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## Inbreeding and Crossbreeding Parameters for Production and Fertility Traits in Holstein, Montbéliarde and Normande Cows

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**ABSTRACT:** Breed differences and non-additive genetic effects for milk production traits, somatic cell score (SCS), conception rate (CR) and days to first service (DFS) were estimated for Holstein × Montbéliarde and Holstein × Normande crossbreeds. The Holstein breed was genetically superior for production and inferior for fertility traits to the two other breeds. Inbreeding depression caused loss of yield for production traits, a small increase in SCS and DFS, and a decrease of CR. Favorable heterosis effects were found for all traits, to such a point that F1 crossbreeds can compete with Holstein cows for milk production and have a better fertility. However, recombination loss indicated that much of the F1 heterosis was lost in second and later generations of crossbreeding.

**Keywords:** dairy crossbreeding; production traits; functional traits; nonadditive effect

### Introduction

With genetic selection primarily focused on yield traits, tremendous gains in milk, fat and protein yields have been achieved especially in the Holstein breed. But this genetic selection combined with a change of herd management also resulted in a decrease of robustness and fertility (Lucy, 2001; Heringstad *et al.*, 2003), combined with an increase in inbreeding (Danchin-Burge *et al.*, 2012). Crossbreeding involving the Holstein breed may be an alternative to counteract these undesirable evolutions (Sørensen *et al.*, 2008). Indeed, first generation crossbreeds (F1) tend to express better functional traits than Holstein cows (Dechow *et al.*, 2007). However, performance of later generations of crossbreeds has received little attention; hence the persistency of crossbreeding effects is poorly known.

French genetic evaluations currently considers data from different breeds separately, excluding crossbred cows' information. Additive genetic effects between breeds and non-additive genetic effects expressed through heterosis, recombination loss and inbreeding depression, have not been estimated. The objectives of this study were to estimate the actual genetic differences between Holstein (HO), Montbéliarde (MO) and Normande (NO) breeds and the effects of inbreeding, heterosis and recombination loss for some production and functional traits.

### Materials and Methods

**Data.** 305-day lactation records on milk, fat, protein and somatic cell score (SCS), conception rate (CR) for

the first three artificial inseminations (AI) and days to first service (DFS) for parities 1 to 3 from 2000 to 2013 were extracted from the French National Genetic Information System. CR was a binary measure (conceived / not conceived after each of the first three AI). Also DFS was calculated as number of days from calving to first service. Breed proportion was computed for each cow and for her parents from the national across breeds pedigree file of 173,025,861 animals. Cows with unknown parents and grandparents were removed. Only cows where the sum of breed proportions between HO and MO and between HO and NO breeds was equal to 1 were retained. Five classes of gene proportions of HO breed were defined as: 0 to 19%, 20 to 39%, 40 to 59%, 60 to 79% and 80 to 100%.

**Inbreeding, specific heterosis and recombination loss coefficients.** Inbreeding coefficients were computed by breeds using the Pedig software (Boichard, 2006) using the method described by VanRaden (1992), which corrects inbreeding using an unknown-parent grouping strategy. Coefficients for heterosis (H) and recombination (R) effects were calculated as in Dechow *et al.* (2007):

$$H = 1 - \sum s_i d_i \text{ and } R = 1 - \sum (s_i^2 + d_i^2) / 2$$

$s_i$  and  $d_i$  are the proportion of sire and dam genes from breed  $i$ .

**Model.** The data were analysed with *Genokit*, an in-house genetic evaluation software (Ducrocq, personal communication) using the official French genetic evaluation model. The effects of inbreeding within classes of HO gene proportions and the regression on heterosis and recombination loss were estimated either overall or across parities. Two populations, HO and MO cows and their crosses (HO × MO) on the one hand and HO and NO cows and their crosses (HO × NO) on the other hand, were analysed separately.

### Results and Discussion

**Raw performances.** A large majority of the records was from purebred HO, MO and NO cows (Table 1). However, the number of F1 crossbreeds and backcross cows was large enough to allow a proper estimation of heterosis and recombination effects. Average 305-d milk, fat and protein yields increased when proportion of HO genes increased from 0% to 100%, except for cows with 20 to 39% of HO genes which produced less milk than the others (Table 2). HO × MO and HO × NO crossbred cows with 40 to

59% of HO genes had a 305-d milk yield respectively 859 and 1411 kg lower than purebred HO cows. These differences are similar to those reported by Heins *et al.* (2012). MO cows had the lowest SCS (3.18) and NO cows had the largest SCS (3.82). HO × MO crossbred cows had lower SCS (3.40, 3.38 and 3.44) than HO cows (3.50), but HO × NO crossbred cows had a higher SCS (3.90, 3.67 and 3.56). Heins *et al.* (2012) found that HO × MO crossbred had a SCS average lower by 0.29 than HO cows whereas HO × NO and HO cows had the same. Such results could be explained by a different sire selection and a more variable herd management in our study. MO and NO cows had a much better CR than HO cows (respectively 51, 45 and 37%). Barbat *et al.* (2010) reported the same breed ranking. Also crossbred cows with 20 to 59% of HO genes had a better CR than the corresponding purebreds (51 and 50% for HO × MO and 51 and 46% for HO × NO). These performances suggest an important heterosis effect. Average DFS was 6 days shorter for MO cows and 2 days shorter for NO cows compared with HO cows. However, when restricting to cows of different breeds which are herd mates, MO (respectively NO) cows, had only a DFS 2 days shorter than (respectively the same DFS as) their HO herd mates. This is clear evidence that DFS is strongly impacted by farmers' decisions. DFS was intermediate between Montbéliarde and Holstein cows for crossbreds except for the 20-39% class which was always better.

**Table 1. Number of cows, lactation records and AI records depending on the proportion of HO genes in the two sub-populations.**

Breed <sup>1</sup>	% HO <sup>2</sup>	Number of cows	Number of lactation records	Number of AI records
MO	0-19	1,185,146	2,615,093	3,629,173
	20-39	5,648	13,260	19,083
	40-59	11,934	24,797	32,074
	60-79	3,157	6,010	8,280
	80-100	6,459,424	13,799,748	21,550,702
NO	0-19	1,001,356	2,085,932	2,978,058
	20-39	2,615	4,777	7,073
	40-59	12,742	24,791	32,962
	60-79	2,586	4,665	6,868
	80-100	6,639,097	13,858,384	21,619,876

<sup>1</sup>HO = HO breed, MO = MO breed, NO = NO breed

<sup>2</sup>0-19 = purebred MO or NO cows and HO × MO or HO × NO crossbred cows with less than 20% of HO genes

20-39, 40-59 and 60-79 = HO × MO or HO × NO crossbred cows with 20 to 39 %, 40 to 59 % and 60 to 79 % of HO genes respectively

80-100 = purebred HO cows and HO × MO or HO × NO crossbred cows with more than 80% of HO genes

**Table 2. 305-d milk, fat and protein (Prot.) yields, somatic cell score (SCS), conception rate (CR) for the first three services and days to first service (DFS) means in 2010, depending on the classes of HO gene proportion (% HO) for the two sub-populations.**

Breed <sup>1</sup>	% HO <sup>2</sup>	Milk (kg)	Fat (kg)	Prot. (kg)	SCS	CR (%)	DFS (d)
MO	0-19	7,970	313	263	3.18	49	86
	20-39	7,881	319	258	3.40	51	85
	40-59	8,878	360	288	3.38	50	88

NO	60-79	9,037	357	290	3.44	42	91
	80-100	9,737	386	313	3.50	37	92
	0-19	7,133	309	250	3.82	45	90
	20-39	7,162	304	245	3.90	51	87
	40-59	8,329	346	278	3.67	46	90
	60-79	8,922	360	291	3.56	44	90
	80-100	9,740	386	314	3.50	37	92

<sup>1</sup>HO = HO breed, MO = MO breed, NO = NO breed

<sup>2</sup>0-19 = purebred MO or NO cows and HO × MO or HO × NO crossbred cows with less than 20% of HO genes

20-39, 40-59 and 60-79 = HO × MO or HO × NO crossbred cows with 20 to 39 %, 40 to 59 % and 60 to 79 % of HO genes respectively

80-100 = purebred HO cows and HO × MO or HO × NO crossbred cows with more than 80% of HO genes

**Table 3. Estimates of genetic, inbreeding and cross-breeding effects for 305-d milk, fat and protein (Prot.) yields, somatic cell score (SCS), conception rate (CR) and days to first service (DFS).**

Genetic effect <sup>1</sup>	Milk (kg)	Fat (kg)	Prot. (kg)	SCS	CR (%)	DFS (d)
Breed diff. (HO-MO)	983	36	23	0.32	-11	1.3
Breed diff. (HO-NO)	2225	80	53	-0.45	-9	-0.2
Inbreeding (%)						
HO	-41	-1.7	-1.3	0.006	-0.27	0.12
MO	-35	-1.4	-1.1	0.006	-0.44	0.12
NO	-32	-1.4	-1.3	0.001	-0.38	0.12
Heterosis						
HO × MO	315	18	10	-0.016	5	-3
HO × NO	466	21	12	-0.03	2	-4
Recombination						
HO × MO	-364	-19	-11	0.074	-5	3
HO × NO	-286	-18	-7	0.37	-14	5

<sup>1</sup>HO = HO breed, MO = MO breed, NO = NO breed, Breed diff. = breed difference, Inbreeding = Inbreeding depression per 1% of inbreeding increase

**Breed difference and inbreeding effects.** Differences in breed average compared with the HO breed were larger for the NO breed than for the MO breed for production traits (Table 3). This is consistent with the average observations. Penasa *et al.* (2010) estimated a breed difference between MO and HO breeds of 731 kg for 305-d milk, 32.9 kg for 305-d fat and 18.2 kg for 305-d protein. These differences are lower than those reported here, possibly because the Montbéliarde cows in the Irish study were a selected sample.

Estimates of inbreeding depression were unfavorable for all traits, as in Miglior *et al.* (1995a) and Wall *et al.* (2005). But we found a larger effect of inbreeding than in Miglior *et al.* (1995b) or Croquet *et al.* (2006) for milk production traits probably because their Holstein cows had a lower average 305-d milk production (respectively 6798 kg and 6020 kg vs 9087 kg here). Inbreeding had a low impact on SCS. This agrees again with Miglior *et al.* (1995a) and Croquet *et al.* (2006). Fertility traits were also negatively impacted by inbreeding with results similar for DFS to those reported by Wall *et al.* (2005).

**Crossbreeding parameters.** Heterosis estimates over all lactations were favorable and larger for HO × NO than for HO × MO crossbreds (Table 3). As heterosis increases with increased genetic distance between the parental breeds (Sørensen *et al.*, 2008), one hypothesis is that HO and NO breeds are more genetically distant from each other than HO and MO. Heterosis estimates increased across lactations from 298 kg (3.4% when expressed as percentage of parental breed averages) in first lactation to 371 kg (4.3%) in third lactation for HO × MO crossbreds and from 460 kg (5.7%) in first lactation to 555 kg (6.8%) in third lactation for HO × NO crossbreds. Dechow *et al.* (2007) also found that heterosis increased over lactations whereas VanRaden and Sanders (2003) found that heterosis was slightly higher in first lactation.

Heterosis estimates for SCS were small but favorable, again as in Dechow *et al.* (2007). For fertility traits, heterosis estimates were favorable as expected and close to theoretical expectations (Sørensen *et al.*, 2008). Heterosis for CR represented 10.7% of the parent breed averages in HO × MO crossbred cows and 5% in HO × NO crossbred cows. In contrast with DFS, even though MO cows were phenotypically superior to the other purebred cows, heterosis was larger in HO × NO crossbred cows than in HO × MO cows (4.4% vs 3.3% of the parental breed averages). In contrast, performance differences for DFS between HO, NO and HO × NO cows were within two days.

Large negative recombination effects were found for all traits indicating that much of the F1 heterosis was lost in second and more generations of crossbreds. This agrees with the results of the experiment described by Sørensen *et al.* (2008). Except for CR, recombination losses were similar in absolute value to heterosis. Varying recombination losses were found per lactation for CR with a loss of 14% in first lactation for HO × MO backcrosses which became a gain in second (+2%) and third (+1%) lactation. One interpretation could be that a limited number of HO × MO crossbred cows (3678) had 3 lactations. Average CR showed a decrease of 1.4% for HO × MO cows with 20 to 39% of HO gene and 1.1% for HO × MO cows with 60 to 79% of HO gene, whereas decreases of 4.1% and 6% were found for MO and HO cows respectively. For HO × NO backcrosses, recombination loss of CR was much larger than heterosis. Average CR showed that HO × NO cows with 20 to 39% of HO genes had a larger CR than both purebreds but HO × NO cows of 60 to 79% of HO genes had a CR close to that of HO cows. In Dechow *et al.* (2007) recombination effects for days open were unfavorable but smaller than heterosis. When they were estimated separately for different types of backcross, a large unfavorable recombination effect was found (+18 days) when F1 cows were mated with HO bulls compared with a large favorable recombination effect (-46 days) when F1 cows were mated with Brown Swiss bulls.

## Conclusion

Results suggest that F1 crossbreds can compete with HO cows for milk production with a small loss in production and better fertility traits. Crossbreeding with the MO breed favored a decrease of SCS whereas crossbreeding with the NO breed tended to increase SCS. However, almost all the heterosis found in F1 was lost by recombination in later generations of crossbreeding. This must be kept in mind when farmers decide to keep crossbred cows as dams of the next generation.

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