Effect of the Holstein crossbreeding on genetic evaluation of the French Black and White cattle population

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Introduction

In France, as in the other European countries, the Black and White population has been crossbred with the North American Holstein strain since the beginning of the 70's. Importations of live females remained limited to several thousand animals and the part of imported semen has always been quite low on the french market (2-5 % according to years). Consequently, this major evolution was achieved through imported Holstein bulls, as live calves until 1983 or as embryos since 1984 following the implementation of new sanitary regulations.

The crossbreeding parameters (heterosis and recombination losses) have often been negliged in dairy data analysis and genetic evaluation. In 1989, Van der Werf & de Boer published estimates of heterosis and recombination losses in the dutch Black and White population. According to these authors, the heterosis effect reached 2-2.5 % of the mean for milk, fat and protein yields, and was zero for protein content and very low for fat content. For yields, recombination losses seemed to be quite important since the 75% Holstein females showed almost no superiority due to crossbreeding. Although these effects are quite low, they may eventually generate significant bias in genetic evaluation, and the consequences of their inclusion in the model of analysis should be investigated.

As the Holstein absorption is going to be completed, this study proposes an overview of the present situation in France, provides other estimates of crossbreeding parameters obtained in the French population and measures the bias generated in the evaluation when these effects are omitted, particularly on the estimated genetic trend and on the genetic differences between strains.

I. Evolution of Holstein genes proportion in the Black and White population

The Holstein gene proportion h_i of each animal was obtained from those of its sire s (h_s) and dam d (h_d) :

$$h_i = (h_s + h_d) / 2$$

When an animal without known pedigree originated from USA, Canada, Italy or Israel, it was considered as pure Holstein. On the other hand, when it originates from France or another European country, it was considered either as pure European Friesian, 50 % Holstein or 75 % Holstein, whether it was born before 1981, from 1981 to 1986, or after 1986 respectively. This choice was motivated by the most frequent genotype observed in the population with known pedigree.

The evolution by birth year of the Holstein gene percentage in the male population is presented in figure 1. For AI males, the Holstein gene part, which was very low before 1970, increased strongly up to 1973. During that period, a significant number of pure Holstein bulls were imported and progeny tested in order to estimate the genetic level of the Holstein strain. From 1973 to 1975, the Holstein level remained stable around 40 %. After 1976, it increased strongly again. In some AI studs, F1 bulls were procreated and progeny tested, because of beef objectives, but this choice was quickly disregarded. Since 1981, the Holstein gene percentage of AI bulls has almost reached 100 %.

For natural mating bulls, the trend is completely different. It is much slower and looks like to that of females.

For females, the evolution is presented also in figure 1. The Holstein percentage increased slowly in the beginning of 70's (by 1-2% per year) and much faster after 1977, up to 8% per year. This trend slowed down gradually as the average Holstein percentage became higher. For females born in 1990, the Holstein percentage reached 83 %, i.e. 3% more than in 1989. This level is much higher than predicted by Colleau & Tanguy (1984), even under the highest hypothesis they have studied.

This trend has been rather similar in whole France, with some differences between regions. The Holstein crossbreeding began sooner in the South East, because of a well-known herd with 800 pure Holstein cows. In the last 70's, the North, Normandy and Loire Valley presented the highest Holstein percentage, while Britany and South West kept a more European Friesian cattle. Since 1980, differences between regions have been very small and are presently less than 2%.

The figure 2 presents the evolution of each female genotype by birth year. European type cows remained predominant until 1978 but decreased rapidly and disappeared in 1984. F1 cows already existed in significant proportion during the 70's, peaked in 1981 and have recently disappeared. 3/4 Holstein cows appeared in 1977-1979, peaked in 1987 and are regressing presently. They still represented 30 % of the females born in 1990. 7/8 Holstein cows appeared in 1982 and are presently predominant (40%) in the population, but they are going to decline gradually. 15/16 cows are increasing rapidly (30% in 1990). Between 1975 and 1984, 25% Holstein cows were born from crossbred bulls but they always represented less than 10-15% of the population. Finally, for a complete description of the population, it should be noted that a large number of genotypes might be found, even the most unlikely, at small frequencies.

II. Estimation of crossbreeding parameters.

Crossbreeding parameters include heterosis, recombination losses and difference in genetic additive levels between strains, which will be presented in part III.

Heterosis and recombination losses were estimated from 12,435,716 records in parity 1 to 3 performed since 1975 by 5,661,106 Black and White females with known pedigree.

Milk, fat and protein yields, and fat and protein contents, were analyzed with an animal model including environmental fixed effects, the breeding value, a permanent environmental effect and a non-additive effect due to the genotype. All relationships were accounted for. Groups were defined for unknown parents, according to sex, birth year and genotype of progeny, and therefore accounted for additive genetic differences between both strains.

Environmental effects were the same as in the French evaluation system (Bonaïti & Boichard, 1990) : herd-year, parity within year and region, month of calving, age at calving and calving interval, within parity, year and region.

The non-additive effect was estimated by a factor which categories were defined according to the percentage of the predominant breed in the genotype of each female with data. Seven categories were defined :

1 - pure animals (24.8% of the data), mostly European Friesian, sometimes Holstein

2 - animals with 1-10% or 90-99% Holstein genes (2.4%), including mainly 15/16 Holstein animals

3 - animal with 11-20% or 80-89% Holstein genes (9.6%), including mainly 7/8 Holstein animals.

4 - animals with 21-30% or 70-79% Holstein genes (26.0%), including mainly 3/4 Holstein animals and, in to a lesser extent, 1/4 Holstein females.

5 - animals with 31-40% or 60-69% Holstein genes (6.5%)

6 - animals with 41-49% or 51-59% Holstein genes (0.9%)

7 - 50% Holstein animals (29.8%), mainly F1 (97.5%), rarely F2.

Results are presented in table 1. They showed a superiority of F1 animals over pure animals of about 135 kg milk, 5.6 kg fat, 4.4 kg protein, while the superiority for fat content was very small (+0.13 g/kg) and almost zero for protein content (+0.02g/kg). The superiority of backcrossed animals (type 4) over pure animals reached only one third of the superiority of F1 for yields : 44 kg milk, 1.7 kg fat, 1.8 kg protein. This effect was equal for fat content (+0.12 g/kg) and larger for protein content (+0.05 g/kg), but remained very low. Intermediate estimates were obtained for genotypes 5 and 6 with 31 to 69 % Holstein (F1 excluded). For animals of genotype 2 and 3, and particularly for 7/8 and 15/16 Holstein animals, the non-additive effects were very small.

These results can be combined to estimate heterosis and recombination losses, under the assumption each category include only one predominant genotype : animals of genotype 7 are F1 and express 100% of the heterosis ; animals of genotype 4 are all backcrossed and express half of heterosis and a quarter of the recombination losses ; animals of genotype 3 are 7/8 and express a quarter of the heterosis and 3/16 of the recombination losses. Estimates obtained from genotypes 4 and 7 only are in table 2. Heterosis estimates are very stable according to the number of genotypes considered and are very similar to results of Van der Werf and de Boer. They represented 2-2.5 % of the yield trait mean obverved in 1982-1985 when F1 females were predominant in the lactating population. For recombination losses, estimates were rather different, whether genotypes 3 or 2 were considered in addition to genotypes 7 and 4, and were in agreement only for milk yield with these authors. However, they remained of small magnitude.

III. Consequences for genetic evaluation

Until now, non-additive effects have been omitted in the French evalution system and have generated some bias. The difference between additive genetic levels of both strains, estimated mainly by the superiority of F1 daughters of Holstein bulls over their European Friesian contemporaries, was overestimated by 115 kg milk. After accounting for non additive effects, the Holstein minus European Friesian difference, based on breeding value estimates of Holstein and Friesian contemporary bulls, reached 943 kg milk (*i.e.* substantially more than estimated by Van der Werf & de Boer), 25 kg fat, 20.5 kg protein, -1.8 g/kg fat content, and -1.25 g/kg protein content.

Consequences on breeding value predictions were complex, but less important than expected. Without accounting for non-additive effects, the first Holstein bulls, progeny tested mainly with F1 daughters, were overestimated by 80 to 100 kg milk, while the evaluation of more recent bulls remained almost unchanged. For milk yield, the bias, noted Δ, can be predicted by the proportion p of F1 daughters in the progeny, but the regression coefficient is relatively small compared to the heterosis effect :

$$\Delta \text{ (kg milk)} = 7 + 0.84\, p\ (\%) \qquad (R^2 = 0.75)$$

The observed bias reached only 40 % of the bias expected if the heterosis effect of F1 daughters would be completely included in their Holstein sire breeding value. Within Holstein, the yearly genetic trend, estimated by averaging by birth year the breeding values of AI sires born from 1972 to 1985, was increased by 5.5 kg milk, 0.22 kg fat, 0.16 kg protein, 0.004 g/kg fat content, and -0.001 g/kg protein content.

The European Friesian bulls proofs were also biased. The younger the bull, the more underestimated his predicted breeding value. While a bull born in 1970 was underestimated by 25 kg milk only, the bias reached 100 kg on average for a bull born in 1978. Consequently, within European Friesian strain, accounting for non-additive effects increased the estimate of genetic trend (obtained from breeding values of AI bulls born from 1969 to 1979) by 9 kg milk, 0.37 kg fat, 0.27 kg protein, -0.004 g/kg fat content and -0.003 g/kg protein content.

However, the pooled estimate of genetic trend in the whole population, which combines the genetic difference between strains (decreased) and the within strain genetic trend (increased), remained unchanged.

The remaining part of the non-additive effects were included in the herd-year effects, which were overestimated by 60-100 kg milk from 1982 to 1987, when lactating cows were mainly F1 animals, in a very large proportion of herds.

Conclusion

Crossbreeding parameters estimated in this study were rather similar to those estimated by Van der Werf & de Boer in the dutch study, particularly for heterosis. Estimates for recombination losses were less in agreement but remained rather low. Heterosis was found to be low for fat and protein contents and reached about 2% of the mean for yield traits.

When these effects are not accounted for in the evaluation model, bias are less important than expected. The main consequence is the overestimation by 10% of the additive genetic difference between the Black and White strains, and the underestimation by 10 % of the within strain genetic trend.

According to its ease of implementation, and in spite of the limited consequences expected on the results, these non-additive effects will be included in the French evaluation.

References

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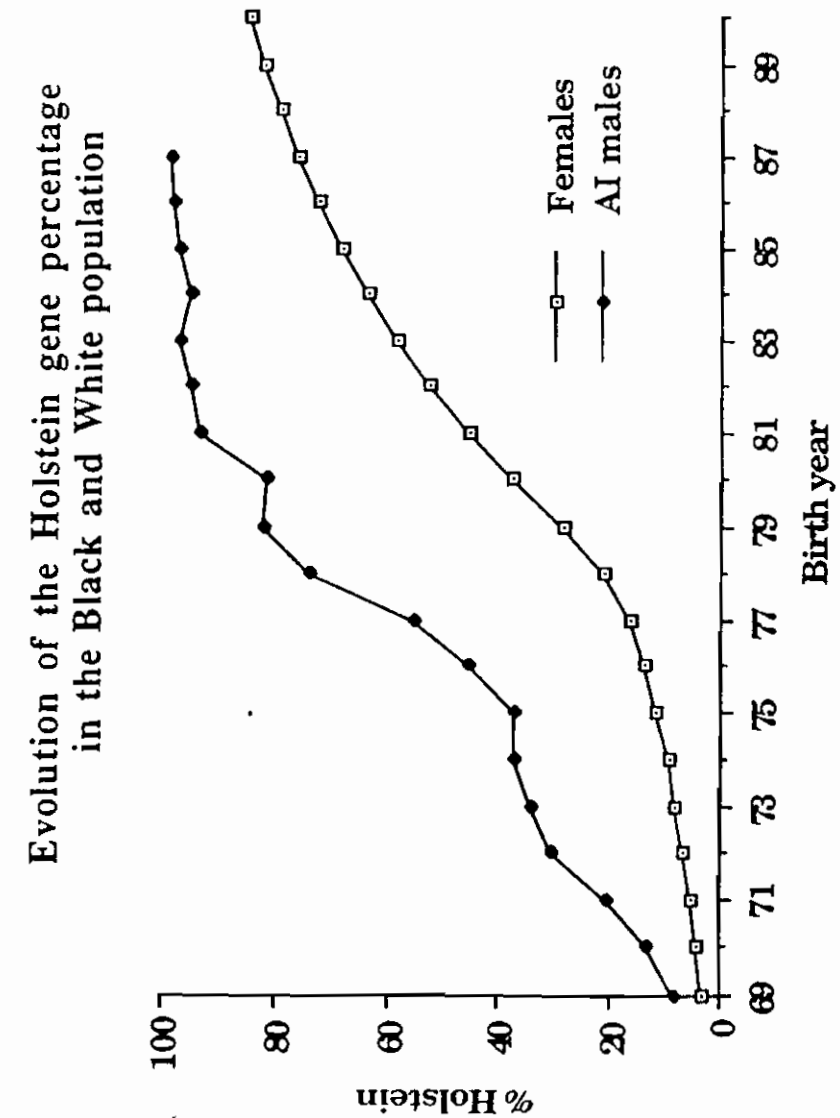
Table 1.
Estimates of non-additive effects for differents genotypes

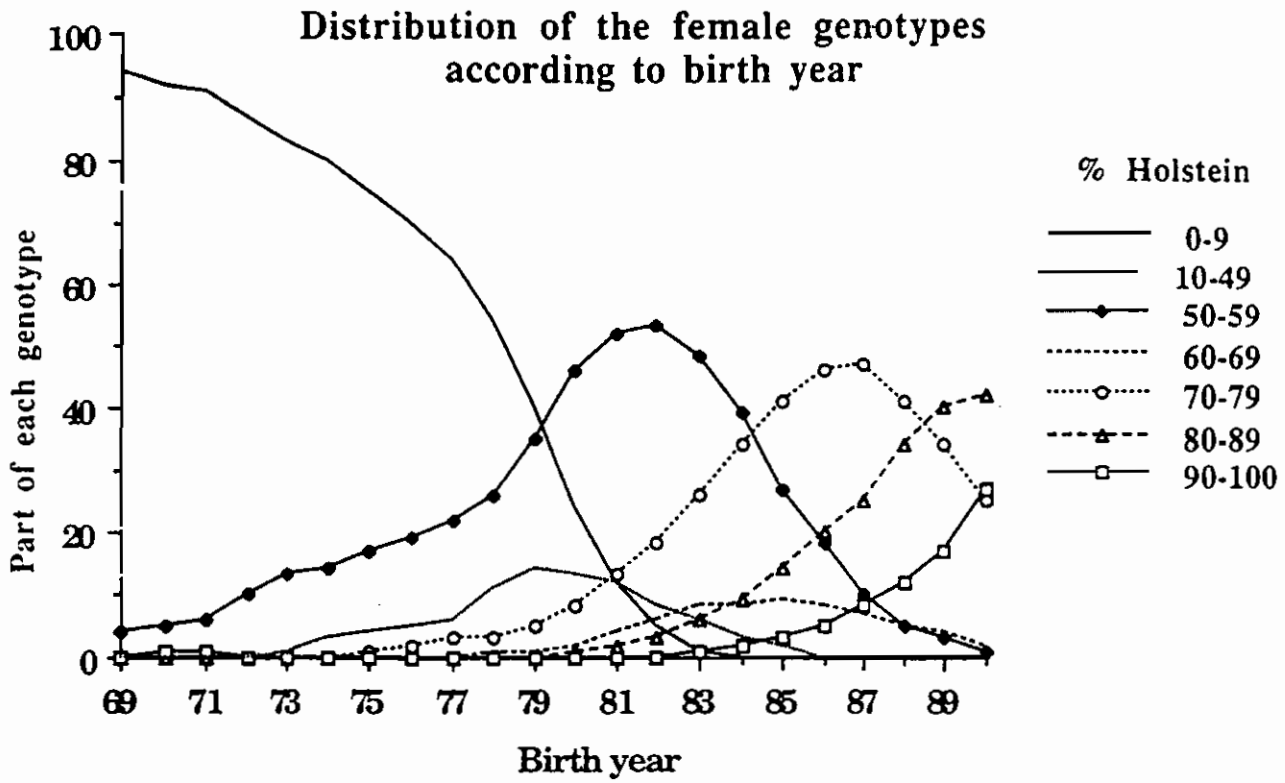
Pourcentage of the predominant breed	Milk yield (kg)	Fat yield (kg)	Protein yield (kg)	Fat content (g/kg)	Protein content (g/kg)
100	0	0,00	0,00	0,00	0,00
90-99	6	0,02	0,91	0,08	0,11
80-89	16	0,47	1,07	0,10	0,08
70-79	44	1,71	1,76	0,12	0,05
60-69	69	2,65	2,47	0,12	0,04
51-59	87	3,62	3,06	0,17	0,05
50	135	5,58	4,39	0,13	0,02

Table 2.
Estimates of heterosis and recombination losses (1)

	Milk yield (kg)	Fat yield (kg)	Protein yield (kg)	Fat content (g/kg)	Protein content (g/kg)
Heterosis	135	5,60	4,33	0,12	0,01
Recombination losses	-94	-4,82	-1,74	0,22	0,16

(1) obtained from genotypes 7 (F1) and 4 (back-cross)




Distribution of the female genotypes
according to birth year
Part of each genotype
100
80
60
40
20
0
69
71
73
75
77
79
81
83
85
87
89
Birth year
% Holstein
0-9
10-49
50-59
60-69
70-79
80-89
90-100