# Genetic Evaluation of Production Traits Across Cattle Breeds in Ireland

V.E. Olori<sup>1</sup> and A.G.F. Harbers<sup>2</sup>

<sup>1</sup> Irish Cattle Breeding Federation, Highfield House, Bandon, Co. Cork, Ireland <sup>2</sup> NRS, P.O. Box 454 6800 AL, Arnhem, The Netherlands

#### Introduction

Dairy cattle production in Ireland is dominated by the Holstein Friesian (HF) breed which is the sire breed of over 90% of dairy cows in Ireland. Current trends however indicate an increase in the number of crossbred and non HF breeds cows that are milk recorded. Yet genetic evaluation to date has been available only for HF bulls and cows. Interest in the genetic evaluation of other dairy breeds of cows and bulls can be attributed to the ICBF philosophy of utilising all available data to supply information useful to farmers. It can also be attributed to the desire for suitable information to guide dairy farmers in the selection of replacement cows within, as well as between, breeds. Where domestic information is absent, farmers have resorted to the selection of bulls of other breed based on foreign information which does not include performance records for the bulls' daughters in Irish herds. Evidence of genotype by environment interactions suggests that ranking of bulls in different environments might be different when genetic evaluation is based on performance records in the different environments.

The decline in fertility of the Black and White population over the years and the perception that crossbred cows might help overcome this problem is another reason why many farmers are increasingly considering crossbreeding. This perception has been supported by some research results (Carrick *et al.*, 2003) which tend to suggest economic benefit from hybrid vigour which may accrue in the crossbred cows for fertility and other fitness traits.

Inclusion of crossbred cows in genetic evaluation without correction for heterosis might bias bull evaluations while exclusion of such cows from the evaluation might reduce the accuracy of bull proofs. The ultimate solution is an across breed evaluation with appropriate correction for the expressions of non additive genetic effects (VanRaden, 1992; Akbas *et al.*, 1993; Wall *et al.*, 2005) such as heterosis and recombination. Heterosis is the increase in the performance of a crossbred animal over and above the mean of the progeny which needs to be excluded in determining the genetic merit of the animal. Recombination loss on the other hand results from inter-breeding between crosses or backcrossing which breaks up epistatic gene combinations in each breed causing a loss in performance. Like heterosis, the decline in performance due to recombination may vary depending on the breed combination (Dickerson, 1969).

The objective of this study was to determine the feasibility an across breed national evaluation in Ireland, that will make it possible to compare all dairy breeds of cattle on the same scale.

# **Materials and Method**

# Data availability

Data was extracted from the ICBF central database for all milk recorded cows calving between 1970 and 2004. Records with no 305-day milk yield were deleted. Erroneous records with wrong birth and calving dates were also deleted. The remaining records numbered about 4million lactation records from 1.6 million cows in 16,990 herds. Table 1 shows the number of cows calving per lactation for Holstein and Holstein crosses (HO) Friesian and Friesian crosses (FR) and other (OT) breeds and crosses. This broad classification was based on the breed with the dominant fraction in the 32 part breed combination of each cow. Holstein Friesian cows and their crosses accounted for about 90% of the total number of cows while cows of other breeds (with no HO or FR genes) made up 10 percent of the records. This distribution of records by breed was similar for each of the first 5 lactations used in the genetic evaluation.

Further edits were carried out to select valid records for the estimation of breeding values. All records from cows with no sires were deleted. Minimum age at calving was set at 640 days while minimum interval between subsequent lactation records was set at 301 days. There was no restriction on lactation length as all records with at least one test day record were projected to a 305day equivalent yield. However cows with milk yield less than 1500 and fat and protein yield less that 40kg were deleted. The majority of the records (1.2 million) were rejected because of missing pedigree information. Figure 1 shows the distribution of available records by breed indicating that records from other breeds were available since the early 1980s.

**Table 1.** Distribution of lactation records by parity and breed showing frequency (top) and row percentage (below) in each parity.

parity	FR	но	ОТ	Total
1	245664	810619	123519	1179802
	20.8	68.7	10.5	
2	203329	657098	88227	948654
	21.43	69.27	9.3	
3	182836	510355	76752	769943
	23.75	66.28	9.97	
4	160861	387346	68331	616538
	26.09	62.83	11.08	
5	136005	285155	61651	482811
	28.17	59.06	12.77	
Total	928695	2650573	418480	3997748
	23.23	66.3	10.47	100

Figure 1. Distribution of available and selected lactation records (a) and available records by breed.



#### Heterosis and recombination

Results of preliminary analysis indicated non random crossing between various breed. For example, 90% of all crossbred cows had various proportions of Holstein Friesian (HF) genes in them while only about 10% were crosses between other non HF breeds. Secondly, there were by far more crossbred cows than purebreds for many of the other dairy breeds. This indicated that accurate estimation of breed effects and heterosis between all combinations of breed will be impossible. To overcome these, all records were grouped into 34 heterosis coefficient and 34 recombination classes irrespective of the breed combination. In order words, all first cross cows were in the same (100%) heterosis coefficient class while all second cross cows where in the same (50%) recombination class. The recombination and heterosis coefficient were computed according to the general equations (Akbas et al., 1993) as follows:

Heterosis =  $\Sigma(P_{is}-P_{is}*P_{id}) + (P_{id}-P_{is}*P_{id})$ 

Recombination= $\Sigma(P_{id}-P_{id}^2)+(P_{is}-P_{is}^2)$ 

where  $P_{is}$  and  $P_{id}$  are the proportions of genes for breed *i*, for the sire and dam respectively, summed over the number of breed (maximum 2) making up the breed fractions of the sire and dam. This approach facilitated the estimation of an average heterosis effect for all breed combination in the same class with the assumption that genetic distance between breeds was the same.

#### Estimation of Breeding values:

Breeding values were estimated with a single trait repeatability animal model using the NRS custom genetic evaluation software. The first 5 lactation records of each cow were included in the analysis. Heritability of 0.35 and repeatability of 0.55 was applied for all traits (305-day Milk, fat and protein Fixed effects in the model include a vields). year\*month of calving effect (YM), Days dry in the previous lactation (DD), Number of days pregnant in the first 305 days of lactation (DP), Age at calving within parity (PAGE), herd-yearseason (HYS), heterosis (HET) and recombination (REC). All effects were fitted across breeds. The model also includes random effects of permanent environment, the animal (including relationship matrix) as well as residual error. Genetic parameters were not re-estimated in this analysis

because data from other breeds were not sufficient for accurate estimates to facilitate comparison with the estimates for the HF population. Fixed effects and breeding values from this analysis were compared with the official evaluation for the HF population which differed only in the absence of correction for HET and REC effects. Breeding values were expressed on the same base defined as all cows born in 1995 with at least one valid lactation record in the selected data.

# **Results and Discussion**

### Phenotypic yield and fixed effects

First lactation milk fat and protein yield for some dairy breeds (purebred and crosses) is presented in Table 2. There was no consistent trend observed because only the dominant breed of the crossbred animals was used in this classification. Within each major breed, proportion of genes had some effect on productivity but this was not statistically tested. There was no significant difference in the fixed effect of age within parity, days dry in previous lactation and days pregnant in the analysis with and without correction for heterosis and recombination. This is because the data set was essentially the same as the bulk of the records were from the HF population.

Table 3 shows the estimated heterosis and recombination effects for milk fat and protein vields. These indicate a heterosis effect of about 68kg in milk yield, 3kg in fat yield and 2kg in protein yield of first cross cows (100% heterosis) across breeds. Recombination loss for a full F2 cross was about 84kg for milk yield, 3 kg for fat and protein yields respectively. The trend in heterosis and recombination estimates for all classes is plotted in figures 3 and 4 for protein yield. The estimates of heterosis for 305-day milk yield from this study (68kg) for 1<sup>st</sup> cross cows is 1.58% of the mean phenotypic milk yield of cows with 50% Holstein genes. This is close to the estimate of 1.49% reported for daily yield of 1st cross HO -FR animals in the UK (Wall et al., 2005). Our estimate is an average effect across breeds. It has been shown that heterosis effects for 1<sup>st</sup> cross cows was different for combinations of Holstein, Angus and Jersey breeds in New Zealand (Harris, 1994). It seems however, that the recombination estimates presented here may be higher than the expectation. For example, considering that the heterosis for an F1 cross was 68kg for milk, the expectation is that recombination loss of the F2 will be a percentage of the heterosis gain of the F1. Because our estimates are average effects across various breed combinations, it is possible that the recombination loss estimates presented here have been biased by spurious estimates from specific breed combinations with few records. It is suggested that further analysis be carried out with data from breeds with sufficient F2 crossbred records, to estimate accurate values.

#### Estimated Sire PTA

The mean PTA for AI bulls with at least 70% reliability and 20 daughters is presented in Table 4 for popular dairy breeds in Ireland. This ranged from -525 for the Jersey breed to 143kg for the Holstein breed. The Jersey as expected had a very high mean fat yield because of the high fat content of the milk. These trends were in line with expectation especially between the Holstein and Jersey. Harris (1994) reported big difference between breeding values for fat yield and protein yield of Jersey bulls similar to the trend in this study.

The correlation between the sire PTAs for these bulls with and without correction for Heterosis and recombination were over 90% for all three traits. Big difference were noticed only for Friesian bulls, which were previously grouped with Holsteins as one breed. Without correction for heterosis, breeding values for Friesian bulls were probably overestimated being the poorer of the two (HO and FR) black and white strains. Genetic trends for the non HF breeds could not be estimated because of two few numbers for each breed.

Mean PTA for protein yield was consistently higher for crossbred cows than for pure breed cows except for the Holstein and MRY breeds as shown in Figure 4. This reflects the fact that most crossbred cows were produced by upgrading the various pure breeds with Holstein bulls rather than the reverse.

### Conclusion

An across breed evaluation with correction for recombination heterosis and has heen implemented for production traits in Ireland. Most of the available crosses were between Holstein and Friesian breeds and between these and other breeds with little or no crosses amongst other non HF breeds. Consequently, average heterosis and recombination effects were estimated across breed combinations. Changes in Holstein Friesian bull proofs was highest for Friesian bulls but that was not sufficient to cause significant re-ranking.

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		Number	Lactation	Mean 305-day yield			Standard deviation (SD)		
	%			Milk	Fat		Milk	Fat	Prot
Breed	Genes	of cows	Length	(kg)	(kg)	Prot (kg)	(kg)	(kg)	(kg)
FR	100	19788	288	4714	176	153	1230	50	44
FR	75	55574	283	4888	185	161	1189	47	40
FR	50	141737	273	4291	159	142	1204	47	40
FR	25	2542	286	4723	185	158	1044	41	34
НО	100	42518	310	6786	257	215	1762	71	68
НО	75	280445	283	5296	201	176	1264	50	42
НО	50	199116	290	5090	193	168	1162	46	39
НО	25	41302	282	4871	181	161	1251	49	42
JE	100	1095	271	3988	214	157	944	57	37
JE	75	120	269	3647	180	140	1008	49	36
JE	50	569	236	4350	199	159	1071	46	36
JE	25	2	277	4131	194	144	990	10	23
MO	100	4161	302	5913	223	200	1568	60	53
MO	75	285	257	5146	194	176	1053	42	35
MO	50	3815	239	5056	193	171	1036	41	34
MO	25	35	195	5264	203	170	1140	48	43

Table 2. First Lactation mean 305-day milk yield for cows by breed and breed fraction.

Figure 2. Estimated fixed effects from models with and without correction for heterosis.



**Table 3.** Estimate of heterosis and recombination across breeds.

Heterosis effects							
Heterosis							
Coefficient	KGMilk	KGFat	KGProt				
12.5%	-15.708	-0.594	-0.383				
25%	17.243	0.692	0.584				
50%	57.179	2.285	1.781				
75%	74.73	2.861	2.345				
87.5%	62.315	2.559	2.045				
100%	67.647	2.963	2.116				
Recombination effects							
Recombination							
Coefficient	KGMilk	KGFat	KGProt				
12.5%	-15.592	-0.431	-0.497				
25%	-32.255	-1.206	-1.111				
37.5%	-100.813	-3.213	-3.176				
50%	-83.66	-3.254	-2.894				

Figure 3. Heterosis and Recombination effects for Protein yield estimated across breeds.

![](_page_5_Figure_3.jpeg)

![](_page_5_Figure_4.jpeg)

		Number	ΡΤΑ	ΡΤΑ	ΡΤΑ	ΡΤΑ	ΡΤΑ
Breed	Stat	of bulls	Milk (kg)	Prot (kg)	Fat (kg)	Fat (%)	Prot (%)
FR	Mean	739	-229.9	-7.26	-9.05	-0.01	0.01
	SD		134.9	4.25	5.96	0.09	0.05
НО	Mean	1601	143.2	3.80	4.25	-0.01	-0.01
	SD		225.0	6.85	7.40	0.11	0.05
JE	Mean	21	-525.3	-5.26	10.33	0.65	0.27
	SD		279.1	8.46	10.39	0.17	0.08
МО	Mean	50	-89.1	-0.55	-3.63	0.00	0.04
	SD		121.2	3.81	5.02	0.06	0.03
MY	Mean	19	-388.4	-8.21	-11.34	0.07	0.10
	SD		192.9	5.58	7.22	0.10	0.07
SI	Mean	14	-330.4	-8.29	-12.11	0.01	0.06
			244.5	7.83	9.20	0.07	0.05

**Table 4.** Summary of sire PTA for AI bulls with 70% reliability or more.

Figure 4. Mean sire PTA for pure and crossbred cows.

Mean protein yield for pure and cross bred cows

![](_page_6_Figure_4.jpeg)