

**PUREBRED AND CROSSBRED INFORMATION IN CROSSBREEDING  
PROGRAMMES IN PIGS**

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**INTRODUCTION**

For the production of pig meat in several countries all over the world crossbred slaughter pigs are used. In crossbreeding programmes in pigs specialized sire and dam lines are used to produce either single crosses (F1), three-way or four-way crosses with F1 dams. In some east European countries synthetic lines or breed-rotation systems have been used where the other European countries prefer specialized sire and dam lines. Pig breeding programmes generally consist of different levels of a pyramid, indicated as nucleus, multiplication and commercial level. In a crossbreeding situation the breeding goal should be defined at the level of commercial growing. In most breeding programmes selection takes place only at the top level (nucleus) based on purebred performances. The influence of the selection at the nucleus level on the rate of genetic change in the production level is highly dependent on the genetic correlation between purebred and crossbred performance for the same trait. This correlation is a good measurement for a possible "genotype x level" interaction in crossbreeding programmes. In this paper some results of estimates of the genetic correlation between purebred and crossbred performance for daily gain and backfat thickness are discussed and consequences for crossbreeding programmes in pigs concerning test procedures and estimation of breeding values are shown.

**LITERATURE REVIEW**

The estimates for the correlation between purebred and crossbred performances out of the literature are summarized in table 1 for production traits and table 2 for reproduction traits. Nearly all correlations in tables 1 and 2 are estimates out of selection experiments or estimates from the relationship between breeding values of sires based on purebred and crossbred progeny. For growth and carcass traits there seems to be a positive correlation between purebred and crossbred performances. For litter size and other reproduction traits there is no correlation or even a negative correlation between the trait measured in purebred and crossbred sows. Only Wong et al. 1971 found a high positive genetic correlation between number of piglets born from purebred and from crossbred sows. This is also the only estimate from a data set with a reasonable number of sires in the analysis. New results from bigger data sets are not known from the literature although most of the litter records from crossbred sows in Germany are available in sow management programmes.

Table 1: Estimates of genetic correlations between purebred and crossbred performances for production traits in pigs

Reference	Method <sup>1</sup>	Number of sires	Trait	Correlation
Robinson et al., 1964	HG	5 and 8	Backfat Weight at 140 days	.21 and > 1 .22 and .72
Stanislaw et al. 1967	HG	89	Backfat Daily gain Weight at 56 days	> 0 > 0 > 0
Standal 1968	HG	40	Backfat Daily gain Meat area	.41 1.33 1.13
Wong et al. 1971	HG	181	Backfat Daily gain Feed conversion Index	> 1 .55 .09 .47
McLaren et al. 1985	ZW	8 to 32	Backfat Daily gain	.88 .56
Englisch et al. 1990	HG	18 and 28	Lifeweight daily gain Daily gain Feed conversion Meat to fat ratio	.10 and .06 .39 and .19 .28 and .28 .80 and .43
Götz and Peschke 1993	ZW	531	Daily gain Feed conversion Meat percentage Meat quality Index	.26 .14 .52 .36 .42

<sup>1</sup> HG = Estimates between half-sib-families ZW = Estimates between breeding values for sires

New methods to estimate the genetic correlation between purebred and crossbred performances directly are described by Wei and Van der Werf 1991 and Kinghorn and Swan 1991. Both papers discuss the possibility of using a multiple trait animal model to estimate breeding values for purebred and crossbred performances as different traits. A similar model could be used to estimate the genetic correlation between a trait in purebreds and in crossbreds directly. To use such an animal model a full pedigree from all purebreds and all crossbreds back to the common parents or grandparents is required. Most of the available crossbred data from field records can not fulfil this requirement. Electronic identification systems could help to solve this problem.

Table 2: Estimates of genetic correlations between purebred and crossbred performances for reproduction traits in pigs

Reference	Number of sires / Number of daughters per sire <sup>1</sup>	Trait	Correlation
Wilson et al. 1962	45	Piglets born alive Piglets weaned	negative negative
Robinson et al. 1964	5 / 6 RZ a. 28 KR	Piglets born alive Piglets weaned	-.74 -1.0
Taylor et al. 1965	35 / 3 RZ a. 2 KR	Piglets born alive 21 Day litter weight 56 Day litter weight	negative .185 .612
Biswas et al. 1971	24 to 29	Piglets born Litter weight at birth	0 - negative 0 - negative
Wong et al. 1971	181	Piglets born alive	.74
McLaren et al. 1985	22	Litter weight at birth	.25 a. .27

<sup>1</sup> RZ = Purebred sows, KR = Crossbred sows

### MATERIALS AND METHODS

The data used in this study were from purebred and crossbred pigs from the Australian Breeder Alan Fyfe. The data included a total of 41239 pigs with backfat measurements and liveweight daily gain, that were measured from 1980 to the end of 1990. The number of tested sows and boars of the different breeds are summarized in table 3. For all animals (purebreds and crossbreds) the full pedigree over several generations was available with a unique identification over all breeds. So the final crosses and the F1-gilts could be traced back to their common parents and grandparents in the nucleus lines. Since 1984 animals from all breeds and both sexes have been tested simultaneously.

Table 3: Number of animals per breed and sex of the Australian data set

	Breed				
	LR	LW	DU	F1	FC
Total number of pigs	15215	13043	3488	5019	4474
Boars	7516	6312	1711	2537	2293
Sows	7699	6731	1777	2482	2181
Pigs tested per litter	6.5	6.3	6.1	7.0	8.0

LR = Landrace, LW = Large White, DU = Duroc  
F1 = 2157 LR★LW and 2862 LW★LR, FC = DU★F1

All animals have been tested at a constant age so there was very little variation for age at test and therefore this trait was not included in the analysis. All breeds showed similar phenotypic standard deviations in all traits of 65 to 68 g in daily gain, 8.0 to 8.3 kg in weight at test and 2.3 to 2.8 mm in backfat thickness.

The following linear model was used in single or multiple trait analysis:

$$y = Xb + Zu + Ww + e$$

with  $y$  vector of observations,  
 $b$  vector of fixed effects,  
 $u$  vector of additive genetic effects of animals,  
 $w$  vector of common litter environment effects,  
 $e$  vector of residuals, and  
 $X, Z$  and  $W$  are known incidence matrices relating observations to fixed and random effects.

The following assumptions are made:

$$E[y] = Xb, E[u] = 0, E[w] = 0 \text{ and } E[e] = 0, \text{ as well as}$$

$$\text{Var} \begin{bmatrix} u \\ w \\ e \end{bmatrix} = \begin{bmatrix} A * G & 0 & 0 \\ 0 & C & 0 \\ 0 & 0 & R \end{bmatrix}$$

The model then results in the following equation system:

$$\begin{bmatrix} X' R^{-1} X & & X' R^{-1} W \\ Z' R^{-1} X & Z' R^{-1} Z + A^{-1} * G^{-1} & Z' R^{-1} W \\ W' R^{-1} X & W' R^{-1} Z & W' R^{-1} W + I * C^{-1} \end{bmatrix} \begin{matrix} x \\ \begin{bmatrix} b \\ u \\ w \end{bmatrix} \end{matrix} = \begin{bmatrix} X' R^{-1} Y \\ Z' R^{-1} Y \\ W' R^{-1} Y \end{bmatrix}$$

with  $A$  = the relationship matrix,  
 $G$  = the matrix of additive genetic variances and covariances,  
 $C$  = the variance- and covariance matrix of the common litter environment and  
 $R$  = the matrix of residual variances and covariances.

As fixed effects for all traits the testing season (month within year) and the sex was included in the model. For backfat thickness the weight at test was included as a linear regression. In the first step the model was used as a single trait animal model within breeds to estimate the variance components for all traits using DFREML from K. Meyer. In a second step the same model was used as a multiple trait model with daily gain or backfat thickness within different breeds as different traits. It has to be known that there is no animal with both traits measured and therefore no covariances for litter and residual effects could be estimated. This model does also not allow to estimate standard errors for genetic correlations between the trait measured in purebreds and in crossbreds. As a comparison to the genetic correlation from the above shown model the correlation between breeding values of dams and sires based on purebred and on crossbred information are calculated. The breeding values were estimated for each trait separately using an animal model.

## RESULTS AND DISCUSSION

For daily gain for all purebred and crossbred lines similar variance components for residual and common litter effects were estimated. Concerning the variance of additive genetic effects the two crossbred lines show higher estimates. This results in heritability estimates of .21 for LR, .22 for LW, .20 for DU, .31 for F1 and .29 for the final crosses. One explanation for the higher heritability could be the expected higher degree of heterozygots in crossbreds which could increase the additive genetic variance. The higher additive genetic variance could also be the result of ignoring nonadditive genetic effects in the model although the individual heterosis estimated for daily gain was only 4.2 percent and 2.3 percent for backfat thickness. For backfat higher heritabilities were found in the pure Landrace (.51) and Large White (.46). The other breeds show lower estimates with .36 for Duroc, .26 for the F1 and .39 for the final crosses. There is more variation in the estimates of variance components for backfat between all breeds than for daily gain. Between daily gain and backfat there is no significant genetic or phenotypic correlation found. There is a tendency of a slightly negative genetic correlation between both traits while the estimates for the phenotypic correlations for all breeds are positive.

The estimates for heritabilities for both traits and also the genetic and phenotypic correlations are in a good agreement with a german data set including purebred and crossbred data of a 4-way crossbreeding scheme. Not only heritabilities but also the different variance components are very similar comparing the Australian with German estimates.

The genetic correlations between the trait measured in purebred and crossbred animals are summarized in table 4. The correlations between breeding values for parents based on the information from different levels are not adjusted for the accuracy of the breeding values, so these estimates are underestimating the true genetic correlations.

Table 4: Genetic correlations between purebred and crossbred performances for daily gain and backfat thickness for different breed combinations

Breed combination	genetic correlation		correlation between breeding values	
	daily gain	backfat	daily gain	backfat
LR - F1	.874	.999	.544	.684
LR - FC	.649	.814	.402	.528
LW - F1	.946	.991	.579	.555
LW - FC	.468	.542	.245	.258
DU - FC	.972	.980	.510	.700
F1 - FC	.736	.716	.389	.310

LR = Landrace, LW = Large White, DU = Duroc, F1 = LR\**LW* and *LW*\*LR, FC = DU\**F1*

The results of table 4 show a clear tendency for higher genetic correlations between purebred and crossbred animals for backfat than for daily gain, which is expected because of the higher heritability for backfat. The correlations between the pure lines and their crossbred progeny is for both traits very high and close to 1.

This holds for Landrace or Large White to F1 but also for Duroc to the final crosses. The correlations between the traits measured in the pure Landrace or Large White and the final crosses is only around .6 for daily gain and .7 for backfat. These results leads to the conclusion that there is a linear relationship between the genetic correlation and the amount of common genes in both breeds considered. The correlations between the traits in F1 and the final crosses show that there are also some nonadditive genetic effects involved. The F1-population and the final crosses have also 50 percent genes in common but the correlation is lower than those between Landrace or Large White and F1 or Duroc and final crosses. The correlations between breeding values based on measurements of the different levels are in a good agreement to the genetic correlations, although all values are somewhat smaller. When average accuracies for breeding values are taken into account these estimates are expected.

In a crossbreeding programme in pigs with the breeding goal defined at the production level with the above shown parameters the effectiveness of direct selection for crossbred performance or indirect selection using purebred performances can be calculated. In 3-way and 4-way crossbreeding systems there will be a higher genetic gain in the production level when selecting on purebred performances for both traits. The main reason is a much longer generation interval for direct selection on crossbred performance. This approach will only use additive genetic effects to increase the production level. A multiple trait approach with purebred and crossbred performances as different traits will give the maximum possible gain in the production level. The combination of purebred and crossbred traits will use additive and nonadditive genetic effects to increase the performance in the final product. The optimum weighting of purebred and crossbred information is dependant on the genetic correlation between both traits. Only the multiple trait approach allows to use different economic weights for purebred and crossbred performances in the case of including both in the breeding goal. This approach can also account for different heritabilities within the breeds.

Within a 2-way crossbreeding system the estimation of breeding values includes 3 traits, a 3-way crossbreeding system includes 5 traits and a 4-way crossbreeding system includes 7 traits. From the above shown parameters the trait in Landrace and in Large White could be seen as one trait, so there would be a reduction from 5 to 4 traits in the evaluation programme. To get an adequate accuracy of breeding values for crossbred and purebred performances for animals in the nucleus lines as early as possible the sires and dams should be used to produce purebred and crossbred progeny simultaneously if possible. The breeding value for a young boar or sow is then based on own performance and possible purebred half- or fullsibs and on crossbred halfsibs. Within breeding programmes run on one farm only there are no organisation problems for such a system. If the different breeds are kept on different farms (the normal situation in german breeding programmes) only the use of artificial insemination would allow the production of purebred and crossbred progeny of sires simultaneously.

#### CONCLUSIONS

For daily gain and backfat thickness there is no "genotype x level" interaction for pigs. The genetic correlations between purebred and crossbred performances are very high. For backfat the correlation is close to 1 and for daily gain between .9 and .95.

Using these correlations the direct selection for crossbred performance will give lower genetic gain in the final products than indirect selection based on purebred performances only.

The combination of purebred and crossbred performances as different traits gives maximum genetic progress and allows different economic weighting and different genetic parameters for the breeds involved.

The production of purebred and crossbred progeny simultaneously will give adequate accuracies for purebred and crossbred breeding values even for young boars and sows without increasing the generation interval.

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