

# EFFECTS OF CROSSBREEDING ON PRODUCTION TRAITS IN GERMAN BLACK PIED DAIRY CATTLE

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## SUMMARY

Data of *German Black Pied Dairy Cattle (SMR)* were used to estimate individual crossbreeding effects. The number of purebred (3) and crossbred (68) genetic groups made it possible to estimate epistatic effects, using models according to Dickerson (1973), Großhans (1993) and Wolf *et al.* (1995). The estimates of additive effects are almost similar for all models. *Holstein-Friesians* showed positive additive effects for milk yield (MY) (+995 to +1,060 kg) and calving interval (CI) (+9.2 to +10.7 days), but negative effects for fat content (FC) (-0.14 to -0.11%); for *Jerseys* the additive effects were negative for MY (-842 to -644 kg) and CI (-15.6 to -6.3 days), but positive for FC (+1.28 to +1.45%). While dominant effects increase the MY (+152 to +272 kg) in all two-breed-combinations, epistatic effects flow in both directions (-358 to +872 kg). The FC is influenced by dominant as well as epistatic effects. For the CI dominant effects did not reach the significance level, whereas epistatic effects of the *Black Pied Cattle x Jersey* combination reduce the calving interval (-18.8 to -4.5 days).

**Keywords:** dairy cattle, milk production, calving interval, heterosis, epistasis

## INTRODUCTION

In the 60's breeding of the *German Black Pied Dairy Cattle (SMR)* has been initiated in East Germany by crossing *Holstein-Friesians* and *Jerseys* with the local *Black Pied Cattle*. The objective of this analysis is to estimate crossbreeding effects for two production traits and the calving interval. Several models with different explanations of epistatic effects will be compared.

## MATERIALS AND METHODS

For the analysis period 1970 to 1984 a dataset was available including milk yield, milk fat content and calving interval (Table 1).

**Table 1. Numbers of records, means and standard deviations**

	1st lactation		
	number of records	mean	s
milk yield (kg)	1,111,013	3,575	632
fat content (%)	1,111,013	4.13	0,32
calving interval (days)	824,412	378.3	58.3

Defined genetic groups have been created using the informations of parents and grandparents. Beside the purebred breeds *Black Pied Cattle (S)*, *Holstein-Friesian (H)* and *Jersey (J)* the material contains 76 crossbred groups. A two-step method was used. In the first step the MME-

means of the genetic groups were obtained. These means were used to estimate crossbreeding effects at the second step. Because of the structure of dataset two different sire models including the paternal relationship matrix for cows and sires were established:

$$\text{milk yield, fat content: } y_{ijklm} = \mu + \text{HYS}_i + \text{AL}_j + s_k + \text{KG}_1 + e_{ijklm}$$

$$\text{calving interval: } y_{ijklm} = \mu + \text{J} * \text{S}_i + \text{AE}_j + s_k + \text{KG}_1 + e_{ijklm}$$

where  $y_{ijklm}$  = milk yield, fat content, calving interval;  $\mu$  = model constant;  $\text{HYS}_i$  = fixed effect of Herd-Year-Season;  $\text{J} * \text{S}_i$  = fixed effect of Year-Season;  $\text{AL}_j$  = fixed effect of age at breeding/ calving;  $\text{AE}_j$  = fixed effect of subunit of herd;  $s_k$  = random effect of sire;  $\text{KG}_1$  = fixed effect of genetic group;  $e_{ijklm}$  = random residual effect.

The MME-means were obtained by applying the iterative procedure by Wiggans *et al.* (1988). Using the GLM-procedure (SAS®) a WLS-model was employed to estimate crossbreeding effects from MME-means ( $\hat{y}_{\text{MME}}$ ):  $\hat{b} = (\text{X}'\text{V}^{-1}\text{X})^{-1}\text{X}'\text{V}^{-1}\hat{y}_{\text{MME}}$ ;  $\text{var}(\hat{b}) = (\text{X}'\text{V}^{-1}\text{X})^{-1}\sigma_e^2$ ;

where  $\text{X}$  = design matrix of crossbreeding coefficients;  $\text{V}$  = diagonal matrix of reciprocal square errors of MME-means. A SAS®-programm has been developed to calculate the crossbreeding coefficients according to the theoretical genetic structure of the parents. *Black Pied Cattle (S)* has been set as the base-population, what means that all additive effects equal to zero. All of the used models are based on the general two-locus-model by Cockerham (1980), a factorial model of gene effects:  $\bar{G} = \mu + \text{A} + \text{D} + \text{AA} + \text{AD} + \text{DD}$

where  $\mu$  describes a general mean,  $\text{A}$  the additive effects,  $\text{D}$  the dominant effects,  $\text{AA}$  the additive x additive interactions,  $\text{AD}$  the additive x dominant interactions and  $\text{DD}$  the dominant x dominant interactions. For a quantitative genetic model an arbitrary number of source populations ( $p$ ) have to be summed up over all loci and averaged over all individuals of the populations included:

$$\begin{aligned} \bar{G} = & \mu + \sum_{i=1}^p \alpha_i \text{A}_i + \sum_{i=1}^p \sum_{j=i}^p \delta_{ij} \text{D}_{ij} + \sum_{i=1}^p \alpha_i^2 \text{AA}_{ii} + 2 \sum_{i=1}^{p-1} \sum_{j=i+1}^p \alpha_i \alpha_j \text{AA}_{ij} \\ & + \sum_{i=1}^p \sum_{j=1}^p \sum_{k=j}^p \alpha_i \delta_{jk} \text{AD}_{i(jk)} + \sum_{i=1}^p \sum_{j=i}^p \delta_{ij}^2 \text{DD}_{(ij)(ij)} + 2 \sum_{i=1}^p \sum_{j=i}^p \sum_{k=1}^p \sum_{l=k}^p \delta_{ij} \delta_{kl} \text{DD}_{(ij)(kl)} \\ & \quad \quad \quad (i \neq k \text{ oder } j \neq l) \end{aligned}$$

While  $\alpha_i$  describes the proportion of genes from the  $i^{\text{th}}$  source population,  $\delta_{ij}$  ( $\delta_{ji}$ ) specifies the probability that one allele is from the  $i^{\text{th}}$  source and one from the  $j^{\text{th}}$  ( $i^{\text{th}}$ ) source population on a randomly chosen locus of a randomly chosen individual. These coefficients are related as follows:

$$\alpha_i = \delta_{ii} + \frac{1}{2} \sum_j \delta_{ij}; \quad j \neq i \quad \text{for} \quad \sum_i \alpha_i = 1 \quad \text{and} \quad \sum_{i \leq j} \delta_{ij} = 1.$$

The different models can be defined in terms of this general two-locus model by introducing reparametrizations. For the models used in this study the equations in terms of the general two-locus-model are represented in the following:

**Model 1: Dickerson (1973):**

$$\bar{G} = m_S + \alpha_{HF}a_{HF} + \alpha_Ja_J + \delta_{SH}d_{SH} + \delta_{SJ}d_{SJ} + \delta_{HJ}d_{HJ} + (4\alpha_S\alpha_H - \delta_{SH})r_{SH} + (4\alpha_S\alpha_J - \delta_{SJ})r_{SJ} + (4\alpha_H\alpha_J - \delta_{HJ})r_{HJ}$$

**Model 2: Model A (Großhans, 1993):**

$$\bar{G} = m_S + \alpha_{HF}a_{HF} + \alpha_Ja_J + \delta_{SH}d_{SH} + \delta_{SJ}d_{SJ} + \delta_{HJ}d_{HJ} + 2\alpha_S\alpha_Haa_{SH} + 2\alpha_S\alpha_Jaa_{SJ} + 2\alpha_H\alpha_Jaa_{HJ}$$

**Model 3: Model I (Wolf *et al.*, 1995):**

$$\bar{G} = m_S + \alpha_Ha_H + \alpha_Ja_J + \delta_{SH}d_{SH} + \delta_{SJ}d_{SJ} + \delta_{HJ}d_{HJ} + 2\alpha_S\alpha_Haa_{SH} + 2\alpha_S\alpha_Jaa_{SJ} + 2\alpha_H\alpha_Jaa_{HJ} + (\alpha_S - \alpha_H)\delta_{SH}ad_{SH} + (\alpha_S - \alpha_J)\delta_{SJ}ad_{SJ} + (\alpha_H - \alpha_J)\delta_{HJ}ad_{HJ} + \delta_{SH}^2dd_{SH} + \delta_{SJ}^2dd_{SJ} + \delta_{HJ}^2dd_{HJ}$$

As a measure of the goodness of fit the coefficients of determination and  $\sigma_e^2$  have been compared among the models used.

**RESULTS AND DISCUSSION**

In Table 2 the estimated individual crossbreeding effects are given. The estimates of breed differences of the production traits clearly reflect the respective main breeding goal of the two breeds in the past: *H* for milk yield (+995 to +1,060 kg), *J* for fat content (+1.28 to +1.45 %). Breed differences have to be interpreted as deviations from the reference breed (*S*). For calving interval positive breed differences have been estimated for *H* (+9.17 to +10.73 days) and negative for *J* (-15.55 to -6.32 days). Using the Dickerson-model significant heterosis effects were obtained in the crosses between *S* x *J* for milk yield and *S* x *H* for fat content. Comparing all models used, significant dominant (heterosis) effects in the range from +152 to +272 kg for milk yield and +0.05 to +0.29 % for fat content meet the expectations of positive estimates. These effects are within the range of the literature. Looking at the definition of the Dickerson-model in terms of the general two-locus-model, heterosis contains the epistatic additive x additive effects. In order to separately estimate dominant and epistatic effects Model A was introduced without increasing the degrees of freedom as compared to the Dickerson-model. The results show the significant implications of additive x additive interactions on heterosis. The dominant effects considerably changed in some instances sign and magnitude. As contrasted to heterosis significant effects are now obtained for dominant effects involving *H* for milk yield (+152, +272 kg) and *J* for milk fat (+0.2, +0.29 %). The recombination loss according to Dickerson is defined as the break down of favourable epistatic interactions between genes on different loci. Through selection mainly on milk yield or fat content desired epistatic interactions should have been enriched in *H* and *J*, respectively. Significant negative recombination effects and additive x additive interactions for milk yield (-358 to -174 kg) and for fat content (-0.72 to -0.22 %) may be explained in this way. However, for calving interval a significant recombination and additive x additive effect has been estimated for the crosses between *S* x *J*. The opposite directions of additive x additive interactions for milk yield and

calving interval in *S* x *J* crosses may be a cause of the genetic antagonism between fertility and milk yield.

**Table 2. Crossbreeding effects for milk yield, fat content and calving interval**

Effect	Dickerson			Model A			Model I		
	MY <sup>A</sup>	FC	CI	MY	FC	CI	MY	FC	CI
a <sub>H</sub> <sup>#</sup>	995***	-0.11***	9.17***	995***	-0.11***	9.17***	1060***	-0.14***	10.73***
a <sub>J</sub> <sup>#</sup>	-644***	1.28***	-6.32 <sup>+</sup>	-645***	1.28***	-6.32 <sup>+</sup>	-842**	1.45***	-15.55***
d <sub>SH</sub> <sup>#</sup>	-22	0.05***	-0.31	152**	-0.01	-2.08	-76	0.02	4.05
d <sub>SJ</sub> <sup>#</sup>	201***	0.03 <sup>+</sup>	-2.35	57	0.29***	2.13	-121	0.02	1.20
d <sub>HJ</sub> <sup>#</sup>	93 <sup>+</sup>	-0.02	-2.60	272***	0.20***	0.44	112	0.19 <sup>+</sup>	-10.82
aa <sub>SH</sub> <sup>#</sup>	-174**	0.06 <sup>+</sup>	1.77	-348**	0.12 <sup>+</sup>	3.53	-352***	0.19**	-1.24
aa <sub>SJ</sub> <sup>#</sup>	144***	-0.25***	-4.48**	288***	-0.51***	-8.96**	872***	-0.72***	12.03
aa <sub>HJ</sub> <sup>#</sup>	-179**	-0.22***	-3.04	-358**	-0.44***	-6.08	-203	-0.29**	-3.79
ad <sub>SH</sub>							330***	-0.11*	-2.16
ad <sub>SJ</sub>							-377***	0.44***	-18.75***
ad <sub>HJ</sub>							-442**	-0.43***	-1.51
dd <sub>SH</sub>							195**	-0.03	-5.09
dd <sub>SJ</sub>							-13	0.28***	-4.94
dd <sub>HJ</sub>							137	-0.04	12.48
R <sup>2</sup>	99%	99%	85%	99%	99%	85%	99%	100%	89%

\*\*\*p<0.001, \*\*p<0.01, \*p<0.05, <sup>+</sup>p<0.1; <sup>A</sup> MY = milk yield, FC = fat content, CI = calving interval

<sup>#</sup> Read 'g' instead of 'a', 'h' instead of 'd', 'r' instead of 'aa' for the Dickerson-model

Beside additive x additive interactions Model I contains epistatic effects describing additive x dominant and dominant x dominant interactions. Especially for milk yield and fat content significant additive x dominant effects have been estimated for all two-breed-crosses. A significant A x D effect for calving interval between *S* and *J* exceeds in absolute size the estimated additive effects. As significant estimations for dominant x dominant interactions indicate, these effects also seem to have some influence on production traits. The general two-locus-model allows to derive most of the models reported in literature to estimate crossbreeding effects. Defining epistatic effects in terms of the general two-locus-model shows that additive and dominant effects can be influenced by interactions of higher order. Nevertheless, even if a full model including all effects isn't estimable, the general two-locus-model enables to find the most important estimable epistatic effects.

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