

Genetic Linking of Pig Farm, Testing Station and Artificial Insemination Centre

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Summary

Growth rate and fat records were analysed from four breeding centres, three farms and a boar testing station. The centres were genetically linked through the use of common AI sires (formal) and other breeding animals (informal). Practical difficulties were experienced in achieving satisfactory levels of formal linkage. Linkage placed the mean breeding merits of the different breeding centres in the correct relativity so breeding values were comparable across centres. Heritability estimates for growth rate and fat in the station were more than twice as high as those on farm and the genetic correlations between these traits were favourable in the station but unfavourable on farm. Correlations between station and farm performance were high. Station testing should give higher response than farm testing to a given amount of selection in farm profit.

Introduction

Northern European countries, particularly Scandinavia, have based their pig improvement programs on coordinating the efforts of many small breeders (McPhee, 1988). Important elements in this coordination have been the testing stations which identify sires likely to improve pig productivity. The widespread use of these sires across many herds using artificial insemination makes it possible also to compare breeding values of animals performance tested on different farms. This is further facilitated by large and fast computers using mixed model (BLUP) statistical techniques (Sehested and Vangen, 1987).

In Queensland and South Australia, pig breeders can performance test their stock both on farm and in testing stations and have access to artificial insemination centres, important elements of the Scandinavian pig improvement program. To use these different elements to best advantage in pig improvement requires deliberate genetic linking using AI between the various farms and stations involved in performance testing and the use of BLUP techniques to compare the breeding values of animals wherever tested. This paper reports a study whose aim was to broaden the choice of superior pig sires by linking 3 Queensland herds with each other and with a boar testing station through the use of common AI sires.

Materials and Methods

In addition to the DPIQ boar performance testing station which performance tested boars from 20 Large White herds, data were drawn from three on-farm performance testing herds, only one of which tested boars in the station during the two years of this study. The three farms f1, f2 and f3 were of sizes 100, 30 and 90 sows respectively.

Linking

Five Large White reference boars selected from the DPIQ boar testing station and standing at the AI centre were used as the reference linking sires. The aim was to inseminate at least every fifth sow presented for service in each of the three herds. These sires were also used by other herds whose boars were tested in the station.

In the event, only one farm, f2, achieved the recommended usage of AI. This farm succeeded in mating every third sow to a reference sire. In the other farms the deficit of

formal genetic linkages was compensated by informal links. For example, farm f1 was expanding, mainly from farm f3, at the time of the study and used semen from the AI centre as needed. It also used, under farm AI, a reference sire discontinued from use in the AI centre and another from farm f2. Combined, these introductions gave farm f1 good links with the other centres.

Data collection and analysis

All three farms routinely performance test their pigs on rations approaching ad lib. They record liveweight and ultrasonic backfat (P2) at tumoff (80 to 100 kg). Test station boars are fed, according to McPhee *et al* 1988), a fixed weight of a rich diet for 12 weeks after 30 kg liveweight. Pig weights are taken weekly and fat at 90 kg. Only farm f2 supplied boars to the station for testing during the study.

A total of 7,660 performance records were analysed. The distribution of these across centres is given in the first row of Table 1. Traits analysed were daily weight gain from birth and fat at tumoff on the farm and 12 week daily gain from 30 kg liveweight and fat at 90 kg in the station. Genetic and environmental variance and covariance estimates were obtained using MTDFREML (Boldman *et al* 1993). The statistical model included farm/test station, time (batch) and sex as fixed effects and litter and animal as random effects. The model for farm data differed from that for station data in having individual farms as an additional fixed effect. Variance and covariance estimates from this analysis were used to produce BLUP breeding values using PEST (Groeneveld, 1990).

Results

Linkage

In Table 1, the testing centres are examined in pairs. Progeny of sires common to both centres of a pair were counted to give an estimate of the degree of genetic linkage. By far the best linkage occurred between farm f2 and the station t with 36 boars siring 96% of 1,278 pigs performance tested in f2 and 26% of 944 pigs tested in t. The poorest linkage occurred between centres f3 and t with 3 common sires producing only 1% and 4% of the pigs tested in both centres.

Table 1. Performance tested pigs linked by common sires in the centres : farms f1, f2 and f3 and the testing station t. The centres are considered in pairs.

Centre pairs	f1/f2	f1/f3	f2/f3	f1/t	f2/t	f3/t
No pigs tested	2686/1278	2686/2752	1278/2752	2686/944	1278/944	2752/944
No sires used	45/42	45/72	42/72	45/227	42/227	72/227
No sires linking	8	13	3	8	36	3
% pigs linked	15/11	16/27	1/8	15/7	96/26	1/4

Parameter estimates

In Table 2 are given the genetic and phenotypic parameters associated with fat and growth rate measurements pooled over farms and in the testing station.

Table 2. Estimates of phenotypic (top triangle) and genetic correlations (bottom triangle), phenotypic standard deviations (s.d.), heritabilities (h^2) and litter effects (c^2).

		Growth rate (kg/d)		Fat (mm)	
		Farm	Station	Farm	Station
Growth rate	Farm	-	-	0.04	-
	Station	0.91	-	-	-0.08
Fat	Farm	0.29	0	-	-
	Station	0	-0.13	0.88	-
s.d.		0.07	0.07	2.17	1.68
h^2		0.14	0.40	0.34	0.70
c^2		0.19	0.14	0.12	0.07

Heritability estimates for gain and fat were more than twice as high in the testing station as on farm and litter effects were higher on farm than in the station. Genetic correlations between farm and station fat and farm and station growth rate were high (0.9). The genetic correlation between gain and fat was positive on farm and negative in the station.

Breeding values

Breeding values for farm growth rate and fat were estimated using PEST for all pigs. These were converted to breeding values for profit per sow using current economic weightings (McPhee, unpubl.). In Table 3 the means of profit breeding values are given for the four breeding centres, taken separately (unlinked) and together (linked).

Table 3. Means of farm profit breeding values of centres genetically linked and unlinked.

Centre		Profit/sow/year (\$)			
		f1	f2	f3	t
Unlinked	mean	3.5	-0.5	3.9	2.9
Linked	mean	12.7	32.0	-0.5	5.3

There was a marked change in the ranking of mean breeding values with the linking of centres. Unlinked, f2 had the lowest mean and f3 the highest. With linking, this order was reversed. The s.d. of the breeding values of farms linked was 31.2 and of the test station alone, 39.4.

Discussion

The study experienced difficulty in maintaining sufficient use of semen from reference AI sires to rely on it alone to form genetic links with the participating herds. Only farm f2, under the control of DPIQ (Table 1), approached the level of AI use of Scandinavian pig herds which participate in well organised genetic linkage programs (Brascamp, 1994). Informal links partly offset this deficiency in the other centres. For example, farm f3 was reasonably well linked with f1 by restocking with minimal disease gilts from f3.

The benefit of genetic linking can be gauged from the change in ranking of the mean profit breeding values of the centres between the unlinked and linked state (Table 3). The true superiority of the breeding values of farm f2 is only revealed when the centre means are placed in the correct relationship with each other by linking. The higher standard deviation of profit breeding values for the station than for farms probably reflects a higher between herd genetic contribution as well as a higher testing accuracy (heritabilities) than for farms. As indicated by the high genetic correlations between station and farm performance, the former was a good indicator of the genetic potential of the latter. This is in line with the findings of a recent similar comparison of farm and station performance testing in Holland by Merks and van Oijen (1994). In addition, the genetic correlation between station gain and fat was economically favourable, in opposition to the unfavourable correlation found between these traits on farm. Relative responses in farm profit from selection using either farm or station performance testing can be gauged from the standard deviation of their economic breeding values, that for station values being 26% higher than that for farm.

The main computer programs used in this study were adequate for the task. MTDFREML was able to estimate genetic variances and covariances both across traits and centres and PEST was efficient in assaying breeding values using these estimates but a widening of the genetic linking program to other herds would necessitate the standardisation of the recording format for all centres.

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