

# Genomic evaluation for litter size in Canadian Yorkshire pigs

Mohsen Jafarikia<sup>1</sup>, Flavio Schenkel<sup>2</sup>, Frédéric Fortin<sup>3</sup>  
Laurence Maignel<sup>1</sup>, Stefanie Wyss<sup>1</sup>, Brian Sullivan<sup>1</sup>



<sup>1</sup>Canadian Centre for Swine Improvement, Ottawa ON Canada

<sup>2</sup>University of Guelph, Guelph ON Canada

<sup>3</sup>Centre de développement du porc du Québec, Québec QC Canada



## Introduction:

➤ Maternal traits are expressed in mature females and generally have low heritability. The reliability of estimated breeding values (EBVs) for maternal traits are therefore very low in young selection candidates.

➤ Simulation and empirical studies have shown the potential of genomic information for increasing the reliability of EBVs.

➤ High-density single nucleotide polymorphism (SNP) panels can be used for predicting genomic EBVs (GEBV) to select breeding animals for various traits including meat quality and other traits that are difficult to measure. GEBVs are also useful to evaluate maternal traits such as litter size and generation interval.

## Objective:

➤ The aim of this study was to investigate the impact of using genomic information on the reliability of EBVs for total number of piglets born per litter.

## Materials & Methods:

### Animals

➤ 542 purebred Yorkshire pigs from herds across Canada were genotyped using Illumina PorcineSNP60 BeadChip.

➤ Animals were divided in two sets:

➤ Training set: 485 pigs born before the end of October 2009 used to estimate SNP effects with an average EBV reliability of 0.47 in 2011.

➤ Validation set: 57 pigs born after October 2009, which had their GEBV predicted based on animals in the training set with an average EBV reliability of 0.31 in 2011.

### Number Born EBVs

➤ Estimated breeding values for total number of piglets born were obtained from the Canadian Swine Improvement Program's genetic evaluation run released on November 2011.

➤ Parental Average (PA) EBVs adjusted to a common base were obtained from the first national genetic evaluation after the birth of each pig in the validation set.

### SNP filtration

➤ 51,198 out of the 62,163 SNPs were included in the analyses:

➤ 1,328 SNPs were excluded because they were located on the sex chromosomes

➤ 9,637 of SNPs were excluded because they had minor allele frequency of less than 0.05

### Genomic EBV (GEBV)

➤ The gebv software by Sargolzaei *et al.* (2009) was used to estimate genomic EBVs, using the VanRaden (2008) equivalent model.

## Validation of GEBV

➤ The squared correlation between the PA or GEBV and the EBV in 2011 was calculated for animals in the training and validation sets.

## Results & Discussion:

➤ GEBV was a better predictor of the number born EBV when compared to the PA EBVs for that same trait for pigs in the validation set.

Data Set	Number of animals	r <sup>2</sup> (PA or GEBV, EBV <sup>1</sup> )	
		PA	GEBV
Training set	485	0.55	0.97
Validation set	57	0.55	0.66

<sup>1</sup>Number Born EBV in 2011

➤ The predictive ability of GEBV may be improved by training SNP effects on more reliable EBVs and by increasing the number of animals in the training set. However, in practice, there is a limit on increased EBV reliability due to the rapid turnover of nucleus pigs.

➤ Options for increasing the number of animals for both training and validation sets include collaboration with other groups to pool datasets and the development of a lower cost SNP panel associated with imputation to the 60K SNP panel to encourage the genotyping of more animals.

## Implications:

➤ GEBVs had 20% greater reliability than PA EBVs for number of piglets born.

➤ Potential benefits obtained from GEBVs for the number born trait were greater than the results reported in a previous study where genomic evaluations for backfat thickness yielded 11% more reliable EBVs when compared to the PA EBVs (Jafarikia *et al.*, 2011).

## Acknowledgements:

**Funding and collaboration from:** Atlantic Swine Centre, Ontario Swine Improvement, Centre de développement du porc du Québec inc., Western Swine Testing Association, and PigGen Canada.

**Funding provided by:** Canadian Swine Research and Development Cluster, a Growing Canadian Agri-Innovation Program - Canadian Agri-Science Cluster Initiative of Agriculture and Agri-Food Canada (AAFC), Agriculture Adaptation Councils of Québec, New Brunswick, Nova Scotia, Manitoba & Ontario, Ministère de l'Agriculture, des Pêcheries et de l'Alimentation du Québec (MAPAQ) & Fédération des producteurs de porcs du Québec (FPPQ).

