

HETEROGENEITY OF VARIANCE AMONGST SWINE HERDS FOR BACKFAT

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SUMMARY

An animal model and DFREML were used to estimate genetic and residual (co)variance components for backfat depth in different herds and for herds grouped by different levels of intraherd backfat variance. Estimates of genetic variance ranged from 1.39 to 9.78 and estimates of residual variance ranged from .88 to 7.05. Additive genetic and residual variances were clearly heterogeneous across herds and SD groups. The genetic component of variance in the high group was more than four times greater than that in the low group. Heritability estimates for backfat ranged from .35 to .73 across herds. Heritability estimates between high, medium and low SD groups were not significantly different. The extent of heterogeneity was such that a potential influence on sire evaluation would be expected. Estimates of genetic correlations between SD groups indicate that sires would be ranked differently in different SD groups and that genetic by SD group interactions did exist.

INTRODUCTION

Current across-herd evaluations for swine in the United States assume that all records come from the same population with constant genetic and residual variances. If variances are heterogeneous, biases will be imposed that become more severe as intensity of selection increases. Hill (1984) demonstrated that heterogenous variance among herds resulted in the selection of a greater proportion of animals from the more variable herds, causing a reduction in response to selection. If heterogeneity of variance is ignored when computing breeding values of boars and sows, high performers in high variance herds are strongly favored over high performers in low variance herds. Adjustment for heterogeneous variance was implemented in 1991 for national dairy evaluations of yield traits (Wiggans and VanRaden, 1991).

The intent of this project was to investigate and characterize the extent of heterogeneity of variance in swine field records of backfat.

MATERIALS AND METHODS

Backfat measurements for 29,977 pedigree Duroc swine collected from 44 herds in the United States were kindly supplied by the United Duroc Swine Registry. Herds recording over 1,000 backfat records were included in further analysis (Table 1). This data set consisted of 21,877 records from 11 herds. Backfat measures were adjusted to 104 kg using adjustment factors recommended by the National Swine Improvement Federation (1987). Contemporary groups were defined by breeders as a group of pigs that were raised in a common herd, year, and seasonal time frame. Two generations of pedigree information were used in the analysis.

Variances were estimated for all records and for individual herds. A multitrait analysis was used to consider backfat at three levels of intraclass backfat SD as three different traits. The low SD trait consisted of records from herd 10. Herds with records considered as a medium SD trait were 1, 3, 5, 6, 8, and 9. Records from herds 2, 4, 7, and 11 were considered to be the high SD trait. The same model was used for all traits and analyses and included a random animal effect and fixed effects of contemporary group and sex. Variance components and heritability estimates were obtained using Multiple Trait DFREML (Boldman et al., 1993). Standard errors for the heritability estimates were obtained by an approximation of the intraclass correlation (Swiger et al., 1964).

Table 1. Description of backfat data

Analysis	Records	Groups	Sires	Mean	SD	CV
All	21,877	522	397	21.15±.03	4.04	21.16
Herd 1	1,305	52	38	21.99±.11	3.87	17.62
Herd 2	1,827	46	37	16.07±.10	4.42	27.47
Herd 3	1,308	42	42	17.10±.11	3.94	23.02
Herd 4	1,048	20	34	17.68±.15	4.71	26.66
Herd 5	2,307	38	33	16.27±.07	3.25	19.97
Herd 6	1,549	112	49	20.51±.10	3.82	18.60
Herd 7	1,611	20	42	20.33±.11	4.60	22.62
Herd 8	2,910	55	38	20.47±.07	3.69	18.04
Herd 9	1,791	20	29	20.16±.09	3.72	18.50
Herd 10	4,793	29	110	19.13±.03	1.79	9.36
Herd 11	1,428	88	51	20.64±.12	4.43	21.47

RESULTS

Estimates of intraherd phenotypic mean, SD and CV for backfat are given in Table 1. Backfat depth ranged from 16.07 mm (Herd 2) to 21.99 mm (Herd 1). Estimates of SD and CV for Herd 10 were generally 50% smaller than those for other herds.

Variance component and heritability estimates are presented in Table 2 for the entire data set, each herd, and the multiple trait analysis. Large differences were found in genetic variance across herds and SD groups. Estimates of genetic variance ranged from 1.39 to 9.78 and estimates of residual variance ranged from .88 to 7.05. Additive genetic and residual variances were clearly heterogeneous across herds. No trends were observed between estimates of either genetic or residual variance and intraherd SD or mean backfat across herds. Heritability estimates for backfat ranged from .35 to .73 across herds. No trend was observed between intraherd SD or mean performance and magnitude of heritability.

Additive genetic and residual variances were clearly heterogeneous across SD groups (Table 2). When herds were grouped by intraherd SD estimates of genetic and residual variance increased as intraherd SD increased. However, the percentage increase from low to medium was greater than that from medium to high. Heritability estimates between high, medium and low SD groups were not significantly different. Moderate genetic correlations were found between low and high (.42) and medium and high (.53) groups. However, a negative genetic correlation was observed between the low and medium (-.55) groups.

DISCUSSION

Additive genetic and residual variances were clearly heterogeneous across herds and SD groups. Differences among herds in variability of performance generally have been thought to result from herd-to-herd differences in regional or local climatic factors and types of herd management

(Vinson, 1987). Herd management factors that create differences in the variability of backfat records may include feeding intensity, diet, measurement procedures, housing, and disease control. The extent of heterogeneity was such that a potential influence on sire evaluation would be expected. The genetic component of variance in the high group was more than four times greater than that in the low group indicating that the greatest reduction in response to selection would occur in Herd 10.

Table 2. Variance component and heritability estimates.

Analysis	Genetic Variance	Residual Variance	Heritability
All	4.49	4.80	.48±.03
Herd 1	7.52	4.79	.61±.14
Herd 2	7.02	6.50	.52±.12
Herd 3	6.23	7.05	.47±.12
Herd 4	4.25	3.04	.58±.15
Herd 5	2.85	3.33	.46±.11
Herd 6	8.74	3.27	.73±.14
Herd 7	6.03	4.90	.55±.12
Herd 8	3.49	6.62	.35±.09
Herd 9	6.32	4.64	.58±.15
Herd 10	1.39	.88	.61±.08
Herd 11	9.78	4.89	.67±.13
Low SD	1.39	.88	.61±.08
Medium SD	5.32	5.49	.49±.05
High SD	6.79	5.64	.55±.07

Estimates of genetic correlations between SD groups indicate that sires would be ranked differently in different SD groups. In addition the difference in sign of the genetic correlations would indicate that genetic by SD group interactions did exist. These correlations are in strong contrast to those found in the evaluation of dairy records (Dong and Mao, 1990), which were near unity between groups split on intraherd variance. The influence of heterogeneous variance on sire evaluation is likely, because of the large differences observed in genetic correlations between SD groups.

As swine from less variable herds may be underevaluated, effects of heterogeneous variance would need to be accounted for in genetic evaluation procedures. A key question for swine breeders is whether the assumption of homogeneous variances that is currently made results in important reduction in genetic gain. Possible approaches for dealing with heterogeneous variances include transformation of records, standardization by intraherd phenotypic standard deviation or by multiple trait methods (Van Vleck, 1987). The expression of a genotype in one herd could be treated as a different trait from the expression in another herd if the covariance structure is known (Gianola, 1986).

This methods is seldom feasible in large data sets. A possible alternative multiple trait methods include herds separated into groups by intraherd variance. Simulation mimicking this population may be one approach to answer the question of whether any of these methods provides for extra genetic gain as compared to the assumption of constant variances.

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