



Analysis on crossbreeding in the Dutch dairy cattle population

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ABSTRACT

This study aimed to estimate heterosis for 305d-milk, fat and protein, and for calving interval in the Dutch dairy cattle population. Six breeds and 11 types of crosses were considered. A total of 5.913.654 and 3.679.183 primiparous cows were used for productive traits and for calving interval, respectively. Pedigree file was used to carry out the evolution by birth year (from 1976 to 2003) of the gene frequency in the Holstein Friesian (HF), Dutch Friesian (DF), and Mosa-Reno-Yssel (MRY) Dutch population. The effects included in the model of analysis, performed using software PEST, were: herd, year-season of calving, age at calving, lactation length, cross and random animal genetic effect. In the model for calving interval lactation length effect was replaced by 305d-milk yield. Means of 305d-milk, fat, and protein were high for HF and equal to 7300 kg, 315 kg, and 250 kg, respectively. Concerning calving interval, the best value was found for MRY (387 days). Non-additive genetic estimates for productive traits ranged from 0.8% (305d-fat) to 10.2% (305d-protein). Heterosis for calving interval appeared higher in crosses involving Brown Swiss (BS) and Montbéliarde (M) breeds, with values between -4.9% and -3.0%, corresponding to -12 and -21 days of calving interval, respectively. In conclusion, for yield traits higher percentages were provided by crosses in which Jersey (J) was present, while for calving interval combinations with BS performed better than others concerning heterosis. Future perspectives could consider the F1 following crossbred cows in order to estimate recombination losses.

(Keywords: crossbreeding, primiparous Dutch cows, heterosis, milk yield, calving interval)

INTRODUCTION

Crossbreeding is used widely in genetic improvement programs for many livestock species (Weigel and Barlass, 2003), in order to improve reproductive performances in female lines and productive characteristics in male ones, exploiting heterosis. This mating system provides a tool to increase health and efficiency in animals (VanRaden and Sanders, 2003), and a well-designed crossbreeding system allows the producer to combine the desirable characteristics of the breeds involved in the cross. Recently, crossbreeding has also become an interesting mating system in dairy cattle for many reasons. First, inbreeding level within each of the major dairy breeds is rapidly increasing, and crossbreeding may be an efficient way to cope with loss of genetic variation in dairy populations under selection, adding variability and reducing the impact of inbreeding depression (Weigel and Barlass, 2003). Second, direct payments for protein as well as fat in many milk pricing systems encourage some producers of the Holstein herds to consider crossbreeding as a tool to improve milk nutrient content, in order to enhance the ability of other breeds and breed crosses to

compete with the Holsteins on an economic basis, especially in those countries where cheese industry is very important. Third, economic weight of functional traits such as reproductive efficiency, health and survival traits has risen in recent decades. Fourth, easy access to genetic material from almost anywhere in the world, strong competition among breeds like the Holstein, Brown Swiss and Jersey, and standardization of sire evaluations are making crossbreeding viable.

Some studies estimated non-additive genetic effects for milk yield traits and productive life in dairy cattle. Estimates of general heterosis in the USA conditions were 3.4%, 4.4%, and 4.1% for milk yield, fat yield, and protein yield, respectively, and 1.2% for productive life, a measure of longevity (*VanRaden and Sanders, 2003*). A Canadian study conducted on the Holstein×Ayrshire cross population (*McAllister et al., 1994*) provided heterosis estimates ranging from 16.5% to 20% for lifetime milk productive traits and estimates greater than 20% for the composite influence of these characteristics and growth, health, and reproductive traits on lifetime annualized discounted net returns (ADNR) (*McAllister, 2002*). In a French study on the Holstein×European Black and White cattle, heterosis reached 2 to 2.5% for yield traits (*Boichard et al., 1993*). Under New Zealand current market values for milk, *Lopez-Villalobos et al. (2000)* demonstrated the superior profitability of the rotational crossbred herds per hectare when compared to purebred ones.

This study aimed to describe the types of crossbreeding schemes currently performed in Dutch dairy cattle population, to analyze the evolution of the gene frequency in the male and female Dutch population, and to estimate heterosis for traits of economic relevance.

MATERIALS AND METHODS

Source of data and editing procedures

Heterosis was estimated in primiparous cows for 305d-milk, fat and protein yields, and for calving interval from the data recorded by NRS between 1980 and 2004. Breeds involved in this study were the Holstein Friesian (HF), Dutch Friesian (DF), Mosa-Reno-Yssel (MRY), Brown Swiss (BS), Montbéliarde (M) and Jersey (J); crossbreds studied were J×MRY, HF×J, DF×J, M×MRY, BS×DF, BS×MRY, BS×HF, DF×HF, DF×MRY, HF×M, and HF×MRY. A total of 6.973.735 data of milk yields distributed in 52.377 herds were available. Records with closed lactation shorter than 240 d or longer than 720 d, with missing sire or dam information, and with age at first calving shorter than 500 or longer than 1500 d were discarded prior to statistical analysis. In addition, for fertility data, calving intervals were restricted between 280 and 820 d.

After editing, yield trait data derived from 3,421,543 crossbreds and 2,492,111 purebreds reared in 39,915 herds, and calving interval data derived from 2,379,598 crossbred cows and 1,299,585 purebreds reared in 33,056 herds.

Pedigree file included 7,906,395 animals. All of them had sire and dam information. Pedigree data were used only for the main breeds (HF, DF, and MRY) in order to obtain gene proportion of each animal and to estimate the birth year variation of these genes.

Statistical analysis

Three classes of age at calving within breed (early, medium, tardive) and 3 classes of lactation length within breed (short, medium, long) were defined. Moreover, 3 classes of milk production levels (low, medium, high) were defined for calving interval.

Statistical analysis was performed using the PEST software (*Groeneveld et al., 1990*) according to a linear model considering the effects of herd, year-season of calving, age at calving, lactation length, cross and random animal genetic effect. All purebreds

and crosses (F1 and following generations) were considered in the model of analysis. NRS provided (co)variance components used in this work. In the model for calving interval lactation length effect was replaced by 305d-milk yield.

Heterosis estimates

Production and reproduction traits solutions of crossbreds (F1) and purebreds were used for heterosis estimation.

RESULTS AND DISCUSSION

Data set composition used for production traits analysis (5.913.654 animals) is shown in *Table 1*. HF, MRY and DF represented the spreadest breeds in the Netherlands, with 21.9%, 10.8%, and 9.3% of the total sample, respectively.

Table 1

**Number of purebred and crossbred primiparous cows for milk yield traits
(n=5.913.654)**

Main breed	Secondary breed					
	BS	DF	HF	J	M	MRY
BS	192	680	3049	26	5	2590
DF	9	549.203	768.431	1096	3	1737
HF	4885	1.634.618	1.297.879	7833	1895	534.681
J	21	1149	1360	3152	7	378
M	48	101	2598	2	320	1756
MRY	4678	18.155	428.243	679	830	641.365

Besides, crossbreds involving these breeds were the most common, especially HF×DF (27.6%), indicating a strong reference to Holstein Friesian in crossbreeding practice. Similar considerations can be done for the data set of calving interval (3.679.183 animals) that is shown in *Table 2*.

Table 2

**Number of purebred and crossbred primiparous cows for calving interval
(n=3.679.183)**

Main breed	Secondary breed					
	BS	DF	HF	J	M	MRY
BS	156	527	2586	2253
DF	6	21.052	237.946	209	...	935
HF	4266	1.308.407	1.097.073	6464	1629	457.620
J	...	403	1022	1885	...	172
M	2160	...	253	1514
MRY	3625	9581	337.253	280	740	179.166

Descriptive statistics for traits studied are shown in *Table 3*. Means of 305d-milk, fat and protein were high for the HF breed, with 7300 kg, 315 kg, and 250 kg, respectively. Fair

production levels resulted for BS and M, with values of 6100 kg for milk, 215 kg for protein, and 265 kg for fat. Concerning calving interval the MRY breed showed the lower value (387 ± 55 days), while other breeds ranged between 398 ± 69 (J) to 422 ± 76 (BS) days. High values of calving interval could indicate the presence of fertility problems with a service period increase, that is probably due to the pregnancy difficulty.

Table 3

Descriptive statistics for 305d-milk yield, protein, fat, and calving interval in purebred primiparous cows

	Milk (kg)		Protein (kg)		Fat (kg)		Calving interval (d)	
	mean	SD	mean	SD	mean	SD	mean	SD
BS	6078	1101	220	42	273	53	422	76
DF	4903	823	165	28	208	36	403	63
HF	7322	1228	250	40	315	50	410	73
J	4105	826	166	31	257	44	398	69
M	6059	1027	210	34	256	40	407	75
MRY	4964	822	172	29	209	37	387	55

The variation per birth year of the HF, DF, and MRY gene percentage in female and male populations are shown in *Figure 1* and 2. The HF genes increased rapidly between 1970s and 1990s from 15% to more than 90%. This variation in the Europe countries was caused to an important introduction of USA genetic materials. Conversely, in the same years the fraction of DF genes decreased in male as well as in female population, passed from high (70%) to small values (5%). In the 1970s the Holstein male population resulted in a major fraction of genes if compared to female one, probably due to the initial importation of Holstein bulls as live calves or embryos in the Europe.

Figure 1

Distribution per birth year of female genes in the HF, DF, and MRY dairy population

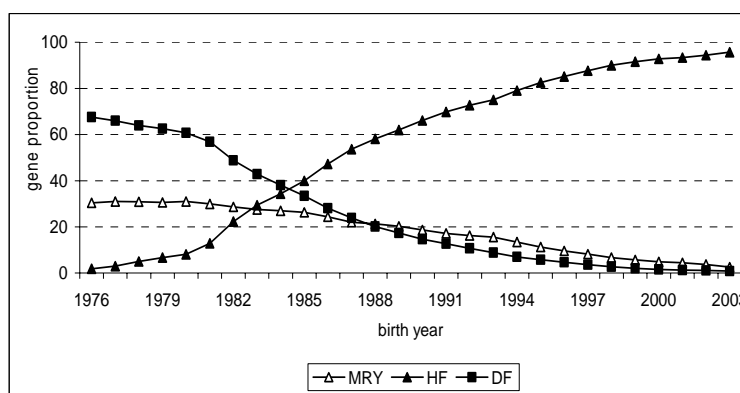
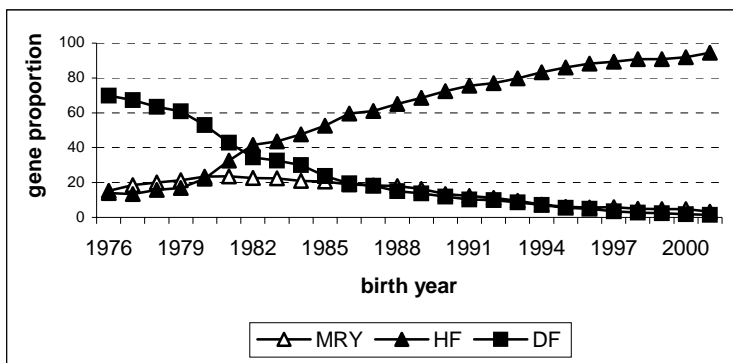


Figure 2

Distribution per birth year of male genes in the HF, DF, and MRY dairy population



Non-additive genetic estimates for yield traits and calving interval for F1 crosses, with at least 100 observations, are shown in *Table 4*. The solutions for 305d-milk yield ranged from 9.8% heterosis for J×MRY to 1.2% for DF×MRY. The solutions for 305d-protein yield ranged from 10.2% for J×MRY to 1.5% for DF×MRY. The solutions for 305d-fat yield ranged from 9.1% for J×MRY to 0.8% for DF×MRY. Finally, calving interval heterosis was higher in the combinations where BS and M were present, with percentage values ranged between -4.9% to -3.0%, corresponding to -12 and -21 days, respectively. Means of heterosis for productive traits were similar to those found by *VanRaden and Sanders (2003)*, and higher percentages were provided by crosses in which Jersey was present.

Table 4

Heterosis estimates for milk yield traits and calving interval

	n.	305d-Milk		305d-Protein		305d-Fat		n.	Calving interval	
		H (kg)	H (%)	H (kg)	H (%)	H (kg)	H (%)		H (d)	H (%)
J×MRY	402	515	9.8	19	10.2	23.0	9.1	110	-6	-1.4
HF×J	3109	376	6.8	16	8.2	23.0	8.8	2549	-6	-1.4
DF×J	1001	503	9.5	16	8.5	23.0	8.9	160	-6	-1.4
M×MRY	508	250	4.3	9	4.5	14.0	5.4	452	-12	-3.0
BS×DF	186	385	6.7	11	5.4	14.5	5.7	115	-13	-3.1
BS×MRY	3004	378	6.6	10	5.0	14.5	5.8	2153	-16	-3.8
BS×HF	1311	241	4.0	6	2.9	11.0	4.2	1086	-21	-4.9
DF×HF	598.100	137	2.3	5	2.4	8.0	2.8	187.448	-3	-0.8
DF×MRY	7759	69	1.2	3	1.5	2.0	0.8	2338	-5	-1.3
HF×M	766	119	2.0	6	2.9	9.0	3.4	621	-14	-3.5
HF×MRY	218.337	131	2.2	5	2.4	8.0	2.9	163.889	-3	-0.8

CONCLUSIONS

HF, DF, and MRY resulted the spreadest breeds in the Netherlands, both as purebred and crossbred, while the others were less represented. In the last 30 years there was an increase of genes fraction for the HF breed, and a decrease for MRY and DF breeds. Regarding calving interval values found for crosses involving BS were interesting with heterosis estimates ranged between -4.9% to -3.1%.

This paper was a preliminary analysis of non-additive effects due to crossbreeding. Future studies will be led to estimate maternal effects of traits studied in this work, and to estimate recombination losses in the F1 following generations. Moreover, heterosis of other functional and sanitary traits (e.g. SCC) could be considered in future perspectives.

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