

Cattle

Michael D. MacNeil¹ (✉), James M. Reecy, and Dorian J. Garrick²

¹ USDA, Agricultural Research Service, Miles City, MT 59301, USA, mike.macneil@ars.usda.gov

² Department of Animal Science, Iowa State University, Ames, IA 50011, USA

1.1 Introduction

1.1.1 History

All contemporary cattle are thought to have been domesticated from the now extinct aurochs, *Bos primigenius*. Evidence from mitochondrial DNA indicates divergence of two cattle taxa, *Bos indicus* and *Bos taurus*, more than 100,000 years ago (Loftus et al. 1994; Bradley et al. 1996). These two taxa were likely domesticated independently (Grigson 1980; Loftus et al. 1994) some 10,000 years before present. Mehrgarh, in modern-day Pakistan, is a strong candidate for the site of domestication of *Bos indicus* cattle. Catal Hüyük, Anatolia, in modern-day Turkey, is a likely site of the Near-Eastern domestication of *Bos taurus* cattle. There is further but less secure evidence for additional domestications of aurochs in the Nile Valley (Bradley et al. 1996; Troy et al. 2001) and in North East Asia (Mannen et al. 2004). These domestications are postulated to give rise to the *Bos taurus* cattle of Africa and contribute to the gene pool of cattle in Mongolia, North China, Korea, and Japan, respectively.

Immigration of *Bos indicus* cattle into Africa appears to radiate from the Horn and East Coast (Hantotte et al. 2002). This immigration may result from local Arabian contacts. Alternatively, it may have been a consequence of long-distance trade on the Indian Ocean that was also responsible for introducing other domestic species into Africa (Clutton-Brock 1993). *Bos primigenius* was distributed throughout Europe at the end of the last Ice Age, and it remains unclear whether or not all European cattle are derived from the stock domesticated in western Asia (Bailey et al. 1996). However, the dominant mitochondrial DNA haplo-

type in European cattle is consistent with their being of Anatolian origin (Troy et al. 2001; Kühn et al. 2005). Genetic relationships among European *Bos taurus*, African *Bos taurus*, African *Bos indicus*, and Indian *Bos indicus* are illustrated in Fig. 1 (Bradley et al. 1998).

Cattle are not indigenous to Australia, North America, and South America. Importations of cattle to these countries followed the respective patterns of human exploration and colonization. Early importations to Australia and North America were predominantly British breeds, whereas early importations to South America were mainly of Spanish origin (Rouse 1970). Subsequently, *Bos indicus* cattle were brought to the more tropical areas of these continents (Rouse 1970) and still later there were substantial importations of *Bos taurus* cattle from continental Europe (Willham et al. 1993).

1.1.2 Economic Importance

Cattle have had a central role in the evolution of human cultures with significant numbers of cattle produced in every continent except Antarctica. From an economic perspective cattle are the most important domestic animal species (Cunningham 1992). In various parts of the world, cattle provide traction, milk, and meat. Worldwide production in 2004 of beef and veal, nonfat dry milk, butter, and cheese were predicted to be 51,191; 3,486; 6,676; and 13,373 thousand metric tons, respectively (USDA 2005).

Following Lush (1945), modern paradigms for genetic improvement of livestock are commonly traced to Robert Bakewell (1725–1795) whose admonitions included: “Like produces like or the likeness of some ancestor; inbreeding produces prepotency and refinement; breed the best to the best.” Historical

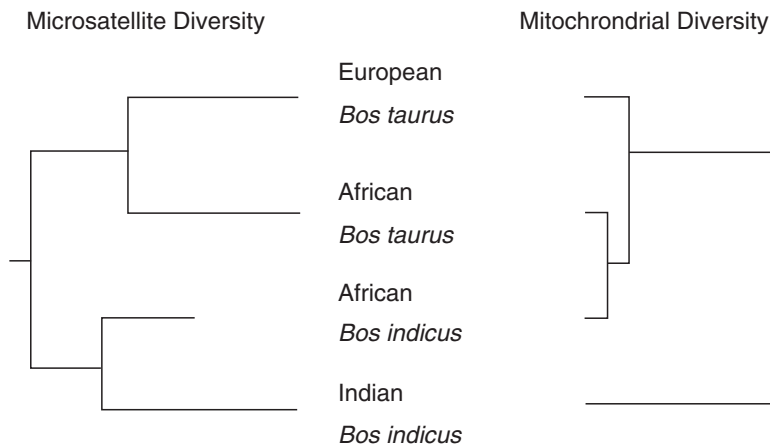


Fig. 1 Phylogenetic tree derived from microsatellite allelic diversity and mitochondrial sequence diversity (Bradley et al. 1998). Note that African *Bos indicus* seemingly derives a majority of their genome from introgression of Indian *Bos indicus* alleles into the African *Bos taurus* maternal background

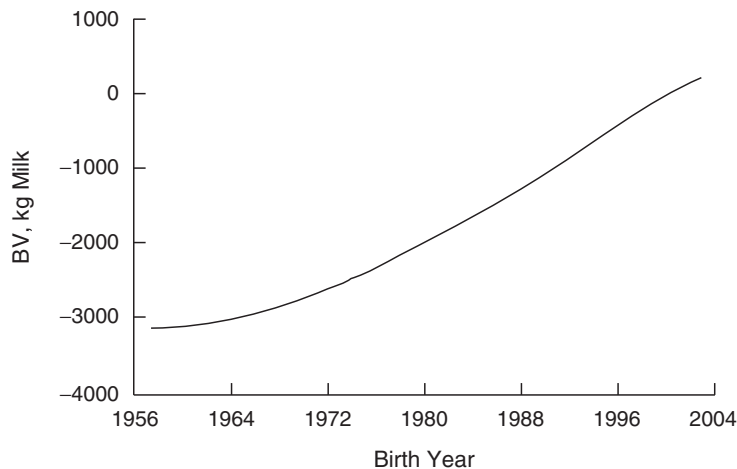


Fig. 2 Genetic trend for fluid milk production of US Holstein cows as of May 2005. From: <http://aipl.arsusda.gov/eval/summary/trend.cfm>

breeding objectives for cattle have focused primarily on increasing yield of milk or milk components in dairy breeds and growth rate, carcass weight, and composition in beef breeds. Success of these efforts in bringing about genetic change can be illustrated by genetic trends in fluid milk production by Holstein cattle in the US (Fig. 2) and growth to weaning by Hereford cattle in Canada (Fig. 3).

Genetic selection for increased production usually, although not always, leads to increased consumption of feed and gross efficiency, while some aspect of fertility is usually impaired (Roberts 1979; MacNeil et al. 1984; Wall et al. 2003). Technology for efficient multiple-trait selection was developed by Hazel (1934) more than 70 years ago and classical applications of

multiple-trait selection for dairy and beef production were put forth in the early 1970s (Norman and Dickinson 1971; Cunningham and McClintock 1974; Dickerson et al. 1974). In regions, where feed costs and land prices are high, breeding objectives have been developed and implemented for dual-purpose cattle that are raised for both milk and meat production (e.g., Niebel 1986; Bekman and van Arendonk 1993). VanRaden (2004) reviewed the changing application of multiple-trait breeding objectives to US dairy production from the early 1970s to the present. Application of multiple-trait breeding objectives and selection indexes to beef production has been relatively more recent (e.g., Ponzoni and Newman 1989; Graser et al. 1994; MacNeil et al. 1994).

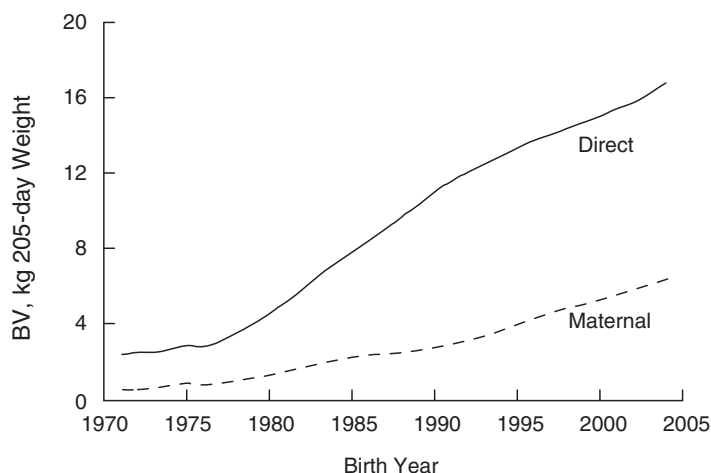


Fig. 3 Genetic trends for direct (solid line) and maternal (dashed line) 205-day weight of Canadian Hereford cattle as of the Spring 2005 Sire Summary. From: http://www.hereford.ca/pdf_files_2008/EPD%20Averages%20Tools%20and%20Trends%202008.pdf

Genetic improvement of cattle is complicated by relatively late attainment of puberty and low reproductive rate, long generation interval, genetic antagonisms, manifestation of economically important phenotypes late in life, and valuable phenotypes that can only be observed post-harvest. Genomic science and its application to selection have the potential to partially overcome several of these obstacles by facilitating selection decisions being made earlier in life without the usual erosion of accuracy. Objectives of this chapter are to review: (1) the current state of genetic mapping in cattle, (2) assignment of economically important phenotypes to those maps, and (3) ongoing development of breeding programs that have been implemented using molecular genetic technologies.

1.2 Molecular Genetics

1.2.1 Genetic-Mapping Resources

The first bovine genetic maps were generated using somatic cell hybrid (SCH) panels and fluorescent in situ hybridization (FISH). Heuertz and Hors-Cayla (1981) and Womack and Moll (1985, 1986) were the first reports on the use of somatic cell hybrids to develop maps of conserved synteny between bovine genes and previously mapped human homologs of these genes. A bovine/hamster somatic cell radiation hybrid panel was

recently developed and used to assign 1,303 previously unassigned expressed sequence tags (ESTs) to chromosome segments (Itoh et al. 2003). Itoh et al. (2005) also used a bovine radiation hybrid panel to map 3,216 microsatellites and 2,377 ESTs. ZOO-FISH mapping has been completed, in which human chromosome-specific painting probes were hybridized to cattle chromosomes (Hayes 1995; Solinas-Toldo et al. 1995; Chowdhary et al. 1996) to produce comparative maps. However, as with somatic cell hybrid panels, gene order could not be addressed with these chromosome pairs.

There are numerous reports on the development of chromosome-specific linkage maps (e.g., Barendse et al. 1993). However, Bishop et al. (1994) were the first to report a genetic linkage map for a majority of the bovine genomes. That map was shortly followed by second-generation medium density maps (Barendse et al. 1997; Kappes et al. 1997). At present, over 3,800 simple tandem repeat polymorphisms have been mapped in cattle by linkage analysis (Ihara et al. 2004). This most recent map comprised 29 sex-averaged autosomal linkage groups and a sex-specific X-chromosome linkage group covering 3,160 centiMorgans (cM). The average interval between markers was 1.4 cM.

Radiation hybrid (RH) mapping (Goss and Harris 1975) has recently been rediscovered as an effective approach to building ordered maps of sequence-tagged sites, regardless of allelic variation. Womack et al. (1997) reported on the generation of a 5,000-rad bovine whole-genome RH panel. This RH panel has served as a resource for mapping the

Genome Mapping and Genomics in Domestic Animals

Cockett, N.E.; Kole, C. (Eds.)

2009, XVI, 280 p. 49 illus., 12 illus. in color., Hardcover

ISBN: 978-3-540-73834-3