Comparisons of Genetic Response of Different Mating Schemes for Improvement of Feed Efficiency, Growth Rate and Percent Lean in Swine

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Abstract

The objective of this study was to compare selection response on three traits (feed conversion ratio, FCR; days to market weight, DAY; and percentage lean content, PCL) based on three mating schemes together with mating criteria for inbreeding control: random mating (RAN), positive assortative mating (AM+), and negative assortative mating (AM-). Only matings that produced less than 10% inbreeding in the offspring would be allowed. Multi-trait animal model simulation software was used for generating pedigree and phenotypes of all traits. The 150 mating pairs from three schemes were selected from current and previous generation animals on their terminal line index (TLI). The results showed that the use of mate selection software could efficiently improve genetic response of FCR, PCL and DAY while controlling inbreeding. All three mating schemes can be applied to improve the genetic response of all growth traits. The AM- gave a slower response, minimum rate of inbreeding, and the most uniformity in offspring phenotypes. However, our result suggested the AM+ accelerated the rate of genetic responses while inbreeding in the population was still in the controlled level. The results of this study have a commercial benefit and could be applied in swine genetic evaluation program with mating selection strategies.

Keywords: Feed conversion ratio, mating schemes, assortative mating, genetic response

Introduction

There is a need for pig farmers to make the best quality animals at minimal cost, especially the feed efficiency. Most terminal line indexes (TLI) were focused on growth rate, feed conversion and composition. In some cases feed efficiency was more emphasized in the TLI selection program instead of growth rate on ad libitum feeding (Hoque et al., 2009). In recent sire-line breeding schemes, the feed conversion ratio (FCR) breeding value has been estimated along with the other traits to construct the TLI using different genetic correlations among traits. FCR is negatively correlated to growth and backfat thickness (Kuhlers et al., 2003). The genetic correlation between FCR and leanness was estimated at -0.23 to -0.49 (Hoque et al., 2007b; Saintilan et al., 2011). There are positive genetic correlations estimates between age (days) to market weight and FCR (Hoque et al., 2007b).

The individual EBV is a commonly used tool for selecting the best sires and dams. With mate selection, nowadays, the corrective parental mating has been proposed, which the several livestock used as a tool to accelerate genetic response together with controlling inbreeding in the population (Henryon et al., 2009; Sonesson and Meuwissen, 2002). Mate selection requires intense computation to generate lists of possible offspring from mating selected parents. The choices of mates will be considered based on the genetic merit and inbreeding levels of offspring generated from different parental combinations (Kinghorn, 2011).

In practical swine nucleus herd management, the best TLI parents are sometimes randomly mated. However, two more types of mating strategies are hypothesized based on the effect to genetic responses, these being positive and negative assortative mating. Therefore, the objective of the study was to examine the different mating strategies for the best genetic response under restricted allowable inbreeding rate using a TLI with FCR, DAY and PCL).

Materials and Methods

Data

The analysis data were generated by multi-trait animal model simulation from the given parameters in Table1. In this study, FCR, PCL adjusted at 105kg and DAY (days to market weight at 105 kg) were considered. At the beginning step, all 50 boars and 150 gilts from base generation (Effective number of population, Ne = 150) were randomly mated to produce next generation offspring. The conditions used were: 1) five contemporary groups (CG) per generation; 2) number of piglets born alive was 8 pigs and ranged 5 to 11 pigs; 3) 15% fallout rate was set every generation to reflect animals with structural and reproductive soundness problems; 4) piglet gender was randomly assign at 50% chance; 5) the live boars and gilts from current and previous generations (overlapping generation) were selected based on TLI to mate to produce new offspring; and 6) one boar was set to mate three sows. The phenotypic data and pedigree information were collected in data file and pedigree file for prediction variance and estimated breeding value usage.

Statistical analysis

Simulation method included fixed effect for gender (female and male) and contemporary groups. The random effects were animals and common litter effect. The variance components were obtained by Restricted Maximum Likelihood (REML) using the BLUPF90 software packages developed by Misztal (2008) to estimate breeding value in each generation under multi-traits analysis (3 traits) using the following animal model:

$$y = X\beta + Za + Wc + \varepsilon \qquad (1)$$

Where y is the vector of observations of the traits; β is the vector of fixed effects; a is the vector of additive genetic effects; c is the vector of litter effects; c is vector of residuals

$\boldsymbol{A}$ is the additive genetic relationship matrix between animals; X, Z, W are the incidence matrices for fixed, random effects, and litter effect for the traits;G, P, R are the (co)variance matrices of vector, a, c and ε with the following structure:

$$Var\begin{bmatrix} \boldsymbol{a} \\ \boldsymbol{c} \\ \boldsymbol{\varepsilon} \end{bmatrix} = \begin{bmatrix} \boldsymbol{G} \otimes \boldsymbol{A} & \boldsymbol{0} & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{P} \otimes \boldsymbol{I} & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{0} & \boldsymbol{R} \otimes \boldsymbol{I} \end{bmatrix}$$

Simulation techniques

Generating base generation (G_0), true breeding value of animal j of trait i were generated with the genetic (co)variance and residual (co)variance from Table 1 under normal distribution as $BV_{ij} \sim MVN(\boldsymbol{0}, \boldsymbol{G})$ and $\varepsilon_{ij} \sim MVN(\boldsymbol{0}, \boldsymbol{R})$ respectively. For the fixed effects, gender effects were generated under uniform distribution where $X_i \sim U(a, b)$ and a, b are parameters of uniform distribution. The effects of CG were generated under normal distribution where $CG_i \sim N(0, \sigma_i^2)$.

Table 1 Parameters used in simulation to generate phenotypic traits, contemporary group variance (σ^2_{CG}), sex variance (σ^2_{sex}), additive variance (σ^2_a), common litter variance(σ^2_c), error variance (σ^2_e) and genetic correlation (r_g)

Traits[1/]	Mean	σ^2_{CG}	σ^2_{sex}	σ^2_a	σ^2_c	σ^2_e	h^2	c^2	r_g	
									PCL	DAY
CR	3.000	0.010	0.017	0.028	0.005	0.050	0.31	0.06	-0.29	0.30
PCL (%)	56.00	1.17	1.76	3.36	0.38	5.86	0.35	0.04	-	0.30
DAY (days)	170.00	35.00	52.00	56.00	40.00	103.00	0.28	0.20	-	-

[1/] FCR= feed conversion ratio, PCL= percentage lean content (%), and DAY = day to market weight (days)

Generating generation 1 to 6, animal breeding values were generated using (2) while animal phenotype for each trait were generated by combining all effects in (3).

$$BV_j = \frac{1}{2}BV_s + \frac{1}{2}BV_d + \varphi_j \qquad (2)$$

$$y_j = \mu + fixed_j + BV_j + \varepsilon_j \qquad (3)$$

Where the y_j is phenotype of animal j for each trait; BV_j , BV_s , BV_d are breeding values of animal j, sire and dam; φ_j is Mendelian sampling of animal j generated under $\varphi_j \sim MVN(\mathbf{0}, \frac{1}{2}\mathbf{G})$.

At the end of each generation, EBVs were estimated by BLUP using multi-trait animal model using previously described genetic parameters. The terminal line index (TLI) with commercial economic value in (4) was also constructed. Inbreeding coefficient were calculated for offspring born from all mated parents using Mate/Selector program developed by Duangjinda (2013).

$$\text{TLI} = 100 - 30 * \text{EBV}_{\text{FCR}} + 2.0 * \text{EBV}_{\text{PCL}} - 1.75 * \text{EBV}_{\text{DAY}} \qquad (4)$$

Mate selection scenarios

In each generation, the best 50 boars and 150 sows based on TLI were selected to be mated to produce the next generation. Three scenarios of parental mating were set for producing next generation offspring: 1) random mating (RAN), 2) positive assortative mating (AM+) and 3) negative assortative mating (AM-). RAN was randomly mated between parents. AM+ was mating the best sows with the best boars. The AM- was mating the best sows with the worst selected boars or vice versa. The inbreeding coefficients were limited to less than 10% for any mating.

Estimation of selection response in inbreeding

Data and pedigrees from six generations of simulation using three mating selection schemes were used to estimate variance components and genetic parameters under tri-variate animal model (1) using AIREML. Genetic responses from each trait were estimated by EBV average in each generation and regression across six generations was also considered.

Individual inbreeding coefficients of animals in the pedigree were calculated. The average BV across generations were plotted to investigate the increasing rate. Each mate selection scenario was conducted for thirty replications.

Results and Discussion

Variance component

The variance components after performing mate selection with three different schemes for five generations were shown in Table 2. RAN gave the most unbiased additive genetic variance (V_A) estimation for all traits while AM+ and AM- gave slight increases in V_A for directional downward selection traits (FCR and DAY), and slight decreases in V_A for directional upward selection trait (PCL). Theoretically, assortative mating could influence the level of additive genetic variance and consequently of heritability (Falconer and Mackay 1996). Hypothetically, offspring genetic variance should be changed to $(1+\frac{1}{2}m)Va$, where m refers to correlation between the breeding values of the mates and Va is the original additive genetic variance. Note on parental BV correlation, AM+ and AM- should have positive and negative correlation, respectively. Therefore, the V_A should be increased in AM+ and V_A should be decreased in AM- according to Falconer and Mackay (1996). In our study, the alteration of V_A did not depend on AM+ or AM- scheme, however, the changing in V_A tentatively depended on the directional upward or downward selection. The result that both AM increased V_A was in agreement with Hohenboken (1985) and Allaire (1993) who showed that both AM+ and AM- increased the V_A. Hohenboken (1985) also explained that V_A would be changed in proportion of population mean for AM- and proportion of selected parental mean for AM+. This study firstly revealed that the increase in genetic variances occurred in the directional downward selection of the trait, while the decreasing occurred in the direction upward selection based on assortative mating selection.

Table 2 Variance component estimates and standard error (in parentheses) after five generations selection from different mating schemes

Traits[1/]	Mating schemes[2/]	Variance component estimates[3/]		
		σ^2_a	σ^2_c	σ^2_p
FCR	RAN	0.029 (0.001)	0.004 (0.000)	0.090 (0.002)
	AM+	0.030 (0.001)	0.004 (0.000)	0.091 (0.002)
	AM-	0.031 (0.001)	0.004 (0.000)	0.091 (0.002)
PCL	RAN	3.38 (0.06)	0.34 (0.01)	9.50 (0.17)
	AM+	3.32 (0.05)	0.33 (0.01)	9.45 (0.17)
	AM-	3.28 (0.06)	0.37 (0.01)	9.47 (0.17)
DAY	RAN	56.1 (1.01)	39.42 (0.70)	198.56 (3.60)
	AM+	57.36 (1.03)	39.19 (0.70)	199.02 (3.61)
	AM-	57.36 (1.12)	39.26 (0.71)	199.06 (3.70)

[1/] FCR= feed conversion ratio, PCL= percentage lean content (%), and DAY = day to market weight (days)
[2/] RAN, random mating after selection; AM+, positive assortative mating; AM-, negative assortative mating
[3/] Variance component (σ_a^2 = additive variance, σ_c^2 = common litters variance, and σ_p^2= phenotypic variance) and numbers in parenthesis are standard errors of the variance

Response to selection

Genetic gains for each generation and selection response across generations for three mating schemes were presented in Table 3. The genetic progress from all selection scenarios followed the expected breeding objectives. Genetic gain per generation was not different for three scenarios in FCR and DAY, however, AM- gave slightly slower genetic progress compared to AM+ or RAN. The result showed that response of DAY was lower than Chen et al. (2003) who reported approximately -32.01 days and -0.40 days/year for average genetic trend. The response of FCR was in the range of -0.51 to -0.54. The response of feed per gain was closed to that reported by Kuhlers et al. (2003). Our results showed that mate selection gave higher response (-0.10 to -0.11) compared to conventional selection in actual breeding from several studies. For example, the average changes in FCR ranged from -0.03 to -0.05 per generation based on selection by BLUP-EBV (Kuhlers et al., 2003; Nguyen and McPhee, 2005).

Table 3 Genetic response after five generations selection from different mating schemes

Traits[1/]	Mating schemes[2/]	Generations						ΔG/generation	SE[3/]
		1	2	3	4	5	6		
FCR	RAN	0.00	-0.13	-0.24	-0.33	-0.42	-0.51	-0.10	0.008
	AM+	0.00	-0.13	-0.24	-0.33	-0.44	-0.54	-0.11	0.007
	AM-	0.00	-0.13	-0.23	-0.32	-0.43	-0.51	-0.10	0.007
PCL	RAN	-0.02	0.24	0.28	0.37	0.75	0.92	0.18	0.170
	AM+	-0.03	0.25	0.33	0.45	0.84	1.01	0.20	0.100
	AM-	-0.02	0.21	0.20	0.26	0.42	0.53	0.10	0.100
DAY	RAN	-0.05	-5.58	-10.68	-15.37	-19.21	-23.68	-4.68	0.039
	AM+	-0.09	-5.68	-10.71	-15.88	-20.49	-25.92	-5.11	0.039
	AM-	-0.07	-5.80	-10.52	-14.85	-19.29	-24.18	-4.72	0.037

[1/] FCR= feed conversion ratio, PCL= percentage lean content (%), and DAY = day to market weight (days)
[2/] RAN, random mating after selection; AM+, positive assortative mating; AM-, negative assortative mating
[3/] SE is standard error of genetic response (ΔG) per generation.

The average response of PCL per generation in this study was lower than the previous reports of Nguyen and McPhee (2005) and they estimated genetic response of lean percentage of 1.24% based on a high line selection for high growth rate. The causes of this loss of genetic improvement in real life compared to simulation, or "leakage", was not clear. It seems that the cause of the different of number of CG, fallout rate, and the accuracy of selection is correlated with true breeding value and estimate breeding value; hence it seems to have affected the selection response as described by earlier investigators (Falconer and Mackay, 1996; Muir, 2000).

This study showed that genetic trend for DAY and FCR was not affected by selection schemes. In contrast to PCL, the increasing rate of genetic trend from AM+ was noticeably higher than RAN and AM-. The result agreed with Quinton and Smith (1995) who reported that AM+ gave higher genetic response in offspring, particularly if inbreeding is ignored. Although, inbreeding rate is limited (less than 10%) in our study but this level is enough to encourage with Quinton and Smith (1995). Likewise, Jorjani et al. (1997) who reported the positive phenotypic assortative mating is the highest cumulative selection response related with negative and random mating.

Note that the directional upward traits of selection have been affected by mate selection scheme more than downward traits. It also found that either AM+ or AM- would give lower SE of the trend (slope) compared to RAN, which revealed that assortative mating increased the accuracy of genetic response for PCL. In general, the mate/selection approach should result in higher genetic response because mate selection improves the accuracy of genetic evaluation for additive effect by choosing the genetic merit of future offspring from parental combinations or specific combining ability (Destefano and Hoeschele, 1992; Uimari and Mäki-Tanila, 1992). Our study has already tested in normality distribution of FCR (prove by normality test, data not show). This is important, because an including ratio trait (FCR) into index selection that does not perform as other normally distribution traits. According to Hoque et al. (2007a, 2007b) who discussed that, the traits measured as rations are small and erratic on selection response. Moreover, the genetic correlation is moderately positive correlated between FCR and feed intake, that selection against feed intake reduces appetite, which might be undesirable. However, the FCR is often set to terminal sire line with backfat thickness, genetic improvement are effectively responded in both traits that reported by Kuhlers et al. (2003). In addition, Chen et al. (2003) showed that the selection on nonlinear index on EBV for lean growth rate is quietly similar responses when compared to the selection based on linear index of EBV.

Uniformity of offspring after selection

The standard deviations of offspring traits in each generation from three mating schemes were shown in Table 4. The variation of phenotypes gradually decreased in each generation due to effect of selection, which generally increases the homozygosity. The higher variation decline was found in AM- compared with AM+ and RAN in all traits. The most variation decline was found in AM-/FCR (23.08%). This study empirically indicated that AM- is a system to improve uniformity of the offspring phenotype. This result is consisted with previous reports (Hohenboken, 1985; Jiang et al., 2013; Lynch and Walsh, 1998).

Effect of inbreeding

The average inbreeding coefficients for each generation under different mating schemes are shown in Figure 1. Increased inbreeding was found in all scenarios from the first to sixth generation, with less than 5% of inbreeding for all mating schemes although all schemes limited inbreeding at 10%. According to Muir (2000) the inbreeding has little effect on the trait in short term selection especially with large effective population size. This study found that assortative mating approaches affected the increasing rate of inbreeding in offspring. It was found that AM- gave lower inbreeding rate compared to AM+ and RAN (Figure 1). This result was supported by Sonesson and Meuwissen (2000) who reported that the assortative mating schemes gave the most efficiency, a delay of inbreeding rate in onset of selection. However, our result found that only AM- that followed their finding empirically. Lynch and Walsh (1998) reported that AM- promotes heterozygosity that can be slow the inbreeding rate, vice versa AM+ can lead to increases homozygosity within loci. Moreover, in general, AM- would be mating of less related animals that implies that the next generation had a minimum of degree of coancestry (Sonesson and Meuwissen, 2000). Therefore, this study revealed that controlling of inbreeding levels of offspring from each parental mating promoted the utilization of homozygosity effects with optimizing the depression.

Table 4 Standard deviation of genetic response in six generations under three mating schemes (average from 30 replicate of simulations)

Traits[1/]	Mating Schemes[2/]	Generations						%variation decline[3/]
		1	2	3	4	5	6	
FCR	RAN	0.13	0.11	0.10	0.11	0.11	0.11	15.38
	AM+	0.13	0.11	0.11	0.11	0.11	0.11	15.38
	AM-	0.13	0.11	0.11	0.12	0.11	0.10	23.08
PCL	RAN	1.36	1.29	1.31	1.40	1.34	1.34	1.47
	AM+	1.29	1.26	1.30	1.33	1.29	1.28	0.78
	AM-	1.29	1.26	1.29	1.31	1.31	1.26	2.33
DAY	RAN	4.20	3.92	3.88	3.80	3.89	3.68	12.38
	AM+	4.65	4.48	4.32	4.23	4.43	4.37	6.02
	AM-	4.67	4.31	4.08	4.21	4.21	3.94	15.63

[1/] FCR= feed conversion ratio, PCL= percentage lean content (%), and DAY = day to market weight (days)

[2/] RAN, random mating after selection; AM+, positive assortative mating; AM-, negative assortative mating

[3/] %Variation decline $= \frac{SD_{G6}-SD_{G1}}{SD_{G1}} \text{x } 100$

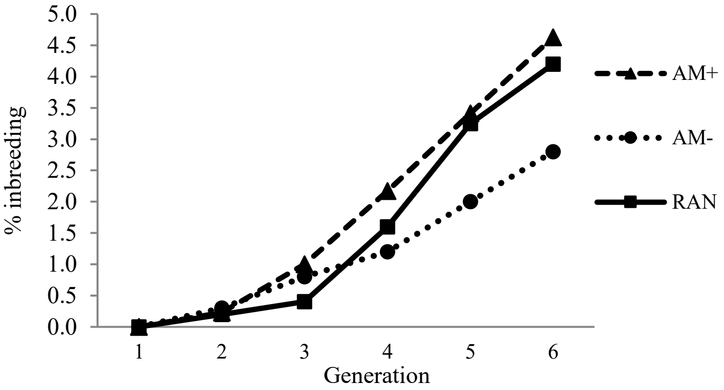

Figure 1 The average inbreeding coefficients (in percentage) for each generation based on mating schemes

Conclusion

The results show that mate selection could improve genetic response of FCR, PCL and DAY and minimize inbreeding rate in short term selection. Positive assortative mating is the most suitable mating strategy due to the most accelerated genetic responses while controlling population inbreeding. It could be applied by selecting the best parental combination in the genetic evaluation program. Selection for Feed conversion ratio together with PCL and DAY as TLI is practically important for commercial swine industry. This study indicates that the genetic response of FCR could be improved along with percentage lean content and day to market weight with appropriate assortative mating selection scheme.

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