

A PRELIMINARY REPORT ON THE INTERACTION BETWEEN GENOTYPE,
FEEDING, AND SEX IN *DUTCH LANDRACE* PIGS

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An experiment with 3 replications was performed to find out if there is an interaction between genotype and feeding level (*ad libitum* versus restricted) in *Dutch Landrace* pigs. Each replication consisted of 120 or 128 animals. These animals were sired, per replication, by 9-11 boars. From each sire 2 or 3 littergroups of 4 animals were usually taken.

From each littergroup 1 gilt and 1 castrate were fattened *ad libitum*, and 1 gilt and 1 castrate were fattened restricted (twice a day using a feeding schema according to age). All animals were housed and fed in single pens, and the fattening period was from 25 to 100 kgs. live weight. The average daily food intake of the restricted fed gilts was about 79 per cent of the daily intake of the *ad libitum* fed gilts. For the castrates, the corresponding figure was 71 per cent.

The data of the first two replications were analysed at the time of reporting. In none of the 3 fattening or 14 carcass traits studied was a significant interaction between genotypes (sires) and feeding levels found. The interaction between genotypes and sexes was only significant at the 5 per cent level for ultrasonically measured backfat thickness. For this trait, the genotype at the 5 per cent level for ultrasonically measured backfat thickness. For this trait, the genotype \times sex \times feeding level interaction was also significant. More information concerning the possible existence of an interaction between genotypes and sexes was provided by data from *Dutch Landrace* pigs in progeny stations during the years 1966-1968. The data consisted of 1869 littergroups of 2 gilts and 2 castrates each, sired by 817 boars. The animals were housed in single pens and were fed twice a day on a restricted level using feeding scale to live weight.

In the analysis of variance a significant sire \times sex interaction was found for backfat thickness and percentage of hams, but not for growth rate, food conversion ratio, and 6 other carcass traits studied. The interaction component of variance accounted for a very small percentage of the total variation in all traits. This is also true for backfat thickness and ham percentage. The genetic correlation between sexes was + 1, or very close to + 1, for most traits studied, except, for backfat thickness ($r_g = + 0.90$), ham percentage ($r_g = + 0.82$), and the score for ham shape ($r_g = + 0.90$).

COMPARATIVE STUDIES ON PROGENY TEST RESULTS FROM
STATIONS AND FIELD DATA

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Butterfat records from 270 *Red Danish* bulls tested on the basis of about 30 000 daughters, partly in farmer herds and partly at the special progeny testing stations in Denmark, were analysed. Only bulls whose sires had at least four tested sons were included in the study.

The material was analysed in two different ways. In the first analysis, the progeny test results of the same bull from field data and from stations were considered to be records of separate characters and the actual and the expected correlations between those were calculated. In the calculation of the expected correlations heritabilities of 0.20 in the field and of 0.75 at the stations were used.

The correlation between field and station results was 0.46 with an expected value of 0.81 and that between two independent field tests was 0.65 with an expected value of 0.69.

In doing so, the accuracy of the test in question can be calculated as four times the intraclass correlation between paternal half brothers.

As regards the station tests the accuracy became very low as compared to the expected. In contrast to that the accuracy of the field tests was in good agreement with expectation.

It was concluded that the large variance component between bulls at the stations and also the low repeatability of a station test in commercial herds are caused by a non-genetic correlation between daughters within groups. This accounts for about 2/3 of the intraclass correlation between half sibs at the stations.

RELATION ENTRE LES PERFORMANCES DE REPRODUCTION
ET LES PERFORMANCES D'ENGRAISSEMENT ET DE CARCASSE
CHEZ LE PORC

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Les corrélations entre les performances de reproduction (taille de la portée à la naissance et au sevrage, poids de la portée à 60 jours) de 1 140 truies de race *Large White* et les performances d'engraissement (gain moyen quotidien de 30 à 100 kilogrammes et indice de transformation) et de carcasse (longueur, épaisseur du lard dorsal, % de morceaux nobles et % de morceaux gras) de 3 de leurs descendants issus de la même portée et contrôlés dans les stations de contrôle de la descendance ont été estimées. Les corrélations phénotypiques intra-verrat et station sont très faibles dans l'ensemble et non significatives. Trois coefficients dépassent cependant légèrement le seuil de signification ($p < 0,05$) : entre la longueur de la carcasse et la taille de la portée à la naissance ($r = -0,09$) et au sevrage ($r = -0,10$) et entre le pourcentage de morceaux nobles et le poids de la portée à 60 jours ($r = 0,11$). Les corrélations génétiques accentuent ces tendances sans qu'il soit possible de leur attribuer une valeur définitive.

En conclusion, les caractères liés à l'engraissement et à la composition corporelle sont indépendante ou faiblement associés aux performances de reproduction. Par conséquent, l'orientation actuelle de la sélection ne devrait pas, du moins à court terme, être préjudiciable à la valeur reproductive des truies.

THE DESIGN OF BEEF BREED COMPARISONS

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In planning the comparison of several breeds of cattle for use as beef crossing sire lines it is necessary to decide how many bulls (N) per breed and how many progeny (n) per bull to measure. Assuming that the breeds are to be compared for a single major trait, the following seven factors need to be taken into account :

h^2 : the intrabreed heritability of the trait.

r : the repeatability or accuracy of the progeny test.

σ : the phenotypic standard deviation for the trait.

d : the true difference between breeds that it is desired to detect.

P : the probability that a true difference of d will be detected.

p_1 : the probability level at which it is desired to test the significance of a difference.

B : the number of breeds to be compared.

If h^2 is presumed known, and a value is specified for r , n becomes fixed. It then becomes possible to use standard experimental design theory to find the minimum value of N which satisfies a given difference, phenotypic standard deviation, probabilities and number of breeds.