Original Article

Genetic Parameters of Semen Quality Traits and Production Traits of Pure-bred Boars in Thailand

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Abstract

The objective of this study was to estimate genetic parameters for semen quality and production traits of pure-bred Finnish-Norwegian boars raised in Thailand. Data used in this study were 9,760 records of semen collection and 108 records of performance tests (from 25 Duroc, 59 Landrace, and 24 Yorkshire boars). Semen quality traits considered per collection were semen volume (SV), semen concentration (SC), total sperm (TS), and total abnormality (TA). Data were recorded from 2001 to 2009, except for TA, which was not recorded until 2003. Production measures from each boar were average daily gain (ADG) and backfat thickness (BF). Results showed that heritabilities varied from 0.29 to 0.49 for semen quality traits; besides, they were 0.40 and 0.18 for ADG and BF, respectively. The repeatability estimates for semen quality traits ranged from 0.30 to 0.61. No significant genetic correlation between semen quality and production traits was observed, except for a relationship between SV and BF (r_g = -0.52 ± 0.19). Among the semen quality traits, significant genetic correlation was observed only between SV and SC (r_g = -0.45 ± 0.18) and between SV and TS (r_g = 0.57 ± 0.16). In addition, ADG had a negative genetic relationship with BF at high magnitude value (r_g = -0.76 ± 0.11). These results suggest that semen quality traits have sufficient genetic variation for selection. Furthermore, traditional selection for AI boar using ADG and BF as selection criteria will not reduce semen quality.

Keywords: average daily gain, back fat thickness, boar, genetic parameters, semen quality

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Introduction

Artificial insemination (AI) has become an important technology in mating system that aims to reduce the number of boars, also the cost of housing, feed, and management. In pig industry, increasing average daily gain (ADG) and decreasing backfat thickness (BF) have generally been set as selection objectives in breeding programs to improve boar production performance (van Wijk et al., 2005; Safranski, 2008). Consequently, semen characteristics are of less interest. However, semen quality can be used to evaluate the efficiency of boar reproduction (Robinson and Buhr, 2005). Moreover, it impacts AI procedure since low quality semen affects conception rate and litter size (Smital et al., 2005; Wolf, 2010).

Oh et al. (2006) found positive genetic correlation between BF and semen traits; they suggested that the selection for production traits had a detrimental effect on semen production. The undesirable genetic relationships among semen quality, ADG, and BF can imply that the selection to improve ADG and BF will adversely affect semen characteristics (Toelle et al., 1984). Hence, effective boar selection should be performed by considering ADG and BF together with semen quality traits. Even though genetic knowledge related to those traits is needed, Smital et al. (2005) and Wolf (2009) reported that only few studies revealed genetic parameters for boar semen quality and production traits. Therefore, it cannot be concluded exactly for further applications. In Thailand, genetic association between semen quality and production traits has not been reported yet. Therefore, the aim of this study was to investigate genetic parameters of semen quality and production traits, as well as relationships between semen quality and production traits of pure-bred AI boars in Thailand.

Materials and Methods

Data: All animals in the current study were accommodated in accordance with the guidelines of the Department of Livestock Development, Ministry of Agriculture and Cooperative, Thailand. In total, 9,760 ejaculates from 108 pure-bred Finnish-Norwegian boars of three different breeds: Duroc, Landrace, and Yorkshire, from a commercial swine farm in Thailand were used in this study. They were reared in individual pens (8 m^2) in an evaporative cooling system building. During the study period, the average temperature in the building was approximately 28°C. Each boar was fed twice daily (2.5 kg/day) on diet containing 16% CP, 3,000 kcal ME/kg, and 0.8% Lysine. On average, male pigs were selected at 5 months of age using a selection index that comprised the estimated breeding value of ADG and BF. In addition to the selection index, physical soundness (body, legs, and movement) of male pigs was also considered. The selected boars were trained to mount a dummy; semen was collected on a weekly basis. At approximately 7 months of age, the selected boars began to be used for breeding.

Data of semen quality were recorded from July 2001 to April 2009, except for total abnormality, which was not recorded until March 2003, including the production data of 108 pure-bred boars, which were also available. Ejaculates were collected once daily (5:00 to 7:00 am) by only one technician throughout the recording period. Semen collections were performed every 7 days for younger boars (<12 months) and every 5 days for mature boars (>12 months).

Studied traits: Semen quality traits were examined for four parameters: semen volume (SV) was measured as the weight of the semen collected, semen concentration (SC) was measured by a spectrophotometer (Minitube Germany, Tiefenbach, Baden-Württemberg), total sperm (TS) was calculated by the multiplication of SV by SC, and total abnormality (TA) was evaluated under a phase-contrast microscope at 100x magnification for head abnormality and at 40x magnification for tail abnormality. Sperm head abnormality was examined by William's staining method (Williams, 1920). Moreover, presence of different sperm head abnormalities, i.e. pyriform head, giant head, micro head, tapering head, and detached head, was recorded. Sperm tail abnormalities, i.e. bent tail, coiled tail, proximal cytoplasmic droplets, and distal cytoplasmic droplets, were evaluated by fixing sperm samples in formal saline solution (Hancock, 1957).

Production traits evaluated were ADG and BF. ADG was calculated individually over the period from 25 to 100 kg live weight of boars as final weight minus initial weight divided by days on test. At approximately 100 kg body weight, BF was measured longitudinally on four different sites: 1) 2.5 cm in front of the last rib, 2) immediately behind the shoulder blades, 3) the highest and 4) the lowest values measured by sliding the probe from loin to ham by an ultrasound scanner (Medata Lean Streak) according to Holm et al. (2004). The average of four BF measured per boar was used in the analyses.

Data edition: Boars with less than four ejaculates were excluded from the analysis. At each collection, SV less than 50 ml or more than 583 ml, SC less than 56×10^6 cells/ml or more than 775×10^6 cells/ml, TS less than 10×10^9 cells or more than 168×10^9 cells per ejaculate, and TA more than 20% were regarded as an outlier and excluded from the analysis. After data edition, a total of 9,760 records of semen characteristics and 108 records of production data from 108 pure-bred AI boars were analyzed.

For statistical analyses, age at each collection was grouped into 17 classes (Kennedy and Wilkins, 1984): 14 classes were collected at 7 to 48 months of age, on a three-month basis (7-9, 10-12, 13-15, …, 46-48 months); 2 classes were collected at 49 to 60 months of age, on a six-month basis (49-54 and 55-60 months), and 1 class was collected at 61 to 72 months of age. Interval of collection was grouped into six classes (3, 4, 5, 6, 7 and >7 days).

Preliminary analyses: Because there were functional relationships among traits, i.e. TS was a product of SV and SC, the parameters estimated might be affected. Furthermore, previous studies showed that one-run analysis for all semen characteristics caused underestimated genetic parameters (Smital et al., 2005; Smital, 2009). In order to find an appropriate model for

genetic parameter estimation, four multi-trait animal models (Table 1) were investigated. In model 1, both SV and SC were included simultaneously. In models 2 and 3, only SV or SC was included and also TS was included concurrently. In model 4, all of the correlated traits (SV, SC, and TS) were included simultaneously.

From the preliminary analyses, the heritability estimates using model 4 were lower than the average heritability estimates from models 1, 2, and 3 (Table 2). However, the percentages of those differences were very low (0.22 to 4.96%), implying that all heritability estimates were not different. Because genetic correlations among semen quality traits were needed, model 4 was chosen for the evaluation of genetic parameters in this study. Therefore, all semen quality traits were fitted in a final model simultaneously.

Table 1 Traits included in the multi-trait animal models to investigate the appropriate model

Multi-trait model	Semen quality traits[1]			
	SV	SC	TS	TA
Model 1	✓	✓	-	✓
Model 2	✓	-	✓	✓
Model 3	-	✓	✓	✓
Model 4	✓	✓	✓	✓

[1]SV = semen volume, SC = semen concentration, TS = total number of sperm, TA = total abnormality

Table 2 Heritabilities for semen quality traits estimated from different multi-trait animal models

Traits[1]	Model[2]					Comparison[3]	
	1	2	3	Ave 1 to 3	4	Difference	%
SV	0.4882	0.5029	-	0.4956	0.4945	-0.0011	-0.22
SC	0.3403	-	0.3315	0.3359	0.3331	-0.0028	-0.84
TS	-	0.3125	0.3055	0.3090	0.2937	-0.0153	-4.96
TA	0.3456	0.3401	0.3477	0.3445	0.3394	-0.0051	-1.49

[1]SV = semen volume, SC = semen concentration, TS = total sperm, TA = total abnormality

[2]1, 2, and 3 = three-trait animal models; TS, SC, or SV was excluded from each model, respectively, 4 = four-trait animal model; TS, SC and SV were analyzed simultaneously, Ave 1 to 3 = average of heritabilities estimated from models 1 to 3

[3]Difference = the difference between Ave 1 to 3 and model 4, % = the difference divided by Ave 1 to 3 and multiplied by 100

Statistical Analyses: Descriptive statistics were examined by MEANS procedure and significance of fixed effects were tested by GLM procedure of SAS program (SAS Institute Inc., 2004). Fixed effects with a significant influence ($p<0.05$) were included in the final models. Although the breed did not significantly affect ADG ($p>0.05$), the dataset used in this study originating from different breeds of boars biologically influenced ADG. Accordingly, the effect of breed should be considered the fixed effect in the model (Hammond, 1992; Swan, 1992). Multivariate analysis was performed for all traits. The following multi-trait animal model was fitted: $\boldsymbol{y = Xb + Za + Wp + e}$, where **y** is the observation vector of studied traits (SV, SC, TS, TA, ADG, and BF); $\boldsymbol{X}$, $\boldsymbol{Z}$, and $\boldsymbol{W}$ are the known incidence matrices for fixed and random effects, respectively; $\boldsymbol{b}$ is the vector of fixed effects; $\boldsymbol{a}$ is the vector of random additive genetic effects; $\boldsymbol{p}$ is the vector of permanent environmental effects; and $\boldsymbol{e}$ is the vector of random residual effects. The random additive genetic effects were assumed to be normally distributed with zero mean and variance $A\sigma_a^2$, where A is the additive genetic relationship matrix between animals and σ_a^2 is the additive genetic variance. The random permanent environmental and residual effects were assumed to be normally distributed with zero mean and variance $I\sigma_p^2$ and $I\sigma_e^2$, respectively, where I is the identity matrix, and σ_p^2 and σ_e^2 are the permanent environmental and the residual variances, respectively

Models used for SV, SC, TS, and TA included breed of boar, age at collection, interval between collection as well as contemporary groups of year-month at collection as fixed effects. The additive genetic effect of boar and the permanent environmental effect of boar were included as random effects. For ADG and BF, breed and birth year of boar were included as fixed effects, and the additive genetic effect of boar was included as random effect. The fixed and random effects included in the final multi-trait animal model are summarized in Table 3. The (co)variance components were estimated by the restricted maximum likelihood (REML) method using REMLF90 program (Misztal et al., 2002). Standard errors of the heritability estimates were calculated by using the equations reported by Lo et al. (1992) and standard errors of genetic correlations were calculated by using the formula given by Falconer and Mackey (1996).

Results

Descriptive statistics: The number of boars, number of ejaculates, and ejaculates per boar, as well as least square means and standard error of the studied traits are presented in Table 4. Landrace was the prominent breed in this study; the average number of ejaculates per boar was 90.37. However, the maximum number of ejaculates per boar was found in Yorkshire. Similarly, the Yorkshire boars had the highest age at collection, followed by the Landrace and Duroc boars, respectively. The ejaculates were collected from each breed with an interval from 5.27 to 5.93 days (average 5.64 days). For semen characteristics, the Duroc boars had the lowest SV and TS, whereas they possessed the highest SC. Yorkshire had the lowest percentage of TA compared to that of Duroc and Landrace. For production performance, Landrace was the best performing genotype with the highest ADG and the thinnest BF.

Genetic parameters: Genetic parameter estimates for semen quality and production traits are presented in Table 5. The heritabilities of semen quality traits were moderate to high. Among the semen quality traits, SV showed the highest heritability (0.49) followed by TA, SC, and TS, respectively. The repeatability estimates of semen quality traits also ranked in the same order as the heritability estimates. For production traits, ADG had moderate heritability (0.40), whereas BF had low heritability (0.18).

Table 3 Fixed and random effects included in the final multi-trait animal model

Traits	Fixed effects[1]					Random effects[2]	
	BR	AC	IC	YM	BY	AD	PE
Semen quality traits							
Semen volume	✓	✓	✓	✓	-	✓	✓
Semen concentration	✓	✓	✓	✓	-	✓	✓
Total sperm	✓	✓	✓	✓	-	✓	✓
Total abnormality	✓	✓	✓	✓	-	✓	✓
Production traits							
Average daily gain	✓	-	-	-	✓	✓	-
Backfat thickness	✓	-	-	-	✓	✓	-

[1]BR = breed, AC = age at collection, IC = interval between collection, YM = combination of year and month at collection, BY = birth year of boar

[2]AD = additive genetic effect of boar, PE = permanent environmental effect of boar

Table 4 Number of boars and ejaculates, as well as mean and SE (in parenthesis) of the studied traits classified by breeds of boar

Variable	Duroc	Landrace	Yorkshire	All breeds
No of boars	25	59	24	108
No of ejaculates	2,382	4,721	2,657	9,760
Ejaculates/boar	95.28 (14.00)	80.02 (9.11)	110.71 (14.29)	90.37 (6.78)
Age[1], months	23.44 (0.24)[c]	24.16 (0.17)[b]	26.89 (0.23)[a]	24.73 (0.12)
Interval[2], days	5.27 (0.14)[c]	5.93 (0.10)[a]	5.47 (0.13)[b]	5.64 (0.07)
Semen quality traits[3]				
SV, ml	175.24 (1.68)[c]	239.44 (1.20)[a]	232.99 (1.59)[b]	221.96 (0.87)
SC, 10^6 cells/ml	349.73 (2.33)[a]	278.10 (1.65)[c]	310.84 (2.20)[b]	304.50 (1.19)
TS, 10^9 cells	59.82 (0.48)[c]	62.18 (0.34)[b]	68.67 (0.45)[a]	63.38 (0.24)
TA, %	4.68 (0.09)[a]	3.93 (0.06)[b]	2.91 (0.09)[c]	3.86 (0.04)
Production traits[4]				
ADG, g/day	994.02 (1.90)[b]	1,015.17 (1.35)[a]	987.11 (1.80)[c]	1,002.37 (0.95)
BF, mm	9.42 (0.03)[a]	6.84 (0.02)[c]	8.60 (0.03)[b]	7.95 (0.02)

[1]Age = age at collection

[2]Interval = interval between collection

[3]SV = semen volume, SC = semen concentration, TS = total sperm, TA = total abnormality

[4]ADG = average daily gain, BF = backfat thickness

[a, b, c]Different superscripts within each row are significantly different ($p<0.05$).

Table 5 Heritabilities (on diagonal), genetic correlations ± standard error (above diagonal), phenotypic correlations (below diagonal) and repeatability (r) for semen quality and production traits of boars

Traits[1]	SV	SC	TS	TA	ADG	BF
SV	**0.49 ± 0.14**	-0.45 ± 0.18	0.57 ± 0.16	-0.03 ± 0.23	-0.05 ± 0.22	-0.52 ± 0.19
SC	-0.21	**0.33 ± 0.12**	0.34 ± 0.24	0.00 ± 0.26	-0.08 ± 0.25	0.24 ± 0.28
TS	0.56	0.63	**0.29 ± 0.12**	-0.03 ± 0.27	-0.11 ± 0.25	-0.17 ± 0.30
TA	-0.23	-0.04	-0.17	**0.34 ± 0.13**	-0.09 ± 0.25	-0.09 ± 0.29
ADG	-0.11	-0.03	-0.15	-0.05	**0.40 ± 0.13**	-0.76 ± 0.11
BF	-0.27	0.25	0.02	0.08	0.41	**0.18 ± 0.08**
r	**0.61**	**0.45**	**0.30**	**0.59**	**-**	**-**

[1]SV = semen volume, SC = semen concentration, TS = total sperm, TA = total abnormality, ADG = average daily gain, BF = backfat thickness

As for the association among semen quality traits, significant genetic correlations were found between SV and SC (-0.45), as well as between SV and TS (0.57). In addition, SV had desirable association with TS, but undesirable with SC. No other genetic relationships among the semen quality traits were remarkable because the estimates of those genetic correlations were not significantly different from zero (due to large standard error). An estimate of not more than two standard errors is often taken as it is insignificantly different from zero. The genetic correlations between the semen quality traits and ADG were rather low and not statistically significant: ADG showed negative genetic correlations with the semen quality traits, ranging from -0.05 to -0.11, whereas both positive and negative genetic correlations were found between BF and the semen quality traits. The magnitude of the corresponding estimates varied from low to high (0.09 to 0.52); however, only the genetic correlation between BF and SV showed a statistically significant relationship ($p<0.05$). Moreover, a highly satisfied

genetic association (-0.76) between ADG and BF was found in this study.

For phenotypic correlations, ejaculates with low SV and TS were taken from high ADG boars, whereas thin BF boars possessed ejaculates with high SV but low SC. The corresponding phenotypic correlations of ADG with SV and TS were -0.11 and -0.15 and of BF with SV and TS were -0.27 and 0.25, respectively. Among the semen characteristic traits, favorable relationships of SV with TS and TA were observed. Moreover, phenotypic correlations between SC and TS together with between TS and TA were preferable.

Discussion

The average SV in the current study except for SV of Duroc fell within the interval reported in previous studies, ranging from 185.11 to 272.16 ml (Suriyasomboon et al., 2005; Oh et al., 2006; Smital, 2009). However, the average values of SC and TS were less than those reported by others, ranging from 401.00 to 525.90 × 10^6 cells/ml of SC and 92.90 to 118.70 × 10^9 cells per ejaculate of TS (Smital et al., 2005; Oh et al., 2006; Wolf and Smital, 2009[a,b]). Possible reasons for our smaller values of SC and TS were the differences in climate condition and the interval between two consecutive collections. According to the study of Smital et al. (2005), which was conducted in Czech Republic, a temperate climate country, the average interval between collections was 8.11 days, with 412.60 × 10^6 cells/ml of SC and 92.90 × 10^9 cells per ejaculate of TS, whereas our data, which were recorded in a tropical country, showed that the average interval between collections was 5.64 days. On the basis of relationships between collection interval and TS, Smital (2009) indicated that the pool of spermatozoa was restored after 5-7 days and fully restored after 10-11 days. Thus, the longer the interval between collections, the larger the amount of spermatozoa collected. The percentage of TA in the present study was less than 19.10 to 20.20% taken from 110 Duroc boars (Suriyasomboon et al., 2005), 10.70 to 11.50% taken from 163 Duroc, 653 Landrace, and 615 Large White (Wolf, 2009), and 10.66 to 11.82% taken from 105 Duroc, 477 Landrace, and 462 Large White (Smital, 2009).

The mean of ADG gathered from all breeds was consistent with that from the studies of Serenius et al. (2004) and Lebret et al. (2006). However, our average ADG was greater than that reported by some of the previous studies (Serenius and Stalder, 2004; Teye et al., 2006; Imboonta et al., 2007; Hoque et al., 2009) since various factors such as testing period and breed of boars can influence ADG. Furthermore, the boars in this study had lower BF (7.95 mm) than literature averages, ranging from 9.48 to 26.08 mm (Chen et al., 2002; Kerr et al., 2003; Serenius and Stalder, 2004; van Wijk et al., 2005; Imboonta et al., 2007). The low value of BF might be the result of the selection of boars born from breeding pigs subjected to continuous BF selection used in this study.

Heritability estimates for SV and SC in this study were higher than those in preceding literatures, which ranged from 0.14 to 0.28 for SV (Brandt and Grandjot, 1998; Wolf, 2009; Wolf and Smital, 2009[b]) and from 0.13 to 0.24 for SC (Brandt and Grandjot, 1998; Oh et al., 2006; Wolf, 2009). It is partly because those heritability estimates were analyzed by data gathered from various farms. Due to the fact that different farms implement different management strategies, the variation among farms might somehow increase the residual variances, resulting in low heritabilities. On the contrary, the heritability estimates of SV and SC in the present study were lower than those reported by Smital et al. (2005), 0.54 for SV and 0.49 for SC. According to Kuha et al. (2000), the heritability estimates obtained from repeatability model are lower than those from animal model. A possible reason might be that our estimates were evaluated using the repeatability model, in which permanent environmental effect was accounted for, whereas the analysis performed by Smital et al. (2005) was based on the animal model.

Although the heritability of TS in this study was quite low (0.29), it fell into the range of 0.06 to 0.42, as published by Smital et al. (2005) and Wolf (2009). Smital et al. (2005) obtained heritability of 0.34 for abnormal sperms (TA). Correspondingly, the heritability of TA calculated in the present investigation was the same value (0.34). All in all, the estimated heritabilities of semen quality traits indicate that these traits were heritable and their genetic variation was sufficient for an improvement.

The estimated heritability of ADG in current study agreed with that in various studies, which ranged from 0.19 to 0.48 (Serenius and Stalder, 2004; van Wijk et al., 2005; Hoque et al., 2009; Akanno et al., 2013). However, the heritability of BF was lower than that from previous observations, which ranged from 0.45 to 0.61 (Chen et al., 2002; van Wijk et al., 2005; Imboonta et al., 2007). The reason for the lower heritability of BF might be due to the low genetic variation in this studied herd. In addition, the boars used in this study originated from breeding pigs selected for reduced BF for a few decades. Furthermore, the present analysis was based only on 108 AI boars with small amount of BF phenotypic variation (SD = 1.77 mm). Small variation of phenotype represented in part the small amount of genetic variation.

The repeatability estimates for semen quality traits were high compared with published values (Brandt and Grandjot, 1998; Oh et al., 2006; Wolf, 2009; Wolf and Smital, 2009[b]), except for TS, which corresponded to previously reported values (Brandt and Grandjot, 1998; Oh et al., 2006; Wolf and Smital, 2009[a]). The results suggest that boars could produce semen with a moderate-to-high consistency of quality during their longevity.

According to the association among semen quality traits, the high genetic correlations of SV with TS and SC indicated that the selection for high SV results in high TS but low SC, as confirmed by various studies (Brandt and Grandjot, 1998; Smital et al., 2005; Oh et al., 2006; Wolf, 2009). SC had no genetic relationships with TS or TA; this is similar to the results of Smital et al. (2005) and Wolf and Smital (2009[a]), who reported that the genetic correlations of SC with TS and with TA were very low (0.01 and 0.06, respectively).

Nevertheless, some literatures showed that the selection for increasing SC also increased TS and TA (Smital et al., 2005; Oh et al., 2006; Wolf and Smital, 2009[b]). Although no genetic association between TS and TA was found in the current study, Smital et al. (2005) revealed slightly unfavorable relationship between them (rg = 0.14).

The low and insignificant genetic correlations between semen quality traits and ADG might be due to the fact that ADG was determined when the boars were around 6 months of age, while the semen quality traits were measured later in the boars' reproductive life. This investigation indicates that the selection for high ADG will not affect semen quality traits. On the contrary, Oh et al. (2006) published significant genetic correlations of ADG with SV (0.12) and with SC (-0.18). In addition, they suggested that the selection to increase ADG caused an increase in SV and a decrease in SC. This conflict might be explained by the difference in genetic background and the number of boars examined; they investigated 843 AI boars, while only 108 boars were used in our study. The highly negative genetic correlation between SV and BF (-0.52) found in the present study was confirmed by the investigation of Toelle et al. (1984), who reported a value of -0.41.

The presence of favorable genetic correlation between ADG and BF (-0.76) indicates that the selection for higher ADG results in lower BF. On the other hand, various literatures showed positive genetic associations between ADG and BF, ranging from 0.27 to 0.59 (Serenius and Stalder, 2004; van Wijk et al., 2005; Oh et al., 2006). This disagreement could be explained by two possible reasons. First, the difference in genetic background used in the studies, reflecting the phenotypic performances of boars. On average, the boars used in this study had low BF (7.86 mm) and high ADG (1,005.51 g/day), measured during 25-100 kg live weight, whereas those from other studies had higher BF (9.48 to 25.10 mm) and lower ADG (533.70 to 695.00 g/day), measured from birth until 100 kg live weight. Second, the different number of boars used in the studies. Our investigation was performed on only 108 boars, while 24,007, 1,645, and 827 boars were used in the studies of Serenius and Stalder (2004), van Wijk et al. (2005) and Oh et al. (2006), respectively. Consequently, the estimated genetic correlations were different with magnitude and direction.

In conclusion, the semen quality traits were heritable and their genetic variations were large enough for selection. Moreover, semen from the same boar could be produced with a moderate-to-high consistency of quality. However, the selection for high semen volume resulted in high total number of sperm but low semen concentration. Therefore, our results suggest that the selection for high ADG will result in low BF without adverse effects on semen quality traits.

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บทคัดย่อ

ค่าพารามิเตอร์ทางพันธุกรรมของลักษณะคุณภาพน้ำเชื้อและลักษณะการให้ผลผลิตของพ่อสุกรพันธุ์แท้ในประเทศไทย

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การศึกษาครั้งนี้มีวัตถุประสงค์เพื่อประเมินค่าพารามิเตอร์ทางพันธุกรรมสำหรับลักษณะคุณภาพน้ำเชื้อและลักษณะการให้ผลผลิตของพ่อสุกรพันธุ์แท้สายพันธุ์ฟินแลนด์และนอร์เวย์ที่ถูกเลี้ยงในประเทศไทย ทำการศึกษาโดยใช้ข้อมูลการรีดเก็บน้ำเชื้อจำนวน 9,760 บันทึกจากพ่อพันธุ์สุกรทั้งหมด 108 ตัว (พันธุ์ดูร็อค 25 ตัว พันธุ์แลนด์เรซ 59 ตัว และพันธุ์ยอร์คเชียร์ 24 ตัว) ลักษณะคุณภาพน้ำเชื้อที่ทำการศึกษาได้แก่ ปริมาตรน้ำเชื้อ (SV) ความเข้มข้นของน้ำเชื้อ (SC) จำนวนตัวอสุจิทั้งหมด (TS) และจำนวนตัวอสุจิผิดปกติทั้งหมด (TA) ข้อมูลทั้งหมดถูกบันทึกตั้งแต่ปี พ.ศ. 2544 ถึง 2552 ยกเว้นข้อมูลของ TA ที่เริ่มบันทึกตั้งแต่ปี พ.ศ. 2546 ลักษณะการให้ผลผลิตที่ทำการศึกษา คือ อัตราการเจริญเติบโตต่อวัน (ADG) และความหนาไขมันสันหลัง (BF) การศึกษาพบว่า ค่าอัตราพันธุกรรมของลักษณะคุณภาพน้ำเชื้อมีตั้งแต่ 0.29 ถึง 0.49 ขณะที่ค่าอัตราพันธุกรรมของ ADG และ BF เท่ากับ 0.40 และ 0.18 ตามลำดับ ค่าอัตราซ้ำสำหรับลักษณะคุณภาพน้ำเชื้ออยู่ในช่วง 0.30 ถึง 0.61 ไม่พบสหสัมพันธ์ทางพันธุกรรมระหว่างลักษณะคุณภาพน้ำเชื้อและลักษณะการให้ผลผลิต ($p>0.05$) ยกเว้นสหสัมพันธ์ทางพันธุกรรมระหว่าง SV และ BF (r_g = -0.52 ± 0.19) เมื่อพิจารณาสหสัมพันธ์ทางพันธุกรรมระหว่างลักษณะคุณภาพน้ำเชื้อแต่ละลักษณะพบว่า มีเพียงค่าสหสัมพันธ์ทางพันธุกรรมระหว่าง SV และ SC (r_g = -0.45 ± 0.18) และ SV และ TS (r_g = 0.57 ± 0.16) เท่านั้นที่มีนัยสำคัญ นอกจากนี้ยังพบว่าค่าสหสัมพันธ์ทางพันธุกรรมระหว่าง ADG และ BF ค่อนข้างสูง แต่มีความสัมพันธ์ในทิศทางตรงกันข้าม (r_g = -0.76 ± 0.11) ผลการศึกษาในครั้งนี้แสดงให้เห็นว่า ลักษณะคุณภาพน้ำเชื้อมีความแปรปรวนทางพันธุกรรมเพียงพอที่ปรับปรุงพันธุกรรมได้จากการคัดเลือก นอกจากนี้การคัดเลือกพ่อพันธุ์สุกรแบบดั้งเดิมโดยใช้ ADG และ BF เป็นเกณฑ์ในการคัดเลือกจะไม่ส่งผลเสียต่อลักษณะคุณภาพน้ำเชื้อของพ่อพันธุ์สุกร

คำสำคัญ: อัตราการเจริญเติบโตเฉลี่ยต่อวัน ความหนาไขมันสันหลัง พ่อพันธุ์สุกร ค่าพารามิเตอร์ทางพันธุกรรม คุณภาพน้ำเชื้อ

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