

GENETIC PARAMETER ESTIMATES FOR REPRODUCTION TRAITS IN PUREBRED LANDRACE PIGS.

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SUMMARY

Estimates of genetic parameters were obtained using REML methods on 5291 all parity and 1416 first parity litter records. Estimates of heritability and repeatability of traits were consistent with those reported elsewhere at 0.1, 0.2 for litter size and 0.21, 0.28 for birth weight respectively. Maternal effects were seen to be very small, particularly in gilts.

INTRODUCTION

The analyses presented here estimate genetic parameters for reproductive traits in British Landrace pigs using REML techniques. Use of an animal model enables full use of the information available, with all relationships accounted for, and comparisons of sows in different units permissible. In order to improve estimates of breeding values of sows it may be necessary to account for maternal genetic effects. These could also bias estimates of heritability if not fitted in the model.

MATERIAL AND METHODS

The data set consists of litter records measured on 1891 Landrace sows born and performance tested in the same nucleus herd. Each sow may have up to 5 consecutive litter records, which need not be from parities 1-5. The data structure is summarised in Table 1.

The sows farrowed on 5 units, the nucleus and 4 multiplier herds in that pyramid, and records in the data set cover parities 1-11.

Table 1: Data structure summary.

Data Set	No. Sows	No. Records	No. Sires	No. Dams	No. FS Groups ¹	No. Litters ²
All Parities	1891	5291	88	552	1001	1095
1 st Parity	1416	1416	81	450	768	834

1 - number of full-sib groups into which the sows were born.

2 - number of litters into which the sows were born.

Means and phenotypic standard deviations of traits analysed are shown in Table 2. Initial analyses of the data suggested that lactation length, farrowing interval and the weaning to service intervals had negative variance components, suggesting that there is little genetic influence on these traits. These were therefore not considered further. Other traits were found to be very highly correlated to each other (e.g. number of boars in a litter, number of gilts in a litter and total number born), representative traits were selected from these groups for inclusion in the DFREML analyses.

The analyses were performed using Univariate Derivative-Free REML programs developed by Dr. K. Meyer, fitting an individual animal model plus other random and fixed effects (Meyer, 1989).

The analyses were performed across all parities and within the first parity. Across all parities a random effect associated with the individual must be included to take account of the repeat record structure. Therefore, the fitting of common family environmental effect and

maternal genotype effects together was not possible because of the number of parameters which would have been required in the model. Common family environmental effects and maternal genotype effects were assessed in separate analyses across all parities. In the analysis of first parity data however, the common family environmental variance was estimated alongside the maternal effects, since it allows improved partitioning of the variance into these components.

Table 2: Phenotypic means and standard deviations of reproduction traits.

Trait	Abbr.*	All Parities	First Parity
No. boars/litter	-	5.213 ± 2.178	4.797 ± 2.115
No. gilts/litter	-	4.989 ± 2.116	4.707 ± 2.037
No. born dead/litter	-	0.406 ± 0.810	0.401 ± 0.816
No. mummified/litter	NM	0.219 ± 0.610	0.219 ± 0.607
Total no. born/litter	NB	10.61 ± 2.939	9.900 ± 2.877
Total no. born alive/litter	NBA	10.20 ± 2.868	9.500 ± 2.848
Total weight of litter (Kg)	LWt	15.08 ± 4.149	13.63 ± 3.977
Average piglet weight (Kg)	PWt	1.444 ± 0.249	1.397 ± 0.237
Gestation length (days)	GL	114.8 ± 1.504	115.2 ± 1.637
Lactation length (days)	-	29.02 ± 7.598	29.31 ± 6.984
Weaning-First service interval (days)	-	6.743 ± 6.830	8.642 ± 9.581
Weaning-Effective service interval (days)	-	9.795 ± 14.67	11.77 ± 16.46
Farrowing interval (days)	-	153.6 ± 15.82	156.2 ± 17.43

* Abbreviations used in later tables.

Two analyses were performed on the data from all parities, fitting the following models:

Model 1: Maternal genetic component included.

$$Y_{ijklmn} = a_i + r_{ij} + d_k + FHP_l + SBP_m + P_n + e_{ijklmn}$$

Where:

- Y_{ijklmn} - is the phenotypic record of individual i for the trait;
- a_i - is the genetic effect of the i^{th} animal;
- r_{ij} - is the random effect of the j^{th} record on animal i ;
- d_k - is the random genetic effect associated with the k^{th} dam, i.e. the dam of sow i ;
- FHP_l - the fixed effect of the l^{th} farrowing herd - 8 week farrowing period combination;
- SBP_m - the fixed effect of the m^{th} 8 week sow birth period;
- P_n - the fixed effect of the n^{th} parity;
- e_{ijklmn} - is the random environmental effect associated with that record, Y_{ijklmn} .

The maternal genotypic effect and the additive direct effect are correlated with one another and variances associated with these effects and the covariance between them ($cov(am)$) are estimated.

Model 2: Sow's litter of birth included in model, maternal genetic effect omitted.

$$Y_{ijklmn} = a_i + r_{ij} + L_k + FHP_l + SBP_m + P_n + e_{ijklmn}$$

Where:

- L_k - is the random effect of the k^{th} litter (i.e. the litter which animal i was born into), from which the common family environmental effect is estimated;
- All other symbols as defined for model 1.

A single model was fitted in the analysis of gilt data in which a common family environmental effect was estimated alongside a maternal genetic effect.

Model 3: Analysis of first parity records; gilt's litter of birth and maternal genetic effect included in model.

$$Y_{ijklm} = a_i + d_j + L_k + FHP_l + SBP_m + e_{ijklm}$$

Where:

d_j - is the random genetic effect of the j^{th} dam ;
Other definitions as for the all parities analyses.

Approximate standard errors of the parameter estimates could not be calculated using the methodology of Graser *et al.* (1987) since the matrix of second derivatives produced using least-squares to fit a quadratic through the estimated points was not positive definite. Therefore, a hierarchical mating structure was assumed and the methodology of Becker (1964) applied.

RESULTS

The results for all analyses consist of variance and covariance estimates given as a proportion of the total phenotypic variance for the trait in question.

The repeatability was estimated as the sum of the (co)variances due to permanent effects (both genetic and environmental) as a proportion of the total phenotypic variance (Falconer, 1981).

Table 2: Estimates of heritabilities (h^2), maternal genetic effects (m^2 and $cov(am)$), common family environmental effects (c^2) and repeatabilities (r) for reproduction traits among all parities.

Trait	$h^2 \pm s.e.$	m^2	$cov(am)$	c^2 *	r
NM	0.019 ± 0.032	0.000	-0.001	0.000	0.069
NB	0.100 ± 0.042	0.019	-0.003	0.034	0.197
NBA	0.092 ± 0.043	0.014	-0.003	0.017	0.189
LWt	0.135 ± 0.047	0.008	0.001	0.024	0.225
PWt	0.211 ± 0.057	0.000	0.002	0.000	0.284
GL	0.197 ± 0.055	0.007	0.000	0.000	0.292

* taken from analysis under model 2, other parameters are from analysis under model 1.

Table 3: Estimates of heritabilities, maternal genetic effects and common family environmental effects for reproduction traits in the first parity.

Trait	$h^2 \pm s.e.$	m^2	$cov(am)$	c^2
NM	0.068 ± 0.047	0.000	0.001	0.007
NB	0.105 ± 0.051	0.000	0.002	0.000
NBA	0.106 ± 0.051	0.000	0.002	0.000
LWt	0.108 ± 0.052	0.000	0.001	0.005
PWt	0.195 ± 0.064	0.000	0.001	0.013
GL	0.206 ± 0.081	0.005	0.001	0.000

Little difference was observed between estimates of h^2 , c^2 and r across analyses.

DISCUSSION

The estimates of heritabilities and repeatabilities are in accordance with previous studies in the literature (Haley *et al.*, 1988).

Common family environmental effects (c^2) and maternal genetic effects (m^2) were found to be low. The estimates of common family environmental effects are lower than those reported for performance test traits in the same population (Crump *et al.*, 1990), and the maternal genetic effects are considerably lower than those reported in Canadian Landrace (Southwood, personal communication). The small size of these effects may be explained by the large amount of cross-fostering practised, often within 24 hours of birth, which means that sows who are littermates at birth do not necessarily share the same post-natal environment. If so, this implies that any maternal genetic effect acts post-natally and *in utero* or cytoplasmic effects could not be a major contributor.

Common family environmental effects and maternal genetic effects were lower in gilt litters than across all parities, when one might expect to see a greater effect in the first litter, subsequently decreasing with time. It is expected that the all parity estimates would be inflated due to confounding of c^2 and m^2 , as these effects were not simultaneously estimated across parities. However, because of the small size of the effects found, sampling error can not be discarded as the probable cause of this.

In conclusion, heritability and repeatability estimates in a population where extensive cross-fostering is being carried out do not appear to be biased by maternal genetic effects and common family environmental effects, which can therefore be omitted from any breeding value estimation models. The precise effect of cross-fostering can not be quantified, but the results presented here may not be applicable in a population where cross-fostering is not in practice.

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