PREDICTIVE ABILITY OF GENOMICS FOR ESTIMATING INTRAMUSCULAR FAT CONTENT IN CANADIAN DUROC PIGS

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Abstract – With the continual development of global markets for pork and competition between major exporting countries, pork quality is becoming more important. One of the major components of pork quality is the amount of intramuscular fat (IMF), a trait which has been shown in previous studies to be associated with various eating quality attributes. It is possible to predict IMF percentage on live animals using ultrasound scanned images. This method prevents having to sacrifice valuable animals to measure IMF on carcasses at the plant. Molecular data can also assist in improving accuracy of genetic evaluation for IMF and marbling. This study was conducted on Canadian purebred Duroc pigs to assess the potential application of high-density SNP panel genotypes for predicting genetic merit for IMF and marbling. Animals were genotyped with the porcine 60K SNP panel and a validation study was carried out. The genomic estimated breeding values for IMF were more reliable than the parental average estimated breeding values. Due to the relatively inexpensive cost of scanning live animals for IMF and the availability of 60K SNP panel, potential application of genomics for improvement of the pork marbling is feasible.

Key Words – GEBV, Marbling, IMF, SNP.

I.   INTRODUCTION

Pork quality is an important issue for competitiveness of the swine industry. In the future, more and more markets will require tailoring pork quality to different criteria. Marbling is a major quality trait for international markets, especially high value markets such as Japan. It also has an increasing value for the Canadian domestic markets and is an important component of sensory quality. Moreover, pigs have been selected very efficiently for leanness in the past decades to address market requirements, and this has likely resulted in a slow decrease in intramuscular fat (IMF) levels. Genetic evaluation and selection on IMF would provide the industry with tools to control the level of marbling.

The ability to measure meat quality on live pigs has been explored for many years, but accurate methods to measure this trait on live pigs have only been developed within the last decade [1]. In an earlier project, the Canadian Centre for Swine Improvement (CCSI) and the *Centre de développement du porc du Québec* (CDPQ) tested a technology based on image and signal-analysis of ultrasound scans, which showed that live IMF predicted using ultrasound measures was highly correlated with chemical IMF measures [2]. Ultrasound technology provides opportunities for breeders to select on meat quality by using routine, non-invasive measures on live pigs.

The estimation of breeding values (EBVs) is highly dependent on phenotypic measurements. More accurate EBVs can be obtained by using molecular data from high-density SNP panels [3]. Genomic breeding values (GEBVs) are of interest for traits that require the sacrifice of an animal or which are costly to measure instead of genetic values obtained via traditional genetic evaluations. The development of high-density SNP panels allows for the genotyping of thousands of SNPs on a genome-wide scale. The Illumina PorcineSNP60 BeadChip (SNP chip) was made available to the swine industry in December 2008. By using this innovative tool, Canadian pig breeders and producers can potentially lower production costs and improve productivity. The 60K SNP panel can also help to differentiate pork products by adding

to classical quantitative selection, which could be available the moment a pig is born. The ability to select animals with more accurate EBVs for IMF early in life using genomic information could be valuable for the Canadian swine industry.

The objectives of this study were to investigate the potential of using GEBVs for prediction of genetic merit for marbling and IMF levels and also discuss the prospective application of genomics for improving pork marbling.

II.   MATERIALS AND METHODS

Animals: This study included IMF estimated breeding values (EBVs) calculated from ultrasonic scan measurements taken on 5,836 Durocs across Canada between September 2009 and February 2012. A total of 892 station-tested pigs and their parents (Table 1) were also genotyped using Illumina porcine 60K panel to investigate the potential of genomics in predicting marbling and IMF levels. Breeders from across Canada on the Canadian Swine Improvement Program contributed animals for central testing and carcass evaluation. This included two trials that were completed in 2005 and 2010, respectively, at the swine testing station located in Deschambault, Quebec, Canada. The data structure, after exclusion of animals with missing information, is presented in Table 1.

DNA extraction and genotyping: DNA extraction and genotyping using the Illumina PorcineSNP60 BeadChip was performed by DNA LandMarks Inc. (St-Jean-sur-le-Richelieu, Quebec, Canada).

Live IMF scan: Technicians from across Canada accredited for intramuscular fat measures scanned live pigs using an Aloka 500 SSD with a 12.5 cm, 3.5 MHz probe. Between 8 and 10 longitudinal images covering the area between the 10th and 13th ribs were saved for each pig. Scanned images were uploaded into the national database for image analysis. Raw IMF values were determined using the Biotronics software and were uploaded into the database for inclusion in genetic evaluations for IMF.

Table 1. Animals used in the study

Source of Information	Number of animals			Total
	Barrow	Male	Female	
Live IMF scan	256	3,302	2,278	5,836
Carcass marbling	240	99	78	417
60K genotype	219	514	159	892[1]

[1]The number of animals with EBV reliability higher than 0.10 was 608 and 591 for live IMF and carcass marbling, respectively.

Loin marbling measurements: A deboned loin was taken from the right side of the carcass 24 hours after slaughter. Loins were sliced perpendicular to the longitudinal axis into one inch chops, corresponding to the 4th last lumbar vertebra. A subjective assessment of the marbling score was performed by a technician on each side surface, using NPPC marbling standards (1 = devoid to 10 = abundant) [4], scored to the nearest 1/2 point and averaged over both sides.

Estimation of live IMF EBVs: EBVs were calculated under the Canadian national genetic improvement program. The model for live IMF breeding value estimation included scanning weight as a covariate, sex and the interaction of farm by scanning date by technician as fixed effects. Litter was included as a random effect.

Estimation of marbling EBVs: The model for estimation of marbling breeding values included carcass weight as a covariate, sex and the interaction of plant by slaughter date by technician as fixed effects. Litter was included as a random effect.

High-density SNP panel genotyping editing: SNPs mapped to sex chromosomes and with low minor allele frequency (MAF) were excluded from further GEBV analyses (Table 2).

Table 2. Number of SNPs used in the study

Trait	Number of SNPs			
	Total	Sex[1]	MAF[2]	Remaining
IMF	62,163	1,328	17,587	43,248
Marbling	62,163	1,328	15,743	45,092

[1]SNPs on the sex chromosome were excluded.
[2]SNPs with MAF of less than 0.05 were excluded.

Estimation of GEBVs: The gebv software [5] was used to compute GEBVs using the equivalent model from VanRaden (2008) [6]. To assess the potential of genomics to predict IMF, direct genomic values (DGVs) were compared to parental average (PA) EBVs. A total of 284 out of 892 genotyped animals with IMF EBV reliabilities lower than 0.10 were excluded from further analyses for IMF. Three hundred and one (301) animals with a marbling EBV reliability lower than 0.10, were also excluded from analyses for marbling. The number of animals included in the training and validation sets for GEBV estimation and average EBV reliability are shown in Table 3. Animals born either in 2010 or later were assigned to the prediction set and the remaining was assigned to the training set. The 60K SNP genotypes and EBVs of animals in the training set were used to estimate the GEBVs of animals in the validation set.

The squared correlation between PA or DGV and the national EBVs published by CCSI in March 2012 was calculated for animals in the training and validation sets [7].

III.   RESULTS AND DISCUSSION

GEBV estimates: For animals in the prediction set, the squared correlations of PA and DGV with EBVs in March 2012 are shown in Table 4. DGVs ($r^2=0.35$) were a better predictor of IMF EBV when compared to the PA IMF EBVs ($r^2=0.21$) in the validation set, with a 67% increase in reliability over PA IMF EBVs.

The 67% increase in GEBV reliability relative to PA may be overestimated, because of the limited number of animals available with parental performance information for the calculation of their PA. Because the technology for live IMF scanning is relatively new, most of the PA do not include the parents' own performance records. This would cause an inflated difference between PA and GEBV reliabilities. The squared correlations of PA and GEBVs in training sets were not reported due to a lack of parental performance data for the estimation of PA (Table 4). There was also limited number of animals with their own performance in the validation set for marbling (37 out of 91, Table 3).

Table 3. Number of genotyped and phenotyped animals and average reliability of EBVs

Trait	Genotyped[1]/ Phenotyped[2]/ Reliability[3]		
	Training	Validation	Total
IMF	500/121/0.35	108/96/0.60	608/217/0.40
Marbling	500/216/0.43	91/37/0.43	591/253/0.43

[1]Number of animals genotyped.
[2]Number of genotyped animals with their own phenotype.
[3]Average reliability of EBVs in each group. Animals with EBV reliability of less than 0.10 were excluded.

The squared correlation of DGV and EBVs was slightly higher in the training set for marbling than for IMF (0.86 *vs*. 0.81, Table 4). This may be due to more animals with their own phenotypic performance for marbling than IMF (216 *vs*. 121, Table 3) and also due to the lower average EBV reliability for IMF (0.35 *vs*. 0. 43). However, the squared correlation of DGV and EBVs was higher in the validation set for IMF than for marbling (0.35 *vs*. 0.22, Table 4). In comparison to IMF EBV reliability, the average marbling EBV reliability of the animals in the validation set was much lower (0.43 *vs*. 0.60, Table 3). The lower accuracy of marbling EBVs for pigs in the validation set could explain the lower correlation between marbling DGV and EBV in the validation set (Table 4).

The relatively small proportion of animals with their own and parental performance was a limiting factor to validate the relative advantage of the GEBV (Table 3). For a trait such as marbling, which requires the sacrifice of an animal that is then no longer available for future breeding, a reliability of 0.22 (accuracy of 0.47) is very promising considering that no loin marbling values can be obtained *in vivo*.

Table 4. Estimated reliability of PA and DGV for predicting genetic merit for IMF and marbling

Trait	Dataset	r^2 (PA or DGV, EBV[1])	
		PA	DGV
IMF	Training	-	0.81
	Validation	0.21	0.35
Marbling	Training	-	0.86
	Validation	-	0.22

[1]March 2012 national IMF and marbling EBVs

For prediction of IMF, GEBVs computed using genomic data clearly show a benefit for improving the selection accuracy of breeding animals. Breeding animals selected based on their GEBV early in life could later be scanned for live IMF scan measurement to obtain a better genetic evaluation for marbling.

The predictive ability of GEBV could be increased by training SNP effects using EBVs with higher reliabilities and by increasing the number of animals in the training set. Both accuracy and number of animals will increase as more data accumulates on the national program. Increasing the number of animals for both training and validation sets could also be achieved by collaborating with other swine research groups to pool datasets as a means of mitigating the high costs associated with 60K genotyping. Another option is the development of a more affordable lower density SNP panel with high accuracy for imputing SNPs on the 60K SNP panel. Low-density SNP panels with high imputation accuracy have been successfully applied in the dairy cattle industry [8].

IV.   CONCLUSION

The results of this preliminary study show the potential value from using high-density SNP panels for improving the accuracy of IMF EBVs. Large-scale application of genomics is feasible due to the rapid progress made in computing resources and the availability of affordable vast genomic data. The development of an economical lower density SNP panel may be necessary to encourage the uptake of genomics technology by the broader industry. A more accurate live IMF and marbling EBV estimation in breeding animals using GEBV could result in a better prediction of marbling levels in market hogs. The available live IMF phenotypes and relatively low investment needed for scanning more breeding animals will facilitate the application of genomics for selection for marbling via live IMF.

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