

Resource Summary Report

Generated by [dkNET](#) on Sep 8, 2026

CaDBase: Genetic diversity in cattle

RRID:SCR_008146

Type: Tool

Proper Citation

CaDBase: Genetic diversity in cattle (RRID:SCR_008146)

Resource Information

URL: <http://www.projects.roslin.ac.uk/cdiv/>

Proper Citation: CaDBase: Genetic diversity in cattle (RRID:SCR_008146)

Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented on July 16, 2013. The objective of the project is the standardization of micro-satellite markers used within participating laboratories, use of DNA markers to define genetic diversity and to enable monitoring of breeds to promote conservation programs where required, and the determination of diversity present in rare and local breeds across Europe. The blood typing laboratories are now beginning to use micro-satellite markers as an alternative to serology for parentage verification, and are selecting a common set to be used from the several hundred micro-satellite markers available that cover the bovine genome, produced as part of the Bovine genome mapping project (See BovMaP). Work with micro-satellite markers has shown that they are valuable tools for examining genetic diversity and phylogeny in many species. However, for work carried out in different laboratories to be comparable, it is essential that the same markers are used. To maintain the compatibility of data generated by the various typing labs, it is essential that all laboratories adopt the same markers and typing protocols. It is therefore of paramount importance that the blood typing laboratories and research labs that are examining the genetic structure of the cattle populations adopt a common panel of the best micro-satellite markers available. Some pilot comparative work has been undertaken through the International Society for Animal Genetics, but so far this has only involved the blood typing laboratories. One objective of this project is to facilitate the comparison of the micro-satellite markers currently in use in the different types of laboratory and determine the efficiency of the markers available in revealing genetic differences within and among breeds. It will also be important to compare the use of markers in different laboratories to determine how robust they are and how easily results can be compared. From comparison of the markers, those that are most suitable will be selected to form a panel which will be recommended for pedigree validation and genetic surveys. Cattle are an important source of food in Europe, and intense selection has resulted in the development of specialized breeds. Selection for high-producing dairy cattle has been successful, but one associated drawback is that the cattle population, both in Europe and North America, has been skewed dramatically

towards one breed, the Holstein/Friesian. So there has been a decline in the number of individuals of other breeds, and hence a general erosion of the genetic base of the cattle population. The progressive move towards the North American-type Holstein animals has also resulted in the requirement for high input/high output farming and intensive management schemes. The impact of this on the environment has been significant, e.g. pollution problems arising from the need for high nitrogen fertilizers to produce sufficient high quality fodder, and disposal problems associated with slurry waste. Poorer areas of the community have been unable to compete with such farming systems, and are more suited to low input/low output farming using traditional stock. It is however the future perspective that is of greatest concern. It is impossible to predict requirements for cattle production - quality, production type, management systems, etc. The ability to switch rapidly to alternative production will be dependent on the genetic base of the population available to selection programs. It is therefore essential to maintain the greatest genetic diversity possible in the cattle population. Whilst current farming practices are perceived to be both efficient and acceptable, the breeds less favored by commercial farmers will dwindle. It is therefore important that on an European scale efficient management of these breeds maintains the widest genetic base possible. This project aims to carry out a survey of the current genetic base of the European cattle population and to provide the tools to assist breeding programs to maintain a broad base. The blood typing laboratories are now beginning to use micro-satellite markers as an alternative to serology for parentage verification, and are selecting a common set to be used from the several hundred micro-satellite markers available that cover the bovine genome, produced as part of the Bovine genome mapping project. Early work to measure genetic diversity used blood groups to show differences between breeds and the diversity present. Unfortunately, the number of loci available are limited, with only the B system being sufficiently polymorphic to be really useful. However, since there is a wealth of information available from such typing, this information can be used to estimate changes in the genetic structure of cattle populations across Europe over the past twenty years. More recently mini-satellite probes have been used to generate "genetic fingerprints" which have been used to show differences between individuals. Such fingerprints have been used to estimate genetic diversity - the greater the number of bands revealed by the fingerprint being equated with greater diversity. This is valid within limits. The main disadvantage of the fingerprint approach is that the chromosomal location and number of loci being sampled, and so the proportion of the genome examined, is unknown. The allelic bands on the gel cannot be easily identified, so allele inheritance cannot be addressed making it impossible to trace ancestry. Through the EC funded BovMaP project, large numbers of highly polymorphic micro-satellite markers have become available, which are being mapped on the bovine genome. These markers are particularly suited to measuring genetic diversity, and markers can be selected to cover the entire genome.

Synonyms: Genetic diversity in cattle

Resource Type: data or information resource, database, portal, topical portal

Keywords: micro-satellite, dna, genetic, diversity, breed, conservation, pedigree, cattle, bovine, cow, blood, typing, serology, parentage, mapping, genome, marker, genetic, structure, population, animal, holstein, farming, fertilizer, locus, polymorphic, allelic, ancestry, people resource

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: CaDBase: Genetic diversity in cattle

Resource ID: SCR_008146

Alternate IDs: nif-0000-20969

Record Creation Time: 20220129T080245+0000

Record Last Update: 20260905T132618+0000

Ratings and Alerts

No rating or validation information has been found for CaDBase: Genetic diversity in cattle.

No alerts have been found for CaDBase: Genetic diversity in cattle.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

Berthouly C, et al. (2010) Revealing fine scale subpopulation structure in the Vietnamese H'Mong cattle breed for conservation purposes. BMC genetics, 11, 45.