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GENETIC AND PHENOTYPIC PARAMETERS ESTIMATED FROM NEBRASKA SPECIFIC-PATHOGEN-FREE SWINE FIELD RECORDS

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Summary

Records collected during 1971 through 1979 from 101,606 hogs raised in 18 Nebraska Specific Pathogen Free herds were analyzed. Traits considered were backfat at 100 kg (BF), weight at 140 d of age (WT) and, in some analyses, number of live pigs/litter at birth (NBA). The phenotypic correlation of BF and WT, averaged across herds, was $-.07$. The correlations between BF and NBA and between WT and NBA were $.04$ and $-.05$, respectively. Average phenotypic standard deviations for BF, WT and NBA were 2.6 mm, 8.8 kg and 2.0 pigs. Estimates of the heritability of BF and WT were lower than most estimates reported from university research herds. Within breed, herd and sex estimates of heritability ranged from $-.22$ and $.51$ (unweighted $\bar{X} = .16 \pm .025$) for BF and ranged from $-.28$ to $.49$ ($\bar{X} = .16 \pm .016$) for WT. Estimates of the genetic correlation between BF and WT were extremely variable ($\bar{X} = -.62 \pm 14.3$, range = -9.42 to 1.30) among breed-herd-sex subclasses. (Key Words: Swine, Heritability, Field Record.)

Introduction

Cumulative genetic improvement in the commercial swine industry is provided entirely by the source of purchased breeding stock (Bichard, 1971). In the United States, these purchased stocks are most often purebred sires. Therefore, it is very important that purebred breeders utilize selection practices that maximize

genetic response.

The heritability of the characteristic in question is an important component of the response from selection. Development of an optimum linear index for multiple trait selection requires knowledge of phenotypic and genetic variances and covariances (Hazel, 1943). Many estimates of the heritabilities of backfat at 100 kg and weight at 140 d of age, and the correlations among these traits, are in the literature (e.g., see reviews by Young et al., 1978; Hutchens and Hintz, 1981). Most of the estimates of genetic parameters found in the literature were obtained from data collected from research herds. Estimates of these parameters from data collected on United States swine farms raising pigs for sale as breeding stock are not available. Reliable estimates would allow for development of optimum linear selection indexes that are directly applicable to on-farm selection programs.

The purpose of this study was to estimate phenotypic variances of, and correlations among, backfat at 100 kg (BF), weight at 140 d (WT) and number of live pigs/litter at birth (NBA) in several Nebraska Specific Pathogen Free (SPF) swine herds. Heritabilities of BF and WT and their genetic correlation also were estimated.

Materials and Methods

Source of Data. Records from 688,250 hogs farrowed in 165 Nebraska SPF herds during the years 1960 through 1979, inclusive, were made available for analyses. Each record may have included information on sire, dam and individual identification, breed, herd, sex, contemporary group, date of birth, NBA and WT. Backfat at about the fourth rib, last rib and last lumbar vertebra was measured on certified hogs, i.e., females with WT in excess of 68 kg and intact males whose WT was at least

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77 kg. Therefore, strict truncation selection on WT was practiced. Backfat was measured by ruler probe. These three values were averaged and adjusted to 100 kg. Adjustment factors for both BF and WT were (Olson et al., 1977):

$$BF = (100) \left(\frac{\text{average of three probes}}{\text{actual weight when probed}} \right),$$

$$WT = \{ [.826 + (\text{actual weight} - 54.43)] .006 \} \\ (140 - \text{actual age}) + \text{actual weight}.$$

The above adjustment for weight was applied if the actual weight fell between 54.4 and 77.1 kg. If an individual was between 77.1 and 113.9 kg when weighed, the factor .006 was replaced by .005.

Data represented swine raised in a broad range of environmental conditions. Housing conditions varied from outside lots to total confinement facilities. Data were collected by the SPF organization on a fee basis. All pigs were weighed and probed at or near 140 d of age. Many of the records did not include sire and dam identification. Only observations with individual and parental identification and breed, sex, herd, contemporary group, date of birth and WT information were utilized. Data from breed-herd-year subclasses with less than 60% of the records complete were not analyzed.

Death loss before measurement of WT accounted for the majority of incomplete records in the subclasses included in the analyses. In addition, herds with less than 1,900 records before editing procedures were disregarded.

This research included a study of selection practices and only herds where on-farm selection had been practiced were useful. A minimum of nine males and 76 females that were raised and subsequently produced offspring reared in herd-year subclasses meeting the edit requirements was considered necessary. These edit procedures yielded 101,606 observations for WT from 18 herds representing three breeds. Of these, 75,661 records included performance data for BF. No herds with data from 1960 to 1970 met all edit requirements and the time period involved in these analyses was 1971 through 1979. The time span, by herd, and the number of observations in each herd-sex subclass are listed in table 1.

Analyses of Data. The phenotypic correlation matrix for each herd-sex subclass was constructed from pooled within contemporary group variances and covariances. Variance of WT was evaluated both in populations of individuals where BF was and was not recorded. Therefore, variance of BF and covariances involving BF were adjusted for truncation based on minimum WT requirements (Robertson, 1977). These adjustments were made with the following formulae:

TABLE 1. TIME SPAN BY HERD, AND HERD-SEX SUBCLASS NUMBERS

Herd	Time span	Males		Females	
		WT	BF	WT	BF
A	1974-1979	1,187	799	1,898	1,279
B	1974-1979	1,255	1,159	1,269	1,212
C	1974-1979	2,285	1,351	2,699	1,790
D	1971-1976	3,603	2,983	4,223	3,908
E	1971-1979	7,472	5,845	12,563	10,300
F	1975-1979	2,583	1,819	4,382	2,904
G	1974-1979	2,714	1,152	3,319	1,965
H	1975-1979	385	191	832	384
I	1974-1979	1,375	1,047	2,098	1,618
J	1971-1977	6,058	4,853	10,862	9,366
K	1974-1979	1,026	794	3,126	2,409
L	1971-1979	1,381	1,095	1,915	1,604
M	1975-1979	1,114	688	1,430	1,025
N	1977-1979	600	149	653	260
O	1971-1976	2,560	1,660	3,299	2,740
P	1974-1979	1,340	1,098	1,852	1,468
Q	1971-1979	2,672	1,193	2,839	1,735
R	1971-1979	1,325	798	1,412	1,020
Total		40,935	28,674	60,671	46,987

$$VBF = VBF/[1 - (RBFWT)^2 (1-Z)],$$

$$CVBFWT = CVBFWT/Z,$$

$$CVBFNBA = CVBFNBA'$$

$$\{RBFNBA/[RBFNBA - (1-Z)$$

$$(RBFWT) (RWTNBA)] \},$$

where

- VBF = estimate of variance of BF in total population,
- CVBFWT = estimate of covariance between BF and WT in total population,
- CVBFNBA = estimate of covariance between BF and NBA in total population,
- RBFWT = correlation of BF with WT,
- RBFNBA = correlation of BF with NBA and
- Z = variance of WT calculated for the population of animals in which BF was measured relative to the variance of WT calculated for all animals.

A prime (') indicates that value as estimated in the population of animals in which BF was measured. The estimation of CVBFWT is straightforward. The VBF and CVBFNBA estimates were accomplished with iterative procedures, because the required correlation coefficients depended on the covariances involved. The mean value of Z across herds and sexes was .57 and the range for the value of Z was .30 to .86.

Estimates of heritability of BF and WT were calculated as:

$$h^2 = 4 \frac{\sigma_S^2}{\sigma_S^2 + \sigma_{D/S}^2 + \sigma_W^2},$$

where

- σ_S^2 = variance between sires,
- $\sigma_{D/S}^2$ = variance between dams within sires and
- σ_W^2 = variance between individuals within dams within sires.

Variance components were estimated by the analysis of variance technique. The completely random model assumed was:

$$Y_{ijkl} = \mu + C_i + S_j + D_{jk} + E_{ijkl}.$$

Here

- Y_{ijkl} = the phenotype of the l^{th} individual raised by the k^{th} dam bred to the j^{th} sire and reared in the i^{th} contemporary group,
- μ = overall mean with equal subclass numbers,
- C_i = effect of the i^{th} contemporary group,
- S_j = effect of the j^{th} sire,
- D_{jk} = effect of the k^{th} dam within the j^{th} sire and
- E_{ijkl} = random error.

Due to the size of herds E and J and the limitations of the computer, variance components were evaluated in five separate subsets of the data. In these herds only, all progeny from each sire were allocated randomly to a subset and data from each subset were fitted to the above model. Average results for herds E and J were obtained by weighting the estimates from each subset by the inverse of their variance.

The standard errors of the estimates of the heritability of BF and WT were approximated by modifying the formula of Dickerson (1969) for unequal subclass numbers (David, 1981).

The genetic correlation between BF and WT (r_G) was estimated from three analyses of variance by the above model of BF and WT and of a variable (F + W) computed as the sum of each individual's BF and WT measurements. Only observations which included BF and WT data were used. Data from three herds were used to test the effect of adjusting genetic correlations for truncation selection on WT. In each case, the adjustment did not change the size of the genetic correlation at the second decimal place. Therefore, no adjustments for truncation selection on WT were made when estimating r_G . The sire component of variance in the analysis of the variable BF plus WT (F + W) has the expectation:

$$E(\sigma_{S_{F+W}}^2) = \sigma_{S_{BF}}^2 + \sigma_{S_{WT}}^2 + 2\sigma_{S_{WT, BF}}.$$

The variance components represent the sire components of variance for BF and WT and the sire component of covariance between BF and WT. The genetic correlation estimate is then:

$$r_G = \frac{\sigma_{S_{BF, WT}}}{[(\sigma_{S_{BF}}^2)(\sigma_{S_{WT}}^2)]^{1/2}}.$$

The standard error of r_G was approximated with the formula for the function of mean squares, again modifying the formula suggested by Dickerson (1969) for unequal subclass numbers.

Results and Discussion

Phenotypic correlations involving BF, WT and NBA are presented in table 2. Within herd estimates of correlation coefficients for males and females were in general agreement. There was a small negative relationship between NBA and WT in most herds. The correlation between BF and NBA was very small, but usually positive. The phenotypic correlation between BF and WT varied from $-.24$ (herd N males) to $.22$ (herd M males). For 29 of the 36 estimates, this correlation was negative. In all herds except N and H, phenotypic correlations with an absolute value greater than $.05$ were different

($P < .05$) from zero. In herds N and H, the correlation needed to be larger than $.10$ to $.15$ to obtain this level of significance. Estimates of the phenotypic correlation between BF and WT were consistent with the literature average of values obtained in research herds (Hutchens and Hintz, 1981). In one field data analysis, the correlation between average daily gain and BF was $.09$ (Puff, 1976). Phenotypic variances and covariances can be calculated from the correlation coefficients and the standard deviations presented in table 3.

Heritability estimates of BF and WT and estimates of genetic correlations between these two characteristics are given in table 4 (females) and table 5 (males). Most estimates of heritability in these data were lower than those obtained from research herds and reported in reviews by Young et al. (1978) and Hutchens and Hintz (1981). Mean literature estimates for heritability

TABLE 2. PHENOTYPIC CORRELATIONS BY HERD-SEX SUBCLASS^a

Herd	Trait	Trait			Herd	Trait	Trait		
		BF	WT	NBA			BF	WT	NBA
A	BF		-.03	.00	B	BF		-.10	.03
	WT	-.10		-.11		WT	-.15		-.07
	NBA	.04	-.14			NBA	-.02	-.01	
C	BF		.11	.01	D	BF		-.15	.06
	WT	.20		-.15		WT	-.01		.03
	NBA	.02	-.15			NBA	.04	.02	
E	BF		-.09	.02	F	BF		-.20	.01
	WT	-.04		-.08		WT	-.10		-.08
	NBA	.02	-.07			NBA	.03	-.15	
G	BF		-.15	.04	H	BF		-.11	.35
	WT	-.13		-.11		WT	-.03		-.06
	NBA	.00	-.12			NBA	.19	-.09	
I	BF		-.14	.10	J	BF		-.07	.04
	WT	-.13		-.09		WT	.03		.00
	NBA	.08	-.15			NBA	-.01	-.01	
K	BF		-.18	.03	L	BF		-.09	.01
	WT	-.16		-.11		WT	-.11		-.12
	NBA	-.02	-.10			NBA	.06	-.14	
M	BF		.22	.09	N	BF		-.24	.03
	WT	.17		-.10		WT	-.07		-.10
	NBA	.01	-.13			NBA	-.04	-.14	
O	BF		-.08	.03	P	BF		-.21	.05
	WT	-.04		.01		WT	-.18		-.07
	NBA	.00	.03			NBA	.05	-.04	
Q	BF		-.09	.02	R	BF		.17	.01
	WT	-.05		-.05		WT	.19		-.02
	NBA	.00	-.04			NBA	-.05	.01	

^aValues above the diagonal are for males, those below for females.

TABLE 3. POOLED WITHIN CONTEMPORARY GROUP PHENOTYPIC STANDARD DEVIATIONS BY HERD-SEX

Herd	Females			Males		
	BF, mm	WT, kg	NBA, no.	BF, mm	WT, kg	NBA, no.
A	2.3	9.6	2.2	1.8	9.8	2.1
B	2.5	8.1	1.9	2.2	9.1	1.8
C	2.5	9.8	2.1	2.2	9.8	2.1
D	3.5	8.1	1.6	3.0	8.4	1.5
E	2.6	9.1	2.1	2.3	9.8	2.1
F	1.9	8.7	2.2	1.7	9.0	2.2
G	2.5	7.8	2.5	2.2	8.5	2.5
H	2.4	7.3	2.4	2.1	7.7	2.4
I	2.2	9.1	2.3	2.0	8.9	2.2
J	3.1	7.7	1.3	2.7	8.2	1.3
K	2.5	8.8	2.6	2.2	8.8	2.7
L	2.5	8.8	2.1	2.1	8.7	2.2
M	2.4	8.3	2.7	2.1	9.0	2.7
N	1.8	7.9	1.5	1.4	8.6	1.5
O	2.7	8.0	1.5	2.5	8.4	1.5
P	2.1	8.7	2.0	2.1	8.3	2.0
Q	2.2	8.7	2.1	2.0	10.0	2.3
R	2.3	9.2	1.9	2.0	10.7	2.0

TABLE 4. ESTIMATES OF HERITABILITY OF BACKFAT (BF) AND WEIGHT AT 140 D (WT) AND THE GENETIC CORRELATION OF BF WITH WT (FEMALES)

Herd	h^2_{BF}	h^2_{WT}	$r^a_{G_{BF, WT}}$
A	.18 ± .09	.49 ± .13	-.09 ± .001
B	.22 ± .12	.01 ± .08	-1.19 ± 1.450
C	.19 ± .08	.21 ± .07	-.43 ± .120
D	.04 ± .03	.06 ± .04	-1.12 ± .982
E	.12 ± .05	.21 ± .02	.13 ± .035
F	.21 ± .06	.16 ± .05	-.54 ± .085
G	.10 ± .07	.29 ± .08	-.05 ± .004
H	-.22 ± .20	.28 ± .17	
I	.25 ± .10	.10 ± .07	-.24 ± .031
J	.02 ± .03	-.04 ± .02	
K	.32 ± .10	.12 ± .05	-.09 ± .005
L	.21 ± .12	.08 ± .08	-1.83 ± 5.388
M	.12 ± .13	.17 ± .11	-.99 ± .740
N	.45 ± .27	.01 ± .08	-1.34 ± 2.588
O	-.01 ± .04	.00 ± .03	
P	.33 ± .13	.28 ± .11	.24 ± .077
Q	.29 ± .11	.22 ± .07	-.82 ± .425
R	.43 ± .17	.21 ± .13	.29 ± .089
Unweighted mean	.18 ± .029	.16 ± .021	-.47 ± .42
Weighted mean ^b	.08 ± .011	.08 ± .011	-.09 ± .00

^aMissing values of r_G are due to negative estimates of sire components of variance for BF or WT in the truncated data set.

^bWeighted by the inverse of the variance of the estimate.

of WT and BF were .26 and .40, respectively. One additional report of note is the research by Cox and Smith (1968). Heritabilities of gain from 98 to 154 d and backfat were .15 and .40, respectively. These data were collected on pigs in an irradiation study at Iowa State University. All sires were a result of repeat sampling of Duroc and Hampshire herds in Iowa. Heritabilities of backfat and average daily gain in German Landrace purebred herds were .30 and .20, respectively (Puff, 1976).

Estimates of the genetic correlation between BF and WT were extremely variable. Negative estimates of the sire component of variance were obtained for BF and for WT (in that portion of the population where BF was measured) in some herd-sex subclasses. Estimates of the genetic correlation were not possible in these herds because the denominator of the estimator includes the square root of the sire component of variance. Little additive genetic variation was found for both BF and WT in a few herds, i.e., those herds with estimates of heritability less than .10. At least 10% of the total variation in both BF and WT was genetic in nature for females and males in eight

herds.

Mean values of heritability and genetic correlation estimates were calculated by weighting the estimate for each herd-sex subclass by the inverse of its variance. This was done within and across sex. Results were $.08 \pm .014$ (h^2 for BF), $.08 \pm .011$ (h^2 for WT) and $-.09 \pm .001$ (r_G) in females. Estimates from boar data were $.07 \pm .016$ (h^2 for BF), $.07 \pm .013$ (h^2 for WT) and $-.03 \pm .020$ (r_G). The overall weighted-least-squares means were $.07 \pm .011$ (h^2 for BF), $.08 \pm .009$ (h^2 for WT) and $-.09 \pm .001$ (r_G). Unweighted means across sex were $.16 \pm .025$ for heritability of BF, $.16 \pm .016$ for heritability of WT and $-.62 \pm 14.3$ for the genetic correlation. Deleting herd D males from the mean changed the average genetic correlation to $-.30 \pm .24$. Mean values of the two heritabilities were similar in boars and gilts. Spearman's rank correlation coefficients between sexes were .29 for the heritability of BF, .24 for the heritability of WT and .40 for the genetic correlation. All rank correlations were nonsignificant, indicating a general lack of agreement between within herd estimates for each sex. Differences between herds in the

TABLE 5. ESTIMATES OF HERITABILITY OF BACKFAT (BF) AND WEIGHT AT 140 D (WT) AND THE GENETIC CORRELATION OF BF WITH WT (MALES)

Herd	h^2_{BF}	h^2_{WT}	$r^a_{G_{BF, WT}}$
A	.17 ± .13	.31 ± .13	-.17 ± .063
B	.08 ± .09	.19 ± .12	-1.11 ± .876
C	.02 ± .07	.29 ± .09	-.96 ± 1.690
D	.03 ± .03	.08 ± .04	-9.42 ± 415.802
E	.19 ± .06	.21 ± .04	-.06 ± .166
F	.10 ± .06	.33 ± .08	.60 ± .239
G	.10 ± .09	.15 ± .06	1.15 ± 1.085
H	-.05 ± .44	-.28 ± .22	
I	.29 ± .13	.17 ± .11	.48 ± .318
J	.07 ± .03	-.04 ± .02	
K	.02 ± .09	.24 ± .11	
L	.11 ± .13	.39 ± .15	-1.13 ± .804
M	.51 ± .23	.26 ± .15	1.30 ± .559
N	-.09 ± .18	-.02 ± .09	
O	.02 ± .06	.02 ± .04	.01 ± .023
P	.29 ± .15	.16 ± .11	-.46 ± .117
Q	.50 ± .14	.09 ± .06	-.29 ± .100
R	.38 ± .19	.27 ± .12	-.21 ± .225
Unweighted mean	.15 ± .037	.16 ± .025	-.73 ± 29.70
Weighted mean ^b	.07 ± .016	.07 ± .013	-.03 ± .02

^aMissing values of r_G are due to negative estimates of sire components of variance for BF or WT in the truncated data set.

^bWeighted by the inverse of the variance of the estimate.

proportion of males castrated could have caused some between-sex within-herd variation. Unequal proportions of males with BF recorded relative to females with BF measurements also could have been a factor in the estimates of the heritability of BF and the genetic correlation of BF with WT.

Weighting estimates of heritabilities and genetic correlation by the inverse of the variances of the estimate may bias estimates of average values. In these data, there is a positive relationship between the absolute value of the estimate and its standard error. Therefore, genetic correlations or heritabilities smaller in absolute value receive more weight than do those statistics larger in absolute value. Funkhouser and Grossman (1982) demonstrated that the bias in the estimate of the standard error of sire variance component estimates of heritability increased as the heritability increased. If their result, based on equal subclass numbers, can be extended to the case of unequal subclass numbers, this phenomenon would introduce the type of bias in the weighted mean discussed above. Therefore, it may be more reasonable to accept the unweighted mean of the estimates because it is unbiased, even though it is not a minimum variance estimate.

The most disturbing result from these analyses was the generally low estimates of heritability. With the amount of introduced breeding stock and the lack of intense selection pressure (David, 1981), depletion of additive genetic variance in these herds was unlikely. The low levels of heritability for BF and WT are probably due to random and environmental variation. Realized heritability estimates in research herds have demonstrated that it is possible to control nongenetic variation so that the portion of the phenotypic variance associated with differences in average breeding values was larger than what was observed in these SPF herds (Hetzer and Harvey, 1967; Rahnefeld and

Garnett, 1976). If seedstock producers want to duplicate that progress, they must mimic the selection and management practices of these research herds.

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