

**Improvement of prolificacy in sows by creation
of a « hyperprolific » line and use of artificial insemination :
principle and preliminary experimental results**

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The possibilities of genetic improvement of prolificacy in a pig population by creation of a line open to exceptionally prolific *Large White* and *Landrace* sows were investigated. Application of the method requires utilization of the boars of the « hyperprolific », line also selected on fattening and carcass traits, in artificial insemination.

The expected theoretical progress was not linear and tended asymptotically towards a maximum, ranging between 5 to 6 p. 100 in purebreeding and 12 to 14 p. 100 in crossbreeding.

The experimental verification of this theory was made by comparing the reproductive ability of the female progeny of 4 *Large White* boars, sons of hyperprolific dams and that of 10 control boars of the same breed. The young females of the experimental line exhibited a significantly higher ovulation rate ($P < 0.01$) than the control line (16.53 vs 13.96 corpora lutea). The mortality of embryos was significantly higher in the hyperprolific line and therefore the number of embryos or piglets alive per litter did not significantly differ between the groups.

Although the hypothesis of a superposing of additive effects (selection) and non additive effects (heterosis) of the genes on prolificacy has not yet been examined experimentally in the pig, the method suggested seems to be better adapted to production of crossbred females than to improvement of purebred females.

Accuracy of « on farm » testing of young gilts

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Heritabilities of performances measured for on-farm testing of young gilts were estimated. This « on farm » test was done when animals from the same test group averaged 85 kg of live weight. Each animal was weighed and probed for backfat thickness in six locations with ultrasonics. Then three criteria calculated :

- The average daily gain from birth to day of test (A.D.G.).
- The average of six backfat measurements, adjusted to 85 kg of liveweight using a correction factor equal to 0.2 mm/kg (B.F.).
- A performance index combining the two above criteria (I).

An analysis of variance of the performances recorded from 4 659 young *Large White* gilts (L. W.) and from 1938 young *Landrace* gilts (LR) was executed considering the following nested model : Herd — Test group — Sire — litter. Heritability coefficients were estimated from sire variance components.

The values found for heritability coefficients of the 3 criteria (A.D.G., B.F. and I.) are the following :

- in L. W. breed : 0.52 ; 0.40 et 0.38 respectively ;
- in LR. breed : 0.29 ; 0.48 et 0.35 respectively.

When all data together were analysed recording to the classification : Breed — Herd — etc..., the estimates obtained were : $h^2 = 0.43$ (A.D.G.), $h^2 = 0.37$ (B.F.), $h^2 = 0.35$ (Index) and $r_G = 0.06 (\pm 0.14)$ for the genetic correlation coefficient between A.D.G. and B.F.

Validity of these estimates is discussed in the paper. Even if values found for heritability of backfat thickness are lower than those usually recorded from backfat measurements in testing stations, economical efficiency of « on-farm » testing of young gilts remains very important.

Comparison of french pig breeding herds for fattening and carcass characteristics

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A sample of 1 432 female *Large White* and *Landrace* pigs, tested in 1973-1974 in five testing stations, has been analysed in order to assess the importance of herd differences and possibility to use the data to compare different breeding herds. Other factors considered were « year », « station », « batch » and « sire ». The year effects are negligible. But important station effects exist for most carcass measurements and for meat quality, the station variance component going up to a maximum of 43 p. 100 for some of these characters. The batch effects are large only for fattening and meat quality measurements. As each herd usually tests the progeny of only one boar in a given batch, the sire effects are confounded with the herd effects. Thus the genetic portion of the between-herd variance may not be estimated from this type of data. If one assumes that the major part of the herd variance is of genetic origin, it would be appropriate to compare herds on the basis of the average breeding value of their breeding animals.
