THE PREDICTED RESPONSES TO GENOMIC SELECTION IN GROWING PIGS

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SUMMARY

The responses to genomic selection in breeding programs for growing pigs were predicted using a selection index approach. Genomic selection increased overall predicted response by 2.6 (500 reference population) to 27.8% (5000 reference population) for a breeding objective consisting of backfat thickness (BFT), average daily gain (ADG), post-weaning survival (PWS) and feed conversion ratio (FCR) in growing pigs. Predicted response in PWS increased by 147% with genomic selection (5000 reference population) at the expense of the other traits like BFT, ADG, and FCR which had 14.5, 1.6, and 2.8% less genetic gain compared to the response in a conventional breeding program without genomic selection. The higher loss in genetic gain for BFT was due to a stronger genetic correlation with FCR in comparison to ADG. The predicted additional responses in the breeding objective is a guideline for the implementation of genomic selection in pig breeding programs.

INTRODUCTION

Genomic selection is a method of predicting genetic merit of selection candidates utilizing dense marker genotyping covering the whole genome and basing predictions on a reference population that has both genotypes and phenotypes (Meuwissen *et al.* 2001). The impact of genomic information on response to selection is mostly determined by an increase in prediction accuracy and a decrease in generation interval. Since the generation interval of pigs is short, the genetic gain will largely be affected by the increased prediction accuracy with genomic information. Tribout *et al.* (2012) predicted 26% additional genetic gain from genomic selection compared to a breeding program without genomic selection. The breeding objective consisted of two genetically independent traits of growing pigs. However, breeding objectives consist of more than two traits in practial pig breeding programs and the prediction of response to genomic selection has not been reported for a broader breeding objective. Moreover, genomic selection is expected to benefit individual traits differently. Therefore, the objective of this study was to investigate how much genomic selection increases the predicted response in a breeding objective consisting of multiple correlated traits in growing pigs.

MATERIALS AND METHODS

A selection index was used to predict the genetic gain in a conventional pig breeding program and compare that with ten different scenarios using genomic selection. The genomic breeding value (GBV) was included as an additional trait with a heritability of 0.99 and had zero economic value in the breeding objective (Dekkers 2007). Genomic selection (GS1 to GS10) was based on a reference population size that varied from 500 to 5000 pigs with an interval of 500. The accuracy of the genomic prediction was derived based on the trait heritability, size of reference population and effective population size according to the formula of Daetwyler *et al.* (2008). Effective population size was assumed to be 100 to provide an estimate of linkage disequilibrium in a historical population. Accordingly, increases in the size of the reference population increased the correlation

between the true breeding value and corresponding GBV (accuracy) of each trait. A deterministic simulation was used to predict the genetic gain per selection round, $R = i\,r_{iA}\,\sigma_A$, where R is the genetic gain, i is the selection intensity of 1, r_{iA} is the selection accuracy (i.e. correlation between the true and estimated breeding value) and σ_A is the standard deviation of the breeding objective. Simulation was done using MTindex software (https://jvanderw.une.edu.au/).

Breeding scenarios. A terminal sire index for growing pigs included four breeding objective traits; back fat thickness (BFT, mm), average daily gain (ADG, g/d), feed conversion ratio (FCR, kg/kg), post-weaning survival (PWS, 0/1). These traits were also used as selection criteria, along with phenotype measurements of insulin-like growth factor 1 (IGF-1, ng/mL), muscle depth (MD, mm) and genomic breeding values for all traits. Base parameters for breeding objective traits and selection criteria are given in Table 1. Heritabilities and correlations were based on studies using Australian pig data. Economic values were taken from the study of Hermesch *et al.* (2014). The breeding objective is summarised in Table 2 including the source of information for each trait at the moment of selection (5 months of age). Sources of information for different traits varied depending on the availability of recording and recording cost. Genomic breeding values were available for the selection candidates before selection.

Table 1: Genetic standard deviation (bold, on the diagonal), heritability (h^2), common litter effect (c^2), economic value (EV), genetic (below diagonal) and phenotypic (above diagonal) correlations of the selection criteria traits (BFT, mm; ADG, g/d; FCR, kg/kg; PWS, 0/1; IGF-1, ng/mL; MD, mm) in a terminal sire line index for growing pigs

Traits[1]	h^2	c^2	EV	Correlations					
BFT	0.33	0.04	-1.7	**1.09**	0.11	0.06	0	0.21	-0.03
ADG	0.31	0.1	0.09	0.02	**39.95**	-0.2	0	0.09	-0.01
FCR	0.12	0.11	-27.44	0.1	-0.37	**0.13**	0	0.15	0
PWS	0.05	0	182.88	0	0	0	**0.04**	0	0
IGF-1	0.22	0.19	0	0.57	0.06	0.65	0	**11.63**	0
MD	0.19	0	0	-0.05	0.28	0	0	0.37	**2.02**

[1]BFT=back fat thickness, ADG= average daily gain, FCR= feed conversion ratio, PWS=post-weaning survival, IGF-1 = insulin like growth factor-1, MD = muscle depth

Table 2: Relative emphasis on the breeding objective traits and the sources of information for the selection criteria traits

Traits	% Contribution to breeding objective	Sources of information				
		Own	Sire	Dam	Fullsibs	Halfsibs
BFT	12.0	1	1	1	5	30
ADG	17.5	1	1	1	5	30
FCR	23.1	1	1	1	1	5
PWS	47.4	0	1	0	0	30
IGF-1	0	1	1	1	2	12
MD	0	1	1	1	5	30

[1]BFT=back fat thickness, ADG= average daily gain, FCR= feed conversion ratio, PWS=post-weaning survival, IGF-1 = insulin like growth factor-1, MD = muscle depth

RESULTS AND DISCUSSION

Selection accuracy. In comparison to a breeding program without genomic selection, overall accuracy of the breeding objective increased in genomic selection scenarios and showed an upward trend with the increase in the size of reference population (Table 3). The accuracy of PWS in the breeding objective increased by 81% in scenario GS10 whereas the accuracy of BFT, ADG and FCR increased by 14, 15, and 20%. Improvement of accuracy for different traits illustrates that traits with limited information prior to selection benefited more due to adding genomic information. Additional carcase and meat quality traits are also expected to benefit from genomic selection but were not considered in this breeding objective because they are not rewarded in most Australian markets.

Table 3. Accuracy of breeding objective traits and the overall terminal sire line index in growing pigs in scenarios with no GS (conventional breeding program) and GS1 to GS10 (assuming different size of reference population starting from 500 to 5000 in increments of 500)

Terminal Sire index	Accuracy										
	no GS	GS1	GS2	GS3	GS4	GS5	GS6	GS7	GS8	GS9	GS10
BFT	0.71	0.72	0.74	0.75	0.76	0.77	0.78	0.79	0.80	0.81	0.81
ADG	0.69	0.70	0.72	0.73	0.75	0.76	0.77	0.78	0.79	0.80	0.80
FCR	0.56	0.57	0.58	0.60	0.61	0.62	0.63	0.64	0.65	0.66	0.67
PWS	0.27	0.31	0.34	0.37	0.39	0.42	0.43	0.45	0.46	0.47	0.49
Overall Merit ($Index)	0.47	0.48	0.50	0.51	0.53	0.55	0.56	0.57	0.58	0.59	0.60

[1]BFT=back fat thickness, ADG= average daily gain, FCR= feed conversion ratio, PWS=post-weaning survival.

Predicted responses. Genomic selection in this study showed the potential to improve overall response in the breeding objective (Table 4). The predicted genetic gain in PWS increased between 23 and 147% using genomic selection compared to the genetic gain in the conventional breeding program. On the other hand, BFT, ADG and FCR had 14.5, 1.65, and 2.89% lower gain in the most accurate genomic selection scenario (GS10). The genetic improvements in PWS were achieved at a diminishing rate from GS3 to GS10.

Relative improvement for the different breeding objective traits is explained by the relative emphasis on breeding objective trait, the accuracy of its estimated breeding values (EBV) and the correlation with EBVs from other objective traits. Back fat thickness had a relative economic value of 12% of the total breeding objective whereas FCR contributed 23.1% while having fewer records available before selection. As a result, FCR did not lose as much gain as BFT. A negative genetic correlation between FCR and ADG (-0.37) prevented ADG from losing as much gain as BFT. However, the different rate of predicted responses for different traits indicates a shift of genetic improvement towards the traits having the limited number of records, a feature of genomic selection that has not been well studied in pig breeding programs but has been reported in a sheep breeding study (van der Werf 2009). The current study illustrated the effects of genetic correlations between breeding objective traits on the magnitude of genetic improvement for different breeding objective traits due to genomic selection.

Genetic gain depends on the GBV prediction accuracy that ultimately depends on the size of the effective population (Daetwyler *et al*. 2008). In this study, effective population size was assumed to be 100 which is slightly higher than the value estimated by D'Augustin *et al*. (2017) that varied from 42 to 98 in three Australian pig breeds. However, genetic gain was predicted deterministically based on selection index theory. This approach provided an approximate figure of additional

1.16$/growing pig in genomic selection with a reference population of 5000 pigs. Further study should be conducted to investigate the long-term economic impact of using genomic selection in growing pigs.

Table 4. Response per round of selection for the breeding objective traits in terminal sire line index in scenarios with no genomic selection (No GS, conventional breeding program) and GS1 to GS10 (assuming different size of reference population starting from 500 to 5000 in increments of 500)

Scenarios	Responses in genetic standard deviation				
	BFT	ADG	FCR	PWS	Overall Merit ($Index)
No GS	-0.311 (100)	0.462 (100)	-0.450 (100)	0.119 (100)	4.17 (100)
GS1	-0.302 (97.1)	0.461 (99.7)	-0.426 (94.6)	0.147 (123.5)	4.28 (102.6)
GS2	-0.291 (93.5)	0.458 (99.1)	-0.421 (93.5)	0.176 (147.8)	4.44 (106.4)
GS3	-0.285 (91.6)	0.456 (98.7)	-0.419 (93.1)	0.199 (167.2)	4.59 (110.0)
GS4	-0.281 (90.3)	0.457 (98.9)	-0.421 (93.5)	0.214 (179.8)	4.71 (112.8)
GS5	-0.278 (89.3)	0.454 (98.2)	-0.420 (93.3)	0.236 (198.3)	4.85 (116.2)
GS6	-0.276 (88.7)	0.458 (99.1)	-0.426 (94.6)	0.246 (206.7)	4.94 (118.4)
GS7	-0.274 (88.1)	0.456 (98.7)	-0.428 (95.1)	0.262 (220.1)	5.06 (121.3)
GS8	-0.272 (87.4)	0.459 (99.3)	-0.428 (95.1)	0.273 (229.4)	5.15 (123.5)
GS9	-0.271 (87.1)	0.461 (99.7)	-0.434 (96.4)	0.284 (238.6)	5.25 (125.8)
GS10	-0.269 (86.5)	0.459 (99.3)	-0.437 (97.1)	0.295 (247.8)	5.33 (127.8)

[1]BFT=back fat thickness, ADG= average daily gain, FCR= feed conversion ratio, PWS=post-weaning survival. Values in parentheses indicate the percentage changes in the responses relative to the base scenario (conventional breeding program).

CONCLUSIONS

This study predicted the additional overall response and additional response in individual breeding objective traits resulting from different scenarios of genomic selection. Overall genetic gain resulting from using GS is motivating for the implementation of GS in growing pigs. Before reaching a final conclusion, it is worthwhile to investigate the cost-benefit analysis of more realistic genomic selection scenarios.

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