Deleterious alleles seem to have been purged in a feral strain of inbred cows. Here we provide support for this hypothesis in a study of the Chillingham cattle, which shows that this viable herd is almost genetically uniform. The homozygosity of this herd far exceeds that of other cattle and that found in wild populations of other mammalian species. This feral herd, which lives in a park in northern England, is thought to have experienced no immigration for at least 300 years (Fig. 1). Despite this genetic isolation, records of calvings and deaths suggest that there has been no drop in fertility or viability. In 1947 the population crashed to five bulls and eight cows; as of 30 October 2000 it numbered 49 individuals. Studies of blood groups and biochemical polymorphisms that represent a small number of genetic loci showed homozygosity for the same alleles at each locus.

We successfully amplified between 3 and 15, respectively, the effective population size of sires and dams per generation of 50% in the population size, and a mean number of 25 markers sampled. These markers are highly polymorphic in cattle, with a heterozygosity of typically 70%, and cover 15 of the 29 autosomes. Three markers are located around the bovine major histocompatibility complex (MHC) region, where selection might maintain polymorphism.

We obtained tissues from calves, adult cows over 6 years old and bulls that died in 1998–99 (n = 13). Family relationships and causes of death were unknown; there was no evidence of infectious disease. DNA from the samples was scored for 25 microsatellite markers. These markers are highly polymorphic in cattle, with a heterozygosity of typically 70%, and cover 15 of the 29 autosomes. Three markers are located around the bovine major histocompatibility complex (MHC) region, where selection might maintain polymorphism.

We observed no significant differences in the genotypes between sampled and untyped animals. The variation was due to the poor quality of DNA extracted from some hair-root samples. All samples showed an identical homozygous genotype for 24 of 25 markers. For one marker (HU616 on chromosome 13, amplified or sequenced from 11 samples), nine individuals were heterozygous for the same alleles at each locus.

The observed genotype frequencies at the segregating locus are not significantly different from Hardy–Weinberg equilibrium (P = 0.057, exact test). Re-typing, re-scoring, and sequencing the single marker HU616 gave the same results, making a procedural artefact or a recent mutation unlikely. Homozygosity could be maintained by selection. Homozygosity was observed at two linked markers on chromosome 13 (9 and 5 animals typed successfully at each). But these markers were 5 and 3 centimorgans from HU616, respectively, too distant to observe a remaining ancestral heterozygous segment.

For the bovine genome (which has a total map distance of 30 morgans), the expected number of crossovers in the genome during meiosis is 30, with random breeding in isolation for 67 generations, initial complete heterozygosity is predicted to result in 30 heterozygous segments with a mean length of only 1.5 centimorgans. But these markers were 5 and 3 centimorgans from HU616, respectively, too distant to observe a remaining ancestral heterozygous segment.

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