



## Efficiency of genomic selection to improve meat quality in pigs using ZPLAN+

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### ABSTRACT

The phenotype or genomic enhanced breeding value (GEBV) of ultrasound intramuscular fat (UIMF) was used as the target trait to improve meat quality. The ZPLAN+ software was employed to calculate and compare the genetic gain and accuracy of each selection scenario. The first scenario reflected the current conventional selection program in which the selection index is composed of average daily gain (ADG), feed conversion ratio (FCR) and ultrasound backfat (UBF). In the second scenario, UIMF was added into the basic selection index as an indicator trait for meat quality. In scenario 3, UIMF was also incorporated into index; however, the GEBV was used instead of phenotype. In scenario 4 and 5, selection was based strictly on the GEBV, and UIMF was included in scenario 5. The results showed that the accuracies of scenario 3, 4 and 5, in which GEBV information was used, increased with increasing accuracy of the GEBV. Moreover, the trends of scenario 4 and 5 changed more rapidly relative to scenario 3. The addition of UIMF to the selection index had a positive effect on the genetic gain of ADG and FCR, but a negative effect on UBF. The addition of UIMF to the selection index led to improvement of other traits and to the overall meat quality, especially when genomic selection was applied.

**Key words:** Genetic gain, Genomic selection, Meat quality, ZPLAN+

### INTRODUCTION

Korean consumers show very strong preferences for particular parts of the pig that are high in fat (Seo *et al.*, 2012). Hence, intramuscular fat (IMF) is one of the most important traits in pork carcass grading in South Korea. Moreover, some breeding companies have included meat quality traits as a fundamental part of breeding selection programs. However, genetic improvement of meat quality under conventional quantitative selection has not been effective because these traits have low-to-moderate heritability and are very difficult and expensive to measure (Miar *et al.*, 2014). Therefore, it is essential to assess the potential for using genomic information in selection of animals. Genomic selection (GS) is currently being discussed as a potential method for improving breeding goal traits in cases in which the accuracy of selection is low, such as low heritable traits and traits that can only be recorded directly in one sex or slaughtered animals. GS simultaneously estimates the effects of dense genetic markers and summarizes these effects across all marker loci used to predict the breeding value of selection candidates (Meuwissen *et al.*, 2001). Herein, the prediction of genetic merit obtained through GS in this way is termed the genomic estimated breeding value (GEBV).

The present study was conducted to compare designs for implementation of genomic selection with scenarios using correlated phenotypes with/or correlated GEBV of traits which are traditionally used for routine

genetic evaluation. Additionally, the potential for use of ultrasound intramuscular fat (phenotype and GEBV) as selection criteria to improve meat quality in pigs was discussed. Scenarios were compared in terms of selection accuracy and genetic gain.

### MATERIALS AND METHODS

**Modeling software:** The ZPLAN+ (Täubert *et al.*, 2010) software was used to simulate and evaluate the different breeding schemes. This deterministic software allows modeling of all related breeding structures, as well as genetic and economic parameters to account for complex breeding programs with a special emphasis on genomic information. ZPLAN+ was developed based on the gene flow method, the selection index procedure for predicting reliabilities, and on complex economic modeling. Schemes were compared in terms of accuracy of the selection index, monetary genetic gain, breeding costs, returns and discounted profit. The costs and returns were not considered in this study due to the complexity of their determination.

**Breeding scenarios:** Traits in the breeding goal considered in this simulation were the average daily gain (ADG), feed conversion rate (FCR), ultrasound backfat depth (UBF), and ultrasound intramuscular fat (IMF), which are the main traits determining meat quality. Heritability, phenotypic standard deviations, and phenotypic and genetic correlations among traits are presented in Table 1. All genetic parameter estimates were adopted from a study conducted by Miar *et al.* (2014). The simulated breeding population used in this

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**Table 1:** Heritabilities (diagonal), phenotypic standard deviation, phenotypic (above diagonal) and genotypic(below diagonal) correlations among simulated traits

Trait	ADG	FCR	UBF	UIMF
ADG, kg/d	0.30	0.27	-0.31	0.32
FCR	-0.19	0.20	0.28	0.00
UBF, in	0.26	0.39	0.45	0.34
UIMF	0.69	0.48	0.00	0.26
SD	0.145	3.17	0.125	0.83

ADG = average daily gain, UBF = ultrasound backfat depth, FCR = feed conversion ratio, UIMF = ultrasound intramuscular fat, SD = standard deviation

study consists of 400 sows with an annual sow replacement rate of 40%. The breeding sows were mated naturally to 30 active boars with a 65% replacement rate every year.

Five scenarios were modeled in ZPLAN+ (Table 2). In the first and second scenarios, genetic evaluations were based entirely on phenotypic information without considering any of the marker information. The first scenario reflected the current conventional selection program, in which the selection index was composed of ADG, FCR and UBF. Methods of measuring these traits were discussed by Cabling *et al.* (2015) and Miar *et al.* (2014) in their studies of genetic associations between production and meat quality traits. The main information source for selection is based only on their own performance. In the second scenario, UIMF was added into the basic selection index as an indicator trait for meat quality. The heritability estimate of UIMF was 0.26, which showed strong genetic correlation with ADG (0.69) and UBF (0.48). In scenario 3, UIMF was also incorporated into the current selection index; however, GEBV was used instead of phenotype. This genomic trait was denoted as gUIMF. This scenario was modeled to assess the impact of genomic value of UIMF alone on the overall genetic gain and accuracy of the selection index. In scenario 4 and 5, the selection was strictly based on the GEBV. The traits in scenario 4 were only the basic selection index traits, which were denoted as gADG, gFCR and gUBF. In scenario 5, gUIMF was added in the index.

For all the scenarios, the accuracy of the selection index was measured depending on the accuracy of the GEBV (0.1-0.9). The accuracy of the GEBV is defined as the correlation between the GEBV and the true breeding value for the corresponding trait. All traits had an economic weight of one monetary unit per genetic standard deviation of the trait.

**Table 2:** Information sources of different simulated scenarios

Scenario	Information Sources
1	ADG + FCR + UBF
2	ADG + FCR + UBF + UIMF
3	ADG + FCR + UBF + gUIMF
4	gADG + gFCR + gUBF
5	gADG + gFCR + gUBF + gUIMF

**Genomic breeding value in ZPLAN+:** Four parameters ( $q$ ,  $N$ ,  $k$ ,  $rTI$ ) were needed to define the GEBV in the program, where  $q$  is the proportion of genetic variance explained by markers,  $N$  is the number of animals in the reference population,  $k$  is the number of independent segregating QTL and  $rTI$  is the accuracy based on the progeny test. Based on these parameters, the genomic information of the trait will automatically be inserted into the same correlation matrices as the other trait. The matrices will automatically be filled using the approach described by Dekkers (2007). In this study, two cases were employed to insert the genomic traits. The first approach was used to attain a certain accuracy ( $q$ =desired accuracy,  $N=1$ ,  $k=0$ , and  $rTI=1$ ). In the second approach, the background for implementing genomic information in the selection index on this basis was developed by Dekkers (2007) and modified by Daetwyler *et al.* (2010; 2008). This approach requires that the correlation between the true value and the GEBV be defined for every genomic trait  $r_{GBV}$ , which was accomplished using the approach developed by Erbe *et al.* (2011) based on an equation derived by Daetwyler *et al.* (2008):

$$r_{GBV} = \sqrt{\frac{N_p r_{TI}^2}{N_p r_{TI}^2 + M_e}} \quad (1)$$

where,  $N$  is the size of the calibration set and  $r_{TI}$  is the reliability of the GEBV of the animals used in the calibration set. In our calculations, we assumed  $N_p = 1000$ , which can be considered the minimum for GS in pigs (Haberland *et al.*, 2013), while the proportion of genetic variance explained by markers ( $q^2$ ) was assumed to be 0.8 for all breeding goal traits as suggested by Erbe *et al.* (2011). The reliability ( $r_2$ ) was assumed to be 0.5 for all traits.  $M_e$  is the number of independently segregating chromosome segments, which was derived by Goddard *et al.* (2011) as:

$$M_e = \frac{2N_e L k}{\log(N_e L)} \quad (2)$$

where,  $N_e$  denotes the effective population size,  $L$  is the average length of a chromosome in Morgans and  $k$  is the number of chromosome pairs.

The first approach was used in all computations, while the second approach was used to test the effects of the increasing reference population and determine the suitable number of animals needed in the reference population to achieve the desired accuracy and genetic response

## RESULTS AND DISCUSSION

**Accuracy of the selection index:** The accuracy of the selection index ( $rTI$ ) for different scenarios depending on the accuracy of the GEBV is presented in Table 3. The target trait under selection in this simulation was UIMF. The accuracy of the selection index was 0.56 and 0.57 for scenario 1 and 2, respectively. The difference in the accuracy of scenario 1 and 2 was small, indicating that inclusion of UIMF in the selection index did not have a strong effect on  $rTI$ .

**Table 3:** Accuracy of the index for each scenario depending on the accuracy of GEBV.

Scenario	Accuracy of GEBV								
	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9
1	0.55	0.55	0.55	0.55	0.55	0.55	0.55	0.55	0.55
2	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56
3	0.56	0.57	0.59	0.61	0.64	0.68	0.73	0.79	0.86
4	0.11	0.23	0.34	0.45	0.55	0.65	0.75	0.84	0.92
5	0.13	0.25	0.37	0.48	0.58	0.68	0.76	0.84	0.92

These results explain the low heritability estimate of UIMF (0.26). As expected, the accuracies of the scenario in which GEBV information was included increased with increasing  $rGBV$ . The  $rTI$  of scenario 3 ranged from 0.56–0.86 depending on the value of  $rGBV$ . The trends of scenario 4 and 5, for which the information source was based mainly on the GEBV, changed more rapidly as the  $rGBV$  increased when compared to scenario 3. The  $rTI$  of scenario 4 and 5 could increase as high as 0.92 when the  $rGBV$  was 0.9. Moreover, the accuracy of scenario 4 and 5 was higher than that of scenario 1 and 2 when the  $rGBV$  was  $e^{0.6}$ . The accuracy of scenario 5 was higher than that of scenario 4 when the  $rGBV$  was 0.1–0.7, but the accuracy was the same when the  $rGBV$  was 0.8–0.9. These accuracies were analogous with those reported by Pimentel and Konig (2012).

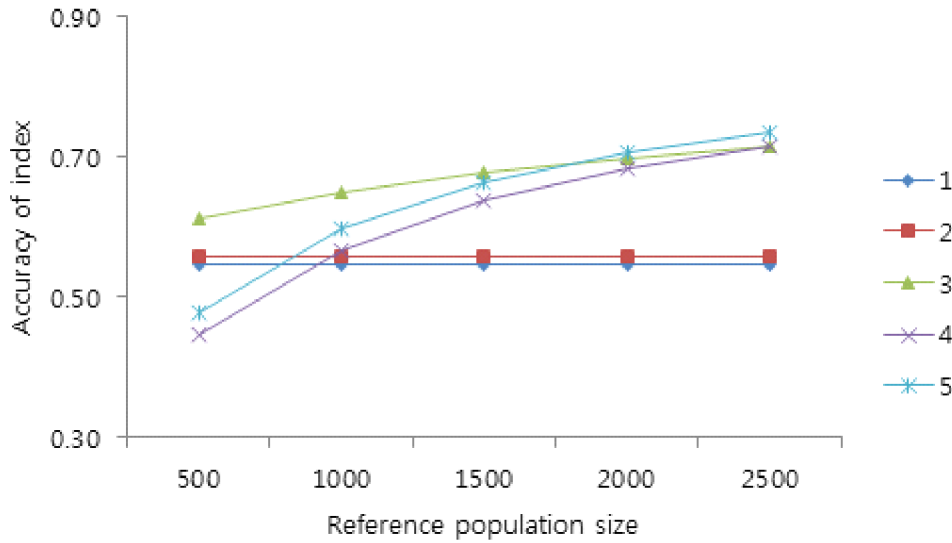
**Annual genetic gain:** The main target in each breeding program is to maximize the genetic gain per generation and year. The overall and per trait monetary genetic gain depending on the accuracy of the GEBV (0.1–0.9) of the breeding goal per year is shown in Table 4. The overall annual monetary genetic gain (AMGG) of scenario 1 and 2 was

0.15 and 0.36, respectively. The AMGG of scenario 2 was 40% higher than that of scenario 1 because of inclusion of UIMF in the selection index. Per trait, the ADG improved by 0.02, while the FCR and UBF were reduced by 0.07 and 0.05, respectively, in scenario 1. The genetic gain of ADG in scenario 2 was higher than in scenario 1, but the reduction in the FCR was lower. Moreover, the UBF in scenario 2 showed unfavorable genetic trends as it increased by 0.02. The addition of UIMF in the selection index favored the genetic gain of ADG because these two traits were positively genetically correlated and showed positive economic value. In the case of UBF, this trait was genetically positively correlated with UIMF, but their economic weight showed the opposite effect.

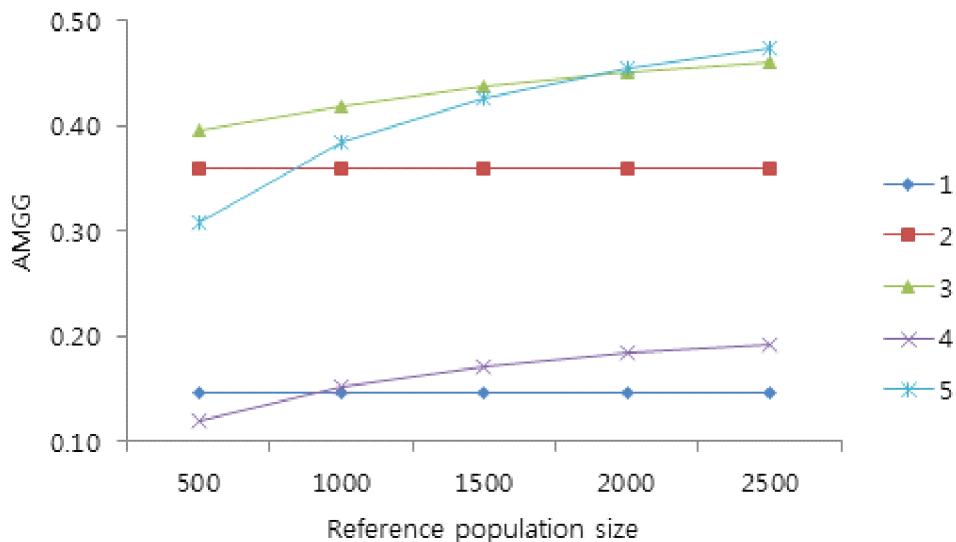
Applying the GEBV of UIMF in the selection index as in scenario 3 may create an AMGG of 0.36–0.55 depending on the accuracy of the GEBV. Scenario 3 further enhanced the AMGG by up to 53% relative to scenario 2. Moreover, the ADG was further improved from 0.02 in scenario 1 to 0.06–0.07 in scenario 3. However, the UBF also showed unfavorable results as in scenario 2. Conducting

**Table 4:** Annual monetary genetic gain for different information sources

Scenario		Accuracy of GEBV								
		0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9
1	AMGG	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15
	ADG	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02
	FCR	-0.07	-0.07	-0.07	-0.07	-0.07	-0.07	-0.07	-0.07	-0.07
	UBF	-0.05	-0.05	-0.05	-0.05	-0.05	-0.05	-0.05	-0.05	-0.05
2	AMGG	0.36	0.36	0.36	0.36	0.36	0.36	0.36	0.36	0.36
	ADG	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.06
	FCR	-0.02	-0.02	-0.02	-0.02	-0.02	-0.02	-0.02	-0.02	-0.02
	UBF	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02
3	UIMF	0.29	0.29	0.29	0.29	0.29	0.29	0.29	0.29	0.29
	AMGG	0.36	0.37	0.38	0.39	0.42	0.44	0.47	0.51	0.55
	ADG	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.07	0.07
	FCR	-0.02	-0.02	-0.02	-0.02	-0.02	-0.02	-0.02	-0.02	-0.02
4	UBF	0.02	0.02	0.02	0.02	0.02	0.02	0.03	0.03	0.03
	UIMF	0.30	0.30	0.32	0.33	0.35	0.38	0.41	0.45	0.49
	AMGG	0.03	0.06	0.09	0.12	0.15	0.18	0.20	0.23	0.25
	ADG	0.00	0.01	0.01	0.02	0.02	0.03	0.03	0.03	0.04
5	FCR	-0.02	-0.04	-0.06	-0.07	-0.09	-0.11	-0.12	-0.14	-0.15
	UBF	-0.01	-0.02	-0.02	-0.03	-0.04	-0.04	-0.05	-0.05	-0.06
	AMGG	0.08	0.16	0.24	0.31	0.37	0.44	0.49	0.54	0.59
	ADG	0.01	0.03	0.04	0.05	0.06	0.07	0.07	0.08	0.08
5	FCR	-0.01	-0.01	-0.02	-0.03	-0.03	-0.04	-0.05	-0.06	-0.06
	UBF	0.01	0.01	0.02	0.02	0.02	0.03	0.03	0.03	0.02
	UIMF	0.07	0.13	0.20	0.25	0.31	0.35	0.39	0.43	0.47



**Figure 1:** Accuracy of selection index for different scenario depending on reference population size.



**Figure 2:** Annual monetary genetic gain (AMGG) for different scenario depending on reference population

scenario 3 would create an annual increase of 0.02–0.03 inches in BF. UIMF increased from 0.29 in scenario 2 to 0.30–0.49 in scenario 3 depending on the accuracy of the GEBV. These findings confirm the results of former studies that showed the value of genetic gain increases when incorporating genomic information in the selection index (Schaeffer, 2006; Täubert *et al.*, 2011). In scenario 4, the AMGG was 67% higher than in scenario 1. All traits in the selection index also showed favorable results. The FCR and UBF were further reduced by 0.15 and 0.06, respectively. The highest AMGG of 0.59 was observed in scenario 5 when the accuracy of the GEBV was 0.9. The ADG increased to 0.08, while it was 0.47 for UIMF. However, scenario 3 improved the UIMF by 4% relative to scenario 5. The FCR

showed a higher favorable response in scenario 5 than scenario 3, with an annual reduction in feed intake of up to 0.06 kg realized per kg body mass gain. The UBF showed unfavorable response in scenarios 2, 3 and 5 in which UIMF was added to the selection index. The overall results showed that genomic selection significantly increased the AMGG. Simianer (2009) reported a 36.7% increase in genetic gain in litter size in pigs under genomic selection when compared to conventional practices.

**Effective reference population size:** The accuracy of the selection index relative to the reference population size ( $N$ ) was also investigated (Fig. 1). A further increase in accuracy of the selection index was possible by enlarging the  $N$  as discussed in many previous studies (Li, 2014; Simianer,

2009; Van Grevenhof and Van der Werf, 2015). The same trend was observed in this study. Scenario 4 and 5 showed lower accuracy than other scenarios if  $N$  was 500. Scenario 3 showed higher accuracy than other scenarios when  $N$  was around 500–2000. These findings indicate that combination of the phenotypic and GEBV in the selection index had an advantage over use of the GEBV or phenotype alone. However, scenarios 4 and 5 could improve the accuracy of scenario 3 when  $N$  was  $\geq 2500$ . Furthermore, scenarios 4 and 5 showed higher accuracy than reference scenarios 1 and 2 when  $N=1000$ . Haberland *et al.* (2013) also investigated the effective size of the reference population and found that  $N=1000$  could be considered the minimum size for a reference population in pig breeding.

The association of annual monetary genetic gain with reference population size is shown in Fig. 2. The AMGG of scenarios in which the GEBV was included in the selection index showed a directly proportional relationship with the reference population size. Scenario 5 showed higher genetic gain than scenario 1 when  $N$  was  $\geq 1000$ . Conversely, scenario 3 had a higher AMGG than scenario 5 when  $N$  was  $< 2000$ . Figure 2 also shows that the increase in AMGG of scenarios 4 and 5 was higher than that of scenario 3. Furthermore, the

increase in scenario 4 and 5 was rapid in the beginning until  $N=1500$ . Sitzenstock *et al.* (2013) reported that genetic gain increased remarkably as the reference population size and number of genotyped males increased.

## CONCLUSION

The addition of UIMF to the selection index had favorable results in terms of accuracy and genetic gain. Moreover, higher results are expected if genomic selection is implemented. The results showed that scenario 5 was the most advisable strategy, followed by scenario 3. The same trends were observed in the relationship of  $N$  with the accuracy of the selection index and AMGG. Both of these values were directly proportional to  $N$ . The minimum size of  $N$  found in this study was  $\sim 1000$ ; however, higher genetic response can be expected for higher  $N$ . It should be noted that this improvement is dependent on the capability of the breeding company and whether customers are willing to pay more for improved genetic quality.

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