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Short communication: Genetic relationships between the Holstein cow populations of three European dairy countries

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ABSTRACT

The degree of relatedness was studied in 3 dairy cow populations from Great Britain (GBR), Italy (ITA), and Ireland (IRL) by using cows born from 2003 to 2006. Effective population size, inbreeding coefficient (F), and average relationship in the top and bottom 4,000 cows ranked on a profit index value (PIV) or milk yield evaluations were studied. Average inbreeding was approximately 2% in GBR and ITA, was 1% in IRL, but was slightly more than 2% when the joint pedigree was used. The average F for the joint population was 10 to 15% higher than estimates averaged across the 3 populations, reflecting the increased completeness of pedigree information in the joint pedigree. Effective population size in the joint pedigree was approximately 12% lower than estimates within the individual countries. The average genetic relationships for the top 4,000 PIV cows were not markedly different from those based on milk evaluation in GBR and ITA, but were approximately 2% lower in IRL. This was due to the use of an index with less weight on production traits in IRL compared with GBR and ITA. However, selection of the top 4,000 cows on PIV reduced the degree of relatedness across the 3 countries. The use of common sires accounted for most of the relatedness across the 3 countries, more than did the use of related sires or common foreign dams.
Key word: genetic relationship, Holstein cow, inbreeding

In the last 30 yr, there has been a steady increase in the importation of foreign genotypes, mainly from North America, to replace commercial dairy Black and White cattle populations in many countries. This "holsteinization" process has been accelerated by improvements in reproductive technology beginning in the 1980s and the availability of international evaluations from Interbull in the last 15 yr (Wickham and Banos, 1998). This has resulted in Holstein bulls with similar parentage being tested simultaneously in several countries and has also resulted in the heavy use of top-ranking bulls in cow populations in several countries.

A major concern about the emergence of the global breeding structure of the Holstein breed has been the apparent reduction in effective population size (**Ne**) and loss of genetic diversity. Wickham and Banos (1998) reported that the average genetic relationship of sires of sons born in 1990 was 6 times greater than that of sons born in 1970. The ratio of Ne to actual population size was approximately 0.22 for sires born in 1990, compared with 0.98 in 1975. Mrode et al. (1998) indicated that, for bulls with progeny test results, the percentage that were the sons of the 5 most used sires increased from approximately 30% in 1981 to approximately 50 to 70% in 1991 in many countries. Fikse and Philipsson (2007) indicated, from an analysis of Interbull pedigree data, that half of all progeny-tested bulls between 1983 and 1985 in the Holstein breed were sired by one bull sire. Weigel et al. (2000) examined the average genetic relationship among a sample of 1,000 Holstein cows with yield records in 15 countries. There were large variations in the estimates of average relationships, with very low values between countries such as Estonia and Finland, Germany and Finland, and Germany and Israel, where there is little or no direct international trade in semen and embryos. In contrast, average relationships were higher between countries such as Canada and Australia, Ireland and the Netherlands, and South Africa and the United States. However, the genetic relationships among top cows ranked on the basis of genetic evaluations for milk or national selection indexes in dairy cattle populations from different countries have not been reported. The use of a unique profit index with broader breeding goals in each country for the selection of bulls for breeding purposes should result in a wider range of bulls being selected across countries and hence a reduction in the rate of decline in Ne. This study therefore examines the genetic relationships among top cows based on an index

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Table 1. The number (N) of cows born in each country, percentage with both parents known (Both), and average number of equivalent generations (Gen)[1] in the year of birth

	Great Britain			Italy			Ireland		
Year	N	Both	Gen	N	Both	Gen	N	Both	Gen
2003	319,510	99	4.95 (5.20)	327,998	95	5.19 (5.46)	80,899	96	4.07 (4.78)
2004	301,873	99	5.08 (5.33)	314,657	94	5.28 (5.61)	62,429	97	4.19 (4.98)
2005	277,957	99	5.21 (5.46)	309,744	95	5.39 (5.74)	42,173	98	3.75 (5.42)
2006	84,749	99	5.28 (5.53)	297,532	95	5.55 (5.89)	115,760	99	4.57 (5.41)

[1]Numbers in brackets are equivalent generations estimated from the joint pedigree.

or on milk evaluations for cows born from 2003 to 2006 in 3 European dairy countries, Great Britain (**GBR**), Italy (**ITA**), and Ireland (**IRL**). In addition, the average levels of inbreeding and Ne within and across the 3 populations over time were studied.

For cows born from 2003 to 2006, national genetic evaluations for milk yield and the profit index value (**PIV**) used in each country and the full pedigree of cows of up to 5 generations were obtained from the Edinburgh Genetic Evaluation Services in GBR; ANAFI, the Italian Holstein Breeders Association in ITA; and the Irish Cattle Breeding Federation in IRL. Some cows born in 2005 and 2006 were too young to be evaluated, so a pedigree index was calculated for these cows. The higher number of cows in 2006 for IRL (Table 1) was due to the inclusion of all females in the database without any requirement that they should be milk recorded.

The composition of the national profit index used in the 3 countries is summarized in Table 2, with GBR, ITA, and IRL placing a relative emphasis, on the basis of economic weights of 77, 59, and 42%, respectively, on production traits. The full descriptions of the national profit indexes have been reported by Stott et al. (2005) for GBR, Biffani et al. (2002) for ITA, and the Irish Cattle Breeding Federation (2008) for IRL. Inbreeding coefficients (F) were computed for each population and for a joint pedigree from the 3 populations. The number of equivalent generations (t) was calculated for all cows in the pedigree as the sum over all known ancestors of the term $(0.5)^n$, where n is the number of generations between ancestor i and the cow (Maignel et al., 1996). Effective population size was calculated for various populations subsets as $1/(2b)$, where b is the regression of F on t for the relevant population subset, and it roughly estimates inbreeding rate.

The computation of average genetic relationship (**AGREL**) for cows within year of birth was not feasible because of the large number of cows. Therefore, AGREL was computed for only the top and bottom 4,000 cows ranked on PIV or milk evaluations both within and across countries. All computations of inbreeding and AGREL were carried out using RelaX2 software (Stranden and Vuori, 2006). To measure the degree of relatedness among the 3 populations resulting from completeness of pedigree and the use of common sires and dams, estimates of F and AGREL from the joint pedigree were compared with values averaged from estimates for the individual countries (referred to as "expected"). For instance, consider the AGREL among the top 4,000 cows calculated initially within each country. Then, AGREL-expected for the 3 populations equals

$$\frac{1}{n}\sum_{i=1}^{3} a_i,$$

where a_i is the sum of nonzero elements of the relationship matrix among the top 4,000 computed within the ith population, and $n = \{0.5[m(m + 1)] - m\}$, with $m = 12{,}000$ (the sum of the top 4,000 in each country).

Table 2. Summary of the national profit index in the 3 countries in terms of percentage emphasis based on economic weights on various traits

Trait	Great Britain	Italy	Ireland
Production (milk, fat, and protein)	77	59	42
Health (lameness, udder, mastitis, or SCC)	6	23	4
Survival	17	8	34[1]
Functional legs and feet		6	
Type traits		4	
Calving traits			11
Beef traits			9

[1]Survival and fertility subindex.