

Genomic Selection of Pork pH in Purebred Pigs for Crossbred Performance

Y. Miar¹, G.S. Plastow¹, H.L. Bruce¹, R.A. Kemp², P. Charagu³, C.Y. Zhang¹, A.E. Huisman⁴, and Z. Wang¹.

¹University of Alberta, Edmonton, AB, Canada, ²Genesus Genetics Inc., Oakville, Manitoba, Canada, ³Hypor Inc., Regina, Saskatchewan, Canada, ⁴Research and Technology Centre, Hendrix Genetics, Boxmeer, The Netherlands

ABSTRACT: Genomic selection (GS) will create a paradigm shift in pig genetic improvement programs. It will be especially useful in genetic improvement of pork quality traits because these traits are not only economically important but also difficult and expensive to measure. Data on 1,948 commercial crossbred pigs genotyped with the Illumina PorcineSNP60 Beadchip were used to develop genomic prediction equations for pork pH using GBLUP method. The accuracy of prediction for crossbred animals was 0.25 after 10-fold cross-validation. Application of the prediction model to the parental Duroc pure lines showed an accuracy of prediction between the EBV and GEBV of 0.21. We conclude that GS can be applied to the parental purebred lines without substantial loss of prediction accuracy. Future investigations including dominance effects in the genomic prediction model will be explored to further improve genomic prediction accuracy in the parental population.

Keywords: genomic selection; pork pH; swine

Introduction

Increased understanding of the genes affecting pork quality could better satisfy consumer demands for excellent eating, healthy and nutritional quality. Genetic improvement for meat quality through traditional quantitative selection has not been effective not only because these traits have a low-to-moderate heritability (Miar et al. (2014)), but also because these traits are very difficult and expensive to measure and often require the harvest of the animal. Therefore, selection of purebreds based on crossbred progeny performance for these traits would be useful in improving pure line parents to produce improved pork quality for their crossbred progenies. Among the pork quality traits, muscle ultimate pH has been recognized as an effective indicator for pork quality traits (Miar et al. (2014)).

Recently, the Illumina PorcineSNP60 BeadChip was developed (Ramos et al. (2009)) and has been used in genome-wide association studies to identify genes that explain variation in meat quality traits. Availability of a high-density SNP panel and new statistical methods, such as genomic best linear unbiased prediction (GBLUP) and Bayesian statistics have made genomic selection (GS) feasible in pigs (Habier et al. (2007)). Habier et al. (2007) used a genomic relationship matrix (G) for implementing genomic selection and demonstrated that this method was good even able to capture the genomic relationships between individuals with poor pedigree records (Hayes and

Goddard (2010)). VanRaden et al. (2009) showed that this method was at least as good as other methods for many traits.

GS can lead to decreased generation interval and improved selection accuracy to accelerate genetic improvement of economically important traits in livestock (Hayes et al. (2009)) if used properly. Improved reliability of genomic prediction has resulted in an increased rate of genetic gain in dairy cattle (VanRaden et al. (2009)). The objective of this study was therefore to develop GEBV prediction equations for pork pH using commercial crossbred animals and to explore the possibility of application of the developed prediction equation in pure parental lines for genomic selection.

Materials and Methods

Animals and Management. The composition of this population has been previously described by Miar et al. (2014). Briefly, the commercial crossbred pigs used in this study were progeny from 139 sires of two Duroc boar lines bred to 429 F1 hybrid Landrace × Large White sows from two breeding companies (Genesus Genetics, and Hypor Inc., Canada). They were a combination of full and half sib families representing a multi-generation family structure drawn from the breeding populations.

Carcass and Meat Quality Measurements. Carcass and meat quality measurements have also been described in detail by Miar et al. (2014). Briefly, pigs were housed overnight at the abattoir with *ad libitum* access to water. The average slaughter weight and age were 124±10 kg and 160±12 days, respectively. Hot carcass weight, cold carcass weight, carcass length, *longissimus dorsi* muscle area, subcutaneous backfat depth, loin depth, texture score, subjective marbling score, and most of the primal and subprimal cut weights were recorded.

Meat quality measurements were taken on the *longissimus dorsi* muscle of the loin. Ultimate or 24 h pH, drip loss, Minolta L*, a*, and b* were taken on both loin and different muscles of ham including *gluteus medius*, *quadriceps femoris*, and *iliopsoas* muscles as described by Miar et al. (2014).

Genotyping and Quality Control. Genomic DNA was extracted from ear tissues using a standard phenol/chloroform method. A total of 2,384 individuals were genotyped using the PorcineSNP60 Beadchip

containing 64,232 SNPs following the manufacturer's protocol (Illumina Inc., San Diego, USA). SNPs were removed from the genotyping data for call rate < 95%, minor allele frequency < 0.05, and Chi-square < 600 of Hardy-Weinberg equilibrium test. A total of 44,507 SNP were retained in the analysis after the filtering.

Statistical and Genetic analysis. The significance of the fixed effects and covariates were determined for pH using the general linear model (GLM) procedure of SAS (SAS Inst., Inc., Cary, NC). The residual from the above adjustment was used as the phenotype for the GEBV model development.

In this study, GBLUP was used to predict GEBVs of individual animals using commercial crossbred pigs as a reference population (n = 1,948) and then the prediction equation that was developed was applied to predict the GEBVs of their parental pure lines (validation population) to explore the model predictability in the pure parental population. A genomic relationship matrix was constructed in the population using 1,948 commercial crossbred and 107 Duroc purebred pigs followed the method described by Habier et al. (2007). The prediction model was then developed using GBLUP for meat pH trait as follows:

$$y = \mathbf{1}_n\mu + \mathbf{Z}g + e,$$

Where y is a phenotypic observation vector for n individuals, μ is the overall mean, $\mathbf{1}_n$ is a vector of ones, \mathbf{Z} is the design matrix for the breeding values, g is a vector of breeding values and e is the residual error vector with an assumed $N(0, \sigma_e^2)$ distribution. In this model, $g = \mathbf{W}u$ where u_j is the effect of j^{th} marker and variance $V(g) = \mathbf{W}\mathbf{W}'\sigma_u^2$. \mathbf{W} matrix contains w_{ij} elements for i^{th} animal which shows the deviation of the number of alleles at the j^{th} marker from the $2p_j$ so that is equal to $0 - 2p_j$ for the homozygous AA, $1 - 2p_j$ for the heterozygous Aa and $2 - 2p_j$ for the homozygous aa. The diagonal elements of $\mathbf{W}\mathbf{W}'$ for m markers would be equal to $\sum_{j=1}^m 2p_j(1 - p_j)$. In GBLUP, the breeding values will be predicted as follows:

$$[\hat{g}] = \left[\mathbf{Z}'\mathbf{Z} + \mathbf{G}^{-1} \frac{\sigma_e^2}{\sigma_g^2} \right]^{-1} [\mathbf{Z}'y]$$

Cross-Validation. For purpose of genomic prediction, we used the correlations obtained from the 10-fold cross validation as a criterion to evaluate the predictabilities of the models in crossbred animals. In the first step of the cross validation, individuals of the population were randomly partitioned into 10 subsamples. In the second step, we used nine parts of the sample to estimate parameters and used these estimated parameters to predict the phenotypes of individuals in the remaining part. The cross validation concluded after all parts have been predicted. The average of the marker effect of all loci from the 10 predictions in the cross validation were used as the marker estimated effects in the final prediction model that were used for the pure parental line GEBV prediction.

Results and Discussion

Prediction of Genomic Estimated Breeding Values. The mean±SD of pH was 5.73±0.18, and pH values ranged from 5.28 to 6.36. The heritability of pH was low (0.15±0.09) (Miar et al. (2014)) and the accuracy of prediction was 0.25 after 10-fold cross-validation in crossbred animals. When the prediction equation was applied in the pure Duroc paternal lines, however, the accuracy of prediction was calculated by using the correlation between EBV and GEBV for the meat pH, which was 0.21. The prediction model was applied to data from the pure Duroc paternal lines (n=107) for each company separately. The GEBV results showed that sufficient variation in GEBV existed in both commercial crossbred animals and pure lines (Figures 1-2), and that selecting animals with known genotypes and unknown phenotypes may be possible so as to completely redesign livestock breeding programs.

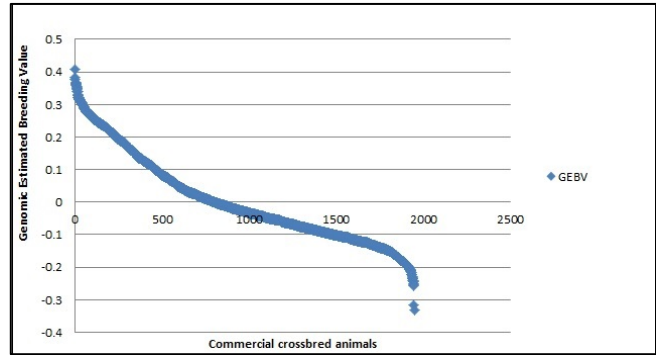


Figure 1. Variation of genomic estimated breeding values in commercial crossbred pigs.

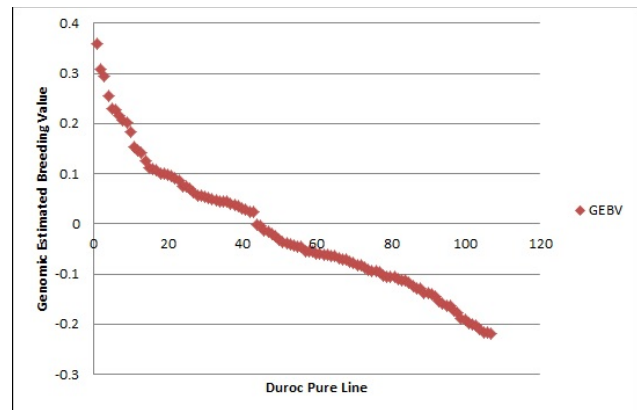


Figure 2. Variation of genomic estimated breeding values in Duroc pure line.

The GBLUP estimation of allele substitution effect for genomic selection in livestock breeding programs is becoming increasingly common (McClure et al. (2012)). The accuracy of the prediction model in this study showed

that a genomic prediction equation generated from commercial crossbred animals could be used to select animals in their parental pure lines for pork pH with known genotypes and unknown phenotypes. This enables pig breeders to predict breeding values of young selection candidates that will result in reducing generation interval with reasonable prediction accuracy and hence accelerate the rate of genetic gain. However, future investigations on including dominance effects in the genomic prediction model should be explored using the data from the commercial animals in an attempt to further improve genomic prediction accuracy in the pure parental populations.

Conclusion

It is apparent that GS has a great potential for the improvement of difficult to measure phenotypes and low heritability traits such as those influencing pork quality. The results showed the potential of genomic selection in the pure parental lines using the prediction models developed from their crossbred progeny.

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