

**ESTIMATION OF GENETIC PARAMETERS FOR
FARROWING TRAITS IN PUREBRED AND
CROSSBRED SOWS AND ESTIMATION OF
THEIR GENETIC RELATIONSHIPS**

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Summary

Data sets from Australia with 11577 purebred and 12127 crossbred sows and from Germany with 54816 purebred and 7807 crossbred sows were analyzed. Heritabilities and genetic correlations were estimated for number of piglets born alive (NBA) under a linear mixed model treating purebred and crossbred performance as different traits to use both purebred and crossbred information. (M. Wei and J. H. J. van der Werf 1992). Estimated heritabilities for NBA (litter 1-3) were .075, .099 and .084 for purebred sows and .084, .069 and .072 for crossbred sows in the Australian data set. In the German data set heritabilities for NBA (litter 1-3) were .07, .075 and .102 for purebred sows and .082, .045 and .103 for crossbred sows.

The genetic correlation between purebred and crossbred performance in the trait number of piglets born alive (litter 1-3) were .98, .689 and .834 in the Australian population and .80, .99 and .81 in the German population.

Keywords: genetic correlation, pigs, reproduction.

Introduction

In crossbreeding programs in swine it is important to know the genetic relationship between purebred and crossbred sows to decide whether selection on purebred or crossbred performance can obtain higher progress. In most crossbreeding programs the selection for purebred performance in the nucleus is the method of choice because the selection for crossbred performance is very expensive and takes a lot of time.

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The calculated parameters in literature vary between -.74 and .74 (Robinson et al. 1964, Taylor et al. 1965, Wilson et al. 1962, Wong et al. 1971), where the analysis with the largest number of animals found the highest value of .74 (Wong et al. 1971). Parameters from newer investigations with higher number of animals are not known, although the use of sow-management-programs became standard in weaner production and so a bigger data set could have been available.

Material and methods

The development of the animal model with the use of a relationship matrix made it possible to build a model for the estimation of the genetic correlation between purebred and crossbred performance. The purebred and crossbred performances are treated as different traits and the analysis is made under a multiple trait animal model as suggested by M. Wei and J. H. J. van der Werf (1992):

$$\begin{bmatrix} y_1 \\ y_2 \\ y_3 \end{bmatrix} = \begin{bmatrix} X_1 & 0 & 0 \\ 0 & X_2 & 0 \\ 0 & 0 & X_3 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \\ b_3 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 & 0 & 0 & 0 \\ 0 & 0 & Z_2 & 0 & 0 \\ 0 & 0 & 0 & 0 & Z_3 \end{bmatrix} \begin{bmatrix} g_{11} \\ g_{13} \\ g_{22} \\ g_{23} \\ g_{33} \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \\ e_3 \end{bmatrix}$$

Y_i = vector of observations for pure line animals ($i=1,2$) and crossbred animals ($i=3$)

X_i = incidence matrix relating the observations to the fixed effects,

b_i = vector of fixed effects for population i ,

Z_i = design matrix that links observations to breeding values,

g_i = vector of random animal effects (breeding values),

e = error term in population.

The crossbred-breeding values for purebred animals (g_{13} and g_{23}) are estimated from the crossbred information under consideration of the relationship between purebred and crossbred performance and their relationship to the breeding values of the crossbred animals.

For the analysis two data sets were available. The first data set was an Australian data set 8341 Large-White sows, 3236 Landrace sows and 12127 Large-White x Landrace crossbred sows. There were both reciprocal crosses available.

The second data set was taken from the German breeding company Bundeshybridzuchtprogramm (BHZP). Records were available from the multiplier herds of the breeding program for 11577 purebred sows and from sow-management-programs in weaner production herds for 12127 crossbred sows. The sows from the multiplier herds could be identified as dams of the crossbred sows, so the relationship between purebred and crossbred sows could be established. Because of the missing reciprocal cross only one purebred dam line and the F1-daughters could be analyzed.

Analyses were made with the program packages VCE3.2/PEST (Groeneveld 1990/1996) and DFREML, (Meyer 1993)

Results and discussion

The results of the estimated heritabilities and genetic correlations between purebred and crossbred performance are shown in table 1 (Australian data set) and in table 2 (German data set).

Table 1. - HERITABILITIES AND GENETIC CORRELATIONS BETWEEN PUREBRED AND CROSSBRED LITTERS IN THE AUSTRALIAN DATA SET

	Purebred $h^2_{(pb)}$	Crossbred $h^2_{(cb)}$	$r_{g(pb-cb)}$
1. litter	.075	.84	.998
2. litter	.099	.069	.689
3. litter	.084	.072	.834

Table 2. - HERITABILITIES AND GENETIC CORRELATIONS BETWEEN PUREBRED AND CROSSBRED LITTERS IN THE GERMAN DATA SET

	Purebred $h^2_{(pb)}$	Crossbred $h^2_{(cb)}$	$r_{g(pb-cb)}$
1. litter	.070	.82	.800
2. litter	.075	.045	.999
3. litter	.102	.103	.810

Heritabilities in both data sets are in the expected range of .05 - .1. The standard errors in table 1 and 2 for the heritabilities of the purebred sows are in the range between .0044 and .0066, for the heritabilities of the crossbred sows in the range between .01 and .012 and for the genetic correlations in the range

between .003 and .12. The heritabilities in the Australian data set are very similar to those in the German data set. In the Australian data set the second litter of the purebred sows has the highest heritability of the three litters, whereas in the German data set the heritability is continuously rising with the number of litters. Both have been noticed in former analyses (Roehe and Kennedy 1995). In crossbred parameters the second litter shows the smallest heritability in both data sets, where in the German data set it nearly amounts to the half of the other two litters. The genetic correlations between purebred and crossbred performance are similar in both data sets and very high. They are, except the value for the second litter in the Australian data set, not significantly different from 1.

Table 3. - GENETIC CORRELATIONS BETWEEN LITTERS IN THE AUSTRALIAN DATA SET

Combination	Purebred		Crossbred
	Large White	Landrace	
litter 1 - litter 2	.61	.77	.88
litter 1 - litter 3	.51	.88	.62
litter 2 - litter 3	.99	.88	.81

Table 4. - GENETIC CORRELATIONS BETWEEN LITTERS IN THE GERMAN DATA SET

Combination	Purebred	Crossbred
litter 1 - litter 2	.80	.66
litter 1 - litter 3	.70	.58
litter 2 - litter 3	.96	1.0

The genetic correlations between the three litters in both data sets are shown in table 3 and 4. In both data sets one can observe, that the genetic correlation between the first and the two other litters are lower than between the second and the third litter, which confirms results from Röhre and Kennedy 1995.

Only the crossbred parameters in the Australian data set do not show this effect. All correlations are above .58 but the results show that for breeding purposes the first and the other litters should be treated as different traits. Second and third litters could be seen as repeated measurements.

Although the analyses show heritabilities and genetic correlations between the litters which are similar to other studies, the genetic correlations between purebred and crossbred litter traits are surprisingly high. In the literature only one analysis with the highest number of sires (Wong 1971) points in the same

direction. Further investigations using modern mixed model estimation procedures are not available yet.

Another remarkable fact is, that nearly similar estimates were found in very different data structures. The Australian data were collected in one farm, the German crossbred data came from 81 different farms and the purebred data from nearly 200 farms.

As conclusion from these estimated correlations between purebred and crossbred performance one has to investigate the use of selection on purebred or crossbred performance in modern crossbreeding programs.

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PROCJENA GENETSKIH PARAMETARA ZA OSOBINE PRASENJA ČISTOKRVNIH I KRIŽANIH KRMAČA TE PROCJENA NJIHOVIH GENETSKIH ODNOSA

Sažetak

Analizirane su skupine podataka iz Australije od 11577 čistokrvnih i 12127 križanih krmača i iz Njemačke 54816 čistokrvnih i 7807 križanih krmača. Nasljednost i genetske korelacije procijenjene su za broj živorođenih praščića pod linearnim miješanim modelom koji obrađuje performancu čistokrvnih i križanaca kao različite osobine za promjenu podataka za čistokrvne i križane životinje (M. Wei i J. H. J. van der Werf 1992.). Procijenjene nasljednosti za NBA (leglo 1-3) iznosile su .075, .099 i .084 za čistokrvne krmače i .084, .069, i 0.72 za križane krmače u australskoj skupini podataka. U njemačkim podacima nasljednost za NBA (leglo 1-3) bile su .07, .075 i .102 za čistokrvne krmače i .082, .045 i .103 za križane krmače. Genetska korelacija između performance čistokrvnih i križanaca u osobini broj živorođenih praščića (leglo 1-3) bile su .098, .689 i .834 u australskoj populaciji i .80, .99 i .81 u njemačkoj populaciji.

Ključne riječi: genetska korelacija, svinje, reprodukcija

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