FIELD TESTING OF YOUNG BREEDING PIGS

II. — THE ACCURACY OF FIELD TESTING [1]

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SUMMARY

The accuracy of the field test, for the individual selection of gilts and for the progeny testing of boars, was investigated.

Data from 4 027 gilts, measured in a farm testing scheme, and being all offspring of AI-boars, were analyzed.

The relative contributions of additive genetic effects (h^2), litter environment effects and farm effects to the total variation were estimated for a performance index, a score for weight, a score for backfat thickness, average daily gain and some conformation traits. The index was a linear combination of both scores.

It was found that the heritability of the index was .22 and that litter environment effects and farm effects contributed 21 p. 100 and 9 p. 100 respectively to the total variation.

It was concluded that this heritability value was high enough to apply individual selection in gilts by means of the field test and that selection within farms would not increase very much the accuracy of the test.

The repeatability of the progeny test of boars, based on data of the field test of their offspring, was estimated empirically as well as theoretically. In an AI breeding population this repeatability was in the order of .6 when about 64 offspring per boar were measured.

INTRODUCTION

Farm testing has some advantages over station testing. Its costs are low and the selection capacity in the field is almost unlimited. For these reasons it is also possible that farm testing may become a substitute for station testing of young

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[1] This article was also part of the study of the first author on the Department of Animal Husbandry, State Agricultural University, Wageningen.

boars, the more so as the risks of spreading diseases are much lower with field testing than with performance testing boars at the stations. A serious drawback of farm testing is of course its lower accuracy. In particular, farm effects may bias the breeding value estimation of animals. The aim of this study was to investigate the accuracy of field testing for individual selection as well as for progeny testing.

MATERIAL AND METHODS

Data of young *Dutch Landrace* gilts, measured in the field testing programme in the provinces Limburg and Noord-Brabant, were analyzed. About 2/3 of the gilts were sired by AI-boars and 1/3 by natural service boars. The numbers of animals measured and their distribution over farms, sires and dams, are listed in table 1.

TABLE I

Numbers of animals measured

Province	Measuring period	AI + Natural service				AI only			
		number of gilts	number of farms	number of sires	number of dams (litters)	number of gilts	number of farms	number of sires	number of dams (litters)
Limburg	XI — '68/IX — '71	3 662	93	227	1 157	2 532	84	90	798
Noord-Brabant	XII — '70/X — '71	2 156	134	178	654	1 495	112	85	442
Total		5 818	227	405	1 811	4 027	196	175	1 240

The gilts were weighed and their backfat thickness was measured at an age between 150 and 295 days. Since January 1970 the animals were given an index, which was a linear combination of a score for weight and a score for backfat thickness. This index was not perfect since older animals systematically got a higher index value. The reason for this was that the score for weight was based on an inaccurate correction for age. For the analysis however all animals were given the new scores and the new index as described in Part I.

In each province farm testing was carried out by one special technician (inspector) of the herdbook. They also judged the animals on conformation. The following characteristics were taken into consideration :

a) muscularity of back and loin,
b) form and shape of hams,
c) legs,
d) size and development.

For each trait a point scale from 1 (poor) to 5 (excellent) was used. Finally total points for conformation were calculated. Each province used a different system.

Limburg : total points L $= 3a + 3b + 3c + d$ (maximum 50 points)

Noord-Brabant : total points NB $= a + b + c + d$ (maximum 20 points)

Estimation of components of variance

Estimation of components of variance was performed for the traits : index, score for weight, score for backfat thickness, average daily gain = weight/age, the four conformation traits and the total points for conformation.

The model chosen to describe the performance traits, was :

$$y_{ijkl} = \mu + \alpha_i + \beta_j + \gamma_{ij} + \delta_{ijk} + \varepsilon_{ijkl}$$

where : y_{ijkl} is the observation on the lth individual of the kth dam and the jth sire on the ith farm ;

  μ is a constant ;
  α_i is the contribution of the ith farm ;
  β_j is the contribution of the jth sire ;
  γ_{ij} is the contribution of the interaction of the ith farm with the jth sire ;
  δ_{ijk} is the contribution of the kth dam mated to the jth sire on the ith farm ;
  ε_{ijkl} is the contribution of the lth individual of the kth dam and the jth sire on the ith farm.

All contributions (except μ)were supposed to be mutually independent and distributed with mean o and standard deviations σ_α, σ_β, σ_γ, σ_δ and σ_ε respectively. Farms and sires form cross classifications ; sires, dams and individuals (daughters) are nested. Since there are many empty subclasses, the data are unbalanced. Therefore the different variance components σ_α^2, σ_β^2, σ_γ^2, σ_δ^2 and σ_ε^2 were estimated according to Henderson's method 1 (e. g. SEARLE, 1971). The sum of these 5 variance components yielded the total phenotypic variance σ_T^2.

The following relative measures of variation, assuming random mating, were calculated for each trait :

h^2 = heritability = relative additive genetic variation = $\dfrac{4 \, \widehat{\sigma_\beta^2}}{\widehat{\sigma_T^2}}$ (e. g. BECKER, 1967)

c_1^2 = relative variation, attributable to common litter environment = $\dfrac{\widehat{\sigma_\delta^2} - \widehat{\sigma_\beta^2}}{\widehat{\sigma_T^2}}$

c_2^2 = relative variation, attributable to common farm environment = $\dfrac{\widehat{\sigma_\alpha^2}}{\widehat{\sigma_T^2}}$

Approximate standard errors were calculated for the heritabilities, according to the for mula

$$\text{SE}(\widehat{h^2}) \approx \frac{4}{\widehat{\sigma_T^2}} \sqrt{ \frac{2}{k^2} \left(\frac{\text{MS}_\beta^2}{s+1} + \frac{\text{MS}_\delta^2}{d-i+2} \right) }$$

where : $\text{SE}(\widehat{h^2})$: standard error of heritability ;
   $\widehat{\sigma_T^4}$: total phenotypic variance ;
   k : « weighted » average number of progeny per sire ;
   MS_β : mean square for sires ;
   MS_δ : mean square for dams ;
   s : number of sires ;
   d : number of dams (litters) ;
   i : degrees of freedom for farm $\times$ sire interaction term.

The formula is a rough approximation of a formula given by LE ROY (1966), which was developed for data from a nested classification.

The estimates were derived for each province separately and within the provinces for data of progeny of all boars as well as for data of progeny of AI-boars only. For the traits : index, scores and average daily gain the estimates were obtained also for both provinces combined. For the conformation traits a combined estimate did not seem to be meaningful, since the subjective judgement could be different for each of both inspectors.

Estimates of components of covariance were obtained in an analogous manner to obtain phenotypic (r_p) and genetic (r_g) correlations between each pair of traits x and y, where :

$$r_{\text{p}} = \frac{\widehat{\sigma}_T(xy)}{\sqrt{\widehat{\sigma_T^2}(x) \cdot \widehat{\sigma_T^2}(y)}}$$

and

$$r_g = \frac{4\widehat{\sigma}_\beta(xy)}{\sqrt{4\widehat{\sigma}_\beta^2(x) \cdot 4\widehat{\sigma}_\beta^2(y)}} \qquad \text{(e. g. BECKER, 1967)}$$

where $\widehat{\sigma}(xy)$ stands for the covariance of traits x and y, and the subscripts refer to the various effects as outlined in the description of the model.

For the computation of the standard errors of the correlations the following approximations were used :

$$\text{SE}(r_p) \approx \sqrt{\frac{1 - r_p^2}{n - 2}} \qquad \text{(e. g. SNEDECOR and COCHRAN, 1967)}$$

where n = number of animals measured

$$\text{SE}(r_g) \approx \frac{1 - r_g^2}{\sqrt{2}} \sqrt{\frac{\text{SE}(\widehat{h}_x^2) \cdot \text{SE}(\widehat{h}_y^2)}{\widehat{h}_x^2 \cdot \widehat{h}_y^2}} \qquad \text{(e. g. LE ROY, 1966)}$$

Daughter-dam regression

A heritability estimate of the index also could be obtained from the regression of offspring (O) on dams (D), since in the province Limburg 127 tested gilts had 458 daughters, that entered the farm test later on. The heritability, estimated as twice the regression coefficient b_{OD}, was calculated over farms as well as within farms. In this regression analysis the number of offspring per dam was weighted according to the method described by FALCONER (1963).

RESULTS

For each province the means ($\bar{x}$) and overall standard deviations (s_x) of the traits are listed in table 2.

TABLE 2

Means of the traits and their overall standard deviations

	Limburg		N-Brabant	
	$\bar{x}$	s_x	$\bar{x}$	s_x
Index (rescaled)	9.222	2.57	9.231	2.54
Score for weight..............................	— .012	1.031	— .115	1.185
Score for backfat thickness	— .426	1.201	— .319	1.129
Age (days)	206.53	18.34	214.65	14.52
Weight (kg)	98.84	12.19	102.13	12.16
Average daily gain (g/day)	480	51	477	59
Backfat thickness (mm)	15.64	3.00	15.90	3.09
Muscularity of back and loins (points)	3.64	.56	3.18	.55
Form and shape of hams (points)	3.86	.60	3.59	.60
Legs (points)	3.19	.57	3.04	.51
Size and development (points)	3.73	.67	3.25	.69
Total conformation score « Limburg » (points)	35.80	3.54	—	—
Total conformation score « N-Brabant » (points) ...	—	—	13.06	1.50

First of all a possible influence of season was investigated by plotting the means against the months of measuring. No systematic season effect could be found on any trait.

However, in both provinces a sudden shift in the average index, scores and daily gain was observed. In Limburg the means of these traits were much better after March 1970, *i. e.* about 3 months after the introduction of the index tables in that province, and in Noord-Brabant after March 1971, that means about 3 months after the beginning of farm testing in that province. The cause of this sudden change was not clear. A possible explanation could be that the technicians as well as the farmers got accustomed to the use of the index after about 3 months, so after this period they were able to apply some pre-selection in order to save costs. So may be the slowest growing animals would not be offered for measuring. Another possibility could be that the farmers found out that they could get a higher index for their pigs by feeding their pigs to a heavier weight. This would raise the index of their animals since the score for weight in the old index was not correct.

Before performing an analysis of variance a correction for this sudden shift was applied for all traits. In each province the observations in the first period were increased by the average difference between the two periods in the respective province. The method of correction applied is debatable if the sudden change was caused by a pre-selection of the animals. However, it turned out that the statistical analysis of the corrected data yielded about the same relative estimates of components of variance as analyses of the data for each period separately.

The estimation of components of variance showed that the contribution of the interaction between farms and sires to the total variance was in most cases low or even negative. So this interaction does not seem to be of much importance.

From the variance components heritability estimates were derived. It turned out that the $\widehat{h^2}$-values in the total material (progeny of AI and natural service boars) were much highter than the $\widehat{h^2}$-values in the AI-population. In natural service there is a strong confounding of farms and sires, so the AI-population provides more reliable estimators of the different variance components. For this reason only the results of the analysis of data from AI-progeny will be given.

In table 3 the heritabilities and the relative contributions of litter environment $\widehat{(c^2)}$ and farm environment $\widehat{(c_2^2)}$ are listed.

The $\widehat{h^2}$-value of .224 of the index is about the average of the $\widehat{h^2}$-values of both scores. The $\widehat{h^2}$ of score for backfat thickness is about 3 times as high as the $\widehat{h^2}$ of score for weight. Average daily gain yields about the same values as score for weight, as would be expected. From the conformation traits the judgement of muscularity of the back and loin and of form and shape of ham have the highest heritabilities. They are of the same order as the $\widehat{h^2}$ of the index. Low values are found for legs and for size and development. From the total conformation scores the method used in Limburg yields the highest $\widehat{h^2}$-value. This is explained by the fact that in the « Limburg total » the first three conformation traits — from which two have a reasonable $\widehat{h^2}$-value — are given three times as much weight as in the « Noord-Brabant total ».

The proportions of variance due to litter environment and due to farm environment are rather high, especially for the score for weight and for average daily gain.

TABLE 3

Proportions of the variance attributed to different causes. (See text)

	Limburg + Noord-Brabant			Limburg			Noord-Brabant		
	$\hat{h}^2 \pm$ SE	$\hat{c}_1^2$	$\hat{c}_2^2$	$\hat{h}^2 \pm$ SE	$\hat{c}_1^2$	$\hat{c}_2^2$	$\hat{h}^2 \pm$ SE	$\hat{c}_1^2$	$\hat{c}_2^2$
Index	.224 ± .063	.209	.088	.245 ± .080	.182	.067	.225 ± .120	.238	.140
Score for weight	.122 ± .062	.261	.248	.207 ± .087	.215	.188	.092 ± .120	.367	.344
Score for backfat thickness	.378 ± .080	.165	.131	.363 ± .100	.151	.130	.440 ± .143	.146	.151
Average daily gain	.108 ± .059	.252	.243	.179 ± .081	.203	.182	.076 ± .117	.368	.341
Muscularity of back and loins				.218 ± .069	.108	.060	.104 ± .077	.110	.043
Form and shape of hams				.224 ± .064	.053	.032	.243 ± .088	.009	.017
Legs				.122 ± .050	.051	.038	.023 ± .057	— .009	.032
Size and development				.055 ± .043	.108	.048	.043 ± .084	.151	.135
Total conformation score « Limburg » ..				.254 ± .069	.042	.070	.187 ± .090	.106	.057
Total conformation score « Noord-Brabant » ..				.205 ± .064	.036	.081	.128 ± .088	.146	.082

About 21 p. 100 of the total variation of the index is due to litter effects. This is about the average of the corresponding values for both scores. Farm effects contribute about 9 p. 100 to the variation of the index and this is much lower than the average of the corresponding values for both scores.

The $\widehat{h^2}$ of .224, derived from the paternal half-sib analysis of the AI-data, is in reasonable agreement with the estimate, derived from the regression of daughters on dams, as is listed in table 4. This regression was done on the index values, corrected for the sudden shift between periods.

TABLE 4

Heritability of index, derived from regression of daughters on dams

	Total	Within farms
$h^2 \pm$ SE	.160 $\pm$ .120	.156 $\pm$ .158

The calculation within farms did not change the $\widehat{h^2}$-value. Often in the analysis of field data of farm animals the within farms regression of daughters on dams is yielding lower but more reliable heritability-estimates than the total regression, which usually is biassed upwards by a correlation between daughters and dams due to their common farm environment. This correlation is eliminated in the within farms regression.

However, as in our analysis daughters are measured at least one year later than their dams, the environment within farms may have changed considerably during this time lag, and consequently may have broken down the environmental correlation between daughters and dams in the total regression calculation.

The phenotypic and genetic correlations between the traits are listed in table 5.

The estimation of components of covariance was based on the AI-data, corrected for the shift differences. In the cells with two values, the upper value refers to Limburg, the lower to Noord-Brabant. In the interpretation of the correlations one has to realize that a negative score for backfat thickness is desirable. The phenotypic correlations between index and both scores are almost of the same size, the genetic correlation between index and score for backfat thickness, however, is much higher than the genetic correlation between index and score for weight. Both scores are phenotypically slightly unfavourable correlated ; the genetic relationship has the same sign but is somewhat stronger. Score for weight and average daily gain are highly correlated and can be considered as same traits. The phenotypic correlations between the index and the conformation traits are all positive. The same holds true for the correlation between the score for weight (or average daily gain) and the conformation traits. The score for backfat thickness is only slightly correlated with the conformation traits ; the correlation with muscularity of back and loins is slightly unfavourable, and with form and shape of hams slightly desirable. The points for legs are almost uncorrelated with the other conformation traits.

The genetic correlations usually have the same sign as the phenotypic correlations, taking into account their high standard errors.

TABLE 5

Phenotypic correlations (above the diagonal) and genetic correlations (below) among the traits
Upper figure Limburg, Lower figure Brabant

	Index	Score for weight	Score for backfat thickness	Average daily gain	Muscularity of back and loins	Form and shape of hams	Legs	Size and development	Total conformation score «Limburg»	Total conformation score «N-Brabant»
Index		.593*	— .674*	.590*	.110* .256*	.227* .318*	.094* .085*	.386* .521*	.317* .410*	.379* .491*
Score for weight	.152		.185*	.990*	.345* .413*	.300* .319*	.117* .153*	.566* .732*	.486* .553*	.573* .672*
Score for backfat thickness	— .868*	.358		.179*	.160* .101*	— .083* — .075*	— .012 .044	.015 .092*	.029 .046	.029 .066*
Average daily gain	.143	.997*	.359		.367* .424*	.308* .328*	.123* .157*	.599* .753*	.509* .567*	.602* .690*
Muscularity of back and loins	— .129 .229	.283 .760*	.299 .140	.220 .855*		.229* .325*	.010 .067*	.263* .341*	.647* .721*	.608* .689*
Form and shape of hams	— .531* .493*	.587* .743*	— .143 — .105	.637* .777*	.490* .938*		.001 — .067*	.222* .212*	.671* .712*	.614* .642*
Legs	.051 — .241	.484* — .196	.292 .110	— .495* — .256	.166 1.438	.321 .450		.080* .120*	.515* .512*	.443* .452*
Size and development	.764* — .443	.891* — .327	— .193 .195	.874* — .144	.239 — .056	.475 .000	.303 — .210		.473* .503*	.698* .713*
Total conformation score «Limburg»	.289 .280	.656* .621	.144 .024	.639* .626	.756* 1 086	.858* .956*	.598* .582	.533* .035		.961* .965*
Total conformation score «N-Brabant»	.385* .186	.738* .544	.098 .063	.722* .586	.722* 1.044	.850* .936*	.591* .544	.644* .211	.991* .986*	

* : Greater than twice their standard error.

FARM TESTING USED FOR PROGENY TESTING OF BOARS

Farm testing could also be used for the progeny testing of AI-boars in the field. A criterion for the accuracy of the progeny test is its repeatability. An empirical estimation of this repeatability was derived from the AI-data.

From the progeny of each AI-boar 2 or more samples of the same size N were drawn. This sampling was done according to the date of measuring of the animals. The first sample comprised the first N measured progeny, the second one the second N measured animals, etc. The sampling was done for various sample sizes : $N = 8$, $N = 16$, $N = 24$, $N = 32$.

The following analysis of variance was carried out on the sample means :

	d.f.	Mean square	Expectation of mean square
Between boars	$v - I$	MS_v	$\sigma_s^2 + k_s\sigma_v^2$
Between sample means within boars	$\sum(s_i - I)$	$MS_{s(v)}$	σ_s^2

where : v : number of boars ;

s_i : number of samples, of size N, drawn from the progeny of boar i;

k_s : « average » number of samples per boar ;

σ_v : variance component between boars ;

σ_s^2 : variance component between sample means within boars.

The repeatability b of the progeny test was estimated as :

$$b = \frac{\widehat{\sigma_v^2}}{\widehat{\sigma_s^2} + \widehat{\sigma_v^2}}$$

The sampling was done in two ways :

A. Sampling per boar within provinces and periods (before and after the sudden shift) and pooling of the respective sum of squares over provinces and periods.

B. Sampling per boar over both provinces, but restricted to the period after March 1971. The results are listed in table 6.

TABLE 6

Empirical estimates of the repeatability of the progeny test

Sample size N	Sampling method A			Sampling method B		
	Repeatability b	Number of samples	Number of boars	Repeatability b	Number of samples	Number of boars
8	.198	264	66	.177	73	26
16	.268	91	27	.367	31	9
24	.338	47	16	.217	14	4
32	.090	28	10	.483	9	3

For larger sample sizes the repeatability estimates are based on less boars, and so are less reliable.

In order to evaluate these findings also a theoretical estimate of the repeatability was derived from a model population, assuming random distribution of the progeny of v boars over farms and litters. Each boar has p offspring per litter, with l litters on each of f farms, so the total number N of offspring per boar is flp.

The analysis of variance of such a hierarchical classification can be written as follows :

Source of variation	d.f.	Mean square	Expectation of mean square
Between boars	$v - 1$	MS_v	$\sigma_p^2 + p\sigma_l^2 + pl\sigma_f^2 + plf\sigma_v^2$
Between farms within boars.......	$v(f-1)$	$MS_{f(v)}$	$\sigma_p^2 + p\sigma_l^2 + pl\sigma_f^2$
Between litters within farms	$vf(l-1)$	$MS_{l(f)}$	$\sigma_p^2 + p\sigma_l^2$
Between progeny within litters	$vfl(p-1)$	$MS_{p(l)}$	σ_p^2

Genetic interpretation of relative components of variance :

$$\frac{\sigma_v^2}{\sigma_T^2} = 1/4h^2 + c_3^2$$

where : h^2, c_1 and c_2^2 are as defined earlier.

$c_3^2 =$ relative proportion of variance due to non genetic differences between progeny groups of boars (e. g. area differences, season differences).

$$\frac{\sigma_f^2}{\sigma_T^2} = c_2^2$$

$$\frac{\sigma_o}{\sigma_T^2} = 1/4h^2 + c_1^2$$

$$\frac{\sigma_p^2}{\sigma_T^2} = 1/2h^2 + e^2$$

where : $e^2 =$ relative proportion of variance due to random environmental differences.

Now the repeatability of the progeny test can be defined as :

$$b = \frac{plf\sigma_v^2}{\sigma_p^2 + p\sigma^2 + pl\sigma_f^2 + plf\sigma_v^2}$$

$$= \frac{1/4plfh^2}{1 + p(lf + 1)\,1/4h^2 - 1/2h^2 + (p-1)\,c_1^2 + (pl-1)\,c_2^2 + (plf-1)\,c_3^2}.$$

With this formula the theoretical repeatability of the progeny test was calculated for various combinations of p, l and f, substituting $\widehat{h}^2 = .22$, $\widehat{c}_1^2 = .21$, $\widehat{c}_2^2 = .09$ and $\widehat{c}_3^2 = 0$ (and also $\widehat{c}_3^2 = .05$).

The results are presented in figure 1 (for $\widehat{c}_3^2 = 0$) and figure 2 (for $\widehat{c}_3^2 = .05$). In both figures the empirically derived values from table 6 are also plotted. It shows that in most cases these values are within the range of the theoretical possibilities.
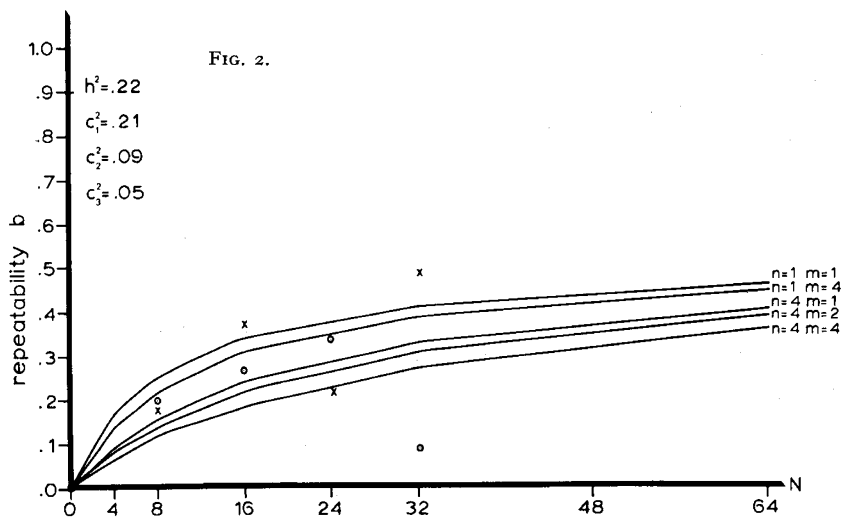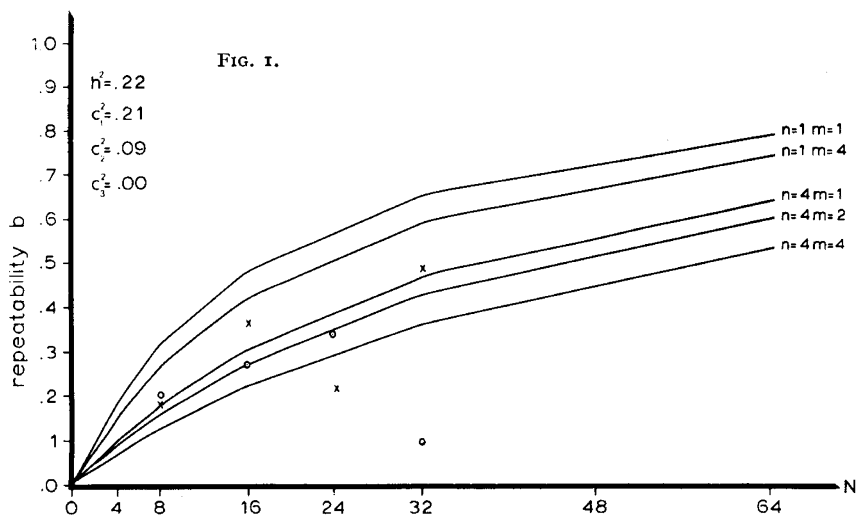
FIG. 1 and 2. — *Theoretical and empirical repeatability of progeny testing boars*

———— : theoretical repeatability b ;
o : empirical estimates of repeatability b, sampling method A (see text) ;
x : empirical estimates of repeatability b, sampling method B (see text) ;
n : number of progeny per litter ;
m : number of litters per farm ;
N : total number of progeny per boar.

DISCUSSION

A $\widehat{h}^2$-value of .22 for the index is rather low, but still high enough to be useful for individual selection of young breeding animals. In fact the value is of about the same magnitude as the h^2 of milk yield in cows. The litter environment contribution to the variation of the index is very high (21 p. 100), much higher than the farm contribution. In practice the selection mainly will be carried out within farms, at least for gilts. However, this increases the accuracy of the breeding value estimation only very little, since the heritability within farms $(\widehat{h}_f^2)$ can be estimated as:

$$\widehat{h}_{(f)}^2 = \frac{\widehat{h}^2}{1 - \widehat{c}_2^2} = \frac{.224}{1 - .088} = .246$$

Selection within litters eliminates the variation due to differences in litter environment, but it also halves the genetic variation, so it does not increase the effectiveness of selection.

Our parameters are based on gilts, and so strictly speaking only applicable to the selection of gilts. Extending of the findings to the selection of boars must be done with reservation.

Keeping this in mind it seems to us that farm testing of young boars will not be a complete alternative to the performance test of the boars on central stations, since the latter has a much higher accuracy and also the food intake can be measured. The heritability of a selection index for boars, tested on stations, usually is in the order of .5—.6.

In a breeding structure, where much AI is applied on the breeding farms, as is the case in the most important pig provinces in the Netherlands, the field test can also be used for progeny-testing AI-boars. If precautions are made to avoid as far as possible environmental differences between progeny groups, the repeatability of the progeny test is .6, when about 64 offspring per boar are tested. This holds true for practical circumstances where on average 2 litters per boar per farm and 4 progeny per litter are measured (see figure 1).

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RÉSUMÉ

TESTAGE EN FERME DES JEUNES REPRODUCTEURS PORCINS
II. — LA PRÉCISION DU TESTAGE EN FERME

Pour étudier la précision du testage en ferme, aussi bien pour la sélection individuelle des truies que pour le jugement des verrats sur la descendance, on a analysé des données recueillies dans un schéma de testage comprenant 4 027 truies, issues d'insémination artificielle.

Les contributions relatives des effets génétiques additifs (h^2), des effets portée et ferme, dans la variation totale, ont été estimées sur un index de performance, un indice de poids, un indice d'épaisseur du lard dorsal, le gain journalier moyen et quelques caractères de conformation. L'index était une fonction linéaire du des deux indices.

L'héritabilité de l'index était de 0,22, alors que l'effet de la portée et l'effet « ferme » contribuaient respectivement pour 21 p. 100 et 9 p. 100 à la variation totale.

On en a conclu que l'héritabilité était suffisamment élevée pour que l'on sélectionne individuellement les truies par le testage en ferme et que la sélection intra-ferme n'augmenterait guère la précision du test.

La répétabilité de la mise à l'épreuve sur descendance des verrats, basée sur le testage en ferme, de leurs progéniture a été estimée aussi bien empiriquement que théoriquement. Dans une population où l'on pratique l'insémination artificielle, cette répétabilité était de l'ordre de 0,6, lorsque l'on mesurait en moyenne 64 descendants par mâle.

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