



Short communication: Is crossbreeding only beneficial in herds with low management level?

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ABSTRACT

The economic benefit of crossbreeding has been well known for many years within dairy production. However, in most countries with an intensive dairy production, an extended use of systematic crossbreeding has not occurred. This may be due to the myth that heterosis is expressed mainly in low-producing herds. The aim of the study was to investigate the effect of heterosis with different management levels in Danish Jersey herds. More than 300,000 records of 305-d milk, fat, and protein yield from first-lactation Danish Jersey cows with different contributions from original Danish and US Jersey were analyzed using an animal model. The herds were distributed in 5 management groups based on production level. First, the results showed a large increase in additive genetic variance from the herds with lowest production level to the high-producing ones, and second, heterosis for all 3 production traits were lowest within the low-intensity management group and tended to be highest in the intermediate management groups. The results, therefore, support that crossbreeding is a breeding system that should be considered valuable for all management levels.

Key words: heterosis, crossbreeding, management, milk production

Short Communication

The benefits of using crossbreeding in dairy cattle production is well documented (Sørensen et al., 2008) and due to heterosis, crossbred animals are more robust and economically efficient compared with the parental breeds (Pedersen and Christensen, 1989; Mäki-Tanila, 2007). Interest has increased in crossbreeding in several countries during the last decade, and systematic crossbreeding programs are now running in, among other countries, Denmark and the United States and, in particular, in New Zealand, where 36% of the dairy cows

are crossbreds (LIC and DairyNZ, 2011). However, many dairy producers are still of the opinion that crossbreeding is only beneficial when management conditions are suboptimal. A few scientific studies show that the animal environment has an effect on the expressed heterosis (Barlow, 1981; Bryant et al., 2007; Penasa et al., 2010). Barlow (1981) and Penasa et al. (2010) found that heterosis generally is larger in a stressful environment than in a supportive environment, which substantiates the myth existing among some dairy producers. Contrarily, Bryant et al. (2007) showed that heterosis was largest in the intermediate environments, when construction of environmental groups was based on herd production level. The population of Jersey cows in Denmark is composed of original Danish and American Jersey (United States), and crosses between these 2 lines of Jersey and the degree of heterozygosity and breed proportion are recorded in the national dairy cattle database. Because we experience a large difference in production level between the herds, our data are very suitable for investigating the effect of environment (defined as herd production level) on heterosis in Jersey cows in Denmark. The aim of the present study was to investigate whether heterosis for milk production traits was more expressed in environments with low production level.

A total of 312,859 first-lactation Danish Jersey cows with different contribution of US genes from 1,746 herds born between 1990 and 2006 were included in the analysis. In the edited data set, the contribution of US Jersey genes increased from slightly below 10% for cows born in 1990 up to 40% for cows born in 2001 (Figure 1). From 2001 and onwards, the contribution of US Jersey genes has been slightly below 40%. Throughout the period, genes not belonging to original Danish or US Jersey lines were below 5%, and decreasing toward zero. Animals with more than 12.5% New Zealand Jersey genes were omitted from the study, and animals with less than 12.5% New Zealand Jersey genes were considered as Danish Jersey, because this contribution originates from an early importation in the 1960s, and many animals have a low contribution of New Zealand genes. Only cows with more than 45 DIM and a calving

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age between 18 and 40 mo were included. Development in degree of breed heterozygosity within the period for the analyzed data are illustrated in Figure 1. Breed heterozygosity was calculated as $sbp_{(breed1)} \times dbp_{(breed2)} + sbp_{(breed2)} \times dbp_{(breed1)}$, where sbp is the breed proportion of a given sire breed and dbp is the breed proportion of the dam. The traits analyzed were 305-d protein yield (**PY**), fat yield (**FY**), and milk yield (**MY**). All analyses in this study were carried out with the AI-REML algorithm (Madsen et al., 1994; Johnson and Thompson, 1995), using the DMU package (Madsen and Jensen, 2010). The convergence criterion used was a change in the norm of the update vector less than 10^{-5} .

To obtain solutions for the fixed herd-year effects, which were used to define the environmental groups considered in this study, a univariate animal model including the following effects was used:

$$Y_{ijkl} = H_i + C_j + M_k + \beta \times het_l + a_l + e_{ijkl}$$

where Y_{ijkl} = 305-d protein, fat, or milk yield; H_i = fixed effect of herd-year i ($i = 1, \dots, 14,159$); C_j = fixed effect of age at first calving in months j ($j = 18, \dots, 40$); M_k = fixed effect of calving month ($k = 1, \dots, 12$);

het_l = degree of breed heterozygosity; β = regression coefficient (heterosis); a_l = additive genetic effect of cow l ; and e_{ijkl} = random residual.

The pedigree was traced as far back as possible in the Danish Cattle Database (Bundgaard and Høj, 2000), and the pedigree file for the full data set included 485,265 animals.

The environmental groups were formed by ranking herds within year (to account for the increase in production level over time) based on herd-year solutions for PY. For each year cohort, 5 groups with approximately equal numbers of herds were constructed. The first group contained the 20% of herds with the lowest herd-year solutions, the second group contained the next 20% of the herd-year solutions, followed by groups 3 and 4, and ending with the fifth group containing the 20% best herds regarding herd-year solutions. Finally, group 1 animals within years were merged into 1 group (I). Group II to V were formed correspondingly. Descriptive statistics (number of animals in each environmental group and production level) are given in Table 1. Each of the 5 groups was then analyzed separately to obtain parameters for the different production environment. The same model as the one given above was used.

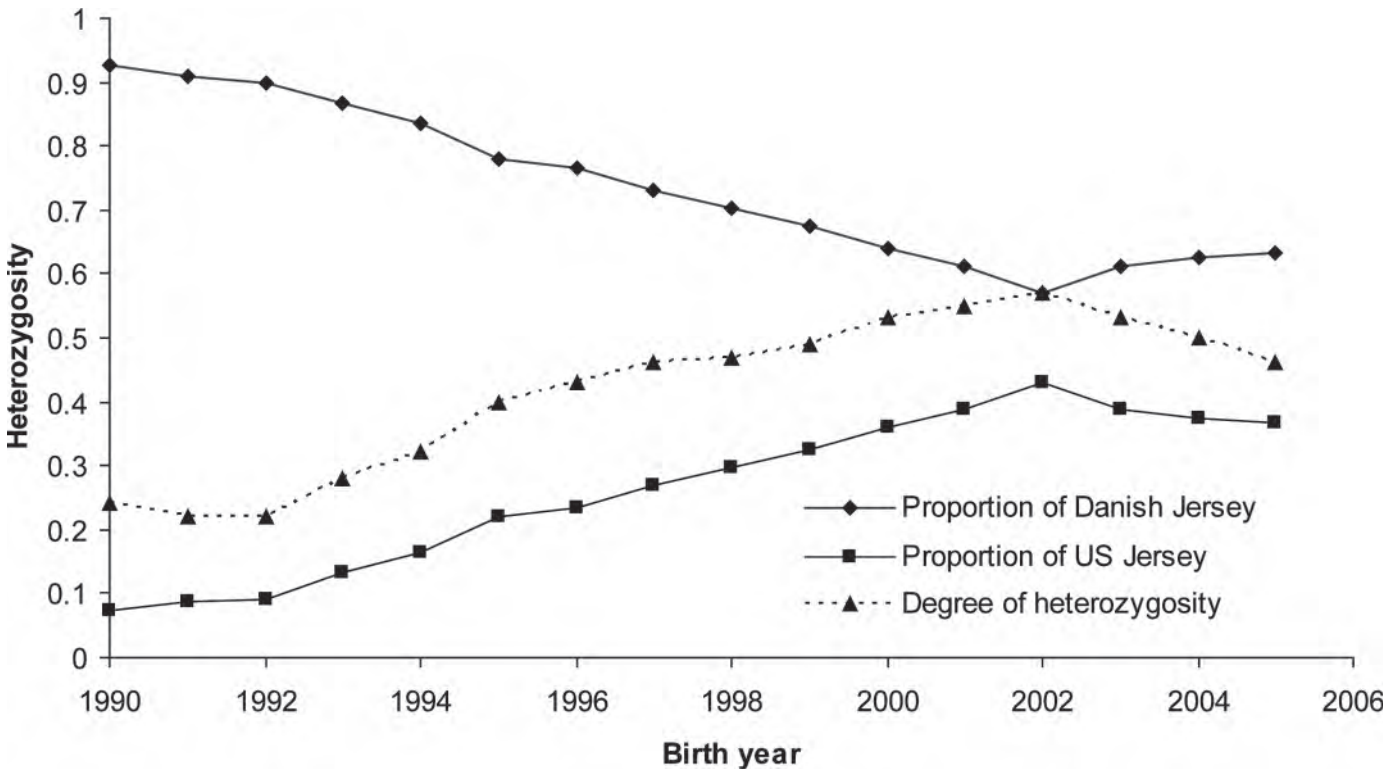


Figure 1. The contribution from original Danish Jerseys and US Jerseys, and the degree of breed heterozygosity for cows kept in the edited data set in different birth years.

Table 1. The number of cows and herds represented in the full data set (All) and in the 5 environmental groups (I–V), and average 305-d protein yield (PY), fat yield (FY), and milk yield (MY) within these groups¹

Group	No. of cows	No. of herds	PY, kg	FY, kg	MY, kg
All	312,859	1,746	195 (38)	291 (54)	4,853 (1,006)
I	54,956	843	164 (30)	247 (45)	4,124 (835)
II	61,122	1,002	183 (31)	275 (45)	4,577 (857)
III	63,886	1,034	194 (32)	291 (46)	4,844 (887)
IV	65,643	951	204 (33)	305 (48)	5,079 (909)
V	67,252	715	221 (36)	327 (51)	5,493 (976)

¹Standard deviations are given in parentheses.

Estimated parameters for genetic and residual variance, heritability, and heterosis (kg) for PY, FY, and MY are presented in Table 2. For all traits, the additive genetic variance is considerably smaller in the lowest-producing herds compared with the highest-producing herds. This may partly be due to the lower average production level in these herds (scaling effect), but could also be because the cows are unable to express their full genetic potential under suboptimal management conditions. The residual variation is similar for all groups. The heritabilities of the 3 traits, estimated for the total data set and the 5 groups are given in Table 2. For PY, the heritability ranged from 0.29 to 0.41, for FY from 0.26 to 0.38, and for MY from 0.36 up to 0.48. As a result of the small additive genetic variation expressed in the groups with the lowest production level, the heritabilities were low in these groups compared with those estimated for the total data set and for the high-producing groups. The results are in agreement with results from both Luxembourg and Tunisia (Hammami et al., 2009), where heritability for 305-d MY in Luxembourg was 0.41 in high-management herds and 0.31 in low-management herds. In Tunisia, the heritabilities were 0.21 and 0.12 in high- and low-management herds, respectively. However, both in Luxembourg and Tunisia, cows were only distributed in 3 management groups, which decreased the differences between the extreme groups. Furthermore, results from Germany support our findings, as heritability for PY given by

Gernand et al. (2007) increased by more than 50% when estimated in high-yielding herds compared with low-yielding herds.

Estimated heterosis in kilograms increased with increasing production level, ranging from 4.4 to 6.4 for PY, from 6.7 to 10.6 for FY, and from 114 to 168 for MY. Heterosis estimated on the total data set was similar to the heterosis level in average- and high-producing groups, which is probably due to different genetic variances within the different management level groups and the total data set. Metzger et al. (1994) estimated heterosis for production traits for crosses between Danish Jerseys and US Jerseys based on production records from both Denmark and the United States. In the current study, heterosis for PY given as a percentage of the mean was 3.3, estimated on the full data set, and varied from 2.7 to 3.4 in the environmental groups. Sørensen et al. (2008) found heterosis estimates for PY in the interval from 1.5 to 8.2%, and Metzger et al. (1994) estimated heterosis to be 2.3% for PY. Heterosis for FY was 3.5% estimated on the full data, which is higher than 1.6% found by Metzger et al. (1994). For FY, heterosis varied from 2.7 to 3.5% estimated in the environmental groups. Heterosis estimates for FY presented in the review by Sørensen et al. (2008) varied from 1.7 to 8.4%. Heterosis was 3.3% for MY estimated on the full data set, and varied from 2.7 to 3.4% estimated in the environmental groups. For MY, Metzger et al. (1994) found heterosis to be 1.8%, which is lower than

Table 2. Estimated parameters for additive genetic (a) and residual (e) variance, heritability (h^2) and heterosis (het; kg, with SE in parentheses and percentage after the semicolon) for 305-d protein yield (PY), fat yield (FY), and milk yield (MY) for the full data set (All) and in the 5 environmental groups (I–V)

Group	Protein yield				Fat yield				Milk yield			
	a	e	h^2	het	a	e	h^2	het	a	e	h^2	het
All	248	480	0.34	6.5 (0.4); 3.3	533	1,100	0.33	10.2 (0.7); 3.5	234,169	329,957	0.42	160 (12); 3.3
I	180	451	0.29	4.4 (1.1); 2.7	379	1,061	0.26	6.7 (1.6); 2.7	175,160	311,199	0.36	114 (29); 2.8
II	206	479	0.30	6.3 (1.0); 3.4	449	1,107	0.29	9.5 (1.5); 3.5	197,195	332,696	0.37	168 (27); 3.7
III	244	485	0.33	6.4 (0.9); 3.3	548	1,103	0.33	9.8 (1.5); 3.4	226,419	335,844	0.40	160 (27); 3.3
IV	258	491	0.34	6.3 (1.0); 3.1	538	1,124	0.32	10.6 (1.4); 3.5	251,422	330,371	0.43	156 (26); 3.1
V	331	479	0.41	6.4 (0.9); 2.9	672	1,094	0.38	10.3 (1.4); 3.1	298,147	329,071	0.48	147 (25); 2.7

the present estimates. The present estimates are in the lower end of the interval when comparing to those presented by Sørensen et al. (2008), which might be explained by the fact that Danish Jersey and US Jersey are lines of the same breed. However, the present estimates are all within the range for heterosis estimates for production traits in crosses between strains (e.g., Metzger et al., 1994; Bryant et al., 2007; Penasa et al., 2010).

For all traits, heterosis (%) was smallest in the low-producing groups (Table 2). This is in agreement with results from New Zealand (Bryant et al., 2007) where heterosis estimates for MY, FY, and PY were below 1% in the lowest management group (defined by production level) for crosses between overseas Holstein and New Zealand Holstein. In the remaining management groups, Bryant et al. (2007) found heterosis estimates at the level of 2.5 to 4%. Contrary to the present study and the study by Bryant et al. (2007), Penasa et al. (2010) found that heterosis was largest in the herds with lowest production level. However, the study by Penasa et al. (2010) was based on fewer animals, and crosses within a breed upgrading from 1 breed (Dutch Friesian) to another breed (Holstein-Friesian) were used. This may create bias, as the animals included in the study were the last animals still being purebred Dutch Friesian, and they could be a selected group. In the present analyses, heterosis was largest in environment group II, and then decreased slightly for the remaining groups. A reason for that could be that the additive genetic variance differs with production level. In addition, many herds changed environment group from one year to another, and this may have an effect. To avoid these concerns, the next step will be to analyze this data with a reaction norm model combining heterosis \times environment with an unknown environmental covariate (Su et al., 2009) and additionally, to include a $G \times E$ interaction with an unknown environmental covariate (Su et al., 2006).

Our study rejected the myth that heterosis for milk production traits decreases with increasing management level, and that crossbreeding is most beneficial for farmers with low production level. This is an important message, because the myth has been a barrier for starting systematic crossbreeding programs for many dairy producers. Based on results from our study, any dairy

producer should consider the economic advantages of crossbreeding.

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