

# Genetic and Genomic Analyses of Vulva Size Traits in Landrace and Yorkshire Gilts

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### Summary and Implications

The objective of this study was to characterize the genetic basis of vulva size (VS). Heritability estimates for vulva area (VA), vulva height (VH), and vulva width (VW) in Landrace were low to moderate, with 0.22, 0.29, and 0.10, respectively, whereas these were moderate to high in Yorkshire, with 0.50, 0.58, 0.33, respectively. For Landrace, we identified a common genomic region on chromosome (chr) 2 (154-157 Mb) associated with VA, VH, and VW. For VA and VH, common genomic regions were identified on chr 7 (107-110 Mb) and 10 (8-19 Mb). For VA and VW, a common genomic region was identified on chr 8 (4-6 Mb). In Yorkshire gilts, we found a common region on chr 1 (282-287 Mb) for VA, VH, and VW. Other regions were found for VH on chr 1 (87-91 Mb) and 5 (67 Mb). Genomic prediction accuracies (GPA) were moderate in Landrace, with 0.47, 0.32, and 0.35, whereas lower accuracies were obtained for Yorkshire, with 0.14, 0.19 and 0.07 for VA, VH, and VW, respectively. Results suggest that selection for VS traits is possible and genetic markers can increase genetic gains for these traits in pre-pubertal gilts.

### Introduction

Reproductive performance is critical for an efficient swine production system. Recent results indicate a strong relationship between the size of the vulva measured at 15 weeks of age in gilts prior to puberty and subsequent reproductive performance. However, there are very few studies available in the literature regarding the genetic basis of VS, and none, to the best of our knowledge, regarding the genomic basis of VS in pigs. Therefore, the objective of this study was to perform genetic and genomic analyses in VS traits to characterize the genetic and genomic bases of these traits.

### Materials and Methods

The data used for this study were collected as part of routine data recording in a commercial breeding program. All farms in this study are operating in line with the regulations on protection of animals.

A total of 1,183 Landrace (n=475) and Yorkshire (n=708) gilts originated from two different lines were used in this study. A 19-generation pedigree including 5,749 individuals was available for these animals. All animals had VS measurements taken at an average 23.8 weeks of age (SD=0.9). Measurements included: vulva area (VA), height (VH), and width (VW). Genotype data (Geneseek GGP-HD) was available for all animals by imputation, for ~40K single nucleotide polymorphisms (SNPs). Genomic regions associated with VS traits were identified using Bayes-B methodology for genomic analysis. Genomic prediction accuracies (GPA) were estimated using three training and validation strategies: between-breed, within-breed (4 and 6 cross-validation folds for Landrace and Yorkshire, respectively), and multi-breed (10-fold cross-validation, using one-fold per breed for validation at a time).

### Results and Discussion

Heritability estimates of VS traits were moderately to highly heritable in Yorkshire, with  $0.50 \pm 0.10$ ,  $0.58 \pm 0.11$ ,  $0.33 \pm 0.09$ , whereas these estimates were low to moderate in Landrace, with  $0.22 \pm 0.12$ ,  $0.29 \pm 0.13$ ,  $0.10 \pm 0.07$  for VA, VH, and VW, respectively. Genetic correlations within VS traits were very high for both breeds, with the lowest of  $0.74 \pm 0.10$  for VH and VW. Genome-wide association (GWA) studies revealed genomic regions associated with VS traits. For Landrace, we identified a common genomic region on chromosome (chr) 2 (154-157 Mb) associated with VA, VH, and VW that accounted for 12.9, 6.2 and 15.8% of the genetic variance (%GV), respectively. For VA and VH, common genomic regions were identified on chr 7 (107-110 Mb) and 10 (8-19 Mb), accounting for 14.0 and 4.7 %GV for VA and 13.5 and 8.7 %GV for VH. For VA and VW, a common genomic region was identified on chr 8 (4-6 Mb), accounting for 11.1 and 10.3 %GV, respectively. In Yorkshire gilts, we found a common region on chr 1 (282-287 Mb) for VA, VH, and VW that accounted for 4.7, 3.4 and 6.9 %GV, respectively. Another two regions were found for VH on chr 1 (87-91 Mb; 4.8 %GV) and 5 (67 Mb; 6.8 %GV). GWA results suggest that different genes may control VS traits in each breed. Within these regions are located genes associated with development of

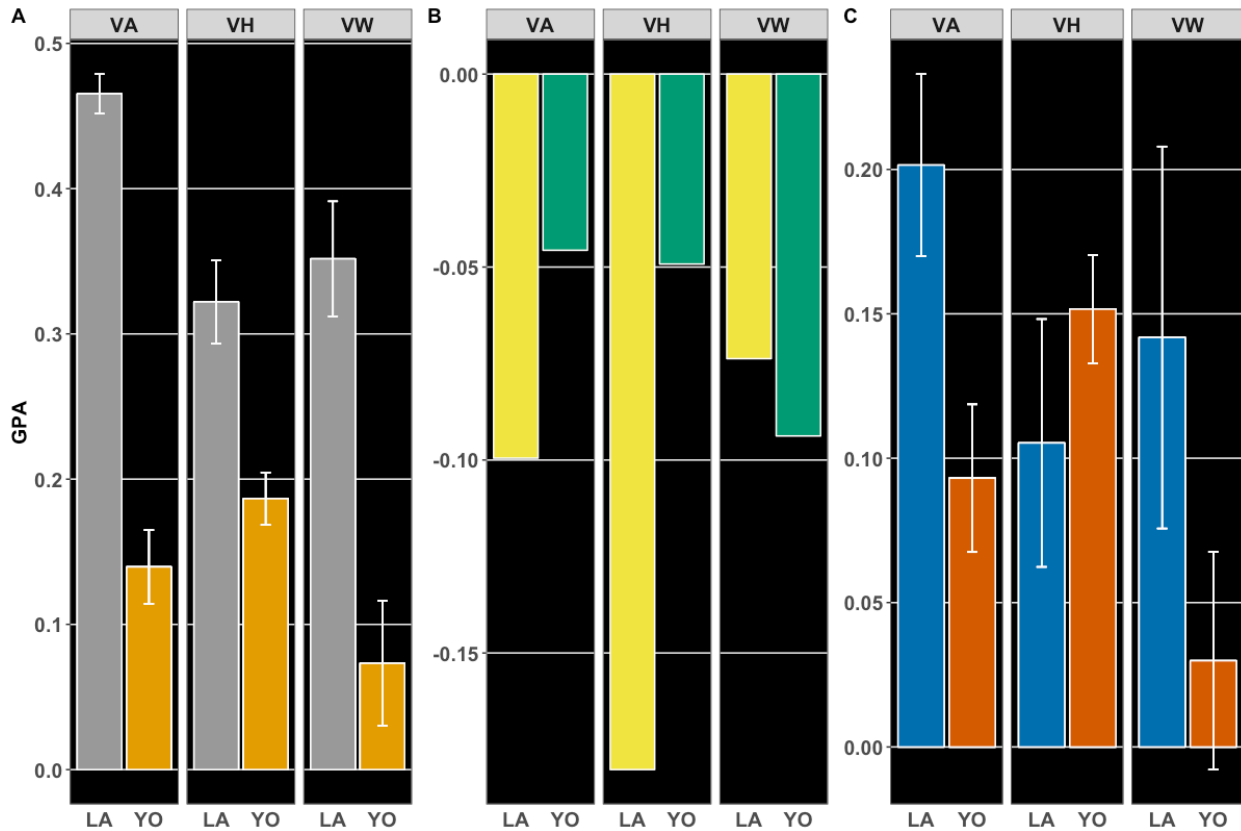
the reproductive organs, reproduction and productive characteristics, like *FLRT2*, a gene that regulates embryonic vascular development. Within-breed GPA (Fig.1A) for Landrace were moderate, with 0.47, 0.32, and 0.35, for VA, VH, and VW, respectively, whereas lower accuracies were obtained for Yorkshire, with 0.14, 0.19, and 0.07, respectively. Between-breed GPA (Fig.1B) were low and consistently negative, with -0.10, -0.18, and -0.07 in Landrace and -0.05, -0.05, and -0.09 in Yorkshire, for VA, VH, and VW, respectively. Multi-breed GPA (Fig.1C) for Landrace were low, with 0.20, 0.11, and 0.14, for VA, VH and VW respectively, whereas these were lower in Yorkshire gilts, with 0.09, 0.15, and 0.03, respectively. In addition to the GWA results, the low and consistently negative between-breed GPA results suggest that VS traits are mostly controlled by different genes in each breed, but some QTL effects for these traits might be being captured between breeds and these might be in opposite phases.

**Conclusion**

Heritability estimates of VS traits were low to moderate in Landrace, whereas moderately to highly heritable in Yorkshire. Genomic analysis results showed different regions associated with VS traits between Landrace and Yorkshire, with similar regions across VS traits within a breed. GPA were moderate in Landrace, but lower in Yorkshire gilts. These results suggest that genomic selection for VS traits is possible in Landrace but limited in Yorkshire gilts.

**Acknowledgements**

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**Fig. 1.** Genomic prediction accuracies (GPA) for vulva area (VA), vulva height (VH), and vulva width (VW). The x-axis represents the breed used as the validation group: Landrace (LA) and Yorkshire (YO). **A.** Within-breed GPA, using 4- and 6-fold cross-validation for LA and YO, respectively, **B.** Between-breed GPA, and **C.** Multi-breed GPA, using 10-fold cross-validation, using one fold per breed for validation at a time. Error bars represent the standard deviation of the GPA across folds.