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ABSTRACT: This study aimed to estimate trends of heterosis for milk yield traits and somatic cell score (SCS) in the Dutch dairy cattle. First lactation data on 305-d milk, fat, and protein yield, and on average 305-d SCS recorded on pure Holstein Friesian (HF), Dutch Friesian (DF), Mosa Reno Yssel (MRY), and F_1 crossbreds (DFxHF and MRYxHF) were considered. According to cows' year of calving, productive records from animals calving from 1980 to 2004 were divided in five periods, while SCS records from animals calving from 1990 to 2004 were divided in four periods. Data were processed using analysis of variance (ANOVA) according to a linear model which included effects of herd, season of calving, age at calving, and the genotype by period of calving interaction effect. Moreover, a linear covariate of sire's estimated breeding value (EBV) for 305-d milk yield was added to the model for yield traits. Heterosis values for productive traits were positive but decreased over time. For 305-d milk yield these values changed from 7.5 to 3.0% in the DFxHF crossbreds, and from 9.0 to 1.0% in the MRYxHF crossbreds. Average heterosis for SCS (-1.2%) was small and negative with a favourable trend over years.

Key words: Crossbreeding, Dairy cattle, Milk yield traits, Somatic cell score.

INTRODUCTION - Crossbreeding is a common practice in beef, sheep, poultry and swine breeding, and these species rely heavily on heterosis via crossbreeding of multiple breeds to improve productivity and efficiency of production (Hansen, 2006). Conversely, this mating system has not been widespread in dairy cattle in temperate climates (Swan and Kinghorn, 1992), mostly because of the superiority of Holsteins for milk production, the economic importance of this trait, and the strong historical influence of purebred breeders and breed associations (Weigel and Barlass, 2003). As a consequence, a purebred system improved by within breed selection is what the dairy industry has practiced for many years. Recently, the interest in crossbreeding aspects has been growing among dairy producers and scientists, and this practice may be used for removing inbreeding depression accumulated in the major dairy breeds, for the improvement of some economically important traits such as fertility, health, longevity and calving ease, and for giving rise to economic gains in those countries where milk pricing systems have put a great emphasis on the volume of milk solids (Weigel and Barlass, 2003). In New Zealand and The Netherlands crossbreeding is common, and all purebreds and crossbreds are used in a combined dataset in order to increase accuracy of genetic evaluations. Information on heterosis trends for productive and functional traits is very scarce in scientific literature. This study aimed to estimate crossbreeding effects over years on milk yield traits and somatic cell score (SCS) in the Dutch dairy cattle population.

MATERIAL AND METHODS - Data of 305-d milk, fat, protein yield, and average 305-d SCS recorded on herdbook registered primiparous cows were analysed. Somatic cell score was expressed as reported by NRS (2005). Purebreds involved were Holstein Friesian (HF), Dutch Friesian (DF), Mosa Reno Yssel (MRY); F_1 crossbreds studied were DFxHF and MRYxHF. Since SCS data collection started in 1990 in The Netherlands, the original dataset was split up in two subsets: one for milk yield traits, with records of cows calving from 1980 to 2004, one for SCS, with data of cows calving from 1990 to 2004. Animals with missing sire and dam information, lactation lengths shorter than 210 d or longer than 600 d, age at first calving shorter than 600 d or longer than 1200 d and without

yield and SCS records were discarded prior to statistical analysis. To estimate crossbreeding effects over time, the interval of 25 years considered for productive traits was divided in five periods, while the interval of 15 years considered for SCS was divided in four periods. Concerning yield traits, only herds that reared at least two different genotypes with at least four cows per genotype within each period were retained, while, for SCS, only herds that reared at least two different genotypes with at least four cows in the whole period, from 1990 to 2004, were considered. This choice largely reduced the number of animals, especially HF purebreds in the last 15 years, but it was necessary to guarantee an equal comparison of genotypes on the same environmental conditions. After editing procedure, subset for yield traits consisted of 289,361 closed lactations recorded on 10,026 herds, and subset for SCS included information from 204,541 cows reared in 4990 herds. Analysis of variance for all traits was conducted using PROC GLM of SAS (SAS Institute, 1999). The linear model included fixed effects of herd, season of calving, age at calving, and the genotype by period of calving interaction effect. Moreover, a linear covariate of sire's estimated breeding value (EBV) for 305-d milk yield, standardized within breed, was included in the model for yield traits. Sire's EBV was required to have at least 10 daughters in 5 herds.

Table 1. Least squares means (LSM) and standard errors (SE) of the genotype by period of calving interaction effect for 305-d milk, fat, protein yield, and somatic cell score (SCS).

Genotype	Period of calving	Milk (kg)		Fat (kg)		Protein (kg)		Period of calving	SCS	
		LSM	SE	LSM	SE	LSM	SE		LSM	SE
HF	80-84	5603	118	240	5.0	186	3.8	-	-	-
	85-89	6473	13	285	0.5	220	0.4	90-92	6.14	0.03
	90-94	6568	8	291	0.3	227	0.2	93-95	6.01	0.01
	95-99	6964	17	307	0.7	242	0.6	96-99	6.01	0.01
	00-04	7089	32	317	1.4	247	1.0	00-04	6.14	0.01
DF	80-84	4848	16	208	0.7	164	0.5	-	-	-
	85-89	5229	11	234	0.5	180	0.3	90-92	6.16	0.06
	90-94	5464	29	251	1.2	193	0.9	93-95	6.04	0.06
	95-99	5791	51	264	2.2	205	1.7	96-99	5.94	0.07
	00-04	5650	76	257	3.2	199	2.5	00-04	6.15	0.09
MRY	80-84	4565	26	192	1.1	158	0.8	-	-	-
	85-89	5183	6	225	0.2	183	0.2	90-92	6.22	0.01
	90-94	5308	7	236	0.3	190	0.2	93-95	5.98	0.01
	95-99	5598	21	244	0.9	201	0.7	96-99	5.95	0.02
	00-04	5743	43	252	1.8	207	1.4	00-04	6.15	0.04
DFxHF	80-84	5630	17	237	0.7	187	0.5	-	-	-
	85-89	6169	7	272	0.3	211	0.2	90-92	6.15	0.01
	90-94	6272	9	284	0.4	219	0.3	93-95	5.98	0.02
	95-99	6631	37	296	1.6	232	1.2	96-99	5.85	0.04
	00-04	6553	92	293	3.9	226	3.0	00-04	6.05	0.08
MRYxHF	80-84	5548	29	229	1.2	186	0.9	-	-	-
	85-89	6156	6	268	0.3	213	0.2	90-92	6.17	0.01
	90-94	6157	7	270	0.3	215	0.2	93-95	5.95	0.01
	95-99	6346	21	279	0.9	222	0.7	96-99	5.93	0.02
	00-04	6498	38	295	1.6	231	1.2	00-04	5.97	0.03

HF=Holstein Friesian; DF=Dutch Friesian; MRY=Mosa Reno Yssel.

Least squares means (LSM) of the interaction effect obtained for each trait were used to calculate heterosis (het), defined as the amount by which the performance (Y) of the F1 cross exceeds the mid parent performance: het = $Y_{F1} - [(Y_A+Y_B)/2]$, where A and B are the two parental breeds. Also, percentage values of heterosis (het%) were obtained as: het% = {het / [($Y_A+Y_B)/2$]} x 100.

RESULTS AND CONCLUSIONS – All the effects included in the model resulted highly significant (P<0.001), and herd and genotype explained the major quota of variability. Least squares means (LSM) and standard errors (SE) of the genotype by period of calving interaction effect for production and SCS are summarized in Table 1. The highest estimates for yield traits were found for pure HF and the two crossbreds, while the lowest were provided by MRY and DF purebreds. Concerning SCS, values ranged from 5.85 (SE=0.04) in DFxHF crossbreds to 6.22 (SE=0.01) in MRY purebreds. Heterosis trends for 305-d milk yield and SCS over years are presented in Figure 1. In both graphs, a decrease of heterosis can be evidenced, and appeared small and favourable for SCS. A possible explanation of this trend for yield traits could be that in The Netherlands the selective evolution of dairy cattle breeds has conducted to a less genetic difference between them. Also, trends for 305-d fat and protein evidenced a decreasing tendency similar to 305-d milk yield. Average heterosis of 4.7, 4.2, 4.3, and -1.2% were found for 305-milk, fat, protein yield, and SCS, respectively, in the DFxHF crossbreds, and of 3.9, 3.7, 3.5, and -1.2% in the MRYxHF combination (data not shown). These results are substantially in agreement with estimates obtained by McAllister *et al.* (1986) on milk yield traits, while a small and positive heterosis was found by VanRaden and Sanders (2003) on SCS. Further researches have to be conducted to investigate non-additive genetic effects for functional traits in the Dutch dairy cattle.

Figure 1.   Heterosis trends over years for 305-d milk yield (a) and somatic cell score (SCS) (b) in the DFxHF and MRYxHF crossbreds.
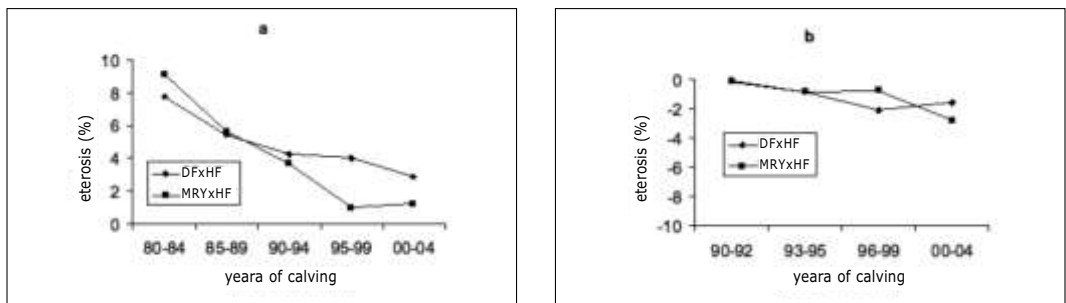
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