

Effect of Sex on Estimates of Genetic Parameters for Daily Gain and Ultrasonic Backfat Thickness In Swine

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ABSTRACT : Estimates were made of genetic parameters for average daily gain (ADG) and average backfat thickness (ABF), and of the effect of sex on estimates of variance-covariance components for average daily gain of boars (DGM) and gilts (DGF) and average backfat thickness of boars (BFM) and gilts (BFF) by residual maximum likelihood (REML) under a bivariate animal model. Data included a total of 2233 records (757 for boars and 1476 for gilts) of the Large White breed born between 1981 and 1986 in Miyazaki and Iwate prefectures in Japan. Heritability estimates for ADG and ABF were 0.43 and 0.69, respectively, with a genetic correlation of -0.08. Heritability estimates for DGM and DGF were 0.54 and 0.46, respectively, with a genetic correlation of 0.79, including that the two traits are influenced by similar but not identical genes. Respective estimates for BFM and BFF were 0.71 and 0.72 with a genetic correlation of 0.95, indicating that identical genes influence backfat thickness in boars and gilts. (*Asian-Aus. J. Anim. Sci.* 1999, Vol. 12, No. 5 : 677-681)

Key Words : Heritability, Genetic Correlation, Genotype, Sex, Pigs

INTRODUCTION

Selection for increased daily gain and reduced backfat thickness has been used to increase production efficiency in pigs (McKay, 1990; Cameron, 1994). Estimates of genetic parameters for daily gain and backfat thickness have been reported (Lo et al., 1992; Li and Kennedy, 1994; Skorupski et al., 1996). However, within a pig population, genetic parameters may differ with respect to sex, giving rise to genotype \times sex interactions. An interaction means that genes influencing a trait in one sex may be different from genes influencing the same trait in another sex. A genetic correlation of less than one indicates the presence of genotype by sex interaction (Robertson, 1959). An interaction may also cause variance heterogeneity (different variances) between sexes.

The effect of sex is currently accounted for in national genetic evaluation programs for pigs by using statistical models that include sex as a fixed effect (Li and Kennedy, 1994) or by adjusting data to one sex (Kennedy, 1984). Although such models have been widely accepted by the animal breeders, the underlying effects of sex on estimates of genetic parameters in pigs have rarely been quantified. One approach to understand the underlying effect of sex on estimates of genetic parameters is to treat a trait measured on one sex and the same trait measured on another sex as different traits. With this approach, it can be determined whether the two traits are genetically the

same. The objectives of this study were to estimate variance-covariance components for post-weaning average daily gain and average backfat thickness and to determine whether daily gain and backfat thickness measured on boars and the same traits measured on gilts are genetically the same traits.

MATERIALS AND METHODS

Data

Data on post-weaning average daily gain and average backfat thickness were obtained from Iwate and Miyazaki prefectures in Japan. The data included a total of 2233 records (757 for boars, 1476 for gilts) for four lines (two lines within each prefecture) of the Large White breed, born between 1981 and 1986 without overlapping generations. Pedigree records were traced back to ancestors born as early as 1979. All animals had the same genetic background and were subjected to the same selection and feeding procedures. In either prefecture, boars were kept and fed separately from the gilts. The animals were selected on an index including daily gain and ultrasonic backfat thickness measured on the animal, and records of loin eye area measured on the carcass of the relatives of the animal i.e. castrates. In this study, only variance-covariance components for daily gain and ultrasonic backfat thickness are estimated, that is only boars and gilts, and records made on them were used. From each litter, one boar and two gilts were selected for test. The test period started when the animals were 30 kg, and ended when they were 90 kg. At the end of the test period, the animals were individually weighed, and ultrasonically scanned for backfat thickness at ten positions (measured along the back of the animal starting 20 cm from the shoulder blade in intervals of 10 cm apart along the vertebra

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column with 5 measurements on each side of the vertebra column at a width of 2 cm apart). The traits of interest were average daily gain (ADG) including all records of boars and gilts defined as the average daily weight gain during the test period, and average backfat thickness (ABF), an average of ten measurements of backfat thickness measured by ultrasonic scanning. To determine the effect of sex on estimates of genetic parameters, data on average daily gain was partitioned and re-coded into average daily gain for boars (DGM) and gilts (DGF), respectively, and treated as different traits in the analysis. Similarly, records of average backfat thickness were re-coded into backfat thickness for boars (BFM) and gilts (BFF), respectively.

Statistical analysis

Data were analyzed using VEC 4.0 (Groeneveld and Garcia, 1998). The basic mixed model was as follows:

$$y = Xb + Za + e$$

where: y is a vector of observations, b is an unknown vector of fixed effects, X is the incidence matrix relating elements of b to y , a is a vector of unknown random additive genetic effects, Z is the incidence matrix relating elements of a to y , e is a vector of unknown random environmental effects peculiar to each observation in y .

The parameters for the random effects were assumed as follows:

$$E \begin{bmatrix} a \\ e \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \end{bmatrix}, \text{var} \begin{bmatrix} a \\ e \end{bmatrix} = \begin{bmatrix} G \times A & 0 \\ 0 & R \times I \end{bmatrix}$$

G and R are respective genetic and environmental variance-covariance matrices, I is the identity matrix and A is the additive relationship matrix. \times denotes the Kronecker product. A bivariate animal model was used to estimate heritabilities for ADG and ABF, and genetic and environmental correlations between the two traits, fitting sex and group (line and generation) as fixed effects (Model I). Under this model, variances and covariances were estimated using all the data available for the two traits. To determine the effect of sex on estimates of genetic parameters, statistical methods used for analysing partitioned data (Lee and Pollak, 1997) were used. Two bivariate animal models were used, the first featuring DGM and DGF (Model IIa) and the second featuring BFM and BFF (Model IIb) and both included the block effect of group as a fixed effect. For each model, the genetic correlation between pairs of traits was computed to determine the level of genotype \times sex interaction. The models IIa and IIb assumed zero environmental covariances between

pairs of traits. All models included 90 kg body weight as a covariate assigned to each trait. The mixed model procedure used considered all the pedigree information available to calculate the inverse of the numerator relationship matrix (A^{-1}), and therefore accounted for genetic trends, nonrandom mating and selection (Kennedy et al., 1988).

RESULTS

Means, standard deviations and coefficients of variation including the number of observations for the traits analysed are presented in table 1. On average boars grew 52 grams faster per day and were 0.8 mm less fat than gilts, an indication that on average a faster growing animal in one sex tend to put on less fat than a slow growing one in another sex when compared at the same body weight.

Table 1. Summary statistics for traits of average daily gain and backfat thickness used for estimating variance components

Trait Unit	Number of observations	Mean	Standard deviation	Coefficient of variation (%)
ADG grams	2233	743.4	109.5	14.7
ABF mm	2233	16.9	2.4	13.9
DGM grams	757	777.6	108.2	13.9
DGF	1476	725.9	105.9	14.9
BFM mm	757	16.4	2.2	13.6
BFF	1476	17.2	2.4	13.8

ADG and ABF are average daily gain and backfat thickness including boars and gilts. DGM and DGF are daily gain for boars and gilts, respectively. BFM and BFF are backfat thickness for boars and gilts, respectively.

Heritability estimates and their standard errors for ADG and ABF from Model I are presented in table 2. The respective estimates for ADG and ABF were 0.43 and 0.69, with respective genetic and phenotypic correlations of -0.08 and -0.14.

Table 2. Estimates of heritabilities, genetic and phenotypic correlations, and genetic variances for average daily gain and backfat thickness from Model I

Trait	Heritabilities and correlations		Genetic variance
	ADG	ABF	
ADG	0.43 ± 0.03	-0.14	2696.3
ABF	-0.08 ± 0.03	0.69 ± 0.02	3.53

Heritabilities and standard errors are in bold along the diagonal, genetic correlation and standard error are below the diagonal and phenotypic correlation is above the diagonal. Refer to table 1 for definitions of notations.

Estimates of heritability for DGM and DGF, and a genetic correlation between the two traits from Model IIa are presented in table 3. The respective estimates for DGM and DGF were 0.54 and 0.46. The genetic correlation between the two traits from Model IIb is presented in table 4. The respective estimates for BFM and BFF were 0.71 and 0.72, with a genetic correlation of 0.95.

Table 3. Estimates of heritabilities, genetic correlation and variances for average daily gain of boars and gilts from Model IIa

Trait	Heritabilities and genetic correlation		Genetic variance
	DGM	DGF	
DGM	0.54 ± 0.06		3730.7
DGF	0.79 ± 0.06	0.46 ± 0.03	2494.7

Heritabilities and standard errors are in bold along the diagonal, genetic correlation and standard error is below the diagonal. Refer to table 1 for definitions of notations.

Table 4. Estimates of heritabilities, genetic correlation and variances for average backfat thickness of boars and gilts from Model IIb

Trait	Heritabilities and genetic correlation		Genetic variance
	BFM	BFF	
BFM	0.71 ± 0.06		3.25
BFF	0.95 ± 0.04	0.72 ± 0.03	3.63

Heritabilities and standard errors are in bold along the diagonal, genetic correlation and standard error is below the diagonal. Refer to table 1 for definitions of notations.

DISCUSSION

Heritability estimates for ADG, ABF, DGM, DGF, BFM and BFF tended to be on the high side of corresponding published estimates for several breeds (Lundeheim et al., 1980; Lo et al., 1992; Li and Kennedy, 1994; Skorupski et al., 1996). The differences between some published estimates and those from the present study can be explained by differences in data samples, methods of estimation and management practices. Hutchens and Hintz (1981), in a comprehensive summary of published research findings, reported pooled estimates of heritability for ADG. In different studies, parameters were estimated by up to 15 different statistical methods, from up to 29 different breeds or groups of pigs and for boars, gilts, barrow, different and mixed sex groups. A total of 79 estimates were listed for ADG ranging from 0.04 to 1.11, with a weighed average of 0.38, which is fairly close to the estimates in this study. In the same study, they reported an average heritability estimate of 0.39

for ABF, with a range of -0.01 to 1.08 for live ABF from 66 studies. This average is smaller than the estimates from the present study. Since in this study ABF was an average of ten measurements, the measuring error may have been smaller than usual. The genetic correlation between ADG and ABF was estimated to be -0.08. The estimate is somewhat lower than the estimate of 0.19 reported by Van Steenberg et al. (1990).

Heterogeneity of covariance components by sex and a genetic correlation of less than unity between DGM and DGF were found. This is consistent with theoretical expectations (Robertson, 1959). It is hard to explain the difference in genetic variances between DGM and DGF. This is probably due to a combination of factors, data structure, population samples and expression of genes. The genetic correlation between DGM and DGF was high and not much different from unity. This indicates that the two traits are likely controlled by similar but not identical genes. Expected genetic gain from selection on two traits is a function of the genetic variances of respective traits, correlation between them and selection intensity. Genetic variances have a scale effect, and therefore can be scaled or transformed. A genetic correlation of less than unity is expected to affect the ranking of animals and expected response to selection is directly proportional to the genetic correlation. However, the high genetic correlation between DGM and DGF indicates weak interactions, therefore, the true ranking of the animals and genetic response will be little affected. How much must the genetic correlation fall before it has biological importance is difficult to tell. Robertson (1959) suggested a value of around 0.8, which is consistent with the value of 0.79 found in this study. The estimate of genetic correlation between BFM and BFF was close to unity (0.95). This indicates that backfat thickness measured on boars and backfat thickness measured on gilts are genetically the same traits.

In the literature, estimates of genotype × sex interaction have been variable and contradictory. Smith and Ross (1965) reported sire by sex interaction for daily gain and backfat thickness in a station test environment. Indications of genotype × sex interaction across environments (station-farm) are given by Roberts and Curran (1981) and Ollivier et al. (1984), who found higher genetic correlations for male to male comparisons than for male to female comparisons. Minkema (1982) and Ollivier (1983) found no indication of genotype × sex interactions within a uniform environment. Merks (1986) investigated genotype × sex interactions for daily gain in Dutch Landrace and Dutch Yorkshire, and found no interaction in the former, but reported interactions and larger genetic variances between boars and gilts in the

latter for daily gain, which is consistent with the results found in the present study.

In this study, a bivariate mixed model methodology based on residual maximum likelihood (REML) was used to estimate variance-covariance components. In the published literature on pigs, there are few studies showing the estimates of variance components for different sexes using bivariate mixed model methodology. Kennedy (1984) used maximum likelihood to estimate the effects of sex on age and backfat thickness to 90 kg in performance tested pigs. However, bivariate mixed model methodologies have been used extensively to estimate the effects of sex on estimates of genetic parameters, and genetic correlations close to unit for weight traits have been reported in beef cattle (Garrick et al., 1989; Rodriguez-Almeida et al., 1995; Lee and Pollak, 1997). Although estimates of genetic parameters from beef cattle are not comparable to estimates on swine, the statistical methodologies are not species specific.

IMPLICATIONS

The practical significance of the results found in the present study lies in the prediction of genetic improvement through selection. The expected genetic change in a population is determined by the heritability of each trait, selection differential and genetic correlations among traits. Partitioning of data by sex produced heterogeneity of covariance components and a genetic correlation of less than unit between measurements of daily gain between males and females. The practical implication of this result is that analysing only male data may not account for selection on females, and vice versa. Therefore, to the extent that differences in sexes can be adequately accounted for in the model as shown in this study, a bivariate animal model including records of both sexes for average daily gain and average backfat thickness would be appropriate and is recommended.

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