

# Identification of Genetic Markers Associated with Sow Reproductive and Longevity Traits

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### Summary and Implications

The length of a sow's productive life (SPL) in a herd is an important component contributing to economic returns to pork producers. Reproductive performance, locomotion, and structural soundness are major factors influencing SPL. Due to low and moderate heritability of reproductive traits, marker assisted selection (MAS) may be an effective tool to reduce the culling rate of sows and thereafter improve SPL. In this study, 119 SNPs from 95 genes were examined in a commercial sow population with recorded reproductive traits for six parities. The association analyses revealed a number of potentially interesting genes associated with total number born, number born alive in the first and later parities, and with gestation length in several continual parities. These associated genes could be considered for marker assisted selection to improve SPL in commercial sow population.

### Introduction

Sow longevity or sow productive life (SPL) has become an emerging concern in the U.S swine commercial industry. It is usually defined as either the number of days that a sow remains in the breeding herd or the number of litters that a sow produces. Length of sow productive life or longevity is evaluated by removal, culling and replacement rates, percent gilts in herd, mean parity of females in inventory and mean parity at removal. According to PigCHAMP™ 2007 report ([http://www.pigchamp.com/summary\\_archives.html](http://www.pigchamp.com/summary_archives.html)), in the last ten years, the average culling rates of breeding females has been 49.7% and sow mortality rate has been 9.2%, which result in significant economic losses for swine producers. The two most prominent reasons for culling of sows from breeding herd are reproductive problems and locomotion disorders, and both of them appear to affect a higher percentage of sows in early parities. Reproductive traits are low to moderately heritable and have low repeatability across parities. Traditional phenotype selection based on reproduction records will be less effective. Marker assisted selection (MAS) is one method to improve lowly heritable traits. The identification of genetic markers significantly associated with high sow longevity would allow breeders to select gilts at early ages prior to the entry of the herd that would have the best opportunity for increased sow

longevity. Breeders could also select on such markers and possibly fix the significantly important genetic markers in the population so that all females have the beneficial alleles. Therefore, our research objective was to identify genetic markers called single nucleotide polymorphisms (SNPs) associated with sow productive traits for future possible use of these SNPs with MAS practices to improve SPL of females.

### Materials and Methods

A commercial population (n = 2066) of gilts from the Newsham Choice Genetics Company was used for this research project. Six reproductive traits were recorded (total number born, TNB; number born alive, NBA; still born number, SBN; mummy number, MN; gestation length, GL and non productive days, NPD) in six different parities that comprised of gradually reduced number of sows. The DNA was isolated using standard procedures. Large scale genotyping was performed using a Sequenom's MassARRAY system. The association analyses between SNPs and the traits was carried out for each parity using the MIXED procedure of the SAS package, and the statistical model treated gilt line, farrowing season and genotype as fixed effects and sire as random effect.

### Results and Discussion

A total of 119 SNPs from 95 genes were successfully genotyped in the analyzed population. In our earlier large scale association studies on body conformation and feet and leg structure traits in pigs, a numbers of associated SNPs were identified from these genes. In this study, a total of 23 genes showed significant ( $P < 0.05$ ) associations with at least three reproductive traits. For parity 1, the genes *COL9A1*, *NST*, *ADAM12*, *WARS2*, *DKFZ* and *LRP5* were significantly ( $P < 0.05$ ) associated with both TNB and NBA. The genes *COL1A*, *CALCR*, *IGFBP2* and *IGFBP5* were highly significantly ( $P \leq 0.01$ ) associated with SBN. The genes *IL6* and *ESR2* were highly significantly ( $P \leq 0.01$ ) associated with MN and NPD, respectively. For the later parities, the genes *CASR*, *ESR2*, *WARS2*, *NST*, *IFN $\gamma$*  and *BMP8* had significant association ( $P < 0.05$ ) with TNB and NBA. The genes *MC4R*, *FBN1*, *IGFBP2* and *SFRP4* were significantly ( $P < 0.05$ ) associated with GL in several parities. The genes *COL9A1*, *IFN $\gamma$* , *MC4R* and *BMP8* were simultaneously associated with reproductive performance, fatness and locomotion traits, implying that these genes have pleiotropic effects on sow longevity related traits. The results showed evidence that there are genes causing variation in sow productive life and offering prospects to the use of marker assisted selection to improve sow longevity.

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