

Potential application of genomics to improve meat colour in Canadian Duroc pigs



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Introduction:

➤ Simulation and empirical studies have shown the potential of genomic information for increasing the reliability of estimated breeding values (EBV) especially for difficult to measure traits such as meat quality.



➤ High-density Single Nucleotide Polymorphism (SNP) chips can be used for computing genomic EBV (GEBV) to select breeding animals for meat quality and other traits.

➤ For important meat quality traits such as meat colour, GEBV can be used to increase the accuracy of prediction and decrease the generation interval.

Objective:

➤ Investigate the impact of using genomic information in prediction of Minolta L* EBV. Minolta L*, an objectively measured trait for pork colour, was chosen because of its importance and relation to other meat quality attributes.

Materials & Methods:

Animals

➤ 1,063 purebred Duroc pigs from herds across Canada were genotyped using Illumina PorcineSNP60 BeadChip.



➤ Minolta L* was measured on *longissimus dorsi* samples from 253 pigs. The average phenotypic value was 50.86±3.19.

➤ 417 pigs with an EBV reliability greater than 10% for Minolta L* were chosen (205 barrows, 104 males and 108 females). Out of the 417 selected animals, 164 pigs did not have their own performance records, but their EBVs were estimated using their relatives' information.

➤ Animals were divided in two sets:

➤ Training set: 334 pigs born in 2009 or earlier were used to estimate SNP effects. The average EBV reliability of the trait was 0.27 in May 2012.

➤ Validation set: 83 pigs born after 2009 had their GEBV for Minolta L* predicted based on animals in the training set. The average EBV reliability for this trait was 0.30 in May 2012.

Minolta L* EBVs

➤ Estimated breeding values for Minolta L* were obtained from the Canadian national genetic evaluation released in May 2012 by Canadian Centre for Swine Improvement.

SNP filtration

➤ 45,166 out of the 62,163 SNPs were included in the analyses:

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

➤ 15,669 of SNPs were excluded because they had a minor allele frequency less than 0.05.

Genomic EBV (GEBV)

➤ *gebv* software (Sargolzaei *et al.*, 2009) was used to estimate the direct genomic values.

➤ Direct genomic values of animals in the validation set were compared to the May 2012 official national EBVs.

Validation of GEBV

➤ The squared correlation between the GEBV and the EBV in 2012 was calculated for animals in the training and validation sets.

Results & Discussion:

	Number of animals	r ² (GEBV, EBV ¹)
Training set	334	0.80
Validation set	83	0.36

¹ Minolta L* EBV in 2012

➤ GEBV was a relatively good predictor of Minolta L* EBV in 2012 with a squared correlation of 0.36. Therefore, genomic values could be valuable for selecting breeding animals when no information from the animal's own performance is available and when meat quality information from the animal's relatives is limited.

➤ The predictive ability of GEBV may be improved by training SNP effects on Minolta L* EBVs with higher reliabilities and by increasing the number of animals included in the training set.

➤ Options for increasing the number of animals in both training and validation sets include collaboration with other groups to pool datasets and using a more affordable lower density SNP panel and imputing genotypes to the 60K SNP panel.

Implications:

➤ Genomics technology can help for pre-selection of breeding animals for meat quality and other economically important traits.

➤ Genomics can help to differentiate Canadian pork.

➤ This study was done using a meat quality trait where phenotypes are not readily available on all animals. Potential benefits from GEBV for animals with phenotypic observation is also expected.

Acknowledgements:

The financial support of Agriculture and Agri-Food Canada, Swine Innovation Porc, the Adaptation councils in Quebec, New Brunswick, Nova Scotia, Manitoba and Ontario, the *Ministère de l'Agriculture, des Pêcheries et de l'Alimentation du Québec* and private financial support from breeders, the *Centre de développement du porc du Québec*, PigGen Canada and the *Fédération des producteurs de porcs du Québec* is gratefully acknowledged and appreciated. Contributions by CCSI's regional centers and participating breeding stock suppliers are also gratefully acknowledged.



Presented at:



Livestock Genetic's 3rd Annual
2012 Conference
Turning Local Production Into Global Advantage