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GENOTYPE BY TRAIT-SPECIFIC SEASON INTERACTIONS FOR FARROWING RATE AND AVERAGE PIGLET BIRTHWEIGHT

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SUMMARY

The aim of this study was to investigate if there are interactions between genotype and trait-specific seasons (GxTrS) for average piglet birth weight and farrowing rate from sow litters. A series of bivariate animal models were used to estimate genetic parameters. The current study found GxTrS for farrowing rate (genetic correlation <0.4), but not for average piglet birth weight (genetic correlation >0.9). Farrowing rate recorded in the least stressful season (low temperature and positive change in day length) was genetically different to farrowing rate recorded in the two most stressful seasons (high temperature and increasing day length or high temperature and decreasing day length). The results of this study showed that seasonal infertility in sows can genetically be improved by using trait-specific seasons. However, the heritability of farrowing rate was very low ($h^2=0.02$) and improving the temperature control in the sow's housing environment and developing effective strategies to minimise the effects of changes in day length on the sows may be more effective to improve seasonal infertility.

INTRODUCTION

The reproductive efficiency of sows is economically important in pig production and has been observed to be affected by seasonal variation; in particular poor reproductive performance in summer (Love *et al.* 1993, Auvigne *et al.* 2010). Previous studies have defined seasons using calendar months or temperature and photoperiod information fitted separately at a single time point to investigate genotype by season interactions (Lewis and Bunter 2011, Sevillano *et al.* 2016). A novel methodology has been developed to define trait-specific seasons (modified from Bunz *et al.* 2019), which accounts for both temperature and photoperiod information simultaneously across multiple important time points. This study hypothesised that interactions between genotype and trait-specific seasons (GxTrS) exist for the reproductive traits of average piglet birthweight and farrowing rate recorded in mature sows.

MATERIALS AND METHODS

The traits investigated were farrowing rate calculated from the first insemination event within each mating cycle (FR1: 0=fail due to reproductive reasons, 1=pregnant) and average piglet birth weight (PWT) using multiparous-sow records. The data from two maternal lines (Large White: LW, and Landrace: LD) and one terminal line (Duroc: DC) were collected from a single farm in southern New South Wales, Australia. Data included 42,248 FR1 records from 14,667 sows (daughters of 1,161sires) and a subset of these sows (N=9,402 sows; daughters of 1,077 sires) with 20,293 PWT records collected between 2013 and 2019. All mating events were performed using artificial insemination with each sow receiving two inseminations from the same boar. Sows were housed in naturally ventilated sheds, during gestation and lactation.

The two steps used to define trait-specific seasons were: 1) A series of single-day models were applied to identify the most informative days ($P < 0.05$) for FR1 and PWT regarding maximum

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temperature (tmax) and change in day length (dl) in a trait-specific time period. The single-day linear mixed models were fitted using the *lme4* procedure in R (R Development Core Team 2022), represented as:

$$y_{\mathrm{ijklm}} = \mu + \mathrm{matingtype}_{\mathrm{i}} + \beta(\mathrm{tmax\ day\ x}) + \beta(\mathrm{dl\ day\ x}) + \mathrm{paritygr}_{j} + \mathrm{lactlength}_{\mathrm{k}} + pe_{l} + \mathrm{quarteryear}_{\mathrm{m}} + e_{ijklm}\ (Model\ 1)$$

where y_{ijklm} are the observations for FR1 or PWT, μ is the overall mean effect, $\mathrm{matingtype}_{\mathrm{i}}$ is the fixed effect of the *i*th mating type (5 levels, LW x LW; LD x LD; LW x LD; LD x LW; DC x DC), $\mathrm{paritygr}_{\mathrm{j}}$ is the fixed effect of the *j*th parity grouping (4 levels, p1;p2;p3; p4), covariate of tmax day x and dl day x, where x is one day in the investigated trait-specific time period, $\mathrm{quarteryear}_{\mathrm{m}}$ is the fixed effect of the *m*th quarter year of trait recording (32 levels over the complete time periods) and the permanent environment of the sow (pe_{l}) was fitted to account for repeated records for FR1 and PWT. The fixed effect of previous $\mathrm{lactlength}_{\mathrm{k}}$, representing the *k*th lactation length grouping (4 levels, quartiles), was significant for FR1 only. For PWT, the time period considered was from 115 days before the farrowing date to the farrowing date and for FR1 the time period was from 45 days before to 18 days post the first mating date. Fitting a generalised linear model with a logit link function for FR1 did not converge; therefore, a linear mixed model was applied to FR1; 2) A cluster procedure (R Development Core Team 2022) was then used to group tmax and dl patterns based on the most informative days for every mating date (FR1) or farrowing date (PWT) which resulted in the definition of four clusters to represent trait-specific seasons (Table 1).

Parameter estimates for each trait were then obtained using an animal model in ASReml (Gilmour *et al.* 2015). Additional to Model 1, the random additive genetic effect of the *n*th sow (animal). Further, the permanent environmental effect of the *o*th service sire (s_{n}) was fitted for FR1. Covariate of tmax and dl was not fitted in the animal model. Random variables were included in models if significant ($P < 0.05$) based on a log-likelihood ratio test. Effects were distributed as var(a)=$\boldsymbol{A}\sigma_a^2$, where $\boldsymbol{A}$ is a matrix describing the relationships between animals (i.e., a numerator relationship matrix), and for the remaining effects: Var(pe)=$\boldsymbol{I}\sigma_{pe}^2$, Var(s)=$\boldsymbol{I}\sigma_s^2$ and Var(e)=$\boldsymbol{I}\sigma_e^2$, where $\boldsymbol{I}$ is an Identity matrix. For each trait-specific season, genetic parameters were obtained. A series of bivariate animal models was applied to estimate genetic correlations between the trait-specific seasons to measure the magnitude of GxTrS for each trait fitting the same fixed and random effects that were fitted in the univariate analyses.

RESULTS AND DISCUSSION

Defining Seasons. Seasons were trait-specific, varied across years and were not the same as the standard four calendar seasons (Figure 1) due to the different informative days for tmax and dl between traits, and the variation in temperature across years. For FR1, high tmax and negative change in dl around the time of mating had the largest reduction in performance, which was Season 2. For PWT, high tmax and negative change in dl during early gestation and low tmax at late gestation had the lowest mean, which was Season 3 (Table 1).

Univariate Analysis. This study found low heritabilities for FR1 (Table 2), similar to those reported by Sevillano *et al.* (2016) and no additive variance was found in Season 3 (Table 2). However, heritability estimates for FR1 differed only marginally between seasons. Moderate heritabilities were found for PWT (Table 2), which were lower than previously reported by (Lewis and Bunter 2011). Season 1 of PWT had a lower heritability (h^2=0.17) than the other seasons due to a lower additive genetic variance, however the phenotypic variance was similar across Seasons.

Bivariate Analysis. Estimates of genetic correlations between the same trait recorded in different trait-specific seasons are shown in Table 2. The standard errors for genetic correlations were high for FR1 due to the low heritability. The genetic correlations were low between Season 4 and the first two seasons, suggesting that FR1 in Season 4 was genetically a different trait than in

Season 1 and Season 2. The first two seasons of FR1 had opposite tmax characteristics compared to Season 4, which could explain the low genetic correlation found in this study. Sevillano *et al.* (2016) found a higher genetic correlation (0.46±0.13) of farrowing rate between opposite environments (stressful and non-stressful) using a bivariate model. Better environmental control for the sows, during lactation, wean to service period and early gestation could reduce the magnitude of the GxTrS. The current study shows that the combined effects of high tmax and dl (Season 2) had the largest GxTrS and therefore it is important to account for both tmax and dl for defining the presence of genotype by season interactions for FR1 outcomes.

Table 1. Data characteristics for farrowing rate (FR1) and average piglet birthweight (PWT) recorded in sows according to trait-specific seasons (Sn), maximum temperature (tmax) and change in daylight length(dl) characteristics

Trait	Sn	Trait-specific season characteristics	N records	Mean(sd)
FR1	1	tmax from medium to high; dl positive	8,130	0.87(0.33)
	2	tmax from high to medium; dl negative	14,497	0.83(0.38)
	3	tmax low; dl negative	6,562	0.88(0.33)
	4	tmax low; dl positive	13,059	0.90(0.30)
PWT	1	tmax from low to high through gestation; dl positive	6,827	1.61(0.25)
	2	tmax from medium to high through gestation; dl negative	5,012	1.59(0.25)
	3	tmax from high to low through gestation; dl negative	5,137	1.56(0.25)
	4	tmax low through gestation; dl positive	3,317	1.59(0.26)

Abbreviations: Mean tmax: high >28ºC; medium 22-28°C; low <22ºC
Mean dl: positive = daylength is increasing;
negative = day length is decreasing

Figure 1. Distribution of calendar days according to the four trait-specific seasons for farrowing rate (FR1) and average piglet birthweight (PWT) over two years 2015 & 2016. Days with missing records were coloured white

Further, there was a high genetic correlation between Season 1 and Season 2 for FR1, indicating that as temperature tolerance is improved, seasonal tolerance will also genetically improve. These results are supported by Sevillano *et al.* (2016), who found that pigs tolerant to decreasing dl are also more tolerant to high tmax. The standard errors for genetic correlations were high for FR1 due to the low heritabilities in all seasons. It was not possible to estimate genetic correlations between Season 3 and other Seasons for FR1 due to the additive genetic variance not being estimable in Season 3.

Genetic correlations between PWT recorded in different Season were high (genetic correlation > 0.9) supporting the result of Lewis and Bunter (2011), which found that PWT was the same trait across all calendar seasons.

Table 2. Heritability estimates (in bold on the diagonal), with genetic (above diagonal) and phenotypic correlations (below diagonal) for farrowing rate (FR1) and average piglet birthweight (PWT) between trait-specific seasons

Trait	Season	1	2	3	4
FR1	1	**0.02±0.01**	0.80±0.36	ne	0.38±0.37
	2	0.04±0.00	**0.02±0.01**	ne	0.22±0.29
	3	ne	ne	**0.00±0.00**	ne
	4	0.04(0.02)	0.03(0.01)	ne	**0.02±0.01**
PWT	1	**0.17±0.03**	0.99±0.03	0.94±0.04	0.97±0.04
	2	0.31±0.02	**0.27±0.03**	1.00±0.04	1.00±0.06
	3	0.35±0.01	0.32±0.02	**0.21±0.04**	1.00±0.03
	4	0.33±0.02	0.34±0.02	0.34±0.02	**0.24±0.03**

CONCLUSION

This study showed that season defined by trait informative days for tmax and dl differed for FR1 and PWT traits, and was accompanied by seasonal differences in mean performances. The study also showed that genotype by season interactions existed for FR1 but not for PWT. Farrowing rates observed in Season 4 versus 1 or 2, which were characterised by opposite mean temperature patterns around mating events, were genetically different traits. The results of this study show that using trait-specific seasons can provide an opportunity to improve seasonal infertility in pigs genetically.

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REFERENCES

Auvigne V., Leneveu P., Jehannin C., Peltoniemi O. and Salle E. (2010) *Theriogenology* **74:** 60.

Bunz A., Bunter K., Morrison R.S., Luxford B. and Hermesch, S.(2019) *Proc. Assoc. Advmt. Anim. Breed. Genet.* **23:** 155.

Gilmour A., Gogel B., Cullis B., Welham S. and Thompson R. (2015) *Hemel Hempstead: VSN International Ltd*

Lewis C.R. and Bunter K.L. (2011) *Anim. Prod. Sci.* **51:** 615.

Love R.J., Evans G. and Klupiec C. (1993) *J. Reprod. Fert.* **48:** 191.

R Development Core Team, 2022.R: A language and environment for statistical

Sevillano C.A., Mulder H.A., Rashidi H., Mathur P.K. and Knol E.F. (2016) *J. Anim. Sci.* **94:** 3185.