Estimates of Genetic Correlations between Production and Semen Traits in Boar

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ABSTRACT : Currently, boars selected for commercial use as AI sires are evaluated on grow-finish performance and carcass characteristics. If AI sires were also evaluated and selected on semen production, it may be possible to reduce the number of boars required to service sows, thereby improving the productivity and profitability of the boar stud. The objective of this study was to estimate genetic correlations between production and semen traits in the boar: average daily gain (ADG), backfat thickness (BF) and muscle depth (MD) as production traits, and total sperm cells (TSC), total concentration (TC), volume collected (SV), number of extended doses (ND), and acceptance rate of ejaculates (AR) as semen traits. Semen collection records and performance data for 843 boars and two generations of pedigree data were provided by Smithfield Premium Genetics. Backfat thickness and MD were measured by real-time ultrasound. Genetic parameters were estimated from five four-trait and one five-trait animal models using MTDFREML. Average heritability estimates were 0.39 for ADG, 0.32 for BF, 0.15 for MD, and repeatability estimates were 0.38 for SV, 0.37 for TSC, 0.09 for TC, 0.39 for ND, and 0.16 for AR. Semen traits showed a strong negative genetic correlation with MD and positive genetic correlation with BF. Genetic correlations between semen traits and ADG were low. Therefore, current AI boar selection practices may be having a detrimental effect on semen production. *(Asian-Aust. J. Anim. Sci. 2006. Vol 19, No. 2 : 160-164)*

INTRODUCTION

The production of a large quantity of high quality semen is important to pork producers since most sows are artificially inseminated (Singleton, 2001). The adoption of artificial insemination (AI) has had a significant impact on the structure of the swine genetics industry. It has been reported that AI now accounts for more than 60 percent of the total swine mating in the United States (Singleton, 2001). This effectively reduces the number of boars required in the U.S. swine breeding herd and at the same time increases the importance of high fertility and genetic merit for each boar. While genetic evaluation procedures (BLUP) to select the top boars for AI are commonplace, the genetic control of semen traits has not been extensively studied. Currently, boars selected for commercial use as AI sires are evaluated on grow-finish performance and carcass characteristics. If AI sires were also evaluated and selected on semen production, it may be possible to reduce the number of boars required to service sows, thereby improving the productivity and profitability of the boar stud. In the past, male fertility traits were not analyzed due to loss of data during natural mating (Brandt and Grandjot, 1998). However, a larger data set can be obtained due to adoption of artificial insemination techniques. Correlation analysis between semen traits and grow-finish performance can be based on these data. The objective of this study was to estimate genetic correlations between production traits such as average daily gain (ADG), backfat thickness (BF) and muscle depth (MD), and boar reproductive traits such as semen volume collected (SV), total sperm cells ($\times 10^9$) (TSC), total concentration of sperm per mL ($\times 10^6$) (TC), number of extended doses (ND), and acceptance rate of ejaculates (AR).

MATERIALS AND METHODS

Data source

Semen collection records and performance data for 843 boars selected for artificial insemination were provided by Smithfield Premium Genetics (Roanoke Rapids, NC). A total of 1,736 individuals were included in the pedigree file. Boars represented three different breeds, and were individually housed at two similar farm locations. Management differences between farms were accounted for by the farm effect in the analysis models. Each farm was also similar in numbers of boars of each breed.

Traits evaluated were ADG, BF, MD, SV, TSC, TC, ND, and AR. Backfat thickness and MD were measured longitudinally by real-time ultrasound using Aloka 500 Ultrasound machine fitted with 3.5 MHz, 12.5 cm linear-alloy transducer (Corometrics; Ithaca, NY). Measurements were collected 7 cm off-midline across the 10th to 13th ribs. Semen traits were recorded as repeated records. Semen volume was measured as the weight of the ejaculate volume.

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Table 1. Statistic of analyzed traits

Traits measured	N	Mean	SD	Min.	Max.
Average daily gain (kg/day)	843	0.695	0.07	0.474	0.920
Backfat (mm)	827	13.39	3.05	6.00	26.00
Muscle depth (mm)	827	57.26	6.28	41.00	77.00
Semen volume collected (ml)	843	206.8	58.87	28.00	410.66
Total sperm cells ($\times 10^9$)	839	104.5	27.93	2.30	188.15
Total concentration of sperm/ml ($\times 10^7$/ml)	839	52.59	15.97	0.25	126.07
Number of extended doses	839	35.22	9.58	1.00	65.46
Acceptance rate of ejaculates (%)	712	90.02	14.36	7.69	100.00

Total concentration was measured using a self-calibrating photometer. Total sperm cells were determined by multiplying SV and TC. Acceptance rate of ejaculates is based on the subjective evaluation of technicians and for an individual collection is binomial. Acceptance rate was calculated over the lifetime of the boar as the number of accepted collections divided by the total collections placing this data on a more normal scale. Technicians discarded ejaculates when blood or urine was present in the collection, when an evaluation of semen morphology presented a large number of abnormal sperm cells or when motility of sperm cells was low. Number of extended doses was calculated using total sperm cells divided by desired number of sperm cells per dose. For these data, each dose averaged 2.7 billion sperm with 100 ml fluid.

For these analyses the arithmetic mean of each semen trait for each individual was calculated to perform the multiple trait analyses with production traits. Therefore, our estimates for semen production traits are repeatabilities since permanent environmental effects were not separated in the model. This also resulted in averaging out the effects of collector, year-season and age of boar.

Genetic parameters were estimated from five four-trait and one five-trait animal models. Five different combinations of four multiple traits were (1) ADG, BF, MD and SV (2) ADG, BF, MD and TSC (3) ADG, BF, MD and TC (4) ADG, BF, MD and ND (5) ADG, BF, MD and AR, respectively. The five-trait analysis consisted of all semen traits, SV, TSC, TC, ND, and AR.

Statistical analysis

Least square means were estimated for fixed effects such as breed and farm, and the differences within fixed effects were compared using least significant differences with PDIFF option in SAS 8.01. The analysis model included fixed effects of farm, test batch, and breed.

Models for single and multiple trait evaluations were as follows:

$$y_{ijklm} = \mu + a_i + f_j + t_k + b_l + e_{ijklm}$$

where, μ is overall mean, a_i is the random additive genetic effect of ith animal, f_j is the fixed effect of jth farm, t_k is the fixed effect of kth test batch, b_l is the fixed effect of lth breed and e_{ijklm} is measurement error. Initial analyses of each trait were conducted using a single trait, animal model. The vector presentation of this model is: $Y = Xb + Zu + e$ where, Y is the vector of observations for all traits, b is a vector of common fixed effects due to farm, test batch and breed, u is a vector of random genetic effects and e is a vector of residuals and X and Z are incidence matrices relating observations to the fixed and animal effects, and E $[y'\ u'\ e']' = [b'X'\ 0'\ 0']'$. Variances of the random variables were:

$$V\begin{bmatrix} u \\ e \end{bmatrix} = \begin{bmatrix} G_o \otimes A & 0 \\ 0 & R_o \otimes I \end{bmatrix}$$

where $\otimes$ denotes a direct product operation, G_0 and R_0 are genetic and residual covariance matrices, with order equal to the number of traits in the analysis, and A is the numerator relationship matrix.

Variance and covariance components were estimated by a derivative-free REML algorithm (Graser et al., 1987) using the MTDFREML computer programs developed by Boldman et al. (1995). Stopping criterion was set as 10^{-10} for the simplex variance. Convergence was achieved after stopping criterion was obtained at the same or larger -2Λ, after a minimum of two cold restarts with the parameter estimates as new starting values.

Using information acquired from univariate analyses of each trait as starting values the multi-trait models were applied to estimate the (co)variance structure. To aid convergence and complete this analysis with available computing resources, the (co)variance structure was estimated from separate four-trait and five-trait analyses. For a four-trait model

$$G_o = \begin{bmatrix} \sigma^2_{a_{11}} & \sigma_{a_{12}} & \sigma_{a_{13}} & \sigma_{a_{14}} \\ \sigma_{a_{21}} & \sigma^2_{a_{22}} & \sigma_{a_{23}} & \sigma_{a_{24}} \\ \sigma_{a_{31}} & \sigma_{a_{32}} & \sigma^2_{a_{33}} & \sigma_{a_{34}} \\ \sigma_{a_{41}} & \sigma_{a_{42}} & \sigma_{a_{43}} & \sigma^2_{a_{44}} \end{bmatrix}$$

Table 2. Coefficient of variation (CV), skewness and kurtosis for each trait

Traits	CV	Skewness	Kurtosis
Average daily gain	10.42	0.160	-0.121
Backfat	22.77	0.736	0.921
Muscle depth	10.97	0.100	-0.178
Semen volume	28.46	0.478	0.402
Total sperm cells	26.73	-0.139	0.504
Total concentration	30.36	0.204	1.000
Number of extended doses	27.20	-0.212	0.298
Acceptance rate of ejaculates	15.96	-2.397	6.713

where $\sigma^2_{a_{ii}}$ is the additive genetic variance of trait i, $\sigma^2_{a_{ij}}$ is the genetic covariance between two traits i and j. Estimation of the genetic and environmental correlations (ρ_{ij}) from the REML (co)variance estimates is straightforward.

Analysis of rank correlations

Correlations between individual breeding values for each trait were obtained from the different multiple traits analyses. Pearson correlation coefficients using SAS 8.01 were calculated and tests of significance were performed under H_0: $\rho = 0$.

RESULTS AND DISCUSSION

Sample means are presented in Table 1 for all traits analyzed in this study. These values were higher for ADG

and lower for BF than those obtained by Smith et al. (1965) and Johnson et al. (2002), but standard deviations were similar. Hermesch et al. (2000) reported that the mean of MD was 37.8 mm recorded with real time ultrasound equipment and 46.6 mm with Hennesy Chong machine. The average MD in this study was greater (57.26 mm). Ejaculate volume in this study was slightly lower than the results of Xu et al. (1998). However, TSC were higher. The distribution of each trait (Table 2) allowed for the assumption of normality, however, AR showed the greatest departure from normality but we considered the distribution to be close enough to normal for the assumptions of the BLUP procedure. Breed 1 had more desirable BF, MD and TC than breeds 2 and 3 (Table 3). Breed 2 had the highest ADG and SV, and Breed 3 had the highest TSC and ND. Breeds 1 and 2 produced more acceptable ejaculates than breed 3. These results indicate that breeds have different roles in breeding programs. Farms 1 and 2 differed only in ADG, ND and AR (p<0.05), which implies that farm location and/or personnel at that location differ in ability to perform and evaluate boar collection.

Table 4 presents the pooled results across all analyses. Heritabilities of production traits have been well documented, and the estimates found for ADG and BF in this study are similar to literature averages (McPhee et al., 1979; Lutaaya et al., 2001), but lower than that reported by Smith et al. (1962) and Mrode et al. (1993). Muscle depth has not generally been considered in the past, with loin eye

Table 3. Least squares means for production and semen traits[1] by breed and farm

	ADG	BF	MD	SV	TSC	TC	ND	AR
Breed 1	0.686[a]	11.88[a]	59.97[a]	176.3[a]	98.83[a]	57.68[a]	33.86[a]	91.78[a]
Breed 2	0.700[b]	14.45[b]	56.64[b]	245.8[b]	100.1[a]	40.35[b]	32.89[a]	90.30[a]
Breed 3	0.695[ab]	14.25[b]	56.55[b]	226.0[c]	110.1[b]	49.64[c]	36.79[b]	86.13[b]
Farm 1	0.702[a]	13.68[a]	58.15[a]	212.4[a]	101.1[a]	49.31[a]	33.07[a]	91.94[a]
Farm 2	0.686[b]	13.37[a]	57.29[a]	219.6[a]	104.9[a]	49.14[a]	35.96[b]	86.86[b]

H0: LSMean (i) = LSMean (j) (Significant level = 0.05).
[1] ADG = Average daily gain; BF = Backfat; MD = Muscle depth; SV = Semen volume;
TSC = Total sperm cells; TC = Total concentration; ND = Number of extended doses; AR = Acceptance rate of ejaculates.

Table 4. Heritabilities, Repeatabilities (diagonal), genetic and phenotypic correlations below and above diagonal between production (ADG, BF, and MD) and semen (SV, TSC, TC, ND, and AR) traits[1]

	ADG	BF	MD	SV	TSC	TC	ND	AR
ADG	0.39*	0.36	0.39	-0.02[ns]	0.14	0.11	-0.01[ns]	-0.08
BF	0.59*	0.32*	0.16	0.19	0.11	-0.09	0.06[ns]	0.03[ns]
MD	0.20*	0.02*	0.15*	-0.12	0.06[ns]	0.16	-0.01[ns]	0.03[ns]
SV	0.12	0.16	-0.94	_0.38*_	0.46	-0.48	0.40	0.09
TSC	0.00	0.35	-0.93	0.74	_0.37*_	0.41	0.91	0.06
TC	-0.18	0.41	-0.49	0.02	0.58	_0.09*_	0.41	0.18[ns]
ND	0.00	0.39	-0.91	0.67	0.96	0.52	_0.39*_	0.02[ns]
AR	-0.22	0.62	0.09	0.22	-0.12	-0.51	-0.14	_0.16*_

* Arithmetic means calculated from parameters of different multiple traits analysis.
Phenotypic correlations were tested under H_0: $\rho = 0$ (Significant level = 0.05).
ns: Not significant. Repeatabilities are underlined.
[1] ADG = Average daily gain; BF = Backfat; MD = Muscle depth; SV = Semen volume;
TSC = Total sperm cells; TC = Total concentration; ND = number of extended doses; AR = acceptance rate of ejaculates.

Table 5. Statistic of breeding value estimates for each semen trait (SV, TSC, TC, ND, and AR)[1]

	SV	TSC	TC	ND	AR
Mean	0.371	0.186	0.008	0.066	0.017
SD	15.40	7.225	1.297	2.497	1.781
Skewness	0.444	0.117	0.165	0.109	-0.807
Kurtosis	3.046	1.565	1.493	1.409	3.502
Percentile					
Max.	95.56	31.52	5.736	11.54	6.885
Upper 1%	44.11	19.36	3.726	6.955	4.185
Upper 5%	26.77	12.52	2.255	4.337	2.715
Upper 10%	18.04	8.909	1.534	3.137	2.012
Upper 25%	8.019	4.044	0.692	1.379	0.967
Median	-0.066	0.000	0.000	0.000	0.077
Lower 25%	-7.908	-3.733	-0.727	-1.315	-0.744
Lower 10%	-16.838	-8.321	-1.540	-2.900	-1.994
Lower 5%	-23.23	-11.68	-2.181	-4.035	-2.912
Lower 1%	-40.43	-18.15	-3.232	-6.270	-5.900
Min.	-63.85	-29.29	-5.431	-10.13	-10.87

[1] SV = Semen volume; TSC = Total sperm cells; TC = Total concentration; ND = number of extended doses; AR = acceptance rate of ejaculates.

area more often reported as a measure of quantity of muscle. However, Hermesch et al. (2000) reported the heritability of MD to be 0.21 when measured by real time ultrasound, which is slightly higher than the heritability (0.15) in this study. Nsoso et al. (1999) also reported that heritability estimates of MD averaged 0.20 in sheep. Heritability and repeatability estimates for ejaculate volume have been reported in Europe, as low as 0.10 (Du Mesnil du Buisson et al., 1974) and as high as 0.35 (Du Mesnil du Buisson et al., 1978). Brandt and Grandjot (1998) found in a study of two selected lines that the mean heritability estimates were 0.16, 0.24, and 0.25 for volume, density, and number of sperm cells, respectively. In this study, the repeatability estimate of SV (0.38) was higher than Brandt and Grandjot (1998), but may be influenced by permanent environmental effects.

Genetic correlations between production traits were 0.59 between ADG and BF, 0.20 between ADG and MD, and 0.02 between BF and MD. The genetic correlation between ADG and BF was higher than that reported by Mrode et al. (1993; 0.32) and Johnson et al. (1999; 0.37). Genetic correlations between MD and ADG, and MD and BF were low or not significantly correlated. Genetic correlations between semen traits were comparatively high. However, genetic correlations between acceptance rate of ejaculates (AR) and TSC, TC and ND were negative which implies that good quantitative semen values don't necessarily result in good qualitative aspects. This negative correlation indicates that boars producing ejaculates with a higher concentration would also be more likely to produce fewer acceptable ejaculates. The high genetic correlations observed between many of the quantitative semen traits are to be expected as these traits are very highly related and often derived from each other. Increased TSC is genetically associated with increased SV, and agrees with Taylor et al.

(1985). Genetic correlation between SV and TC was 0.02, which is in contrast with the previously reported estimate of -0.49 (Brandt and Grandjot, 1998).

Genetic correlations between ADG and semen traits were generally low and not different from zero. Genetic correlations may be biased downward due to the inability to properly account for permanent environmental effects associated with semen traits. Genetic correlations between BF and semen traits were positive in sign and therefore selection for BF would have an adverse effect on semen traits. Conversely, genetic correlations between ADG, BF, SV, and TC reported by Brandt and Grandjot (1998) were negative. Strong negative genetic correlations were observed between MD and semen traits, excluding AR. Genetic correlations between BF and MD and semen traits in this study would indicate that current selection objectives would be expected to result in reduced male fertility. There was a consistent negative genetic relationship between lean content (MD and BF) and semen traits. Nestor (1976) reported in turkeys that body weight of a genetic line selected for semen yield at sexual maturity tended to be lower than the control line after six generations of selection. He proposed that this result may be due to loose linkage of the genes involved in growth and semen production, which may have broken up in a few generations of selection.

Statistics of breeding values for each reproductive trait from the five-multiple traits analyses are presented in Table 5. Breeding value estimates for the various semen traits would indicate that there is an opportunity to select for genetically superior boars that would produce ejaculates that are more acceptable and would yield more extended doses. The range in breeding values shows that from best to worst there is an 18% difference in acceptance rate and nearly 22 more extended doses per ejaculate. Pearson correlations between breeding values from different multiple traits analysis for each semen trait were

Table 6. Pearson correlations between breeding values estimated from multiple trait analyses with different combinations of traits

Comparison[1]	Pearson correlation coefficients
ABM_SV vs. SV	0.76
ABM_TSC vs. TSC	0.75
ABM_TC vs. TC	0.60
ABM_ND vs. ND	0.77
ABM_AR vs. AR	0.45

[1] Comparison of breeding values for semen traits estimated from a four-trait model including ADG, BF, MD, and one semen trait, and a five-trait model including all semen traits.

A = Average daily gain; B = Backfat; M = Muscle depth; SV = Semen volume; TSC = Total sperm cells; TC = Total concentration; ND = Number of extended doses; AR = Acceptance rate of ejaculates.

significantly different from zero ($p<0.0001$), but not approaching one (Table 6). This result is expected due to the genetic correlations between BF and MD and the semen traits and genetic correlations among semen traits. Therefore to implement genetic selection for semen traits the most efficient evaluation procedure needs to be determined. This may be a separate genetic evaluation of semen traits and then appropriate weightings with BF and MD in the development of breeding objectives.

IMPLICATIONS

Genetic selection for semen traits is possible. However, selection for increased muscle depth and reduced backfat may result in reduced boar fertility as measured by semen volume, total sperm cells, and total concentration of sperm per mL. Therefore, current swine industry selection practices would be expected to result in reduced male fertility. Additional work is needed to understand the relative economic importance of semen traits in the development of breeding objectives.

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