between weaning and grower-finishing phase.

Analysis II. Validation of infection challenges captured by the environmental descriptors based on contemporary group estimates. The first two environmental descriptors examined based on CG estimates of ADG were derived in Guy et al. (2017a), using the following linear mixed animal models

using restricted maximum likelihood in ASReml (Gilmour et al., 2009):

Model I. Unadjusted CG estimates:

$$ADG_{ijkl} = \mu + \text{Sex}_i + \text{Animal}_j + \text{CG}_k + \text{Litter}_l + e_{ijkl}$$

Model II. CG estimates adjusted for MinT:

$$ADG_{ijkl} = \mu + \text{Sex}_i + \beta_1 \text{MinT} + s(\text{MinT}) + \text{Animal}_j + \text{CG}_k + \text{Litter}_l + e_{ijkl}$$

where ADG was defined for the j th animal from the k th birth month–year CG, and l th Litter; μ is the overall mean across all animals. Both models contained the fixed effect of i th Sex (two levels, female, and entire male), and the random effects of CG, Animal as the additive genetic effect, Litter as the common litter environment, and e_{ijkl} as residual effect unique for each animal. The genetic effects of animals were assumed to be $N(0, A\sigma_A^2)$ where σ_A^2 is the additive genetic variance and A is the numerator relationship matrix based on the pedigree, CG was assumed to be $N(0, I\sigma_{CG}^2)$ where σ_{CG}^2 is the CG variance and I is the identity matrix, Litter effects were assumed to be $N(0, I\sigma_L^2)$ where σ_L^2 is the litter variance, and residual effects were assumed to be $N(0, I\sigma_e^2)$ where σ_e^2 is the residual variance. For Model II, the average minimum monthly air temperature of test month (MinT) was fitted as a random cubic smoothing spline, denoted as $s()$, and also as a linear covariate as a fixed effect, where β_1 is the regression coefficient of MinT. The CG

estimates unadjusted for climatic effects (Model I) were assumed to capture all known and unknown challenges in the environment, while the CG estimates adjusted for MinT (Model II) can be seen as a measure of environmental challenges other than climatic effects captured by MinT.

The last three environmental descriptors examined were derived by Guy et al. (2017b). Seasonal-trend decomposition based on locally weight regression (STL) was used to decompose the CG estimates adjusted for MinT (from Model II above) into the trend, seasonal, and residual time-series components. The ‘stl’ function in R (R Core Team, 2016) was used. The locally weighted neighborhood window to extract the seasonal component parameter was set to the mean (defined as ‘periodic’), the locally weighted neighborhood window to extract the trend component was set to a lag of 25, and the degree of the locally fitted polynomials to extract the seasonal and trend components was set as linear. This empirical technique provided values for the long-term trend component, short-term perturbations as the residual component, and a seasonal component. Although there is possible confounding, the trend and residual components, together and individually, can be seen as a measure of the environmental challenges other than seasonal effects.

The summary statistics for these five environmental descriptors examined in this study are summarized in Table 2. While these environmental

Table 1. Categories of health challenges using producer-recorded medication records from an Australian commercial piggery between 2011 and 2016 ($n = 2,854$)

Category	Health challenges
Farrowing issues	Internal, discharge, retained, assisted farrowing, abort
Tail bite	
Lameness	Includes legs, feet, lame, claw injury, toe injury
General illness	Unwell to a non-specific illness, including unwell, anorexia, off-colour, underweight, fever, vomiting, pain, panting
Diarrhea	
Skin	Includes spots
Other	Reasons with <50 records. Includes ear infections, mastitis, urinary infection, arthritis, ulcers

Table 2. Summary statistics of the five environmental descriptors¹ based on contemporary group (CG) estimates of ADG (g/d), unadjusted and adjusted for minimum monthly temperatures (MinT), and from decomposed time-series components

Environmental descriptor based on CG estimates	Mean	Range	SD
Unadjusted	−4.6	−47.6 to 33.2	19.7
Adjusted for MinT	−3.6	−29.1 to 18.8	13.3
Decomposed trend component	−3.3	−18.8 to 6.2	8.5
Decomposed residual component	0.8	−32.9 to 33.6	11.9
Decomposed trend + residual component	−2.5	−27.0 to 26.3	14.9

¹Derived by Guy et al. (2017a, b) from between September 2010 and December 2013, $n = 39$.

descriptors were derived using all performance records from 1997 to 2013, only the years from which both CG estimates and medication records were available were used. That is, from between September 2010 and December 2013 ($n = 39$).

The monthly frequency of medication records for growing pigs was compared to the five environmental descriptors based on CG estimates described above. Pearson's correlations were used to determine the strength of the linear relationship between the frequency of monthly medication records for growing pigs and the five definitions of the environment based on CG estimates of ADG.

Analysis III. An alternative definition of health using medication status. There were insufficient medication records to derive health traits for each health challenge category. Consequently, the health trait developed was on overall health, defined as a binary trait based on medication status, Y , where pigs were classified as $Y = 1$ if medicated (case) or $Y = 0$ if not medicated (control). This outcome variable was analyzed as a binomial variable using a generalized linear mixed model, which was fitted on a sire level with a logistic link. Consequently, a logistic distribution was assumed for the underlying liability scale. Variance and covariance components were estimated using penalized quasi-likelihood method in ASReml (Gilmour et al., 2009).

For health analyzed using the pedigree constructed using reduced-control numbers, the model was as follows:

$$\log_e \left(\frac{\pi}{1 - \pi} \right) = \mu + \text{Sex}_i + \beta_1 \text{PostWeanDead} \\ + \text{Sire}_j + \text{CG}_k + \text{Litter}_l$$

where $\pi = P(Y = 1)$ is the probability of progeny from Sire j born in the k th month-year CG and l th Litter being medicated. Fixed effects included Sex_i (two levels, female, and entire male), and linear covariate of litter characteristics of number of postweaning deaths (PostWeanDead) with regression coefficient of β_1 . Random effects included Sire_j , birth-month CG_k , and common litter effect (Litter_l). The relationships between sires and their progeny were taken into account using the pedigree constructed using reduced-control and full-control numbers. For the full-control health trait, only the number of PostWeanDead was fitted as a fixed effect because Sex could not be inferred for the littermates that were not performance recorded. Although animal models are theoretically preferable to sire models, sire models were used for analysis to provide clearer links between medication

frequencies, where sires could be seen as having repeated observations or records for medication through their progeny.

Additive genetic variance was calculated as four times the estimated sire variance. The residual variance was specified as $\pi^2/3 \approx 3.29$ because a logistic link function was used in the model (Gilmour et al., 2009). Phenotypic variance was calculated as the summation of the sire genetic variance, common litter variance and the residual variance. Heritability and common litter effect was calculated as the proportion of the phenotypic variance attributed to the estimated additive genetic variance and common litter variance, respectively, expressed on the underlying liability scale.

The association between medication status and the genetic merit for growth was also explored in additional models, with the estimated breeding value (EBV) for growth fitted as a linear covariate. These EBVs were derived from Model I in Guy et al. (2017a). Mid-parent EBVs were used if the EBV for an individual was not available.

RESULTS

Analysis I. Characterization of Health Challenges Using Medication Records

The number of medication records available for each unit and the reasons for medication are presented in Figure 1. The majority of the medication records were taken from the farrowing unit (46%), followed by grower unit (22%). There were approximately equal number of records taken at the dry sow, DMA, weaner and porker units (6% to 8%). There were very few medication records from the gilt unit and records of medicated piglets still on the sow (1% to 2%).

Overall, the most common reason for medication for this herd was due to farrowing issues (44%), followed by tail bite (22%), issues with feet and legs (categorized as lameness) (11%), generally unwell (10%), other ailments (10%), diarrhea (3%), and skin conditions (1%). The number of pathogen-specific health challenges in this herd was low and was included in the 'Other' category.

For the weaner, porker, and grower unit records combined, the reasons for medication treatments indicate that the dominant health challenge in this herd was due to tail bite ($n = 480$), followed by 'generally unwell' ($n = 85$), issues involving feet and legs ($n = 85$), and skin conditions ($n = 60$). All other health challenges were recorded <25 times over the 5.5 yr period.

Monthly prevalence of medication for growing pigs. To calculate the monthly prevalence of medication, the date of birth, or at least the month of birth, of the medicated pigs needed to be known. This required the pig IDs in the medication records to align with the IDs in the pedigree and production records, which was not always possible. From the 1,012 treatments that were recorded in the weaner, porker, and grower units, there were 812

IDs of medicated pigs that aligned with IDs of pigs recorded in the pedigree. The analysis included only one medication record per pig.

The distributions of the medication prevalence differed depending on the number of control (nonmedicated) pigs used to quantify the number of pigs on farm each month (Figure 2). Using the reduced-control numbers, which included only performance-tested pigs, the medication prevalence was

Figure 1. Percentage of medication treatment reasons as described by medication records, across dry sow, detection mating area (DMA), gilt, farrow, piglets in farrowing unit, weaner, porker and grower units between 2011 and 2016 ($n = 2,854$).

Figure 2. Distribution of monthly prevalence of medication of pigs (%) born between October 2010 and March 2016, using a representative sample of littermates with available performance records (reduced-control; $n = 8,835$) and full number of nonmedicated control pigs which included all piglets weaned per litter (full-control; $n = 22,164$).

highly positively skewed, and ranged from 1.7% to 58.0% of pigs medicated per month, with a median of 7.5%. Meanwhile, use of the full-control numbers, constructed using litter records to include performance-tested and non-performance-tested pigs, resulted in monthly medication prevalence estimates ranging from 0.15% to 10.9% with a median of 2.2%.

Analysis II. Validation of infection challenges captured by the environmental descriptors based on contemporary group estimates. Five environmental descriptors based on CG estimates of ADG were examined (Table 2). The medication frequency was quantified as the number of growing pigs born in each birth-month CG which were medicated, in the weaner, grower, or porker units. Figure 3 shows the quality of environment over time as described by the five environmental descriptors and the medication frequency.

The medication frequency of growing pigs was negatively correlated with all five environmental descriptors, with Pearson's correlations ranging from -0.29 to -0.12 (Table 3). The standard error for all correlations was 0.16. The environmental descriptor based on the unadjusted CG estimates had the strongest negative linear relationship with the medication frequency ($r = -0.29$, $p = 0.08$), which is shown in Figure 4. A 10 g/d increase in the CG estimate for ADG was predicted to decrease medication frequency by 0.9 ± 0.5 ($p = 0.08$). While only marginally significantly different from 0, this indicates that better growth environments are associated with better health.

Analysis III. An Alternative Definition of Health Using Medication Status

Two health trait definitions were explored, which differed in the number of control (nonmedicated) pigs per litter. For health defined by medication status, the estimated intercept, which reflects the expected odds of medication, was higher for reduced-control health trait compared with the full-control health trait. The odds of medication was 0.11 (confidence interval, CI: 0.08, 0.15) for the reduced-control health trait compared with 0.03 (CI: 0.03, 0.04) for the full-control health trait. This reflects the estimated prevalence using the two control numbers described in Analysis I. However, the risk factors and their direction were the same. The number of postweaning deaths increased the odds of medication, estimated at 1.20 (CI: 1.04, 1.37) per death for the reduced-control health trait, and 1.36 (CI: 1.21, 1.57) for the full-control health trait. That is, in this herd, litters with higher number of postweaning deaths were more likely to be medicated. Using the reduced-control health trait, the estimated odds of a female pig being medicated was 0.61 times compared with a male pig (CI: 0.51, 0.73). Therefore, pigs in this herd were more likely to be medicated if they were male and from litters with higher number of postweaning deaths.

The genetic parameter estimates were consistent for both health trait definitions (Table 4). Heritability on the underlying liability scale was calculated at 0.06 ± 0.04 for the reduced-control

Figure 3. The quality of environment as described various environmental descriptors based on contemporary group estimates of growth (primary y-axis) (Guy et al., 2017a, b) and medication frequency for each birth-month contemporary group (CG) (secondary y-axis) over time.

Table 3. Pearson's correlations between medication frequencies and the five environmental descriptors,¹ based on contemporary group (CG) estimates of ADG (g/d), unadjusted and adjusted for minimum monthly temperatures (MinT), and from decomposed time-series components

	Unadjusted	Adjusted for MinT	Decomposed trend	Decomposed residual	Decomposed residual + trend
Medication frequency	-0.29	-0.19	-0.17	-0.12	-0.20

¹Derived by Guy et al. (2017a, b) from between September 2010 and December 2013, $n = 39$.

Figure 4. The relationship between quality of environment, quantified through contemporary group (CG, $n = 39$) estimates of ADG, and the frequency of medication of pigs born in that CG ($n = 812$ medicated pigs, $r = -0.29$, $P = 0.08$).

health trait and 0.04 ± 0.03 for the full-control health trait. To compare the use of the two trait definitions, the health EBVs of sires that had a minimum of 100 performance-tested progeny were examined. The EBVs for the reduced-control health trait and the EBVs for the full-control health trait had a Pearson's correlation of 0.74.

Postweaning survival was taken into account in this study by including the number of pigs that died in each litter. Postweaning survival as a trait of the sow reflects the maternal genetic component for postweaning survival. This requires examination and could be analyzed as number of piglets surviving after weaning as a trait of the sow, which is beyond the scope of this study. However, when postweaning death was excluded from the model, the heritability calculated for health remained stable ($\hat{h}^2 = 0.06 \pm 0.05$). This indicates that when health is defined as a trait of the growing pig, postweaning litter deaths do not contribute to the genetic variation in health. Therefore, postweaning deaths in a litter is an independent risk factor to medication status.

The nongenetic variation was partitioned between the CG and litter effects. For the reduced-control health trait, the CG variance component accounted for 0.28 ± 0.06 of the phenotypic variance, compared with 0.08 ± 0.02 of the phenotypic variance for the full-control health trait. Since the entire litter was represented in the full-control health trait, there was a larger

common litter effect estimate ($\hat{c}^2 = 0.18 \pm 0.02$) compared with the reduced-control health trait ($\hat{c}^2 = 0.09 \pm 0.03$). Nevertheless, the proportion of variability attributed to the environment of litters and the environment of CGs was greater than the proportion of variability attributed to the additive genetic variance. This indicates that more variation in health is explained by nongenetic effects than genetic effects.

In separate models to evaluate the association between health and the genetic merit for growth, a 10 g/d increase in the EBV for growth was estimated to decrease the odds of medication by 8% for the reduced-control health trait (odds ratio = 0.92), and by 4% for the full-control health trait (odds ratio = 0.96). This indicates that the animals with higher EBVs for growth are less likely to be medicated.

DISCUSSION

This study investigated the use of producer-recorded medication records to provide insight into the health challenges experienced in a pig herd. The extent to which CG estimates of growth capture the infection challenges was determined to assess the potential use of CG estimates for the genetic evaluation of disease resilience. In addition to this, a simple alternative health trait of the growing pig was provided for the genetic analysis of health using these medication records.

Table 4. Genetic parameter estimates¹ (on the underlying liability scale) for two health traits defined by medication status, which differed in the number of control (nonmedicated) pigs per litter; the ‘reduced-control’ health trait had a representative sample of littermates with performance records, and ‘full-control’ health trait included all piglets weaned per litter (i.e., performance-tested and nonperformance-tested pigs)

	$\hat{\sigma}_A^2$	$\hat{\sigma}_{CG}^2$	$\hat{\sigma}_P^2$	$\hat{\sigma}_\varepsilon^2$	$\hat{h}^2$	$\hat{c}^2$	pV_{CG}
Reduced-control	0.21 (0.17)	1.03 (0.21)	3.68 (0.19)	3.29	0.06 (0.04)	0.09 (0.03)	0.28 (0.06)
Full-control	0.17 (0.14)	0.38 (0.10)	4.07 (0.12)	3.29	0.04 (0.03)	0.18 (0.02)	0.08 (0.02)

¹ $\hat{\sigma}_A^2$ = additive genetic variance, $\hat{\sigma}_{CG}^2$ = contemporary group variance, $\hat{\sigma}_P^2$ = phenotypic variance, calculated as the summation of the sire genetic variance, common litter variance, and residual variance, $\hat{\sigma}_\varepsilon^2$ = residual variance, $\hat{h}^2$ = heritability estimate, $\hat{c}^2$ = proportion of total variance attributed to the common litter variance, pV_{CG} = proportion of total variance attributed to the contemporary group variance component (where total variance = $\hat{\sigma}_{CG}^2 + \hat{\sigma}_P^2$).

Characterization of Health Challenges Using Medication Records

Medication records are a readily available source of information about the health status of a piggery, and there is potential for use for the genetic evaluation of health. The prevalence of medication treatment of growing pigs in the weaner, porker, and grower units was estimated using two ways to quantify the number of control (nonmedicated) pigs. Since not all pigs that were on farm were taken into account in the reduced-control numbers (which included only performance-tested pigs), the medication prevalence calculated using the reduced-control numbers is an overestimation. On the other hand, because the full-control numbers was derived using numbers weaned and dummy IDs had to be created to include performance-tested pigs as well as non-performance tested pigs, there may have been medicated pigs that were not appropriately aligned to the pedigree. Therefore, the measure of medication prevalence using the full-control numbers may be an underestimation. Nevertheless, because the full-control numbers pedigree presents a more precise measure of the total number of pigs on farm each month, use of the full-control numbers provides a more accurate estimate of medication prevalence compared with using the reduced-control numbers.

The pigs with available performance and pedigree records for this herd were a representative sample of litter mates, which was decided at weaning. While there is a potential bias due to only healthy animals being selected to be performance recorded, this may be a reflection of preweaning health status. It was attempted to account for this potential bias in the health trait models with the inclusion of the number of preweaning deaths in the litter. In addition to this, the performance-tested animals may have also been affected by subclinical diseases present prior to weaning. Both aspects counteract any potential bias caused by selection of healthy animals for performance testing.

In this herd, the main reason for medication treatment of growing pigs was due to tail biting. The ‘generally unwell’ symptoms may have been caused by undiagnosed pathogenic agents, and the exact cause may not be identified without clinical laboratory testing. There was no additional information in the medication records to indicate that these ‘generally unwell’ health challenges were caused by an infection challenge. It must also be acknowledged that the information provided by medication records may be difficult to interpret as there are complex interdependencies between health challenges and the illness may be caused by several things simultaneously. While estimates are available on the proportion of Australian piggeries using various antimicrobials (Jordan et al., 2009), there is no literature currently available the proportion of individual pigs actually being medicated. Therefore, no comparisons can be made on an industry level. Nevertheless, because these medication records indicate that there have been minimal pathogenic challenges in recent years, this herd can be classified as a high-health herd.

The utility of medication records for the genetic evaluation of health relies on the producer’s ability to firstly recognize that there is a health issue, then their ability to correctly identify the issue at hand and to record it. The correct identification of health challenges can be improved with the training of veterinarians or staff who administers the medication treatments. Since medication treatments are routinely recorded for quality assurance programs, these records also have the potential to be used for monitoring the health status of the farm, and to take stock of medication supplies and their associated costs. However, medication records are often hand-written and entered by various farm managers, resulting in inconsistencies with the health challenges recorded. Recording medication treatments electronically, with standardization of health challenge categories will improve use of these records.

The electronic recording of medication treatments also applies to the identification of pigs electronically. The prevalence of health challenges was estimated using pedigree and performance records, which provide an indication of the number of growing pigs in production during a period of time. The pigs that were considered as ‘controls’ were the pigs that had a performance record but no medication record. However, these control pigs also included any medicated pigs whose IDs could not be aligned with production records, or pigs that were culled or died. Therefore, this is part of the uncertainty for this health trait definition, which may contribute to the lower heritability estimate and the reported prevalence of medication may be an underestimate. In addition to this, remixing occurred after weaning. This aspect could not be considered in our models as pen information for individual pigs was not available. The use of electronic ID, information on pen allocation and changes, and direct linkage of medication records to herd performance databases will reduce errors in data entry, and increase accuracy in estimation of medication prevalence. In turn, this may enable better estimation of the genetic source of variation in health, facilitating the inclusion of health aspects in genetic improvement programs.

Contemporary Group Estimates of Growth as Proxy for Environmental Infection Challenges

There were weak-to-moderately strong negative relationships between the environmental descriptors based on CG estimates of ADG and the corresponding medication frequency of pigs born in that CG. This means that as the quality of environment described by CG estimates for growth increases, the frequency of medication decreases. This suggests that all environmental descriptors derived by Guy et al. (2017a, b) partially describe the quality of environment in terms of health challenges. However, the best descriptor appears to be CG estimates unadjusted for other effects. While seasonality challenges may have been partitioned from other challenges captured in CG estimates, the strength of the unadjusted CG estimates supports the complex interdependency, and possible cumulative effects, of challenges that pigs may encounter.

A proxy measure of infection challenge of porcine respiratory and reproductive syndrome (PRRS) through CG estimates of reproductive traits has been demonstrated by Lewis et al. (2009). This proxy has been used for the identification of disease outbreaks and has been validated for

PRRS challenge loads through molecular diagnosis (Mathur et al., 2014). These measures of PRRS challenge load have been used to estimate variation in sow response to PRRS outbreaks (Rashidi et al., 2014) and to identify the most resilient and sensitive animals to PRRS (Herrero-Medrano et al., 2015). While this proxy measure is available for a specific disease with a marked effect on the reproductive performance of sows, the performance of growing pigs when faced with a range of nonspecific and endemic infectious challenges for more generalized disease resilience is not currently available.

While CG estimates are able to capture the health issues experienced by growing pig, the ability to measure disease resilience for this herd using routinely collected production records is limited due to the minimal pathogenic challenges experienced in this herd. This is because the majority of these challenges were not caused by infectious agents. To better define disease resilience, this requires sufficient infection challenge caused by pathogenic agents. Nevertheless, as the quality of environments described by CG estimates increases, the pigs tend to be less medicated. Therefore, CG estimates of growth can be used as environmental descriptors to evaluate the robustness of sire lines against overall environmental challenges.

A Simple Health Trait of the Growing Pig

Since disease resilience could not be evaluated for this herd, this study proposes the use of medication status as a practical and simple way to define health of the growing pig. This health trait was defined as a simple binary trait of absence/presence of disease or health incident. In pigs, Henryon et al. (2001) also used medication treatment records to derive a disease resistance trait. This health trait was defined by the number of days from the start of performance test until first treatment and diagnosis of a clinical or subclinical disease, and was estimated to have a heritability of 0.10. Mathur et al. (2018) recently used health inspection data from a pig abattoir to estimate the prevalence of health events. Logistic regression models, similar to that used in this study, were used to derive genetic parameter estimates for health traits. However, heritability estimates for health were much larger, ranging from 0.09 ± 0.02 for pleuritis to 0.24 ± 0.03 for liver lesions. To our knowledge, there have been no other studies in the pig that have quantified health status as a simple binary trait (presence/absence) using medication records. It would be beneficial to further explore health defined this way for other herds of varying health status.

Two health-trait definitions were explored, which differed in the number of control (non-medicated) pigs per litter. Genetic parameter estimates were consistent for both traits. While the full-control health trait provided a more accurate estimate of medication prevalence, the reduced-control health trait with only performance-recorded pigs appears sufficient to derive genetic parameter estimates for health. Further, the Pearson's correlation between sire EBVs from the reduced-control health trait and the sire EBVs from the full-control health trait of 0.74 provides an underestimation of the genetic correlation. While the genetic correlation threshold to distinguish traits has traditionally been 0.80 (Robertson, 1959), Mulder et al. (2006) argues that the threshold should be 0.60. Considering that this Pearson's correlation was derived using only 26 sires, and there are known errors with both health trait definitions, it is not known which health trait definition is better to use. Ultimately, it will be up to the breeder to choose which control group to use for the most reliable health trait.

While there appears to be limited genetic variation in the health trait defined through medication status for this herd, there was evidence that sires varied in the number of progeny that were medicated. Sires had on average 60 progeny, with an average of 6 (10%) that were medicated. Examining the 26 sires that had a minimum of 100 performance-recorded progeny, there were between 3.5% and 24.3% progeny medicated. The high standard error associated with the heritabilities estimated in this current study may reflect the low number of pigs that were medicated. Nevertheless, the heritability estimates align with those estimated in literature for other species. There are numerous examples of health defined as a binary trait in other species. Examples include farmer-reported health events dairy cattle, where the heritability of the overall disease trait was estimated at 0.02 ± 0.004 (Abdelsayed et al., 2017). In rabbits, the heritabilities ranged from 0.011 ± 0.002 for digestive syndromes to 0.043 ± 0.004 for infectious mortalities, using visual assessment of disease syndromes (Gunia et al., 2015). Despite these low heritability estimates for health, selection for health defined this way is currently being implemented (M. Gunia, personal communication). Therefore, combined with ensuring ideal environmental conditions for good health, selective breeding for good health in pigs may be possible, even using a simple measure of absence/presence of a health incident or medication status.

While the accuracy of genetic parameter estimates will improve with more data, the frequency

of a health issue may not necessarily be reflective of the ability to detect genetic variation in trait. For example, Gunia et al. (2015)'s health trait for infectious mortalities exhibited the most genetic variation with 4.7% of rabbits were diagnosed with the syndrome. On the other hand, the health trait for digestive syndromes exhibited the lowest genetic variation, even though more rabbits (7.1%) were diagnosed with the syndrome. Similarly, the overall health trait derived by Henryon et al. (2001), which resulted in the greatest frequency of disease due to combining numbers from all diseases, exhibited the smallest amount of genetic variation compared with disease-specific health traits. Therefore, the prevalence of disease may affect the accuracy of health parameter estimates, but not necessarily affect the ability to detect genetic variation. Nevertheless, similar to mortality traits, genetic gain in the health traits derived in this study will be low. Although these traits are important in the breeding objective relative to the genetic standard deviation, response to selection will be low due to limited information available for selection candidates (Hermesch et al., 2015a).

Since the prominent reason for medication treatment for growing pigs was due to tail bite, the health trait derived inadvertently may have been for tail bite. Although genetic variation of the trait may have been captured by the models used in this study, biting behavior is a behavioral trait (Camerlink et al., 2015) and individuals who bite may have an effect on their group mates, i.e., social genetic effects. While the methodology is available to genetically improve socially affected traits in the growing pig (Ellen et al., 2014), more information about the interactions between pigs through group structure and pen allocation is required to more accurately derive a health trait specifically for tail bite. In turn, this may increase the ability to detect genetic variation in the health traits derived. Since this information was not readily recorded for this herd, this could not be further explored in this study.

Health was defined as medicated or not medicated, regardless of the number of times they were medicated. This was decided because most of the growing pigs in this herd were medicated once, with a maximum of three times. However, a piggery of lower health status may have a greater rate of repeated medication treatments. If there are sufficient pigs that were treated more than once, a health trait can also be defined as the number of separate health incidences per pig. In turn, whether the subsequent treatments are separate health incidences needs to be determined. The minimum

period between repeated treatments before the next treatment occurrence can be considered a separate disease case can vary with each disease (Stevenson, 2000). For example, Abdelsayed et al. (2017) allowed for a minimum of 7 d for mastitis and metabolic disorders before a second treatment was considered a separate health event. On the other hand, a minimum of 14 d was allowed for lameness, reproductive, and miscellaneous disorders. While this was not required for this herd because there were limited repeated treatments, this is a consideration for other herds with repeated medication treatments. This may also be a consideration if a health trait of a sow was derived using medication status because they were medicated more frequently.

The Association Between Health and Growth in the Pig

The association between health challenges and growth traits has been well demonstrated in the pig, and has been shown across various types of challenges in a meta-analysis by Pastorelli et al. (2012). Growth also has the advantage of capturing response to subclinical infections which may not be directly observable (Clapperton et al., 2009). Therefore, a positive phenotypic association between good health and good growth is expected.

Several reviews have claimed that selection for productivity alone has been detrimental to health of the pig, and impacted the ability of pigs to cope with challenges (Prunier et al., 2010; Rauw and Gomez-Raya, 2015). While health should be included as a breeding objective trait in pig breeding programs to ensure optimum health and welfare of the pig, we question this claim that poor health is a result of selection for high productivity. It can be argued that a biological system will simply not function if the physiological and immunological mechanisms responsible for health functions are placed under too much pressure: muscle deposition and weight gain simply will not occur. More evidence is required to determine whether high productivity is directly associated with poor health.

The use of growth as an indirect indicator for health is supported by the association between higher EBVs for growth and lower odds of medication found in this study. This association was also found by Guy et al. (2018), where the genetic correlation between health and growth for the same herd as this current study was estimated to be 0.26 ± 0.34 . The large standard error associated with this preliminary estimate can be attributed to the insufficient data for this herd to provide an

accurate estimate. Nevertheless, although the direction of the genetic relationship between growth and health appears unknown, health and growth appear to be distinct traits. In pigs, the genetic correlation between growth traits at different production stages and several elbow joint disorder traits was estimated by Jørgensen and Nielsen (2005), which ranged from -0.34 ± 0.12 to 0.27 ± 0.07 . Both positive and negative genetic correlation estimates of moderate strength have also been found between health events and various growth traits in dairy cattle by Brotherstone et al. (2007). The inconsistency in direction of these correlations suggests that the association between growth and health is dependent on the type of health challenge. Productivity has only been examined with various robustness traits and not direct measures of health (reviewed by Hermes et al. (2015b)). For example, low residual feed intake selection lines have been found to be less environmentally sensitive than less-efficient high residual feed intake lines (Gilbert et al., 2014). However, more feed efficient lines have also been found to be more sensitive to heat stress (Renaudeau et al., 2013). This again demonstrates that the association between productivity and environmental and/or health stressors may be stressor dependent. To more accurately assess the association between health and productivity of the pig, more specific measures of health should be evaluated. Nevertheless, health should be included as a breeding objective trait in pig breeding programs, without fitting a genetic association with growth until sufficient data are available for re-evaluation of the genetic association between growth and health.

CONCLUSIONS

The ability to measure disease resilience using medication records for this herd was restricted due to the minimal pathogenic challenges experienced. Nevertheless, environmental descriptors based on contemporary group estimates of growth still provide a measure of the overall health challenges experienced by pigs, and also a measure of the robustness of sire lines. While results may be specific for individual herds depending on health status, these estimates align with those presented in literature for other health traits. Together, these results demonstrate that routinely collected medication records may be useful for pig breeding programs and their economic importance and genetic background should be explored further.

Conflict of interest statement. None declared.

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