

Conservation of the Existing Domestic Animal Populations of the Fertile Crescent Region of Southwest Asia

Monali Rathod*

Department of Microbiology, University of Science and Technology of China, Anhui, China

DESCRIPTION

Bos primigenius, the precursor of modern cattle, was domesticated by humans for the first time around 10,000 years ago in the Fertile Crescent region of Southwest Asia. Existing domestic cattle, which involve humpless taurine (*B. taurus*), humped zebu (*B. indicus*), and numerous *B. taurus/indicus* hybrid populations, have evolved into more than 1,100 recognized breeds through genetic drift and natural and artificial selection. More than 200 locally adapted landrace or native cow breeds have been threatened with extinction and increased vulnerability as an outcome of socioeconomic preferences for huge, highly productive dairy, beef, and dual-purpose breeds starting in the middle of the twentieth century.

North-western Europe's agro-ecological habitats will unavoidably experience major change over the course of the next century as an outcome of the onset of rapid climate change, notably in the Arctic and circumarctic regions. Thus, it is becoming increasingly clear that the conservation and management of livestock genetic resources in this area are necessary for the long-term viability of animal production systems and food security. For quantitative health, reproductive, and production variables, locally adapted native cattle breeds will have accumulated novel genetic variation and haplotype combinations due to their different microevolutionary histories and low levels of external gene flow. Therefore, these populations might be crucial to breeding programmes in the future with the goal to adapt European livestock to new agro-ecological and production contexts.

Animal geneticists and conservation biologists are provided with the ability to characterize genomic variation and estimate population genetic parameters in threatened or endangered livestock breeds using powerful and affordable tools for genotyping large numbers of single nucleotide polymorphisms. The strategies for managed breeding and biobanking of these populations will be supported by these studies which are already supplying crucial baseline data for genetic conservation.

Kerry cattle are regarded as valuable culturally to Ireland as a native breed with a reportedly ancient heritage. In harsh upland

regions with low-quality feed, which are typical of southwest Ireland, where the Kerry breed emerged, this landrace cow herd continues to be productive. The Kerry breed is also thought to be the remains of which was once a much larger and more widespread historical population; these cattle were frequently referred to locally in Ireland as the "poor man's cow" due to their capacity to produce relatively large quantities of milk on very little fodder. Genetic information has been used to assess levels of inbreeding, and the total amount since the herd book's founding in 1887 reached 15% in 1985. Due to altering socioeconomic and agricultural conditions, the Kerry cattle breed has had substantial population variations in recent decades. When the number of breeding females decreased to less than 200 in the 1980s, the Irish agricultural authorities decided to implement a Kerry cattle conservation scheme. The scheme is still in place today under the Department of Agriculture, Food, and the Marine Kerry Cattle Premium Scheme.

As an outcome of the institutional conservation policies and supports initiated during in the early 1990s, the population of Kerry cattle increased significantly, reaching more than a thousand animals by 2007 (Food and Agriculture Organization, 2007). The Kerry cow population, however, has significantly decreased recently as an outcome of the deteriorating economy in Ireland following the 2008 financial crisis. As a result, the breed is now considered endangered and undergoes a serious risk of extinction or extinction through interbreeding with other breeds. One of the first European heritage cattle breeds to be studied utilizing molecular population genetics methods was the Kerry breed of cattle. We have previously conducted comparative evolutionary analyses of the genetic diversity in Kerry cattle as well as other British, European, African, and Asian breeds using autosomal microsatellite genetic markers and mitochondrial DNA control region sequence variation. More recently, investigations of medium- and high-density SNP genotypes made using genome sequence data from a British *B. primigenius* subfossil that is extinct have demonstrated that Kerry cattle still contain a strong wild aurochs genomic signature. This outcome highlights the Kerry population's genetic individuality and has significant implications for the preservation and management of the breed.

Correspondence to: Monali Rathod, Department of Microbiology, University of Science and Technology of China, Anhui, China, Canada, E-mail: Monali123@gmail.com

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