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The Bovine Genome Sequencing Project

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In approximately 20 years, bovine genomics has progressed from synteny mapping of protein gene products to a nearly completed 7.5X whole genome sequence. Sequencing of the bovine genome began in December, 2003 and the high-quality genome sequence with 2,000,000 DNA markers was released in August, 2006. A single animal from the Hereford breed was used to generate the bulk of the sequence. Animals from additional breeds, specifically Holstein, Angus, Jersey, Limousin, Norwegian Red, and Brahman were sequenced at low coverage to facilitate single nucleotide polymorphism (SNP) discovery. The cattle genome map serves as a prototype for genomic studies in other bovids such as goats, sheep, and river buffalo in which chromosome arms are totally conserved at the current level of cytogenetic and map comparison. Cattle genomics has contributed to the discovery of genes underlying economically important phenotypes including quantitative traits, to the development of bovine models of human diseases, and to our understanding of mammalian chromosome evolution.