Genetic parameters for health of the growing pig using medication records

S.Z.Y. Guy[1], L. Li[2], P.C. Thomson[1,2] & S. Hermesch[2]

[1] School of Life and Environmental Sciences, University of Sydney, Sydney, Australia
sarita.guy@une.edu.au (Corresponding Author)
[2] Animal Genetics and Breeding Unit, a joint venture of NSW Department of Primary Industries and University of New England, University of New England, Armidale, Australia

Summary

The objective of this study was to estimate genetic parameters for health of the growing pig. Pedigree, production and medication records were available for an Australian herd of Large White pigs, which had 812 growing pigs medicated between 2011 and 2016. The number of pigs in the herd was quantified through birth-month contemporary groups using two pedigrees – a reduced pedigree based on available performance records, and a full pedigree, constructed using numbers weaned per litter. Since the full pedigree provides a more precise measure of the number of pigs on-farm, the estimated medication prevalence of 2.2% using the full pedigree is more accurate than the 7.5% estimate using the reduced pedigree. There were minimal pathogenic challenges described in the reasons for medication, and so the herd can be classified as high-health. Genetic parameters for health, which was defined as a binary trait of medicated (case) or not medicated (control), were estimated using the reduced and full pedigree. Significant fixed effects included sex (2 levels; reduced pedigree only) and linear covariate of number of post-weaning deaths in the litter. In this herd, male pigs from litters with a higher number of post-weaning deaths were more likely to be medicated. Genetic parameter estimates were fairly consistent using either pedigree, with heritability estimated at 0.06 ± 0.04 (± SE) using the reduced pedigree, and 0.04 ± 0.03 using the full pedigree. Therefore, the reduced pedigree available from performance recording may be sufficient to derive genetic parameter estimates for health. Further, animals with higher estimated breeding values for growth were less likely to be medicated, which supports the use of growth as an indirect indicator for health. This study highlights the use of on-farm medication records to provide insight into the health status of a herd, and its potential use for the genetic improvement of health in growing pigs.

Keywords: disease, welfare

Introduction

Although pig breeding programs have been successful in increasing growth rate and reducing backfat, selection for productivity alone has impacted on the ability of pigs to cope with challenges (Prunier *et al.*, 2010). Consequently, selection for pigs that also respond appropriately to challenges has become an important issue for breeding programs (Hermesch *et al.*, 2015). Selection for health will not only produce healthier pigs, but also reduce the risk of antibiotic resistance, reduce on-farm costs and increase farm profitability.

Medication records are routinely collected in most Australian piggeries as they are required for quality assurance programs, and provide insight into the health status of a herd. The prevalence of disease reported on Australian piggeries have been disease-specific, and

the extent of medication use to manage these diseases have only been determined by subjective farmer surveys (Jordan *et al.*, 2009). Therefore, the objective of this study was to use on-farm medication records to estimate genetic parameters for health of the growing pig.

Materials and methods

Medication records were available between January 2011 and March 2016 from the University of Queensland piggery in Gatton, Queensland, Australia. Information included the date of medication, pig identification (ID), medication(s) used, dose, and reason(s) for treatment. There were 812 pigs that were born between October 2010 and March 2016, and medicated at some point between weaning to finishing phase.

The number of animals in the herd each month was quantified through birth-month contemporary groups, using two pedigrees. A reduced pedigree was based on performance recording, where there were on average 3.3 animals per litter and roughly equal numbers of male and female pigs. This reduced pedigree contained 8,835 pigs, with an average birth-month contemporary group size of 134 pigs. A full pedigree was constructed using additional information on the number of pigs weaned in each litter, which included a record for all siblings in the litter. This resulted in a total of 22,164 pigs, with an average birth-month contemporary group size of 339 pigs. Any pig in the pedigree without a medication record was assumed to not have been medicated. The monthly prevalence of medication was calculated as the percentage of pigs born each month which were medicated at some point during production.

An overall health trait was developed, defined as a binary trait of medicated (case) or not medicated (control). This was analysed as a binomial variable using a generalised linear mixed model, which was fitted on a sire level with a logistic link in ASReml (Gilmour *et al.*, 2009). For health analysed using the reduced pedigree, significant fixed effects included sex (2 levels) and linear covariate of number of post-weaning deaths in the litter. For health analysed using the full pedigree, only the number of post-weaning deaths was fitted as a fixed effect since sex could not be inferred. Random effects for both traits included sire, common litter effect and birth-month contemporary group. 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 (derived in Guy *et al.* (2017)). Mid-parent EBVs were used if the EBV for an individual was not available.

The additive genetic variance was estimated as four times the estimated sire variance. The phenotypic variance was calculated as the summation of the sire variance, common litter variance and the residual variance (specified as $\pi^2/3$). Heritability and common litter effect were estimated as the proportion of the phenotypic variance attributed to the estimated additive genetic variance and common litter variance, respectively.

Results and discussion

The reasons for medication treatment 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 less than 25 times over the 5.5 year period. While there are complex interdependencies between health challenges, and the 'generally unwell' symptoms may have been caused by undiagnosed infectious agents, these medication records indicate that there were minimal pathogenic challenges and that this herd can be classified as high-health.

Using the reduced pedigree, the monthly prevalence of medication was highly positively skewed, and ranged from 1.7% to 58.0% of pigs medicated per month, with a median of 7.5%. Since not all pigs that were on-farm were taken into account in the reduced pedigree, this medication prevalence is overestimated. On the other hand, the monthly prevalence of medication treatments using the full pedigree ranged from 0.15% to 10.9%, with a median of 2.2%. This measure of medication prevalence did not include the medicated pigs that were not performance recorded, and so may be an underestimation. However, since the full pedigree presents a more precise measure of the total number of pigs on-farm each month, use of the full pedigree provides a more accurate estimate of medication prevalence compared to using the reduced pedigree.

For the health trait defined by medication status, the estimated intercept was higher using the reduced pedigree. This reflects the estimated prevalence using the two pedigrees (Table 1). However, the risk factors and their direction were the same. The number of post-weaning deaths increased the odds of medication, estimated at 1.20 per death using the reduced pedigree, and 1.38 using the full pedigree. That is, in this herd, litters with higher number of post-weaning deaths were more likely to be medicated. Using the reduced pedigree, the estimated odds of a female pig being medicated was 0.61 times compared to a male pig.

Table 1. Fixed effect estimates[1] and (95% confidence interval, CI) for health defined by medication status, derived using a reduced pedigree (Reduced) and full pedigree (Full).

	Intercept	Sex[2]	Post-weaning deaths
Reduced	0.11 (CI: 0.08, 0.15)	0.61 (CI: 0.51 , 0.73)	1.20 (CI: 1.04, 1.37)
Full	0.03 (CI: 0.03, 0.04)	-	1.38 (CI: 1.21, 1.57)

[1] reported as odds for intercept, and odds ratios for sex and post-weaning
[2] male as reference level

The genetic parameter estimates were consistent using both pedigrees (Table 2). Heritability on the underlying liability scale was estimated at 0.06 ± 0.04 using the reduced pedigree, and 0.04 ± 0.03 using the full pedigree. Due to the litter having full representation in the pedigree, there was a larger common litter effect using the full pedigree, which also reduced the contemporary group variance. With a large proportion in variability attributed to the environment of litters and the environment of contemporary groups, this indicates that more variation in health is explained by non-genetic effects than genetic effects.

Table 2. Genetic parameter estimates[1] for health (on the underlying liability scale) defined by medication status, derived using a reduced pedigree (Reduced) and full pedigree (Full).

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

[1] $\hat{\sigma}^2_A$ = additive genetic variance, $\hat{\sigma}^2_{CG}$ = contemporary group variance, $\hat{\sigma}^2_P$ = phenotypic variance, $\hat{\sigma}^2_e$ = residual variance, $\hat{h}^2$ = heritability estimate, $\hat{c}^2$ = common litter effect

To compare the use of the two pedigrees, the health EBVs of sires that had a minimum of 100

progeny were examined. The EBVs from the reduced pedigree and the EBVs from the full pedigree had a Pearson's correlation of 0.74. While this provides an underestimation of the genetic correlation (Calo *et al.*, 1973), this indicates that the health trait analysed using the two pedigrees are the same trait. Therefore, while use of a full pedigree provides a more accurate estimate of medication prevalence, the reduced pedigree available through performance recording may be sufficient to derive genetic parameter estimates for health.

In separate models to evaluate the association between health and the genetic merit for growth, a 10 g/day increase in the EBV for growth was estimated to decrease the odds of medication by 8% using the reduced pedigree (odds ratio = 0.92), and by 4% using the full pedigree (odds ratio = 0.96). This indicates that animals with higher EBVs for growth are less likely to be medicated, and which supports the use of growth as an indirect indicator for health.

Health can be defined as a simple binary trait of absence/presence of disease. Health traits of the growing pig defined as binary traits through health records have not been widely explored. Henryon *et al.* (2001) defined a health trait of the pig as the time until first treatment and diagnosis of a clinical or subclinical disease. With an overall disease prevalence of 24%, heritability for this trait was estimated at 0.18 ± 0.05 on the log-frailty scale. In other species, the presence/absence of reported health events have been widely used to estimate genetic parameters for health. Examples include dairy cattle, where a heritability estimate of 0.02 ± 0.004 was reported for overall disease incidence (Abdelsayed *et al.*, 2017). In rabbits, health traits derived from carcase assessment ranged in heritability estimates from 0.01 ± 0.002 for digestive syndromes to 0.04 ± 0.004 for infectious mortalities (Gunia *et al.*, 2015). Therefore, simple health traits can be derived from medication or disease status. These medication records allow for the routine monitoring of health on farms, and provides a practical approach for the inclusion of health in breeding objectives.

Conclusions

This study highlights the use of medication records to provide insight into the health status of a herd, and its potential use for the genetic improvement of health in growing pigs. While use of a full pedigree provides a more accurate estimate of medication prevalence, the reduced pedigree available from performance recording may be sufficient to derive genetic parameter estimates for health.

Acknowledgement

S.Z.Y. Guy is a recipient of a Pork CRC postgraduate scholarship. The authors thank Gatton piggery for providing data, and GaoYu Xu and Baukje Hollema for assisting data preparation.

List of References

Abdelsayed, M., M. Haile-Mariam & J.E. Pryce, 2017. Genetic parameters for health traits using data collected from genomic information nucleus herds. J. Dairy Sci. 100(12): 9643-9655.

Calo, L.L., R.E. McDowell, L.D. VanVleck & P.D. Miller, 1973. Genetic Aspects of Beef Production among Holstein-Friesians Pedigree Selected for Milk Production. J. Anim. Sci. 37(3): 676-682.

Gilmour, A.R., B.J. Gogel, B.R. Cullis & R. Thompson, 2009. ASReml User Guide Release

3.0. VSN International Ltd., Hemel Hempstead, UK.
Gunia, M., I. David, J. Hurtaud, M. Maupin, H. Gilbert & H. Garreau, 2015. Resistance to infectious diseases is a heritable trait in rabbits. J. Anim. Sci. 93(12): 5631-5638.
Guy, S.Z.Y., L. Li, P.C. Thomson & S. Hermesch, 2017. Contemporary group estimates adjusted for climatic effects provide a finer definition of the unknown environmental challenges experienced by growing pigs. J. Anim. Breed. Genet. 134(6): 520–530.
Henryon, M., P. Berg, J. Jensen & S. Andersen, 2001. Genetic variation for resistance to clinical and subclinical diseases exists in growing pigs. Anim. Sci. 73(3): 375-387.
Hermesch, S., L. Li, A.B. Doeschl-Wilson & H. Gilbert, 2015. Selection for productivity and robustness traits in pigs. Anim. Prod. Sci. 55(12): 1437-1447.
Jordan, D., J.-C. Chin, V.A. Fahy, M.D. Barton, M.G. Smith & D.J. Trott, 2009. Antimicrobial use in the Australian pig industry: results of a national survey. Australian veterinary journal 87(6): 222-229.
Prunier, A., M. Heinonen & H. Quesnel, 2010. High physiological demands in intensively raised pigs: impact on health and welfare. Animal 4(6): 886-898.