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Abstract

Performance test records from on-farm tests of young Polish Large White boars and reproductive records of Polish Large White sows from 94 nucleus farms during 1978 to 1987 were used to estimate population parameters for the measured traits. The number of boar performance records after editing was 114,347 from 3,932 sires, 21,543 dams, 44,493 litters and 1,075 herd-year-seasons. Reproductive performance records of sows involved 41,080 litters from 2,348 sires, 18,683 dams and 1,520 herd-year-seasons. Both data sets were analyzed by using restricted maximum-likelihood programs. The model used for the performance records included fixed herd-year-seasons, random sires, dams and error effects, and covariances for the year of birth of sire and year of birth of dam. The model used for the reproduction data set was the same as the performance data with parity as an additional fixed effect. Estimated heritabilities were .27, .29, .26, .07, .06, .06 for average daily gain standardized to 180 d (ADG), backfat thickness standardized to 110 kg BW (BF), days to 110 kg (DAYS), litter size at birth born alive (NBA), litter size at 21 d (N21) and litter weight at 21 d (W21), respectively. Estimated common environmental effects for the same traits were .09, .10, .09, .06, .07 and .05, respectively. Genetic correlations were .68 (NBA and W21) and .80 (N21 and W21). The respective phenotypic correlations were .23, -.99, -.20, .88, .75, .86. These population parameters for Polish Large White pigs are similar to those for breeds in other countries.

Keywords

Pigs, Growth Traits, Reproductive Traits, Heritability, Genetic Correlation, Phenotypic Correlation

Disciplines

Agriculture | Animal Sciences | Genetics

Comments

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POPULATION PARAMETER ESTIMATES FOR PERFORMANCE AND REPRODUCTIVE TRAITS IN POLISH LARGE WHITE NUCLEUS HERDS^{1,2}

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ABSTRACT

Performance test records from on-farm tests of young Polish Large White boars and reproductive records of Polish Large White sows from 94 nucleus farms during 1978 to 1987 were used to estimate population parameters for the measured traits. The number of boar performance records after editing was 114,347 from 3,932 sires, 21,543 dams, 44,493 litters and 1,075 herd-year-seasons. Reproductive performance records of sows involved 41,080 litters from 2,348 sires, 18,683 dams and 1,520 herd-year-seasons. Both data sets were analyzed by using restricted maximum-likelihood programs. The model used for the performance records included fixed herd-year-seasons, random sires, dams and error effects, and covariances for the year of birth of sire and year of birth of dam. The model used for the reproduction data set was the same as the performance data with parity as an additional fixed effect. Estimated heritabilities were .27, .29, .26, .07, .06, .06 for average daily gain standardized to 180 d (ADG), backfat thickness standardized to 110 kg BW (BF), days to 110 kg (DAYS), litter size at birth born alive (NBA), litter size at 21 d (N21) and litter weight at 21 d (W21), respectively. Estimated common environmental effects for the same traits were .09, .10, .09, .06, .07 and .08, respectively. Genetic correlations were .25 (ADG and BF), -.99 (ADG and DAYS), -.21 (BF and DAYS), .91 (NBA and N21), .68 (NBA and W21) and .80 (N21 and W21). The respective phenotypic correlations were .23, -.99, -.20, .88, .75, .86. These population parameters for Polish Large White pigs are similar to those for breeds in other countries.

Key Words: Pigs, Growth Traits, Reproductive Traits, Heritability, Genetic Correlation, Phenotypic Correlation

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Introduction

Reliable estimates of variance components are of great importance in any livestock improvement scheme. Estimates of heritability

or common environmental effects are a function of variance components and are, in general, specific for a particular population and period of time. Hence, reliable and specific population parameter estimates are essential in developing an efficient, long-term improvement scheme.

The parameter estimates in the literature for many traits often are quite variable (Hutchens and Hintz, 1981). Utilization of parameter estimates from the literature to set up a breeding program for a specific population can be very misleading when the values used are not the true values. Estimates from large field data sets are not always in agreement with those from designed research projects or controlled test stations. Pig improvement programs presently in use in Poland are based either on estimates from relatively small size

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samples from the active (nucleus) population or on results in the literature.

The major objective of this study was to estimate components of variance, heritabilities, common environmental effects (c^2) and phenotypic and genetic correlations for the performance and reproductive traits of Polish Large White pigs in the nucleus population. These estimates can be utilized to change pig improvement programs in Poland.

Materials and Methods

Data

Performance test records from on-farm (home) tests of young Polish Large White boars and reproductive records of Polish Large White sows were obtained from the National Research Institute of Animal Production in Poland. Animals were measured from 1978 to 1987 on all nucleus state farms. The data sets did not include results from private nucleus farms because the average size of the private farms was less than five sows and because fewer than 25 boars were tested yearly per farm. In contrast, the average size of the state farms was about 70 sows, with about 350 boars performance tested yearly.

Performance Test of Young Boars. The raw data contained 126,637 records on boars from 94 farms. Each record consisted of the herd, region (Regional Breeding Office) of origin and dam, sire and the tested animal registration number. Also included were date of birth, date of test, age at day of test, body weight at day of test, average daily gain over the pig's entire life, average backfat thickness, average daily gain standardized to 180 d of age (ADG) and backfat thickness standardized to 110 kg BW (BF). According to the test procedures, all boars were measured at the home farm when they were from 170 to 210 d of age. Age adjusted to 110 kg was defined as DAYS. Backfat thickness was measured ultrasonically by the Kraut Krammer USM2⁶ apparatus at four sites: over the shoulder, on the midback (10th rib) and twice at the last rib. Three measurements were taken 3 cm away from midline. The second measurement at the last rib was taken 8 cm away from the midline. All

measurements were done on the right side of the animal. Measurements generally were done by the same group of people (Regional Breeding Office) within a region. The test period was considered to be the period from birth until the day of measurement; some selection may have taken place at the end of the test period. Results from the test period generally are not used to compare animals across farms.

The data were edited to eliminate all records with missing information and to remove records when only one sire progeny group was represented in a single herd-year-season (HYS) or when a sire had only one progeny. A total of 114,347 records of the original 126,637 were used. The number of records, farms, dams, litters and HYS are presented in Table 1.

Reproductive Performance Test of Sows. The data contained 53,630 litter records, of which 22,583 were first-parity litters. Records were collected from 97 farms. Each progeny record consisted of region and farm identification number and dam, sire, maternal grandsire and maternal granddam registration number. Also included was information about year of birth, date of birth of dam, parity of dam, date of farrowing, number of piglets born alive (NBA) measured at d 1 to 3, litter size at 21 d (N21), litter weight at 21 d (W21) and age at first farrowing. Little or no selection took place prior to first farrowing. Crossfostering was not practiced routinely.

The data were edited to eliminate all progeny records with missing information and to remove data in which all records in a single HYS were from one sire progeny group only and when a sire progeny group had only one litter. A total of 8,203 records were eliminated because of missing information; 4,347 additional records were eliminated for other reasons. This left 41,080 litter records from 81 farms. The number of records, farms, dams, litters and HYS are presented in Table 1.

Methods

The data were analyzed separately for the performance test of young boars and the reproductive performance test of sows. Variance components were estimated by restricted maximum-likelihood (REML) methods (Thompson, 1962; Patterson and Thompson, 1971, 1974; Harville, 1977; Thompson and

⁶Kraut Krammer, Inc., Cologne, Germany.

TABLE 1. NUMBER OF RECORDS AND DATA STRUCTURE

Regions ^a	Performance data						Reproductive data				
	Farms	HYS ^b	Sires	Dams	Litters	Records	Farms	HYS ^c	Sires	Dams	Litters
1	10	120	604	3,390	6,846	15,718	14	241	405	3,478	7,555
2	18	163	578	3,328	6,972	16,428	13	197	332	2,506	5,701
3	16	187	629	3,440	7,793	19,755	13	234	355	3,092	6,847
4	20	182	538	3,232	5,712	14,182	10	178	279	2,449	5,258
5	16	203	632	3,639	7,510	21,936	20	399	501	4,107	8,858
6	7	115	458	2,267	5,760	17,440	11	271	476	3,051	6,861
7	7	105	493	2,201	4,005	8,888					
Total	94	1,075	3,932	21,543	44,498	114,347	81	1,520	2,348	18,683	41,080

^aRegional subsets were achieved by combining some relatively similar regions together.

^bHerd-year-seasons with season of birth defined as November to April and May to October.

^cHerd-year-seasons with season of birth defined as January to April, May to August and September to December.

Meyer, 1986; Meyer 1987). The REML method maximizes only the part of the data vector that is independent of the fixed effects and accounts for loss of degree of freedom due to fitting fixed effects. This method produces biased estimators, but these estimates are within the parameter space. Gianola and Fernando (1986) proved that REML estimates are unaffected by selection and assortative mating. Such desirable properties make REML the preferred method to estimate population parameters from field data (Henderson, 1986; Meyer, 1986; Searle, 1989) because other methods available are biased due to selection and culling (Rothschild et al., 1979; Meyer and Thompson, 1984; Sorensen and Kennedy, 1984). The REML program (Meyer, 1987) that was used to process the data was kindly provided by K. Meyer (Inst. of Animal Genetics, Edinburgh).

Models

For the performance test data of young boars, the assumed model was as follows:

$$Y_{ijkl} = \mu + h_i + s_j + d_{ijk} + b_s p_{ijk} + b_d q_{ijk} + e_{ijkl}$$

where y_{ijkl} is the performance trait, μ is the population mean, h_i is the fixed effect of the i^{th} HYS of birth of the pig, s_j is the random effect of the k^{th} sire $\sim(O, I\sigma_s^2)$, d_{ijk} is the random effect of the ijk^{th} dam $\sim(O, I\sigma_d^2)$, b_s is the partial regression of y_{ijkl} on the year of birth of the sire (p_{ijk}), b_d is the partial regression of y_{ijkl} on the year of birth of dam (q_{ijk}) and e_{ijkl} is the random residual associated with the $ijkl^{\text{th}}$

pig $\sim(O, I\sigma_e^2)$. The regressions on year of birth of the dam and sire were included to adjust for trends that may not have been accounted for otherwise by the analysis. Seasons for the HYS of birth groups were defined as November to April (cold part of the year) and May to October (warm part of the year). Large HYS were needed to have sufficient data within each subclass for variance component estimation.

For the reproductive data of sows, the model assumed was the following:

$$Y_{ijkl} = \mu + h_i + s_j + d_{ijk} + b_s p_{ijk} + b_d q_{ijk} + b_p z_{ijk} + e_{ijkl}$$

where Y_{ijkl} is the progeny's reproductive record, μ is the population mean, h_i is the fixed effect of the i^{th} HYS of birth of the litter, s_j is the random effect of k^{th} sire of the progeny $\sim(O, I\sigma_s^2)$, d_{ijk} is a random effect of the ijk^{th} dam of the progeny $\sim(O, I\sigma_d^2)$, b_s is the partial regression of y_{ijkl} on the year of birth of the sire (p_{ijk}), b_d is the partial regression of y_{ijkl} on the year of birth of the dam (q_{ijk}), b_p is the partial regression of y_{ijkl} on the subsequent parity of the dam (z_{ijk}) and e_{ijkl} is the random residual associated with the $ijkl^{\text{th}}$ litter $\sim(O, I\sigma_e^2)$. No effect of service sire was included. The regressions on year of birth of the dam and sire were included to adjust for trends that may not have been accounted for otherwise by the analysis. Seasons for HYS of birth groups were defined as January to April, May to August and September to December. This creation of three seasons was necessary because smaller seasons did not contain

TABLE 2. MEANS FOR PERFORMANCE AND REPRODUCTIVE TRAITS

Regions	Performance records			Reproductive records		
	ADG ^a , g	BF ^b , mm	DAYS ^c	NBA ^d	N21 ^e	W21 ^f , kg
1	512	15.28	218.15	8.96	8.57	52.05
2	528	15.93	210.70	9.12	8.82	58.47
3	545	16.08	204.06	9.11	8.84	54.26
4	527	16.33	211.09	9.18	8.74	55.18
5	537	15.70	207.11	9.66	9.35	60.33
6	520	14.91	214.21	9.30	8.97	56.73
7	515	15.02	215.68			
Overall	529	15.54	215.68	9.24	8.82	56.38

^aAverage life daily gain standardized to 180 d.

^bAverage backfat thickness (4 measurements) standardized to 110 kg.

^cNo. of days needed to achieve 110 kg of body weight.

^dNo. of piglets born alive (measured at 1 to 3 d of life).

^eLitter size at 21 d.

^fLitter weight at 21 d.

enough data to estimate the variance components accurately, but sufficient data were available such that two HYS were not used, as was necessary for the performance analysis. Litters were divided into three groups: first-parity litters (18,683 observations), second-parity litters (11,679 observations) and third- and older-parity litters (10,718 observations). Sire birth years ranged from 1975 to 1986.

Covariances between litters of the same sire, dam or relatives were assumed to be zero. This may have reduced heritability estimates slightly but it was necessary for computational use. The estimate of the sire component of variance represents the variance between paternal half sibs, i.e., $E(\hat{\sigma}_s^2) = \text{COV}(\text{PHS}) = \sigma_a^2/4$, where σ_a^2 is the additive genetic variance. The dam nested within sire component of variance represents the covariance between contemporary full sibs (littermates), i.e., $E(\hat{\sigma}_d^2) = \text{COV}(\text{FS}) - \text{COV}(\text{PHS}) = \sigma_a^2/4 + \sigma_{\text{dom}}^2/4 + \sigma_{\text{ce}}^2$, where σ_{dom}^2 is the dominance variance and σ_{ce}^2 is the variance due to common environmental effects. We assumed further that dominance, overdominance and epistatic effects were zero, i.e., that an additive genetic model was appropriate. Given that a large number of the records were first farrowings and that later farrowing data were limited within HYS, a model with repeatability equal to 1 was assumed. Paternal half-sib heritability was estimated as $\hat{h}^2 = 4 \hat{\sigma}_s^2 / (\hat{\sigma}_s^2 + \hat{\sigma}_d^2 + \hat{\sigma}_e^2)$.

Common environmental covariance among littermates (c^2) relative to the phenotypic variance (assuming $\sigma_{\text{dom}}^2 = 0$) was estimated as $(\hat{\sigma}_d^2 - \hat{\sigma}_s^2) / (\hat{\sigma}_s^2 + \hat{\sigma}_d^2 + \hat{\sigma}_e^2) = \hat{\sigma}_{\text{ce}}^2 / (\hat{\sigma}_s^2 + \hat{\sigma}_d^2 + \hat{\sigma}_e^2) = \hat{c}^2$.

Computing Strategy

Both data sets were too large to be analyzed at once. Each data set included results from 17 regions run by the separate Regional Breeding Offices. This structure was used to divide both data sets into several subsets such that each subset had nearly equal numbers of sires. This was accomplished by grouping some relatively similar regions together. The boar performance data were divided into seven subsets, and the sow reproductive performance data were divided into six subsets. The size of the subsets and the distribution of sires, dams, litters and HYS across these subsets are presented in Table 1.

Separate analyses were performed within each subset for each trait. Estimates of variances across subsets were obtained by pooling weighted averages from each data subset. Sire components of variance were weighted by the number of sires, and the dam component of variance was weighted by the number of dams. The residual components were weighted by the degrees of freedom for residuals within each subset. Total variance was estimated by summing all three weighted components of variance. Covariances were

estimated by the method of using the variances of the sum of two traits and the variances of the individual traits to compute the covariances between the traits. The convergence criterion for each component of variance in the program was .10000E-03. Depending on the subset and trait, the program required from 17 to 238 rounds of iterations to fully converge.

Results

The means for performance and reproductive traits for each region and pooled across regions are presented in Table 2. Production level differences among regions were large for all traits measured. The sire, dam and residual estimates of components of variance are given in Table 3. Variance component estimates for all performance and reproductive traits were extremely different across regions.

The estimates of genetic and phenotypic correlations, heritabilities and c^2 effects for performance test data are presented in Table 4. Phenotypic correlations for all three traits generally were consistent across regions. The estimates of the genetic correlations between ADG and BF, and BF and DAYS ranged from -.30 to .74 and from -.68 to .34 across regions and varied more than the phenotypic correlations. The genetic correlation between DAYS and ADG was similar to the phenotypic correlation. The heritability estimates for ADG, BF and DAYS were .27, .29 and .26, respectively. Estimates of heritabilities ranged from .13 to .47 for BF and from .14 to .46 for DAYS. The c^2 effects for ADG, BF and DAYS were .09, .10 and .09, and ranged from .01 to .11, .05 to .14 and .01 to .42 for ADG, BF and DAYS, respectively.

The estimates of genetic and phenotypic correlations, heritabilities and c^2 effects for the reproductive data are presented in Table 5. Phenotypic correlations for all three reproductive traits were large, positive and similar to the performance data in that they were consistent across the regions. Heritability estimates were .06 for N21 and W21 and .07 for NBA. The highest c^2 effect was for W21 (.08) and the smallest was for NBA (.06).

Discussion

Comparison between variance component estimates from the literature is difficult because these estimates depend on the population and traits measured and on the data collected.

TABLE 3. ESTIMATES OF SIRE, DAM AND ERROR COMPONENTS OF VARIANCE FOR ANALYZED TRAITS

Trait	Source of variation					
	Sire		Dam		Residual	
	Pooled ^a	Range ^b	Pooled ^a	Range ^b	Pooled ^a	Range ^b
Average daily gain ^c (ADG) standardized to 180 d, g ²	163.5	82.8 to 286.2	374.2	286.9 to 417.5	1,923.8	1,674.4 to 2,156.8
Backfat thickness ^d (BF) standardized on 110 kg, mm ²	.14	.06 to .33	.32	.13 to .48	1.44	.71 to 2.31
Days to 110 kg (DAYS), d ^e	26.2	12.9 to 53.7	60.7	48.4 to 67.5	311.2	280.8 to 362.1
No. of piglets born alive (NBA) ²	.055	.003 to .091	.297	.202 to .394	3.342	3.095 to 3.745
Litter size at 21 d (N21) ²	.058	.012 to .094	.330	.214 to .484	3.660	3.307 to 4.359
Litter wt at 21 d (W21), kg ²	2.00	.85 to 3.06	12.00	7.68 to 18.67	126.44	92.92 to 171.19

^aWeighted averages across regions.

^bLowest and highest values across the six or seven regions.

^cAnimal birth weight is assumed to be zero, gain standardized to d 180.

^dAverage of four ultrasonic measurements, standardized to d 180.

^eTrait represents litter size at d 2 or 3 after farrowing.

Estimates of sire, dam and residual components of variance for backfat thickness generally were smaller than those in the literature (Kennedy et al., 1985; Takahashi, 1989; Van Diepen and Kennedy, 1989). Estimates for backfat thickness will depend in part on origin of the data, number of measurement sites, location of sites, type of equipment, sex, preselection before and during the test period, weight at which BF was standardized and, finally, on the chosen method of estimating of variance components. Relatively smaller estimates of the variance components for BF in the present report seem to be a function of number of sites (four) at which backfat was measured and the relatively heavy weight of standardization (110 kg). Most other research has been based on fewer measurements and standardized to lighter weights (90 to 105 kg). No estimates of components of variance for average daily gain over the pig's life (180 d) were found in the literature, but estimates for DAYS generally were larger than those previously reported for the trait days to 105 kg (Hutchens and Hintz, 1981). This may be a result of scaling because in this case DAYS was to 110 kg and was not days to 105 kg, as is commonly reported.

The estimates of heritability for BF and DAYS were smaller than those presented by some researchers, but they were within the range of estimates seen in the literature (Schaeffer, 1979; Hutchens and Hintz, 1981; David et al., 1983; Kennedy et al., 1985; Keele et al., 1988; Van Diepen and Kennedy, 1989; Stewart and Schinckel, 1990). The smaller estimates could have resulted from the fact that field data were used and that no relationships among parents were assumed in our study.

The estimates of c^2 for DAYS were smaller than those of Kennedy et al. (1985) and, for backfat thickness, they were similar to those of Kennedy et al. (1985) for Canadian Yorkshire pigs and of Van Diepen and Kennedy (1989) for boars tested on-farm. Our estimates for both traits also were similar to those reported by Takahashi (1989). These results suggest that maternal and common environmental influences on DAYS may not be as substantially important as suggested by Kennedy (1984). Common environmental effects in the present study, especially for DAYS, may be overestimated if some preselection of boars existed on the basis of body weight (growth rate) at the day of measurement. In these data,

as in those reported by Kennedy et al. (1985), only three out of an average of four boars per litter were performance-tested. One difference between the study of Kennedy et al. (1985) and our study was that, in our data, boars were preselected on the basis of their entire life growth until the day of measurement and they were measured at much heavier weights. This, according to Kennedy et al. (1985), may have resulted in our estimates being less affected by preselection than those for Canadian pigs.

The average estimates of genetic and phenotypic correlations between ADG and BF, ADG and DAYS and DAYS and BF were in agreement with those reported by Stewart and Schinckel (1990) and in the range of those presented by other researchers (Hutchens and Hintz, 1981; David et al., 1983; Bereskin, 1984; Kennedy et al., 1985). The values also were similar to values recommended by National Swine Improvement Federation (1987). The large range of the estimates in the literature reviewed probably was due to differences among experiments in measuring the traits, breeds and sexes or in methods of estimating of variance components. Differences between regions in the present research were only slightly less variable.

Estimates of sire, dam and residual components of variance for reproductive traits generally were smaller than those reported previously (Strang and Smith, 1979; Hutchens and Hintz, 1981; Bereskin, 1984; Irgang and Robison, 1984; McCarter et al., 1987). The smaller estimate for NBA in our study may be because this trait in our study was measured either at d 1, 2 or 3 after farrowing. Pig losses during the first 2 d reduced the phenotypic variance for NBA.

The estimates of heritability of number born alive and litter size at weaning were similar to those of the review of literature presented by Lamberson (1990) from 21 different experiments based on 138,248 observations. However, the weighted heritability estimate (Lamberson, 1990) for litter weight at 21 d was twice as large as in our present work. Our estimates were similar to those of previous researchers (Strang and King, 1970; Strang and Smith, 1979; Bereskin, 1984) but smaller than those reported by McCarter et al. (1987).

Genetic and phenotypic correlations between reproductive traits were large and positive and were in general agreement with most estimates from the literature (Omtvedt et

TABLE 4. ESTIMATES OF GENETIC^a AND PHENOTYPIC^b CORRELATIONS, HERITABILITIES (h^2) AND COMMON ENVIRONMENTAL COVARIANCE (c^2) FOR PERFORMANCE TEST OF YOUNG BOARS

Item	ADG ^c		BF ^d		Days ^e	
	Pooled ^f	Range ^g	Pooled ^f	Range ^g	Pooled ^f	Range ^g
ADG			.25	-.30 +.74	-.99	-.98 -1.00
BF	.23	+.11 +.42			-.21	-.68 +.34
DAYS	-.99	-.98 -1.00	-.20	-.03 -.39		
h^2	.27	.15 to .42	.29	.13 to .47	.26	.14 to .46
c^2	.09	.01 to .11	.10	.05 to .14	.09	.01 to .42

^aAbove diagonal.^bBelow diagonal.^cAverage daily gain standardized on 180 d.^dAverage backfat thickness standardized to 110 kg of body weight.^eNumber of days needed to obtain 110 kg of body weight animal.^fWeighted averages across seven regions.^gLowest and highest values across seven regions.

al., 1966; Edwards and Omtvedt, 1971; Lamberson, 1990). The phenotypic correlations between NBA and N21 and between NBA and W21 were much larger than those reported by Young et al. (1978), Bereskin (1984), Irvin and Swiger (1984) and Ferguson et al. (1985). Much lower estimates for all correlations between the same traits were reported by McCarter et al. (1987), but their estimates were based on records adjusted for subsequent parity. Both pooled and specific region phenotypic and genetic correlations were within the

range of estimates from the literature. Measurement of NBA on d 2 and 3 after farrowing reduced the phenotypic variation of this trait and resulted in overestimating phenotypic correlations between NBA (d 1 to 3) and the other two reproductive traits.

Implications

A relatively large range of estimates across regions for almost all the measured traits suggests that even reasonably large regional

TABLE 5. ESTIMATES OF GENETIC^a AND PHENOTYPIC^b CORRELATIONS, HERITABILITIES (h^2) AND COMMON ENVIRONMENTAL COVARIANCE (c^2) VALUES FOR REPRODUCTIVE PERFORMANCE OF SOWS

	NBA ^c		N21 ^d		W21 ^e	
	Pooled ^f	Range ^g	Pooled ^f	Range ^g	Pooled ^f	Range ^g
NBA			.91	.87 to .98	.68	.49 to .89
N21	.88	.87 to .92			.80	.41 to .97
W21	.75	.72 to .80	.86	.81 to .92		
h^2	.07	.04 to .09	.06	.03 to .08	.06	.03 to .10
c^2	.06	.03 to .11	.07	.05 to .12	.08	.04 to .42

^aAbove diagonal.^bBelow diagonal.^cNumber of piglets born alive (measured at d 1 to 3).^dLitter size at 21 d.^eLitter weight at 21 d.^fWeighted average across six regions.^gLowest and highest values across given data subsets.

samples from the country's population may give quite different estimates compared with those from the whole population. Present research gives additional evidence that genetic correlations among performance traits seem to be different from zero and need to be considered when developing genetic evaluation programs. At present, no correlation between average daily gain, days to 110 kg and backfat thickness standardized to 110 kg BW is assumed in breed improvement programs in Poland; this may have reduced genetic progress in these traits. Therefore, the use of correlations among traits for future breed improvement programs is recommended.

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