

REALIZED GENERATION INTERVALS, SELECTION DIFFERENTIALS AND PREDICTED GENETIC PROGRESS IN THE SWEDISH PIG BREEDING PROGRAMME

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SUMMARY

Data from the national Swedish pig progeny station testing scheme from the 1980s have been analysed in order to estimate the realised generation intervals and selection differentials for the Landrace and Yorkshire breeds. The average generation interval was close to 2 years for both breeds. Selection differentials were, on average, higher for growth rate during test period than for lean percentage in carcass. Selection differentials for osteochondrosis, recorded after slaughter and included in the progeny test index, do not indicate any negative genetic trend.

INTRODUCTION

In the national Swedish pig breeding scheme, progeny evaluation at testing stations plays a central role. Every year, about 4000 pigs are transported from the elite herds and fattened at the testing stations. At present, there are 2 testing stations in use, and about 50 approved elite herds. One third of the testing capacity is allocated to the Landrace breed, one third to the Yorkshire breed, and the remaining capacity is devoted to Hampshire and Duroc. Most of the boars and sows that are progeny tested have parents themselves, which are tested in this system. Only a minor fraction of the progeny tested animals, e.g. imported boars and sows, have parents that are not progeny tested in this system. Thus one can define the active pig breeding population in Sweden as those boars and sows that have a progeny test index.

In the tests, 2 fullsibs are penned together, and a testing interval from 35 to 104 kg is used (before 1991, 30 to 104 kg). Since spring 1993, the fullsib group has constituted one entire male and one gilt, whereas earlier the gilt has been accompanied by one castrated male. The pigs are fed on a group basis, at a high intensity, according to the average weight of the group.

Carcass meatiness (lean percentage) is estimated by partial dissection. Since 1982, all pigs in this testing scheme have been scored, in connection with the partial dissection, for the presence and severity of osteochondrosis in one elbow joint (medial humeral condyle) and one knee joint (medial femoral condyle). These scores range from 0 (best) to 5 (worst) (Lundeheim, 1987).

To obtain an official progeny test index, each sow has to be tested with one progeny group and each boar with four groups. The index includes information on growth rate and feed efficiency during the test period, lean percentage, meat colour and, since 1988, leg weakness (clinical scoring) and the presence and severity of osteochondrosis in the two joints scored. The constitutional traits are included in the index with the aim of keeping the genetic level of leg weakness score constant, and to some degree improve the osteochondrosis scores.

The aim of the present investigation was to estimate realised generation intervals and selection differentials for the Landrace and Yorkshire breeds on basis of data from the Swedish pig progeny testing scheme, and to predict annual genetic change for some of the traits of importance in Swedish pig breeding.

MATERIALS AND METHODS

Data originate from the official Swedish pig testing scheme and comprise:

- 1) pedigree information on all boars and sows born in 1982 or later, that have a progeny test index
- 2) data on Landrace and Yorkshire pigs, born from 1982 to 1992, and tested at the progeny testing stations. Test groups with incomplete data were excluded, whereafter information on 35 500 pigs remained for analysis.

The calculations carried out were as follows:

- a) For all progeny tested boars and sows born from 1982 to 1986 and having sons and daughters that also are progeny tested, mean generation interval was calculated within breed, path (F-S; F-D; M-S; M-D) and birth year of parent. For each parent - progeny path, for which both parent and progeny were progeny tested, the age of the parent when the progeny was born, was included in the mean.
- b) Data recorded in the progeny testing scheme, i.e. growth rate from birth to slaughter and during the test period, lean percentage in carcass, and osteochondrosis in elbow and knee joints, were pre-corrected according to a model including the effects of breed, sex and a combination of test station, year and season of arrival to test station. Progeny test means were thereafter calculated for each boar and each sow, whereby boars represented by less than 4 progeny groups were omitted. Also, for boars represented by more than 4 progeny groups and sows represented by more than one progeny group, the additional groups were randomly omitted. For every breed, sex and birth year of parent (1982 to 1986), means (M1) and standard deviations (SD) of the progeny group means were calculated.

Thereafter, a corresponding mean (M2, within breed, path and birth year of parent) was calculated for those sows and boars, having progenies that also were progeny tested. Here, as in the calculation of generation interval, a boar/sow was included in the mean, according to how many progenies that had been progeny tested.

Standardised selection differentials were calculated within breed, path and birth year of parent according to:
 $(M2 - M1) / SD$.

RESULTS AND DISCUSSION

During the 1980s, about 150 Landrace boars and 700 sows and the same numbers of Yorkshire were progeny tested every year. Of the boars, about 50 had sons that were progeny tested, and 100 had daughters that were progeny tested. Of the sows, about 90 had sons that were progeny tested, and 280 had daughters that were progeny tested. Roughly half of the selected boars had only one son each, and 70 % of the selected sows had only one son each. Of the selected boars, about 30 % had one daughter each, and 45 % of the selected sows had one daughter each.

The average generation intervals within path, presented in table 1, vary between 21 and 28 months. On an individual basis, the range is, however, huge (from 10 to 90 months). This wide range might have caused a minor underestimation of the generation intervals for parents born in 1986, since the data available only included progeny tested boars and sows born 1991 or earlier. For both breeds, the average generation interval was close to 2 years.

The realised selection differentials for the two main production traits included in the progeny test index (growth rate during test and lean percentage) were between +0.5 and +0.9 SD. The selection pressure being higher for growth rate than for lean percentage. Growth rate from birth to slaughter has a selection differential of about two thirds of that for growth rate during test period. For the osteochondrosis scores, the selection differentials are, on average, somewhat below zero, and no inferior genetic trend can be expected in spite of unfavourable genetic correlations that have been found between osteochondrosis and production (Lundeheim, 1987). It seems as if the inclusion of these constitutional traits, with certain restrictions, into the progeny test index has been successful.

To predict the annual genetic change for the production traits analysed, the growth rates were assessed the heritability of 0.3 and lean percentage the heritability of 0.65. σ_G were assessed the values of 23 g/day (daily gain from birth to slaughter); 44 g/day (daily gain during test) and 2.0 %-units (lean percentage). The predicted annual genetic trends are similar for both breeds: approximately + 2.5 g/day (from birth to slaughter); +8 g/day (during test) and +0.35 %-units lean meat in carcass. The trends for growth rate during test and lean percentage are of the same magnitude as those found in earlier Swedish studies (Lundeheim & Eriksson, 1984). The predicted genetic trend for growth rate from birth to slaughter is only about one third of that for test period. However, expressed as 'saved days', both these trends corresponds to ~ -0.7 days/year.

Finally, it should be kept in mind that the outcome of these types of calculations, as well as the outcome of mixed model estimations of genetic trends are highly dependent on the parameters being used.

CONCLUDING REMARKS

The results of this study indicate a genetic progress of expected magnitude for the traits studied. However, there seems to be potential for further enhancements, which would increase the annual genetic change: e.g. a decrease of the average generation interval from 2 years to 1.5 years would increase the annual genetic change by 30 %.

REFERENCES

- LUNDEHEIM, N. (1987) *Acta Agric Scand*, 37 : 159 - 173.
LUNDEHEIM, N. and ERIKSSON, J.-Å. (1984) *Acta Agric Scand*, 34 : 97 - 106.

Table 1. Realized generation intervals and selection differentials within path (average of parents born 1982 to 1986)

Trait	F - S.		F - D.		M - S.		M - D.	
	Landrace	Yorkshire	Landrace	Yorkshire	Landrace	Yorkshire	Landrace	Yorkshire
Gen. interval, days								
1982-parents	649	638	752	749	799	753	879	872
1983-parents	612	757	768	869	681	767	846	824
1984-parents	640	660	745	759	662	668	818	763
1985-parents	711	600	782	700	686	710	779	781
1986-parents	632	592	741	720	660	579	828	754
<i>Av. 1982 to 1986</i>	<i>649</i>	<i>649</i>	<i>758</i>	<i>759</i>	<i>698</i>	<i>695</i>	<i>830</i>	<i>799</i>
Daily gain								
Birth to slaughter	+0.46	+0.59	+0.42	+0.49	+0.51	+0.61	+0.34	+0.41
During test	+0.82	+0.72	+0.69	+0.67	+0.91	+0.79	+0.60	+0.58
Lean percentage	+0.60	+0.56	+0.53	+0.53	+0.66	+0.59	+0.50	+0.49
Osteochondrosis*								
Elbow	-0.11	+0.02	-0.04	-0.01	-0.06	-0.04	0.00	+0.03
Knee	-0.05	-0.02	-0.11	0.00	-0.03	-0.11	+0.03	-0.03

* score 0 (best) to 5 (worst)