

# Identification of Genomic Regions Associated With Lactation Performance in Yorkshire Sows

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### Summary and Implications

Lactation is an economically important phase in the lifecycle of sows, and events that happen during that period have a big impact on longevity of the sow and therefore profitability of the operation. The difficulty in collecting accurate phenotypes that are required to assess lactation performance, and the inability to evaluate longevity of sows in nucleus herds, highlight the importance of using genomic tools to examine the underlying genetics of these traits. The goal of this project was to conduct genome wide association studies (GWAS) of traits related to lactation in Yorkshire sows using 60k SNP marker information. A 1 Mb region on chromosome 2 (SCC2), which showed strong evidence of linkage disequilibrium, explained around 50% of genetic variation for total weaning weight of litter and litter weight gain for sows in parity 2 and also affected parity 3 phenotypes. These results are extremely encouraging and may be useful in marker assisted or genomic selection to improve lactation performance, especially litter weaning weight of sows in parity 2 and higher.

### Introduction

Lactation is an energy demanding process for sows and better performance during lactation results in increased litter weight gain, decreased body tissue loss and minimization of weaning to estrus interval. Improving sow performance during lactation can decrease culling rates, increase longevity and thereby increases profitability of the commercial operation. Some of the traits used to measure sow lactation performance are total weaning weight of litter (TWW), litter weight gain (LWG), sow body weight loss (SWL), sow back fat loss (BFL), sow loin loss (SLL) and sow feed intake during lactation (SFI). Genetic improvement of lactation performance is, however hampered by the low heritability of most of these traits and the need to collect accurate data on feed intake and body composition during lactation. These limitations could be overcome if we can identify genetic markers associated with these traits and can explain the variation contributed by these markers. Thus, the objective of this study was to

identify genomic associations for these traits, which in the future can be utilized for genomic or marker assisted selection.

### Materials and Methods

The data were provided by Genesus Inc. from pureline Yorkshire sows maintained at one of their nucleus breeding facilities. Complete details on 1,309 farrowings from 843 sows recorded between August 2011 and September 2013 were utilized to estimate genetic parameters. The sows were weighed and scanned for back fat and loin depth before farrowing and at weaning and piglets were weighed at birth, at the time of fostering (if any) and at death or weaning. Daily feed intake of sows was measured using the Gestal<sup>®</sup> feed recording system. Heritabilities were estimated with a single trait linear mixed model analysis using the software ASReml. All models included the fixed effects of parity (3 levels), contemporary group based on week of weaning (97 levels), random animal effects and permanent environment effects. Covariates included in the model were lactation length, average birth weight of weaned pigs, sow body weight, back fat and loin depth at the time of farrowing, proportion of male piglets in the litter, and piglet load, which was a daily sum of the number of piglets nursed by the sow.

Of the sows described above, 531 (with 868 litters) were genotyped using the Illumina porcine 60k bead chip which contains 60,000 gene markers. The GWAS was conducted separately for parity 1 (n=414) and 2 (n=340) phenotypes using the statistical software GenSel. Based on GWAS results, the genotype of the most significant marker was used as a fixed class effect in the animal model described above as an interaction with parity, and LSmeans and allele substitution effects of that marker were estimated.

### Results and Discussion

Heritability estimates were moderate for SWL ( $0.24 \pm 0.06$ ) and SFI ( $0.29 \pm 0.06$ ), but low for TWW ( $0.14 \pm 0.05$ ), LWG ( $0.14 \pm 0.06$ ), BFL ( $0.11 \pm 0.05$ ) and SLL ( $0.15 \pm 0.05$ ). A one Mb region on chromosome 2, which exhibited strong linkage disequilibrium, explained 59% of the genetic variance for TWW and 48% for LWG for parity 2 phenotypes but less than 0.1% of genetic variation for parity 1 records. For BFL, the same region explained the highest, though low, proportion of variance for parity 2 records (0.33%) but less than 0.2% of genetic variance for traits SLL, SWL and SFI in both parities. The genomic EBVs calculated for TWW and LWG for parity 2 sows, based on the 35 SNPs in this window, showed that the animals could be grouped into three distinct classes, suggesting the presence of a biallelic quantitative trait locus

(QTL) in this region. Further investigation showed that one particular SNP in that window captured all variation contributed by this region. The favorable allele of this SNP had a frequency of 0.6 and the genotypes were in Hardy Weinberg equilibrium.

Fitting the genotype of this marker as a fixed class effect in the animal model analysis showed that the effects of genotype were significant for traits LWG, TWW, SLL ( $P < 0.001$ ) and BFL ( $P < 0.01$  and  $0.09$ ) for parities 2 and 3 but were not significant for these traits in parity 1 ( $P > 0.32$ ). The estimates of allele substitution effects summarized in table 1 support these findings. Positional candidate genes identified at this region were associated with the monosaccharide metabolic process.

### Conclusions

It can be concluded that a region on SCC2 carries a QTL that has a significant impact on litter growth traits for Yorkshire sows in parity 2 and later. These results can potentially aid in marker assisted selection for traits such as weaning weight. Absence of effects of this region for parity 1 traits also corroborates the assumption that parity 1 and 2 traits should be considered as different traits. The results need further validation for different traits in additional data from this and other breeds.

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**Table 1. Estimates of allele substitution effects of the significant genetic marker on SSC2 by parity**

	Parity		
	1	2	3
Total weaning weight of litter (TWW, kg)	0.64 ± 0.72	5.37 ± 0.94	1.39 ± 1.59
Litter weight gain (LWG, kg)	0.47 ± 0.67	5.10 ± 0.85	2.28 ± 1.47
Sow back fat loss (BFL, mm)	0.29 ± 0.26	0.75 ± 0.36	0.62 ± 0.59
Sow loin loss (SLL, mm)	-0.05 ± 0.42	1.18 ± 0.55	2.44 ± 0.93
Sow feed intake (SFI, kg)	0.21 ± 1.23	0.88 ± 1.40	4.01 ± 2.50
Sow body weight loss (SWL, kg)	1.33 ± 1.06	0.17 ± 1.30	0.29 ± 2.20