

## Genomic analysis of reproductive traits in health challenged commercial sow herds

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### Summary

Reproductive traits are difficult to select for due to low heritability and late expression of the traits. However, genomic information can be used to detect quantitative trait loci (QTL) for these traits, which may improve the accuracy of selection. In addition, acclimation strategies for gilts that enter the herd can affect reproductive performance. The objectives of this study were to estimate genetic parameters, to identify QTL associated with reproductive traits in commercial crossbred sows, and to determine the impact of acclimation on reproductive performance.

Performance data from 1 to 4 parities and genotypes (40K SNPs) were available from 21 commercial farms on Large White x Landrace sows from 7 breeding companies (PigGen Canada). Traits analyzed included total number of piglets born (TB), number of piglets born alive (NBA), number of stillborn piglets (SB), number of mummified piglets (MUM), number of piglets weaned (NW). In addition, gilt average daily gain during acclimation (ADG) and PRRS vaccination status (Vx) were available. Genetic parameters (heritabilities) were estimated using ASReml v.4 and genome-wide associations were performed in GenSel.

Heritabilities for TB ranged from  $0.12 \pm 0.04$  (parity [p] 1) to  $0.21 \pm 0.04$  (p2), NBA from  $0.05 \pm 0.06$  (p4) to  $0.15 \pm 0.04$  (p2), SB from  $0.08 \pm 0.04$  (p2) to  $0.11 \pm 0.05$  (p3), MUM from  $0.00 \pm 0.00$  (p3) to  $0.05 \pm 0.03$  (p1), NBD from  $0.06 \pm 0.06$  (p4) to  $0.10 \pm 0.04$  (p1), and NW  $0.00 \pm 0.00$  (p1) to  $0.27 \pm 0.07$  (p4). There were significant effects of ADG on TB and NBA for parity 1. In parity 1, regions associated with TB, NBA, and SB explained 13.9% (chromosome [SSC]1 and SSC6), 10.8% (SSC2 and SSC10), and 20.9% (SSC13) of the genetic variance (GV), respectively. For parity 2, regions associated with SB, MUM, and NW explained 3.9% (SSC11), 3.8% (SSC4), and 10.7% (SSC15) of the GV. In parity 3, regions associated with NW accounted for 4.7% (SSC7) of the GV. In parity 4, regions associated with TB and NW explained 10.6% (SSC13) and 15.8% (SSC13) of the GV, respectively.

These results indicate that reproductive traits are lowly heritable. Greater ADG during acclimation positively affected TB and NBA during parity 1. The GWAS revealed QTL that correspond to corpus luteum number, teat number, age at puberty, TB, NBA, SB, and MUM, all traits that are related to reproduction.

*Keywords: genome-wide association study, reproductive performance, gilt acclimation*

## **Introduction**

Sow reproduction is a key component of profitability in the swine industry. High producing sows that stay in the herd through productive parities produces enhances profitability. Reproductive traits (e.g. number of piglets born alive; NBA) are difficult to select for and change using genetic selection due to low heritability (~10%; Lamberson, 1990), expression after normal selection age and sex limited expression. However, genomic information can be used to detect quantitative trait loci (QTL) for these traits, which can be used to improve the accuracy of selection.

Another important aspect that may affect reproductive performance is the procedures used during the gilt acclimation period, which is the time when a gilt is brought onto a farm and vaccinated and/or exposed to pathogens that are common to the farm (Serão *et al.*, 2016). Different acclimation procedures can have positive or negative effects on reproductive performance, especially in parity 1. Therefore, the objectives of this study were to estimate genetic parameters, to identify QTL for reproductive traits in commercial crossbred sows, and to investigate the impact of gilt acclimation procedures on reproductive performance.

## **Materials and Methods**

### **Description of data**

The data used in this study was provided by 7 breeding companies that are members of PigGen Canada (Guelph, ON, Canada). A total of 3,015 White x Landrace F1 replacement gilts were sourced from 17 multiplier herds (2 or 3 per breeding company) and these were sent out to 23 commercial farms (1 to 3 per multiplier) with a history of disease problems and a range of acclimation procedures. The gilts were introduced into commercial herds in groups (contemporary group; CG) that ranged in size from 10 to 63 animals, for a total of 106 CG. All gilts followed the standard acclimation and gilt rearing procedures that routine for each farm.

Reproductive data was available from 1 to 4 parities with a total of 7,635 farrowing events from 2,604 sows that were used in this analysis. The acclimation period included the first 30 days after the animals entered the farm, at which time they weighed between 100 and 165 kg. Average daily gain (ADG) during the acclimation period was available for 2,511 gilts. Vaccination records were available for 2,894 gilts. A total of 3,615 animals (including some of the parents of the gilts) were genotyped using one of three versions of the Illumina PorcineSNP BeadChip, which had 42,145 SNPs in common. After quality control, 38,191 SNPs were used in analysis.

### **Data analysis**

Traits analyzed included total number of piglets born (TB), number of piglets born alive (NBA), number of stillborn piglets (SB), number of mummified piglets (MUM), number of piglets born dead (NBD), number of piglets weaned (NW), average daily gain during acclimation (ADG), and gilt acclimation status(Vx). Each trait was analyzed separately by parity. Genetic parameters (heritabilities) were estimated using a genomic relationship matrix (GRM; VanRaden, 2008) in

the following model in ASReml4 (Gilmour *et al.*, 2015):

$$(1)$$

where  $y_{ijk}$  is the phenotype;  $\mu$  is the intercept;  $CG_i$  is the fixed effect of the  $i^{\text{th}}$  level of contemporary group;  $YM_j$  is the fixed effect of the  $j^{\text{th}}$  level of farrowing year-month;  $u_{ijk}$  is the breeding value; and  $e_{ijk}$  is the residual error. Breeding values and residuals were assumed to be normally distributed with  $\sigma^2$  and  $\sigma^2$ . For NW, the net number of piglets fostered was added to the model as a covariate. The effect of gilt acclimation was tested by adding ADG (covariate) and PRRS vaccination status separately as effects in the model for each trait.

Genome-wide association studies (GWAS) were performed using Bayesian methods in GenSel v. 4R (Fernando *et al.*, 2009). The same fixed effects described above were used in this step. Bayes-C $\pi$  was used to obtain an estimate for the number of SNPs that had zero effect on the trait ( $\pi = 0.995$ ), which was then used for analysis with Bayes-B to find the location of QTL and estimate amount of variance explained by the identified QTL.

## Results and Discussion

Heritability estimates for parities 1 to 4 are found in Table 1. Heritabilities for TB ranged from  $0.12 \pm 0.04$  (parity [p] 1) to  $0.21 \pm 0.04$  (p2), NBA from  $0.05 \pm 0.06$  (p4) to  $0.15 \pm 0.04$  (p2), SB from  $0.08 \pm 0.04$  (p2) to  $0.11 \pm 0.05$  (p3), MUM from  $0.00 \pm 0.00$  (p3) to  $0.05 \pm 0.03$  (p1), NBD from  $0.06 \pm 0.06$  (p4) to  $0.10 \pm 0.04$  (p1), and NW  $0.00 \pm 0.00$  (p1) to  $0.27 \pm 0.07$  (p4). These results indicate that reproductive traits are overall lowly heritable, but heritability increased after parity 1 for TB, NBA, and most significantly for NW.

*Table 1: Heritabilities for reproductive traits by parity.*

| Parity | TB          | NBA         | SB          | MUM         | NBD         | NW          |
|--------|-------------|-------------|-------------|-------------|-------------|-------------|
| 1      | 0.12 (0.04) | 0.09 (0.03) | 0.11 (0.04) | 0.05 (0.03) | 0.10 (0.04) | 0.00 (0.00) |
| 2      | 0.21 (0.04) | 0.15 (0.04) | 0.08 (0.04) | 0.04 (0.04) | 0.07 (0.04) | 0.01 (0.03) |
| 3      | 0.20 (0.06) | 0.14 (0.05) | 0.11 (0.05) | 0.00 (0.00) | 0.07 (0.05) | 0.02 (0.05) |
| 4      | 0.12 (0.06) | 0.05 (0.06) | 0.08 (0.06) | 0.01 (0.05) | 0.06 (0.06) | 0.27 (0.07) |

TB = Total number piglets born; NBA = Number piglets born alive; SB = Number stillborn piglets; MUM = Number mummified piglets; NBD = Number piglets born dead; NW = Number piglets weaned

PRRS vaccination was not associated ( $P > 0.05$ ) with subsequent reproductive performance. However, acclimation ADG had an impact ( $P < 0.05$ ) on TB and NBA at parity 1, in which animals have estimates of 0.11 and 0.15 kg per day, respectively, indicating that greater ADG is associated with greater TB or NBA at parity 1.

The results of the GWAS are presented in Table 2. In parity 1, regions associated with TB, NBA, and SB explained 13.9% (chromosome [SSC]1 and SSC6), 10.8% (SSC2 and SSC10), and 20.9% (SSC13) of the genetic variance (GV), respectively. For parity 2, regions associated with SB, MUM, and NW explained 3.9% (SSC11), 3.8% (SSC4), and 10.7% (SSC15) of the GV. In parity 3, regions associated with NW accounted for 4.7% (SSC7) of the GV. In parity 4, regions associated with TB and NW explained 10.6% (SSC13) and 15.8% (SSC13) of the GV, respectively. The GWAS revealed QTL that correspond to corpus luteum number, teat number, age at puberty, TB, NBA, SB, and MUM, all traits that are related to reproduction. A novel QTL was also found for NBA for parity 1.

*Table 2: Amount of genetic variance explained and location of QTL by trait within parity*

| Parity | Trait <sup>1</sup> | %Variance | Location   | Parity | Trait | %Variance | Location |
|--------|--------------------|-----------|------------|--------|-------|-----------|----------|
| 1      | TB                 | 13.9      | SSC 3 & 6  | 3      | NW    | 4.7       | SSC 7    |
|        | NBA                | 10.7      | SSC 2 & 10 |        |       |           |          |
|        | SB                 | 20.9      | SSC 13     |        |       |           |          |
| 2      | SB                 | 3.9       | SSC 11     | 4      | TB    | 10.6      | SSC 13   |
|        | MUM                | 3.8       | SSC 4      |        | NW    | 15.8      | SSC 13   |
|        | NW                 | 10.7      | SSC 15     |        |       |           |          |

TB = Total number piglets born; NBA = Number piglets born alive; SB = Number stillborn piglets; MUM = Number mummified piglets; NBD = Number piglets born dead; NW = Number piglets weaned

Future research includes investigation of QTL for sow longevity, lifetime performance and lifetime productivity traits as well as genomic prediction.

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