

A SELECTION EXPERIMENT FOR INCREASING LITTER SIZE OF LANDRACE PIGS IN SPAIN

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SUMMARY

We report the status and prospectives of an ongoing 'hyperprolific' selection experiment in Landrace pigs in Spain. Around 3500 females were available for selection. The whole population was evaluated using a BLUP animal model. Two selected lines of 175 females were founded. Males were obtained from best 25 matings. A control line consisting of 200 females and 15 males was established as well. All animals were allocated in a single breeding farm. One female offspring from each dam will be produced and there will be two measurements of litter size on each of these offspring. A parallel simulation study suggests that a genetic increase of about 0.35 - 0.40 piglets can be expected.

INTRODUCTION

Economic value of litter size (LS) has recently increased in pig breeding schemes after tenacious selection for growth traits has resulted in animals with an almost optimum lean content. Increasing LS by conventional selection has, nonetheless, proved to be a difficult task in most domestic species. There are not many reported selection experiments that have succeeded in increasing prolificacy in swine, in spite of optimistic theoretical predictions (e.g., Avalos and Smith, 1987). The French 'hyperprolific' experiment resulted in an initial increase on the female side of one piglet. Annual genetic gain was much smaller, however, because of the need of backcrossing (Le Roy et al., 1987). In a Danish experiment, the best 30 and 150 matings out of 5392 contributed young boars and gilts to the selected line (Sorensen, 1990). Preliminary results indicate a response in the first parity of 0.3 piglets (Sorensen and Vernersen, 1991). This is approximately 50% of the expected response.

In general, two main causes have been signalled as responsables for the small (or lack of) response. First, heritability of LS is low. Average figure found in the literature is 0.10 (Lamberson, 1990) but realized heritabilities - a measure of genetic progress - have been even smaller. Second, selection differentials actually effected have been low. This can be a consequence of animal management, e.g., not all candidates for selection are available at the same time, but also of setting some type of restriction in inbreeding or to maximize the number of genetic origins in the selected population.

The objectives of the experiment reported are to provide further evidence of the feasibility of increasing LS in pigs by direct selection, record different physiological parameters that may allow us to explain genetic and phenotypic changes in prolificacy, and evaluate economically the interest of 'hyperprolific' schemes in swine.

SELECTION EXPERIMENT

The experiment commenced in 1993. The whole data bank consisted of 34512 records of number piglets born pertaining to 10636 females. The total number of animals controlled was 15576. The number of females alive and available for selection was 3537. Animals were evaluated using a BLUP animal model. Model included herd-year-season, parity order and genetic group as fixed effects and breeding value and permanent environment as random effects. Genetic parameters used were estimated by REML in the population, and were 0.06 for heritability and 0.13 for repeatability.

There were two genetic groups that corresponded to two distinct genetic sublimes. About 2900 females pertained to group H and about 700 to group I. Two lines were thus selected, line H formed with the best 175 females from one group and line I with best 175 females from the other group. Males were selected from the best 25 litters of the H group. A control line consisting of 200 females and 15 males was also established. All selected and control females were allocated in a single breeding farm, which can lodge up to 628 animals.

The difference in mean estimated breeding value between the control and selected population, was 0.53 in females and 0.22 in males (line H). One female offspring from each selected female will be obtained and their first two parity performances will be recorded. Management will assure that there are farrowings from all three origins (H, I and control) in each batch. Measurements of ovulation rate in control and selected females and their offspring will be obtained in order to estimate correlated response and genetic parameters of ovulation rate and prenatal survival. Blood samples will be taken in order to analyze the frequency of gene Hal in both selected and control population.

Among offspring of control animals, best 25% females and best 10% males will be selected for average daily gain (ADG) and backfat thickness (BF). This would allow us to estimate the economic loss for not selecting for growth traits in the 'hyperprolific' line. In successive generations, the 'hyperprolific' line will be selected using a global economic criterion that weights ADG, BF and LS.

SIMULATION STUDY

A computer simulation was carried out. It was aimed at reflecting the selection process operating in the breeding population that was screened for hyperprolific animals.

A nucleus of 696 dams and six males was simulated. Each breeding season, each dam provided a female offspring and 80 dams randomly chosen provided additionally a male offspring. ADG and BF were recorded in these offspring. Animals were evaluated using a bivariate animal model for ADG and BF. Economic weights were 0.84 and -31.289 for ADG and BF, respectively. Litter size records were generated but they were not used in selection. Best 174 female offspring and best 3 male offspring replaced an equivalent number of dams and sires, that were culled at random. This is supposed to be close to reality as major reasons for culling in this herd were extra-productive problems: disease, low fertility, leg problems, etc. After four cycles of selection for growth traits, the multiplication herd (2088 females) plus the nucleus population were evaluated for LS using all available information. Best (in terms of prolificacy) 175 females and male offspring from best 25 matings were selected. Twenty five replicates of the whole process were run.

Genotypes and residuals were generated following a trivariate (ADG, BF and LS) infinitesimal model. Heritabilities were 0.27, 0.47 and 0.06 for ADG, BF and LS, respectively. Genetic and environmental correlations between ADG and BF were 0.38 and 0.68, respectively. Two cases were considered, either LS was assumed to be uncorrelated with growth traits or genetically correlated. In the latter case, genetic correlations of -0.14 and -0.20 between LS and ADG, and LS and BF, respectively, were taken.

The Table shows mean genotypic differences between the females of the hyperprolific line and those of the nucleus in the previous generation, for the two sets of genetic parameters considered. Note that there is a loss in growth traits in the hyperprolific line. This is due to the genetic lag as females in the multiplier level were also candidates for selection. When a genetic correlation between growth and reproductive traits was assumed, relative loss in lean percentage was smaller but it was larger in ADG. Simulation indicated that the standard error of the phenotypic difference in LS between nucleus and hyperprolific females was 0.2.

Table. Simulated genetic differences in ADG, BF, LS between females of the hyperprolific line and nucleus females

	Δ ADG	Δ BF	Δ LS
LS uncorrelated	-0.31 \pm 1.98	0.57 \pm 0.11	0.41 \pm 0.04
LS correlated	-1.15 \pm 2.20	0.39 \pm 0.13	0.35 \pm 0.05

DISCUSSION

This experiment should provide evidence about the feasibility of increasing LS in pigs. Simulation results show that a gain of about 0.35 - 0.40 piglets per litter can be expected. This is slightly larger than the response actually obtained in a similar experiment (Sorensen and Vernersen, 1991). The gain in prolificacy will result in an increase of mean aggregate economic value, showing the interest of selecting for LS.

The main difficulty in this experiment is likely to be the detection of significant differences and ascertaining the actual genetic response. Two factors contribute to this problem. First, the heritability estimated in this population was smaller than that currently reported in the literature. This makes its response smaller than previewed when the experiment was designed. Second, the standard error associated with the response will be large, a consequence of the small effective size of the base population (only six sires were kept at a time) together with the additional increase in genetic drift due to intense selection.

Forecoming results should also shed light on the underlying changes in LS components, i.e., ovulation rate and prenatal survival. This evidence will be useful as the genetic relationship among LS and its components is uncertain and there is an important discrepancy between expected and attained responses when selection has been practiced on ovulation rate or on an index combining ovulation rate and prenatal survival.

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