GENETIC DIVERSITY AMONG EUROPEAN CATTLE BREEDS

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Over the centuries since mankind first started farming, genetic variation has allowed the selection of the improved crops and livestock that have fed an ever increasing population. Maintaining genetic variation is crucial if we want to continue to improve our livestock and respond to changes in climate, disease or consumer preferences. This article describes work at the Roslin Institute on the evaluation of genetic diversity in European cattle breeds.

The efficiency of modern breeding methods can lead to the rapid propagation of particular desirable genotypes and hence to the loss of diversity. This is particularly the case in plants: in the US, for example, only 8-9 cultivars account for almost all the maize crop. In many developing countries, native livestock breeds that are less competitive under current market conditions are being interbred or replaced by improved Western breeds. The preservation of different breeds is important if they have genetically unique characteristics (Hall and Bradley, 1995). Native West African breeds, for example, are much more resistant to heat stress and trypanosomiasis than imported cattle.

Genetic conservation programmes are, however, costly to implement and it is not possible to conserve all genetic variation in all populations. An essential first step is the evaluation of genetic resources and the selection of appropriate populations for conservation. A strategy is then required that will maintain the widest possible level of genetic variation across the species (FAO,1996).

Maintaining genetic variation within a breed is also important for its commercial future. Loss of variation within a breed can cause inbreeding depression and hence markedly reduce performance, particularly for fertility traits. There is often an associated increase in the incidence of specific genetic disorders. In the Holstein population, for example, widespread use of a few sires has led to an increased incidence of BLAD (bovine leukocyte adhesion deficiency), mulefoot and DUMPS (uridine monophosphate synthase deficiency).

Characterisation of genetic resources

Appearance is not necessarily a good guide to genetic variation. Members of a breed of cattle may look outwardly similar but be quite different genetically. Conversely, breeds may look very different but be genetically closely related. A more reliable measure of differences between breeds is *genetic distance*, which can be estimated from the difference in the frequencies of different genetic variants (alleles) at a number of marker loci. Breeds which share the same alleles at similar frequencies are genetically closely related, whereas those having the same alleles at different frequencies (or different alleles altogether) are further apart. Distances or relationships between breeds can then be summarised using a phylogenetic tree or by multidimensional scaling.

Variation *within* a breed can also be estimated by examining the number and frequency of alleles. If there is much variation, most animals will be heterozygous (i.e. have two different alleles at each locus). If there is little variation most animals will be homozygous (i.e. have two copies of the same allele).

Genetic variation between European breeds

In a recent study, we have used data on cattle blood types to evaluate the genetic relationships among thirty-seven European cattle breeds present in the UK. Our analysis used information accumulated by the Cattle Blood Typing Service at Roslin over 30 years. A subset of data was used, representing a random sample drawn from pedigree populations in the UK since 1980. With a total of about 18 000 animals and up to 50 loci per animal, our study is the largest of its kind to date.

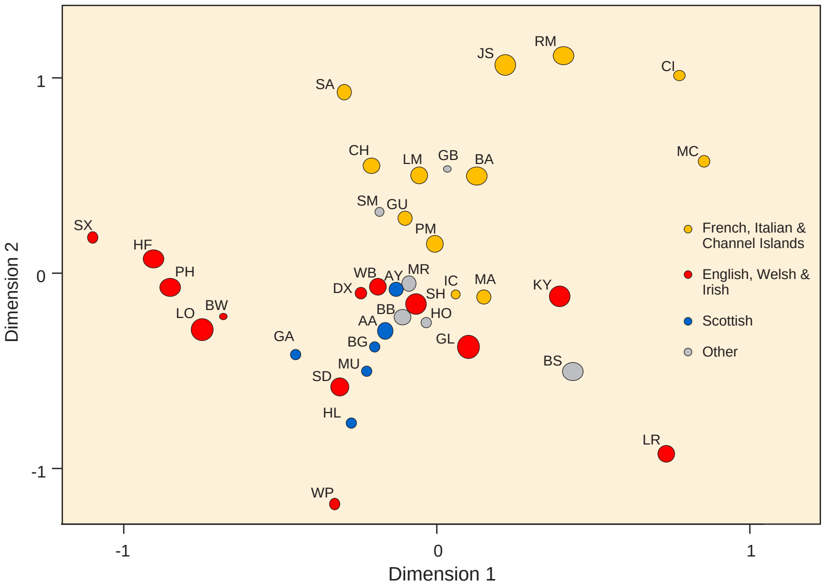

Figure 1. Genetic distances between European cattle breeds. The complex table of genetic distances between pairs of breeds has been simplified and presented as a 3-d plot. Each breed is plotted in a 3-dimensional cube, with the size of the circle indicating the distance from the front of the cube. French, Italian and Channel Island breeds (orange) tend to cluster in the top right-hand side of the diagram, whereas British breeds (red and blue) are towards the lower left. A few breeds from Germany, Switzerland, and the Benelux countries are towards the centre of the diagram (grey).

A simplified version of the relationships that we found between breeds is shown in Figure 1. We identified two major groups: the first, a group of continental breeds from France and Italy which also contained the Channel Island breeds; the second, a group of breeds from mainland Britain and North Western Europe. In general, the relationships between breeds reflected their geographical origin (and most probably a common ancestry) rather than their primary use (i.e. dairy and beef breeds did not form separate groups). Breeds from mainland Britain tended to have less genetic variation (i.e. lower heterozygosities) than continental breeds such as the Limousin, Charolais and Blonde D'Aquitaine. This is probably related to the smaller effective population size of British breeds and possibly their longer history.

Genetic changes within breeds

During the last century a number of pre-eminent British breeds (e.g. Jersey, Aberdeen Angus, and Hereford) were exported to other countries around the world. Successful breeding in some of these locations has led to re-importation into the UK. Among some European breeds, there has been an increasing influence of Holstein cattle from North America. This influence is not only on black-and-white cattle populations (e.g. Friesians), but now also on red-and-white breeds, such as the Ayrshire, Shorthorn and Meuse-Rheine-Yssel , in which red-and-white Holstein sires have been used. Analysis of relationships between breeds based on blood type data confirms that the Ayrshire, Shorthorn, Meuse-Rheine-Yssel and Holstein-Friesian are now very close genetically.

The widespread use of sire lines from the United States and Canada is common in other breeds. Since the mid-1970s, British Hereford breeders, for example, have been importing Canadian animals for breeding and around 90% of the British Hereford population now have some Canadian ancestry. Data from the Cattle Blood Typing Service has allowed us to look at the impact of this importation on the genetic diversity in the UK population. We compared Hereford populations from five countries (Britain, Ireland, Sweden, Canada and New Zealand) with each other and with six other breeds. Data from the British populations were divided into animals with no known overseas ancestors ('traditional' British Herefords) and those known to have ancestors from overseas ('modern' British Herefords). Canadian and British populations were further divided according to year of birth and polled or horned status.

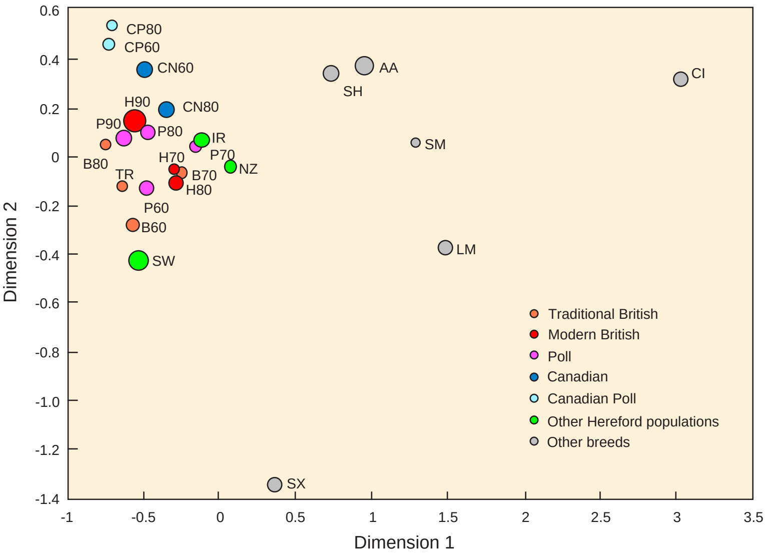

Figure 2. Genetic distances between Hereford populations. Genetic distances between pairs of populations have been simplified in a similar way as in Figure 1 . The Hereford populations (red) all cluster together in the top left-hand side of the diagram, with the overseas populations (blue and green) around the perimeter of those from the UK. Other breeds (grey) lie some way away from this cluster of Hereford populations.

KEY

Abbreviation	**Breed**
AA	Aberdeen Angus
AY	Ayrshire
BB	Belgian Blue
BA	Blonde d'Aquitaine
BG	Belted Galloway
BS	Brown Swiss
BW	British White
CH	Charolais
CI	Chianina
DX	Dexter
GA	Galloway
GB	Gelbvieh
GL	Gloucester
GU	Guernsey
HF	Hereford
HL	Highland
HO	Holstein-Friesian
IC	Icelandic
JS	Jersey
KY	Kerry
LM	Limousin
LO	Longhorn
LR	Lincoln Red
PH	Poll Hereford
MA	Maine-Anjou
MC	Marchigiana
MR	Meuse-Rhein-Yssel
MU	Murray Grey
PM	Piemontese
RM	Romagnola
SA	Salers
SD	South Devon
SH	Shorthorn
SM	Simmental
SX	Sussex
WB	Welsh Black
WP	White Park

We found that all the Hereford populations clustered together and were significantly different from other breeds based on their blood types (Fig. 2). There was also a pattern associated with the geographic origin of the Hereford populations, so that horned and polled groups from the same geographic region were closely related. The extent of Canadian admixture in the modern British Hereford population, estimated from blood type data, was about 65% and this is close to the value expected from the known breeding history of the population. This result is important because it demonstrates that we can now estimate genetic admixture without the use of herdbooks, which are often not available for many threatened breeds.

Variation within traditional Herefords of purely British ancestry has declined over the last 30 years: there may be no more than 400-500 animals of purely British descent left in the UK, compared with tens of thousands in the 1960s. The modern Hereford population in the UK contains genes that are mostly from animals of Canadian and British origin. Interestingly the Canadian Herefords were found to be less variable genetically than other Hereford groups (Fig. 3) and importation of genotypes from this particular group may have accelerated the loss of genetic diversity in the UK.

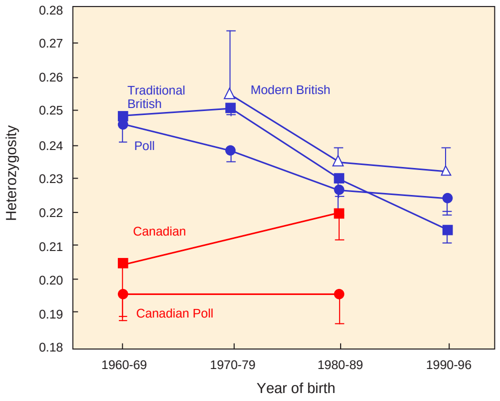

Figure 3. Heterozygosity within Hereford populations. Genetic variation has declined in British populations since the 1960s. Samples of Canadian animals in the UK are significantly less variable than those from other countries.

The changes seen in the Hereford population are likely to be mirrored in other breeds in the UK and elsewhere. This study also illustrates how the substitution of native populations by animals from another national population may result in a loss of genetic variation, despite there being a relatively large number of Herefords left in the UK. These results were partly instrumental in persuading the Rare Breeds Survival Trust to instigate a new category of 'Native' breeds, of which the Hereford was the first to be identified as under threat.

Future work

Further studies are required to assess the long-term effects of population substitution and to evaluate whether the benefits of improved performance outweigh the costs in, for example, reduction in fertility. This could be achieved by a statistical analysis of the past and current pedigree structure, or by analysis of genetic variation as illustrated here or a combination of both. Ongoing research at Roslin Institute is directed towards developing new tools to measure and assess genetic variability and devising breeding plans that maximise genetic progress whilst maintaining genetic variation (see article by John Woolliams in 1994/5 Annual Report). One limitation of the use of blood groups is that they represent loci that are clustered on only nine of the chromosomes. Molecular markers such as AFLPs and microsatellites can now be used to provide information on the whole genome and are potentially much more useful.

Improving performance is essential for the commercial producer to remain competitive and preservation of genetic diversity is often regarded as somebody else's problem. We would argue, however, that it is in the breeders' long term interest to take into account the need for gene conservation, and to evaluate their breeding strategies accordingly. Breeders and breed societies first need to understand the present position of their breed: this can be determined from an analysis of historical records supplemented with data from genetic markers.

Further information on genetic diversity in cattle is available from the EC Cattle diversity database which is maintained by Roslin Institute and available via www.ri.bbsrc.ac.uk/cdiv.www/homepage.htm.

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