The Usage of Heterosis Correction in a Multiple Breed Genetic Evaluation

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Introduction

Heterosis occurs when breeds with different gene-frequencies are crossed to produce offspring. The amount of heterosis is the difference between the offspring and the parental means. Heterosis depends on dominance. Loci without dominance cause no heterosis (1). Furthermore heterosis depends on the genetic distance between the breeds. The amount of heterosis becomes higher if the genetic distance between the breeds becomes bigger.

Next to heterosis, recombination can become important if an original breed is replaced by another breed by backcrossing. Recombination is mostly negative because of the positive gene interactions in the original breeds through selection.

Estimates for heterosis and recombination in several different crossbred populations are summarized in Table 1.

Table 1. Estimates (kg) for heterosis and recombination.

Country	Breed	Trait	Hetersosis	Recombination	Reference
NL	HF*DF	Kg Milk	120.0	-100.0	(2)
		Kg Fat	6.0	-1.3	
		Kg Protein	4.4	-3.5	
D	HF*RD	Kg Milk	210	-2382	(3)
		Kg Fat	10	-77	
		Kg Protein	7	83	
UK	HF*F	Kg Milk	100	-156	(4)
		Kg Fat	4.5	-2.1	
		Kg Protein	3.6	-3.8	
NL	HF*MRY	Kg Milk	140	-295	(5)
		Kg Fat	6.0	-11.1	
		Kg Protein	5.3	-8.2	

Countrycodes :   NL = Netherlands, D = Denmark, UK = United Kingdom
Breedcodes :   HF = Holstein Friesian, DF = Dutch Friesian, RD = Red Danish, F = Friesian,
MRY = Dutch MRY.

Most of the estimates are quite similar, except the estimate for recombination in the Danish research. However the standard error of these estimates were high. The estimate for recombination in the Dutch research using HF and MRY data also had an high standard error. Estimates for heterosis and recombination are around 2% of the population mean for the production traits.

According to (2) biased estimates of breeding values are found by not accounting for heterosis and recombination in genetic evaluations of crossbred populations. Therefore in the Dutch multiple breed genetic evaluation a correction for heterosis and recombination is done. The objective of this paper is to describe this correction.

Materials and methods

In the Netherlands the original black & white breed (DF) are mostly replaced by holstein friesians (HF). This started in the middle of the 1970s and nowadays most of the cows are Holstein Friesians. The original red & white breed (the MRY) is being replaced by red Holstein Friesians. This replacement started in the middle of the 1980s and is still going on. Because of these breed replacements a lot of cows are crossbreds and therefore a correction for heterosis and recombination is necessary.

Breed codes from each animal and the proportions of the genes from each breed code are stored on database. The proportions of the genes from each breed are stored in classes from 1 to 8. Each class represents 12,5% of genes. Coefficients for heterosis and recombination can be computed using the following formulaes:

$$h = [p_s (1 - p_d) + p_d (1 - p_s)]$$
$$r = [p_s (1 - p_s) + p_d (1 - p_d)]$$

were

h = coefficient for heterosis
r = coefficient for recombination
p_s = percentage of genes of a breed present in the sire
p_d = percentage of genes of a breed present in the dam

Table 2 gives some examples of the coefficients.

Table 2. Coefficients for heterosis and recombination.

Cross	P_s	P_d	h	r
A * A	1.0	1.0	0.0	0.0
A * B	1.0	0.0	0.5	0.0
A * (A *B)	1.0	0.5	0.5	0.25
(A * B) * (A * B)	0.5	0.5	0.5	0.5

The coefficients are calculated in every evaluation and all breed combinations are assigned the same heterosis coefficients. This is a simplification because it assumes the same amount of heterosis between all the breeds. However, in the Netherlands most of the crossbred animals are either HF * DF of HF * MRY. The estimates for heterosis for these crossbreds are almost the same as can be seen in Table 1. The estimates for recombination differ somewhat but because of the larger standard error of the estimate for recombination in the HF * MRY data the estimate for recombination in the HF * DF data is used. If different heterosis coefficients for different breed combinations would be used then estimates for the smaller crossbred populations can be unreliable because of the small amount of data that can be used for the estimation.

The correction for heterosis and recombination is a pre-correction. Advantages of a pre-correction are that it reduces computational time. If an in-model estimate would be done every genetic evaluation then the estimates would probably be very similar every evaluation because of the same data that is used for the estimation.

In the genetic evaluation first the coefficients for heterosis and recombination are computed.

After that these coefficients are multiplied by the estimates for heterosis and recombination. The total sum of these multiplications are substracted from the 305-day yield for the specific trait. Table 3 gives an example for the crosses given in Table 2 for kg milk.

Table 3. Correction for heterosis and recombination for milk production.

Cross	h	r	heterosis	recombination	total [1]
A * A	0.0	0.0	0	0	0
A * B	0.5	0.0	120	0	120
A * (A *B)	0.5	0.25	60	-25	35
(A*B) * (A*B)	0.5	0.5	60	-50	10

[1]The total is substracted from the 305 day yield.

Two evaluations were performed, one with the pre-correction for heterosis and recombination and the other without the pre-correction. Per birth year of 100% HF-sires some characteristics have been calculated. Next to that the ranking based on Inet, the Dutch production index calculated as -0.15 * kg milk + 2 * kg fat + 12 * kg protein, of the top-10 bulls in both evaluations has been compared in the evaluation without and the evaluation with correction for heterosis.

Results and discussion

Table 4 gives the average breeding value for milk-production calculated in the evaluation without correction for heterosis and the evaluation with correction for heterosis per birth year of a sire. Also the maximum difference in the breeding value for milk production between the two evaluations is given.

Table 4 shows that average breeding value for kg milk of 100% HF sires is considerably higher in the evaluation without correction for heterosis compared to the evaluation with correction for heterosis. Especially in the birth years between 1973 and 1981 the breeding value for milk production in the evaluation with correction for heterosis is lower compared to the evaluation without correction for heterosis. The reason for this might be that in the early years of the breed replacement (middle of the 1970s) a lot of farmers tried the HF bulls on a few of their DF cows. So only a few cows on their farm are 50% HF and the rest still is 50% DF. In the genetic evaluation daughters of bulls are compared in herd-year-season (HYS) classes. Daughters of the HF bulls have HYS-mates that are 100% DF. This means that in a genetic evaluation with correction for heterosis the 305-day yield of the daughters of HF bulls are corrected for heterosis. The daughters of the DF bulls do not have heterosis so the difference between the daughters of the HF bulls and the daughters of the DF bulls becomes smaller. This leads to lower breeding values of the HF sire in an evaluation with correction for heterosis.

The maximum difference in breeding value for milk production between the two evaluations also shows that the early HF bulls were used only at a small scale. Theoretical the maximum difference can be 120 kg milk (this is the estimate of heterosis for milk production). This situation occurs when daughters of a HF bull have HYS-mates who are all 100% DF. As can be seen from Table 4 the maximum difference in the breeding values between the two evaluations is high between the birth years 1973 and 1981.

Table 4. Average breeding value for milk production per birth year of sires.

Birth year	Number of sires	Average BV without correction	Average BV with correction	Maximum difference in BV
73	22	392	359	104
74	22	623	585	84
75	29	538	498	94
76	43	596	551	81
77	57	494	460	89
78	47	440	402	101
79	64	366	323	104
80	90	382	328	111
81	98	430	384	109
82	134	356	345	71
83	107	533	540	73

Bulls born after 1981 show something completely different. At the time those bulls were used the breed replacement was going very fast. Those bulls show almost no difference in breeding value for milk production in the evaluation without and with correction for heterosis because the daughters of those bulls had HYS-mates that had the same breed composition. In such a situation the difference between HYS-mates is not influenced by a correction for heterosis compared to no correction for heterosis because all the animals in a HYS-class get the same correction. The maximum difference in breeding value for milk production between the two evaluations is also smaller for bulls born after 1981 compared to bulls born before 1981.

Table 5 gives the ranking of the top-10 bulls based on the evaluation without correction for heterosis and the rank of these bulls in the evaluation with correction for heterosis.

Table 5 shows that the ranking of the bulls is different between the two evaluations. Furthermore some indexes are also different, but not all bulls get different indexes. One reason for this can be that

the daughters of these bulls have coefficients for heterosis and recombination equal to 0. Another reason can be that the effect of heterosis in the evaluation without correction has been taken care of by the HYS-class of these daughters. If daughters of a certain bull all have the same breed-composition as their HYS-mates then a correction for heterosis does not change the difference between the HYS-mates because all of them get the same correction. In such a situation the index of the bull does not change in the two evaluations.

Another situation can be seen looking at the first and the second bull in Table 5. These bulls get higher indexes in the evaluation with correction for heterosis. The reason for this may be that those bulls have daughters with higher percentages of HF-genes. If the HYS-mates of the daughters of those bulls are 50% HF and the daughters of the bulls themselves are 75% HF then the correction for heterosis is bigger in the HYS-mates. This leads to bigger differences between the HYS-mates and the daughters of the bulls, resulting in higher indexes of the bulls.

Table 5. Ranking of top-10 bulls with and without correction for heterosis.

Rank without correction	Index without correction	Index with correction	Rank with correction
1	509	522	1
2	495	512	2
3	487	487	3
4	468	483	4
5	452	451	7
6	445	447	8
7	444	454	6
8	443	436	11
9	443	455	5
10	433	445	9

Conclusions

Heterosis has an impact on the ranking of bulls in an genetic evaluation. The change in ranking depends on the amount of heterosis and on the breed composition of the population in which the bulls are used.

In a population with breed replacement and a multiple breed genetic evaluation a correction for heterosis in the evaluation is recommended.

References

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