Accuracies of Genomic Prediction of Traits Associated with Lactation and Reproduction in Yorkshire and Landrace Sows

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Summary and Implications

Genomic prediction involves statistical methods to estimate the genetic merit of selection candidates based on genetic markers spaced across the genome. The benefit of genomic prediction depends on the accuracies with which we can predict the genomic estimated breeding values (GEBV) of selection candidates based on their marker genotypes. The objective of this study was to estimate the accuracies of GEBV for traits associated with lactation and reproduction in Yorkshire and Landrace sows. Across both breeds, genomic predictions had greater accuracy than pedigree-based predictions. This result suggests that accuracy of selection can be improved by genomic prediction and, thereby, increase selection response compared to pedigree based genetic evaluation.

Introduction

Genetic improvement involves selection of superior animals as parents of future generations. Traditionally, animals are selected based on estimated breeding values (EBV) based on phenotypic records and pedigree. This method has been very successful for easy to measure production traits, but not for traits that are difficult to measure or for traits with low heritability. Many of these difficult to measure traits (e.g. feed efficiency, disease resistance, etc.) are of high economic importance. Genomic prediction is a method for estimation of breeding values based on marker information (GEBV) from high-density SNP chips and can be used to overcome these limitations. Most traits associated with lactation and reproduction in pigs are either less heritable, or appear later in life, or are difficult to measure on a routine basis. So for these traits, genomic prediction can be an attractive alternative to traditional pedigree based methods. Before practical implementation of genomic prediction methods, accuracies of GEBV over traditional pedigree-based EBV have to be examined. In this report, accuracies of EBV for traits associated with lactation and reproduction obtained using genomic methods are compared with those of traditional pedigree based methods.

Materials and Methods

Data on 1,532 sows (821 Yorkshire and 711 Landrace sows) farrowed between August 2011 and January 2014 were used in this study. Sows were weighed and scanned for back fat and loin depth at around 5 days before farrowing and at weaning. The piglets were weighed immediately after birth, at fostering and at death or weaning. Daily feed consumption of each sow was measured using automatic feed recording equipment. All sows were genotyped using the 60k Chip. Genomic prediction methods involve estimating marker effects on a training data set and then testing the effects on a validation group. Within each breed, a subset (~15%) of younger animals was allocated to the validation group. Accuracies of the predicted EBV were estimated as the correlation between EBV and phenotypes corrected for fixed effect of the animals in the validation data set, divided by the square root of heritability of the trait.

Results

In Table 1 the accuracies are presented of EBV based on genomic and pedigree based methods for Yorkshire and Landrace sows for multiple reproductive and lactation traits. In both breeds and for most traits, accuracies of EBV based on genomic prediction methods were higher than the accuracy of EBV from pedigree based methods, and these differences were greater in the Yorkshire breed.

Conclusions

These results are promising, especially for traits associated with lactation and reproduction. These traits are economically important and are difficult to measure, and the results reiterate the importance of incorporating genomic selection methodologies into routine genetic evaluation programs in pigs.

Table 1. Accuracies of EBV for traits associated with lactation and reproduction in Yorkshire and Landrace sows using genomic prediction and pedigree-based genetic evaluation.

	Yorkshire			Landrace		
	Pedigree method	Genomic method[#]	% Increase[*]	Pedigree method	Genomic method[#]	% Increase[*]
Body weight at farrowing	0.39	0.53	36.8	0.28	0.28[C0]	0
Back fat at farrowing	0.37	0.71	90.0	0.26	0.28	6.3
Loin depth at farrowing	0.40	0.50	27.3	0.58	0.53	-7.1
Body weight loss during lactation	0.26	0.18	-30.1	0.32	0.41[C0]	27.8
Back fat loss during lactation	-0.03	0.16	600	0.48	0.43	-10.5
Loin depth loss during lactation	0.31	0.47	54.5	0.43	0.61	40
Feed intake during lactation	0.42	0.40	-4.5	0.51	0.51	0
Litter weight gain	0.65	0.92	46.1	0.49	0.59	19
Net energy balance at weaning	0.03	0.19	600	0.42	0.44	5
Total litter size at farrowing	0.12	0.54	350	0.24	-0.07	-130

[*]% increase in accuracy using genomic method compared to pedigree based methods
[#]All genomic accuracies without any super script are obtained from Bayesian regression method Bayes B
[C0]Genomic accuracies obtained using Bayes C0 method