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Genetic and phenotypic trends in Polish large white nucleus swine herds

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Abstract

Performance test records collected from 1978 to 1987 from on-farm tests of young Polish Large White boars from 94 herds and reproductive records of Polish Large White sows from 81 nucleus farms were used to estimate the phenotypic, environmental, and genetic trends. There were, after editing, 114,347 boar performance records and 41,080 litter records on sows. Both data sets were analyzed by use of an animal model. Estimated annual phenotypic and environmental trends were relatively large and desirable and were, respectively, .17 +/- .05, .11 +/- .05 (number born alive); .16 +/- .04, .10 +/- .04 (21-d litter size); 1.86 +/- .63, 1.43 +/- .62 (21-d litter weight, kg); 6.80 +/- .60, 6.76 +/- .72 (average daily gain, g/d); -.065 +/- .007, -.058 +/- .023 (backfat thickness, mm); -2.76 +/- .28, -2.75 +/- .29 (days to 110 kg). In contrast, all estimated genetic trends were relatively small and not always favorable. The genetic trends estimated from animal, sire and dam genetic values were, respectively, .01 +/- .01, .02 +/- .01, .01 +/- .01 (number born alive and 21-d litter size); .04 +/- .06, .10 +/- .05, .05 +/- .04 (21-d litter weight, kg); .04 +/- .04, .50 +/- .10, -.43 +/- .05 (average daily gain, g/d), -.009 +/- .001, -.015 +/- .002, -.004 +/- .0004 (backfat thickness, mm); and -.01 +/- .01, -.17 +/- .04, .19 +/- .02 (days to 110 kg). Neither examination of selection practices nor boar utilization provided an explanation for the lack of genetic progress.

Keywords

Pigs, Genetic Trend, phenotypic Trend, Reproductive Traits, Performance Traits

Disciplines

Agriculture | Animal Sciences | Genetics

GENETIC AND PHENOTYPIC TRENDS IN POLISH LARGE WHITE NUCLEUS SWINE HERDS[1,2]

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ABSTRACT

Performance test records collected from 1978 to 1987 from on-farm tests of young Polish Large White boars from 94 herds and reproductive records of Polish Large White sows from 81 nucleus farms were used to estimate the phenotypic, environmental, and genetic trends. There were, after editing, 114,347 boar performance records and 41,080 litter records on sows. Both data sets were analyzed by use of an animal model. Estimated annual phenotypic and environmental trends were relatively large and desirable and were, respectively, .17 ± .05, .11 ± .05 (number born alive); .16 ± .04, .10 ± .04 (21-d litter size); 1.86 ± .63, 1.43 ± .62 (21-d litter weight, kg); 6.80 ± .60, 6.76 ± .72 (average daily gain, g/ d); −.065 ± .007, −.058 ± .023 (backfat thickness, mm); −2.76 ± .28, −2.75 ± .29 (days to 110 kg). In contrast, all estimated genetic trends were relatively small and not always favorable. The genetic trends estimated from animal, sire and dam genetic values were, respectively, .01 ± .01, .02 ± .01, .01 ± .01 (number born alive and 21-d litter size); .04 ± .06, .10 ± .05, .05 ± .04 (21-d litter weight, kg); .04 ± .04, .50 ± .10, −.43 ± .05 (average daily gain, g/d), −.009 ± .001, −.015 ± .002, −.004 ± .0004 (backfat thickness, mm); and −.01 ± .01, −.17 ± .04, .19 ± .02 (days to 110 kg). Neither examination of selection practices nor boar utilization provided an explanation for the lack of genetic progress.
Key Words: Pigs, Genetic Trend, Phenotypic Trend, Reproductive Traits, Performance Traits

Introduction

Genetic progress in a classical, tiered pig improvement program depends exclusively on the rate of genetic progress achieved in the nucleus level and proper multiplication in the

lower levels of the pyramid (Bichard, 1971). The yearly improvement rate of performance traits at the nucleus level, within some efficient selection schemes, may be as large as 2% of the mean value of the traits and will result generally in changes of about 1% within the whole population (Smith, 1962, 1963, 1965, 1984; Cox and Smith, 1968; Hill, 1971; Ollivier, 1974, 1988; Dickerson et al, 1976, 1977; Puff, 1976; Standal, 1979; Mitchell et al., 1982; David et al., 1985; Hudson and Kennedy, 1985; Ronningen, 1988; Sellier and Rothschild, 1990).

For reproductive traits, quite sophisticated improvement schemes have to be applied to achieve a similar rate of progress. Some of them potentially can result in a 5% yearly improvement for litter size when applied to the development of maternal lines (Bichard and Siedel, 1982; Bichard and David, 1985;

Legault, 1985; Healey et al., 1986; Avalos and Smith, 1987).

Estimation of genetic progress in traits gives an important evaluation of the efficiency of applied improvement schemes. It also supplies the animal breeder with the essential information to develop more successful programs in the future.

The objective of this study was to investigate the nature and magnitude of changes in performance and reproductive traits in Polish Large White nucleus swine herds.

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 Large White state swine farms. The raw performance data contained 126,367 records on boars from 99 farms. A total of 114,347 records from 94 farms were used. The records included in the performance data were average daily gain from birth to 180 d of age (ADG) and backfat standardized to 110 kg (BF). The raw reproductive data contained 53,630 litter records collected on 97 farms. A total of 41,080 records from 81 farms were used. The reproductive records included the number of pigs born alive (NBA), litter size at 21 d (N21) and litter weight at 21 d (W21). The number of records, farms, dams, litters, and herd-year-seasons (HYS) for both data subsets are presented in Table 1. A detailed description of both data subsets and editing procedures is given elsewhere (Kaplon et al., 1991).

A classical, three-tiered pig improvement scheme is used in Poland. In this scheme, selection for reproductive performance was made at the nucleus and multiplier levels. The sows and gilts were selected on the basis of their own reproductive performance by using independent culling levels associated with NBA, N21, W21 and number of teats. This selection has been carried on since the establishment of the Polish Large White breed.

In the farm test, backfat thickness and

[6]Kraut Krammer, Ind., Cologne, West Germany.

TABLE 1. NUMBER OF RECORDS AND DATA STRUCTURE

Item	Performance data	Reproductive data
Farms	94	81
HYS	3,031[a]	2,594[a]
Sires	3,932	2,348
Dams	21,543	18,683
Litters	44,493	41,080
Records	114,347	41,080

[a]Herd-year-seasons with seasons of birth defined as subsequent 2-mo periods.

average daily gain were measured only on boars whose age ranged from 170 to 210 d. The test was considered to be the time period from birth until the day of measurement. Backfat thickness (BF) was measured ultrasonically by using the Kraut Krammer USM2[6] 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 the midline. The second measurement at the last rib was taken 8 cm from the midline. The average of the four measurements was standardized at 110 kg of body weight. Estimated average daily gain (ADG) was standardized to 180 d of life. DAYS was defined as number of days to 110 kg. Average daily gain and BF were used to calculate an index that was used to evaluate animals within their home farms. In this index, the economic value of average daily gain to backfat was assumed to be 2:1 and the genetic correlation between the traits was assumed to be zero. The boars with index values above average for their test were registered; only these could be utilized at any tier of the pig improvement scheme. The test has been conducted continuously since 1973.

Statistical Analysis. The performance test data on young boars and the reproductive data of the sows were analyzed separately. For the performance test data the individual animal model assumed was:

$$Y_{ijk} = \mu + h_i + l_{ij} + a_{ijk} + e_{ijk},$$

where:

Y_{ijk} = a performance trait recorded on the ijk^{th} pig,

μ = the population mean,

h_i = the fixed effect of the ith herd-year-season (HYS) of birth,

l_{ij} = the random effect of the jth litter in the ith HYS $\sim(0, I\sigma_l^2)$,

a_{ijk} = the random additive genetic effect of the kth pig in the ij^{th} litter $\sim(0, A\sigma_a^2)$, where A represents relationships among animals through their sires,

e_{ijk} = a random residual associated with the ijk^{th} pig $\sim(0, I\sigma_e^2)$.

For the reproductive performance test data of sows, the individual animal model assumed was:

$$Y_{ij} = \mu + h_i + a_{ij} + bz_{ij} + e_{ij},$$

where:

Y_{ij} = a reproductive trait (NBA, N21, W21) recorded on the ij^{th} litter,

μ = the population mean,

h_i = the fixed effect of the ith HYS of birth of the litter,

a_{ij} = the random additive genetic effect of the jth female in the ith HYS $\sim(0, A\sigma_a^2)$, where A represents relationships among animals through their sires,

b = a partial regression of Y_{ij} on parity of the dam (z_{ij}),

e_{ij} = the random residual associated with the ij^{th} female $\sim(0, I\sigma_e^2)$.

In both models, seasons for HYS of birth groups were defined as 2-mo periods. All covariances among random elements of the model except the relationship among animals were assumed to be zero. Sows were identified by litter number. Therefore, it was not possible to combine information on repeated litters by the same sow or progeny with own performance on the sows. Boars, however, were uniquely identified across all litters and herds. Estimates of components of variance were taken from the pooled analysis reported by Kaplon et al. (1991).

The data were analyzed separately for each trait by region and also combined across region. Regions were defined as herds with the same Regional Breeding Office. Some combining of these was made to aid in analysis. Analyses of the data were done by using an

iterative program (Misztal, 1987; Misztal and Gianola, 1987) kindly provided by Ignacy Misztal. Means were calculated for predicted breeding values of animals and their parents (weighted by number of progeny) by years and across regions to predict genetic trend for the performance and reproductive traits. These means were regressed across years to predict yearly genetic trend. Simple correlations between predicted breeding values and phenotypic and index values for the traits also were computed.

Results

The annual phenotypic, environmental and genetic trends for reproductive and performance traits are presented in Tables 2 and 3, Figure 1, and Figure 2, respectively. Estimated phenotypic and environmental trends for all traits were relatively large $(P < .05)$ and favorable. The exceptions were phenotypic and environmental trends for BF (Table 3, Figure 2b) and environmental trend for NBA (Table 2, Figure 1a). For each performance trait, certain regions had large and undesirable phenotypic and environmental trends. The rate of annual phenotypic and environmental trends for the performance traits were quite linear, especially for ADG and DAYS after 1982 and BF before 1983. A similar situation was seen for the reproductive traits for the phenotypic and environmental trends. In a number of instances, however, regional trends were significant. The range of differences among regions was quite large; therefore, different trends existed for the traits. Phenotypic and environmental trends in the same traits generally were linear except for the last 2 yr.

In contrast to the phenotypic and environmental trends, all the estimated genetic trends in both data sets were relatively small and sometimes undesirable (Tables 2 and 3, Figures 1a, 1b, 1c, 2a, 2b, and 2c). Although some of the trends were desirable and significant, the magnitude of the change over time was of limited practical importance.

All estimated genetic trends (sire, dam, and animal) for the reproductive data were small; none was significantly different from zero (Tables 2, Figures 1a, 1b, and 1c). Genetic trend estimated from the weighted sire genetic values for each reproductive trait were twice as large as those calculated from the dam values. All regional estimates of genetic trends from

Number Born Alive
(a)

Litter size at 21 days
(b)

Litter Weight at 21 days (kg)
(c)
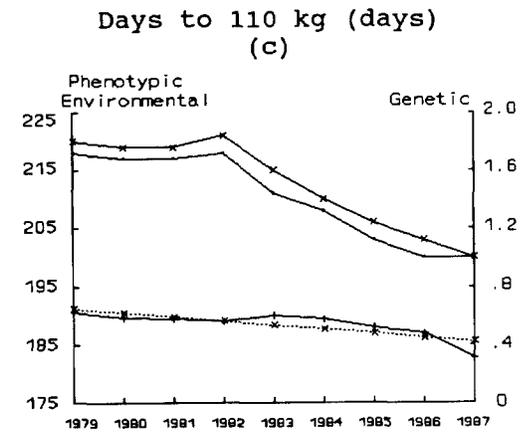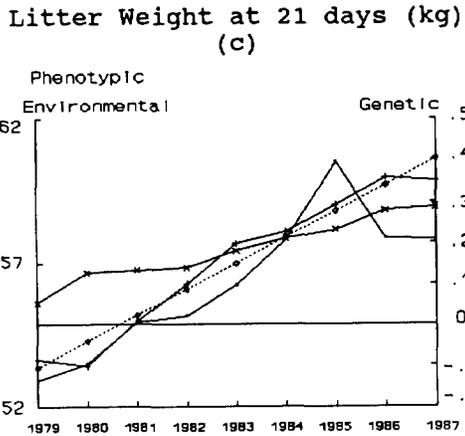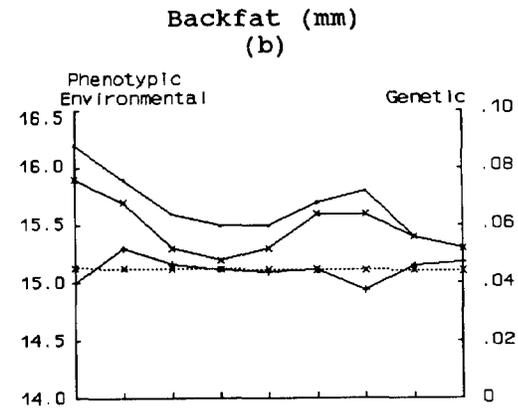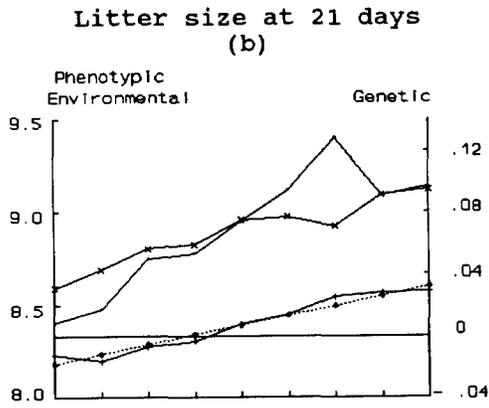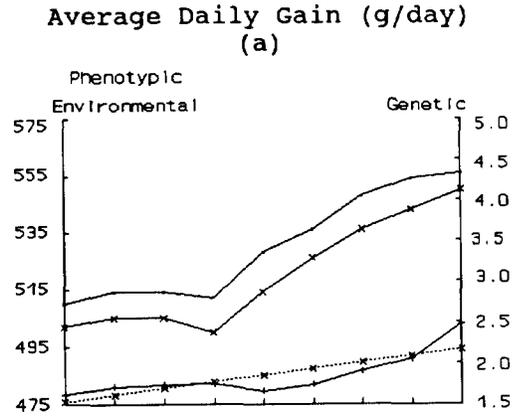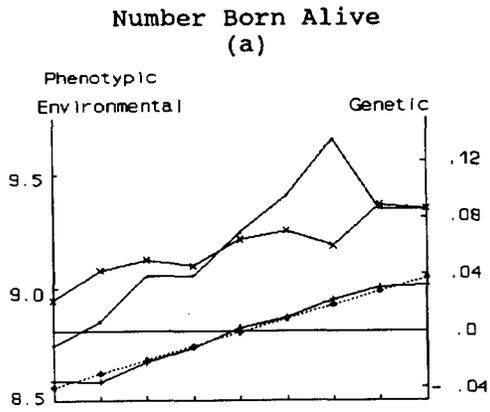
———•——— trait (P)
———X——— herd (E)
———|——— sow (G)
•••X••• sow regression

Average Daily Gain (g/day)
(a)

Backfat (mm)
(b)

Days to 110 kg (days)
(c)

———•——— trait (P)
———X——— herd (E)
———|——— pig (G)
•••X••• pig regression

Figure 1. Annual phenotypic (P), environmental (E) and genetic (G) trends for reproductive traits; number born alive, (1a); litter size at 21 d, (1b); 21-d litter weight (kg), (1c).

Figure 2. Annual phenotypic (P), environmental (E) and genetic (G) trends for performance traits; average daily gain (kg/d), (2a); backfat (cm), (2b); days to 110 kg, (2c).

TABLE 2. ANNUAL PHENOTYPIC, ENVIRONMENTAL, AND GENETIC TRENDS
FOR REPRODUCTIVE PERFORMANCE TRAITS OF SOWS

Trend	NBA[a] Pooled[d]	Range[e]	N21[b] Pooled[d]	Range[e]	W21[c] Pooled[d]	Range[e]
Phenotypic	.17 ± .05**	-.17 to .23	.16 ± .04**	-.18 to .23	1.86 ± .63*	-2.11 to 2.40
Environmental	.11 ± .05	-.34 to .17	.10 ± .04*	-.34 to .12	1.43 ± .62*	-3.14 to 1.95
Genetic[f]						
Animal	.01 ± .01	.012 to .035	.01 ± .01	.01 to .09	.045 ± .06	-.07 to .18
Sire	.02 ± .01	.006 to .043	.02 ± .01	.00 to .044	.10 ± .05	-.09 to .22
Dam	.01 ± .01	.01 to .026	.01 ± .01	.01 to .030	.05 ± .04	-.12 to .15

[a]Number of piglets born alive (measured at d 1 to 3).

[b]Litter size at 21 d.

[c]Litter weight at 21 d (kg).

[d]Averages across regions.

[e]Lowest and highest values across regions.

[f]Estimated using animal, sire, or dam genetic values.

*$P < .05$.

**$P < .01$.

sire, dam, and animal genetic values for NBA and N21 were positive and variable across regions. Only one of the 15 regions analyzed had an estimated negative genetic trend for W21 as estimated by the dam values. The rate of annual genetic progress was nearly linear for all reproductive traits, especially after 1982 (Figures 1a, 1b, and 1c). Prior to 1982, annual trends estimated from sire and dam genetic values were undesirable and small.

All estimated genetic trends (sire, dam and animal) for BF were favorable but not important (Table 3, Figure 2b). The annual rate of

genetic progress in backfat thickness estimated from the sire genetic values was four times as large as that estimated from the dam genetic values. Both sire and dam trends were, however, in desirable directions (Table 3). Estimated trends for ADG and DAYS (Figures 2a and 2c), using sire and dam genetic values, were linear and similar in absolute value but different in sign. All of them were significantly different from zero. Almost all the genetic progress achieved in both these traits from the selection of sires was canceled by the lack of progress as measured by the dam values. As a

TABLE 3. ANNUAL PHENOTYPIC, ENVIRONMENTAL, AND GENETIC TRENDS
FOR PERFORMANCE TRAITS

Trend	ADG[a] Pooled[d]	Range[e]	BF[b] Pooled[d]	Range[e]	DAYS[c] Pooled[d]	Range[e]
Phenotypic	6.80 ± .60**	-.18 to 26.40	-.065 ± .007	-.58 to .55	-2.76 ± .28**	-13.54 to .05
Environmental	6.76 ± .72**	-.83 to 25.75	-.058 ± .023	-.53 to .55	-2.75 ± .29**	-13.30 to .37
Genetic[f]						
Animal	.04 ± .04	-1.53 to .85	-.009 ± .001**	-.04 to .06	-.01 ± .01	-.36 to .67
Sire	.50 ± .10**	-3.95 to 2.05	-.015 ± .002**	-.05 to .13	-.17 ± .04**	-.92 to 1.70
Dam	-.43 ± .05**	-.50 to .88	-.004 ± .0004**	-.009 to .016	.19 ± .02**	-.35 to .22

[a]Average daily gain standardized on 180 d (g).

[b]Average backfat thickness standardized to 110 kg of body weight (mm).

[c]Number of days needed to obtain 110 kg of body weight animal.

[d]Averages across regions.

[e]Lowest and highest values across regions.

[f]Estimated using animal, sire, or dam genetic values.

**$P < .01$.

TABLE 4. PERCENTAGE OF BOARS SELECTED TO BE SIRES ON THE BASIS
OF INDEX VALUE AND BREEDING VALUES FOR BF[a] AND ADG[b]

Trait for ranking	Percentile class[c]				
	1	2	3	4	5
Index[d]					
No. tested	21,999	22,250	23,766	22,451	22,130
% Selected	3.03	2.27	1.57	.93	.36
% Progeny	38.24	29.73	19.20	10.16	2.66
ADG[e]					
No. tested	22,298	22,499	22,593	22,611	22,613
% Selected	2.62	1.71	1.27	1.21	1.20
% Progeny	34.52	20.41	14.20	14.48	16.38
BF[f]					
No. tested	22,494	22,564	22,588	22,566	22,405
% Selected	1.70	1.45	1.28	1.41	2.15
% Progeny	21.96	17.95	15.76	17.71	26.64

[a]Average backfat thickness standardized to 110 kg of body weight.

[b]Average daily gain standardized on 180 d.

[c]From the best to the worst, each class contained about 20% of boars tested.

[d]Description of index given in material and methods.

[e]Expected breeding values for average daily gain.

[f]Expected breeding values for backfat thickness.

Discussion

result, the estimated genetic trends from the animal breeding values for ADG and DAYS were small and not significant.

The study revealed generally small but desirable changes in the performance traits. Because only boars were tested for ADG and BF, the rate of improvement in the whole population may have been reduced. Although some response to selection was expected in these traits, this study did not demonstrate large improvement on the Large White nucleus swine farms.

The assumed ratio of the economic weights for ADG and BF was 2:1 in the original on-farm index. The heritabilities for these traits recently were estimated to be .27 and .29, respectively (Kaplon et al., 1991). Use of the on-farm index would have been expected to yield a larger response to selection for ADG than for BF. The present study did not confirm this expected response in ADG. Selection on data from boars was expected to result in favorable changes in the sows. Analysis of the backfat data partly supports this, but the magnitude of the changes of sire and dam genetic values for BF were small and significant. The opposite situation was seen for ADG and DAYS; selection on boars did not result in

direct, favorable changes in sow genetic values.

In an attempt to explain the lack of observable genetic changes across the years in the performance data, an analysis of the selection practices of the sires and their utilization was conducted. These results are presented in Table 4. All tested animals were divided into five classes on the basis of their percentile ranking. Each class contained approximately 20% of the animals. The classes were constructed on the basis of their ranking on either the index score or the genetic values for BF and ADG. The number of sires selected from each class and the contribution of these sires in terms of the progeny produced were examined. About 76% of the sires used had above average index values, and 62% and 48% of the sires used had above average genetic values for BF or ADG, respectively. These above average sire, as measured by index, BF, or ADG, sired 79.3, 61.5 or 47.85% of the progeny, respectively. The average selection differentials for ADG, BF, and the index were 42 g, −.21 mm and 9 index points, respectively. The correlation between the predicted genetic values for ADG and the index was .57, whereas the correlation between the genetic value for BF and the index was −.15. Kaplon et al. (1991) estimated that the genetic and phenotypic correlations between ADG and BF

were .25 and .23, respectively. Given this information and the lack of progress seen, the index must not have accounted correctly for the antagonistic relationship between BF and ADG; this contributed to a lack of selection progress. A possible explanation for the lack of favorable genetic trend for ADG for dams was that dams were selected on the basis of their reproductive performance only. Nevertheless, the general lack of progress is disappointing given the selection practiced.

For the performance traits, a temporary change in trends appeared after 1983 or 1984. During this period, genetic progress for ADG and DAYS had stopped and was substantially slowed to reduce BF. This may be the result of a change in personnel performing the test, which occurred in 1983 and 1984. Until 1983, the test was conducted by groups of workers from the National Research Institute of Animal Production. After 1984 the test was run by personnel of the Central and Regional Breeding Offices. This change, it seems, affected the results of the test. Without this change, the rate of genetic progress over time for the performance traits could have been substantially larger.

The rate of progress, however small, was positive for all six performance and reproductive traits analyzed. This has not always been true in other populations (Skiervold, 1979; Kennedy, 1984; Nougera and Legault, 1984; David et al., 1985; Kangasniemi and Maki-Tanila, 1986; Cox and Smith, 1968). There were small but positive genetic trends in the reproductive traits. This also may explain the lack of progress in the performance traits if these are antagonistically correlated. The rate of genetic progress seemed to accelerate during the last 4 to 5 yr, especially for the reproductive traits. The annual rate of genetic trend, as measured by the sire genetic values for NBA, N21 and W21 was .06, .07, and .35 kg, respectively. This rate was smaller for sow genetic values. The rate of improvement in the whole nucleus population was much smaller than would be expected. The progress achieved in this population was made by using independent culling levels for NBA, N21, W21, and number of teats. A similar rate of progress was seen in the Quebec Records of Performance Sow Productivity Program for litter size at birth and litter size at weaning (Southwood and Kennedy, 1989).

The present study provides additional evidence that the genetic progress realized may be

substantially smaller than expected. The lack of extensive ties among both farms and animals may have reduced genetic progress. Ties were not very complete in the early years of the two data sets analyzed. Because of the truncation of the data, many sires did not have their own performance records included in the analysis and dams never received credit for their own performance. Also, there may have been an insufficient number of ties to evaluate the genetic trend using this model. Unlike the results of Hudson and Kennedy (1985), central test data were not available; therefore, additional ties from such data could not be acquired. The genetic trend remained relatively constant during the first years of the evaluation, and the trend began to develop only after sufficient ties had accumulated. This seems to have been true for the reproductive traits and may have been true to the performance traits, but the change in test personnel may have hidden this result.

Implications

Genetic trends estimated from these data sets suggested that selection practices have not been very successful for performance traits and only slightly successful for reproductive traits. These results would suggest that adherence to previously defined selection practices and goals would be more productive. Selection practices need to be monitored so that progress is in the correct direction and of practical importance.

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