

IMPLICATIONS OF GENOTYPE X ENVIRONMENT INTERACTION FOR THE DESIGN OF NATIONAL PIG BREEDING PROGRAMMES

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SUMMARY

Genotype x environment interaction for the traits daily gain and ultrasonic backfat is estimated as genetic correlation between two homologous traits at nucleus and multiplication level of the pig breeding programme. The implications of the knowledge about genotype x environment interaction in the national pig breeding programme is discussed.

INTRODUCTION

A pig breeding programme generally consists of different levels of a pyramid, indicated as nucleus, multiplication and commercial level. Although selection takes place at all levels, only selection at the top level (nucleus) influences the rate of annual genetic change.

Selection at nucleus level for growth and carcass traits is generally based upon performance test, supplemented with sib information. In national programmes these tests generally take place under special conditions, as a central test, which deviate from the conditions of commercial growing. Interaction of genotype and level of the breeding programme decreases the efficiency of pyramidal programmes to a large extent (e.g. Standal, 1977; Brascamp et al., 1985; Webb and Curran, 1986; Merks, 1988; Cameron, 1991).

In the Netherlands the Stamboek breeding programme has been adapted in order to overcome genotype by environment interaction (GxE), e.g. group housing and ad libitum feeding in central test. These adaptations were of help to improve the genetic correlations between the genotypic values in different environments, but further adaptations are introduced to optimize the national pig breeding programme.

The aim of this paper is to review the latest estimates of genetic correlations across levels in the Netherlands and to discuss the implications of the present knowledge about GxE interaction for the national pig breeding programme.

MATERIALS AND METHODS

Data of Dutch Landrace (NL), Dutch Yorkshire dam line (GY-d) and Dutch Yorkshire sire line (GY-s) tested between June 1991 and July 1993 are analysed. Animals are tested either in the herdbook field testing programme (FT) or at the central test station (CT) (Knap, 1990). In the on-farm test pigs are tested in groups and on ad libitum feeding. They are weighed to calculate daily gain on live period (DGL) and their backfat thickness is measured ultrasonically (UB FT) at an age of about 190 days. At the central test pigs are tested in groups and on ad libitum feeding. The test starts at an age of about 12 weeks and takes 13 weeks. Daily gain on test (DGT) is calculated and ultrasonic

backfat thickness at the end of the test is measured ultrasonically (UB CT). In total 58413 numbers of records from FT and CT are analysed. Records analysed are from 3 breeds.

Heritabilities are estimated by derivative free restricted maximum likelihood analysis of univariate animal models with complete relationship matrix (Meyer, 1989a). Ancestors are traced back four generations. The models used for daily gain are:

$$\text{FT: } Y_{ijkl} = \mu + S_i + H_j + a_{ijkl} + t_{ijl} + e_{ijkl}$$

$$\text{CT: } Y_{ijkl} = \mu + S_i + B_j + a_{ijkl} + t_{ijl} + e_{ijkl}$$

where:

Y_{ijkl}	=	record of daily gain
μ	=	general mean
S_i	=	fixed effect of sex i
H_j	=	fixed effect of herd-year-season j
B_j	=	fixed effect of batch j
a_{ijkl}	=	random additive genetic effect of animal l
t_{ijk}	=	random litter effect of litter k
e_{ijkl}	=	random residual effect of animal l

For the analysis of ultrasonic backfat thickness the following models are used:

$$\text{FT: } Y_{ijkl} = \mu + S_i + H_j + a_{ijkl} + t_{ijk} + \beta LW_{ijkl} + e_{ijkl}$$

$$\text{CT: } Y_{ijkl} = \mu + S_i + B_j + a_{ijkl} + t_{ijk} + \beta LW_{ijkl} + e_{ijkl}$$

where:

Y_{ijkl}	=	record of ultrasonic backfat thickness
β	=	regression coefficient
LW_{ijkl}	=	live weight of animal l
other symbols as in previous model		

Genotype environment interaction is estimated as the genetic correlation between homologous traits in the two environments by derivative free restricted maximum likelihood analysis of multivariate models (Meyer, 1989b).

RESULTS

Estimates for heritabilities for daily gain on live period (DGL), daily gain on test (DGT) and ultrasonic backfat in the on-farm test (UB FT) and in the central station test (UB CT) are presented in Table I for all three breeds.

Table I. Heritability (h^2) estimates for daily gain and ultrasonic backfat in the on-farm test and in the central station test (standard deviations in brackets).

	NL	GY-d	GY-s
DGT (CT)	0.09 (0.06)	0.17 (0.06)	0.27 (0.05)
DGL (FT)	0.20 (0.02)	0.20 (0.04)	0.14 (0.02)
UB CT	0.25 (0.08)	0.44 (0.10)	0.15 (0.05)
UB FT	0.37 (0.02)	0.48 (0.05)	0.22 (0.03)

The estimates for daily gain on test are lower than on live period for NL and GY-d. For GY-s daily gain on test has a higher estimate than daily gain on live period. The estimates for ultrasonic backfat thickness are higher in the field testing programme than in the central station test for all three breeds. At the central test GY-s has the highest heritability for daily gain, followed by GY-d and NL. For ultrasonic backfat GY-d has the highest heritability in both environments, followed by NL and GY-s.

Estimates of genetic correlations between daily gain in the field testing programme and in the central station test and between ultrasonic backfat measurements in both environments are given in table II.

Table II. Estimates of genetic correlation between homologous traits in two environments for all three breeds.

Trait	NL	GY-d	GY-s
Daily gain	0.96	0.96	0.70
Ultrasonic backfat	0.87	0.95	0.97

The estimates for genetic correlation range between 0.70-0.96 for growth and between 0.87-0.97 for ultrasonic backfat. For growth NL and GY-d have similar estimates and GY-s has a lower estimate of 0.70. For ultrasonic backfat GY-d and GY-s have about similar estimates and NL has a lower estimate of 0.87.

DISCUSSION

The estimates of genetic correlations between genotypic values in CT and FT are close to one. Merks (1988) estimated lower correlations for daily gain (0.3-0.6) as well as for ultrasonic backfat thickness (0.5-0.7). At the same time the estimated heritabilities in central test are similar or lower than those estimated in on-farm test. Apparently the adaptations of central test environment (from individual to group housing and ad libitum instead of restricted feeding) improved the genetic correlations across environments. However these adaptations reduced uniformity of environment in central test and consequently reduced the genetic efficiency of central test. As indicated by Sehested and

Ianssen (1991) model calculations with these parameters show that a national breeding programme without central test but with the same number of animals tested in on-farm test results in a higher rate of genetic progress.

Generally, national breeding programmes with performance testing in central test (with or without full sibs to be slaughtered) are accepted as the best, while programmes with progeny testing are considered to achieve less progress due to a prolonged generation interval. In a commercial situation most fattening pigs are crossbred pigs. Because of this, the programmes that make use of the results of fattening pigs, become a combination of individual and reciprocal recurrent selection. In other studies (e.g. McKay and Rahnefeld, 1984; McLaren et al., 1985) no clear advantage for reciprocal recurrent selection over mass selection is reported for daily gain and backfat thickness due to the prolonged generation interval with progeny testing. However, this disadvantage is not present if paternal half sibs are used. Reciprocal recurrent selection may even be part of the answer to GxE in pig breeding programmes because the low genetic correlations between nucleus and commercial fattening environment may partly be due to the comparison of pure-bred and crossbred animals. In any case will the possibilities of including reciprocal recurrent selection in pig breeding programmes on, open new dimensions for exploiting non-additive genes (Ming, 1992).

Generally, it may be concluded that national breeding programmes should make more use of the sib and progeny data gathered in the different levels of the breeding programme by use of animal models. This helps to overcome the problems of GxE and also enables the exploiting of non-additive genes. Central test has lost its effectiveness because of more effective evaluation methods and because of veterinary risks that are unified with bringing together piglets of 50-100 different breeding farms.

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