

INFLUENCE OF MANAGEMENT EFFECTS AND COMPARISON GROUP SIZE ON THE PREDICTION OF BREEDING VALUES FOR LITTER SIZE IN PIGS.

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SUMMARY

The influence of lactation length, weaning to conception interval and reduction in the contemporary group size on the prediction of breeding values for litter size in pigs is analyzed.

The inclusion in the prediction model of the effects mentioned above does not entail relevant variations either in the ranking of the animals or in the estimates of genetic trend. The loss of expected response caused by the omission of these effects in the model is always lower than 2 %.

INTRODUCTION

The prediction of breeding values using the mixed model methodology has been considered preferable to other traditional methodology. However, the use of incorrect models will lead to the obtaining of predictors which are neither optimal in a minimum squared errors sense nor unbiased. Including effects of little relevance increases the variance of prediction error as well as the computational costs (Henderson, 1975).

In practice the genetic evaluation of animals for reproductive characteristics in pigs is done in most countries using a repeatability animal model including as fixed effects the parity order and comparison group (Ducos et al, 1992). The effect that other factors related with the management of sows may have on litter size is not considered, but there are results which suggest that its importance is not negligible (Clark and Leman, 1986).

The aim of this study is to present the incidence of the effects of lactation length, weaning to conception interval and the reduction in the contemporary group size on predicted breeding values for litter size.

MATERIAL AND METHODS

The data used in the analysis have been obtained from GTEP-IRTA data bank (Noguera et al, 1992). It corresponds to the reproductive information produced between 1987 and 1992 in a Landrace (LD), and another Large White (LW) populations, belonging to the same breeding organization. The number of live-born piglets has been analyzed as this is the criterion currently used in the breeding objective. The characteristics of the data used can be seen in Table 1.

Table 1. Description of the data sets used in the analysis.

| Item | Landrace | Large White |
|-------------------------------------|-------------|-------------|
| N ^o of litters | 13092 | 2760 |
| N ^o of animals | 6150 | 1246 |
| N ^o of active animals | 3208 | 429 |
| N ^o of sows with records | 3616 | 683 |
| N ^o of sires | 299 | 104 |
| N ^o of dams | 1290 | 298 |
| Piglets born alive (s.d.) | 9.7 (2.52) | 9.5 (2.87) |
| Lactation Length (s.d.) | 20.0 (11.8) | 21.4 (12.0) |
| Weaning-conception-interval (s.d.) | 9.8 (15.3) | 9.7 (14.8) |

Currently the model used to explain the number of piglets born alive (Y) is a repeatability animal model which includes as random effects the animal (a), the permanent environmental effect (p) and the residual effect (e). The fixed effects include the parity class (PC) effect (with 9 levels; grouping farrowings produced in parities greater than 8) and the herd-year-season (HYS3M) effect (grouping births produced every three months; 105 levels in LD and 32 levels in LW). From this model, and keeping the random effects, alternative models were defined (Table 2):

1 - Including as covariates lactation length in the preceding parity (L), or preceding weaning to conception interval (WCI). It is assumed that their effect is linear and affects equally all parity orders superior to the first.

2 - Reducing comparison group size by grouping together births produced every two months (HYS2M), every month (HYS1M) or every two weeks (HYS2W).

Table 2. Fixed effects considered in the different models.

| EFFECT | MODEL | | | | | | |
|--------|-------|---|---|---|---|---|---|
| | 1 | 2 | 3 | 4 | 5 | 6 | 7 |
| PC | X | X | X | X | X | X | X |
| L | | X | | X | | | |
| WCI | | | X | X | | | |
| HYS3M | X | X | X | X | | | |
| HYS2M | | | | | X | | |
| HYS1M | | | | | | X | |
| HYS2W | | | | | | | X |

For the estimation of fixed effects and the prediction of breeding values, the PEST package (Groeneveld et al, 1990) was used. For each model the variance components estimated from the data using the DF-REML program (Meyer, 1989) were considered. The criterion for finalization of the iterative process was established in all cases for a variance of value $-2\ln(\text{likelihood})$ of 10^{-8} .

The models were compared statistically by means of an approximate F-test. To contrast the incidence of the different models in the genetic evaluation of the animals, three criteria were used:

- The Spearman rank correlation coefficient between animals.
- The loss of response expected by choosing the animals using as prediction model 1 against the models with greater statistical significance.
- The variation in genetic trend predicted by means of the different models, expressed as a regression of the breeding values on the year birth.

RESULTS AND DISCUSSION

The heritability values obtained vary noticeably between populations. Within population the estimates of the genetic parameters are not significantly affected by the different explanatory models analyzed. Thus, in the LW population the values range between 0.081 ± 0.031 and 0.092 ± 0.031 , being close to the average values referred to in the bibliography (Haley et al, 1988). In the LD population, lower values were obtained, between 0.053 ± 0.012 and 0.056 ± 0.012 , similar to those recently obtained using the same methodology (Kaplon et al, 1991). The repeatability is practically constant in both populations, and is around 0.15.

The inclusion in the prediction model of the variable L supposes a statistically significant improvement in both populations ($p < 0.05$). In Table 3 the regression coefficients associated to each variable are shown, as is their significance level.

Table 3. Regression coefficients (b_i) and of the variables lactation length (L) and weaning to conception interval (WCI) in the two populations.

| Model | Variable | LD | LW |
|-------|----------|-------------------------|-------------------------|
| | | b_i | b_i |
| 2 | L | $0.0310 \pm 0.007^{**}$ | $0.0360 \pm 0.016^*$ |
| 3 | WCI | 0.0002 ± 0.001 | 0.0070 ± 0.004 |
| 4 | L | $0.0310 \pm 0.006^{**}$ | $0.0360 \pm 0.016^{**}$ |
| 4 | WCI | 0.0003 ± 0.001 | 0.0070 ± 0.004 |

(* $p < 0.05$; ** $p < 0.01$)

The statistical comparison by means of the approximate F-test of the models with different comparison groups leads to a monthly parity grouping in the LD (average number of litters for HYS1M equal 43), with a three monthly grouping being better for LW (average number of litters for HYS3M equal 86).

In the LD population the reduction in comparison group size proposed in models 5, 6 and 7 carries with it a reduction in the residual variance estimate. On the other hand, in the LW population this supposes an increase in the same estimate in the three models. Given that both populations are subjected to similar environmental conditions, the different behaviour could be partially explained by the difference in population size.

The Spearman rank correlation coefficients between breeding values predicted under different models range from 0.97 to 0.99 in both populations.

The loss of response expected and the response expected by selecting on the genetic values predicted with the model 1 assuming as correct the other models is negligible. Practically nil for models 2, 3 and 4 and of about 2 % for the herd-year-season variable models.

The genetic trend estimated in the last seven years is similar for all the models contrasted. In the LW population it is around 0.07 piglets per year, and in the LD one it is 0.01 piglets per year.

In the population analyzed, some of the proposed modifications to the fixed effects vector suppose an improvement in the explanatory model for the number of live born piglets. However this improvement in the model does not lead to relevant variations in the prediction of breeding values, which suggests no need to modify, for the factors considered here, the univariate model currently used in the genetic evaluation of the animals.

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