

# The Chosen One

How a single cow and the Hereford breed continue to impact the world.

by **Will Fiske**

**L**1 Dominette 01449 (L1 Dominette) was born April 14, 2001. She was a product of the Line 1 (L1) Hereford cattle breeding program at the Livestock and Range Research Station at Miles City, Mont. USDA animal scientists first developed L1 Herefords in 1934 as part of a strategic effort to introduce successful linebreeding to beef cattle production systems. Recognized as being at the forefront of beef cattle breeding research, the Line 1 Hereford population's contribution to procedures for performance testing is historic. Data from Line 1 was fundamental in developing the first estimates of heritability and genetic correlation for beef cattle.

As for L1 Dominette, approximately 70 years of disciplined and well-defined breeding resulted in her possessing a high level of inbreeding (30% inbreeding coefficient) and a 93% genetic relationship with her sire, L1 Domino 99375 (31% inbreeding coefficient). Such high inbreeding coefficients were nontraditional to the Hereford breed but a unique focus of the Line 1 breeding program. Over her productive life L1 Dominette reared five calves, but it wasn't the genetic contribution to her progeny that established her as a matriarch of the Hereford breed. In fact, the impact of L1 Dominette and her genomic profile reach far beyond the American Hereford Association (AHA) registry.

On April 24, 2009, nearly eight years after L1 Dominette was born, the field of animal genomics reached a significant milestone: the bovine genome was officially sequenced, as reported in the *Journal of Science*. And it was L1 Dominette 01449's genome that was sequenced. From the *New York Times* to BBC News, this scientific achievement made headlines around the world — marking a major breakthrough for the scientific community.

“Understanding the cattle genome and having the sequence will allow researchers to understand the genetic basis for disease in domestic cattle and could result in healthier production of meat and milk while reducing producers' dependence on antibiotics,” United States Secretary of Agriculture Tom Vilsack said in a statement.

## Groundbreaking genomic research

At the time, the bovine genome was one of the largest animal genomes ever sequenced. Sequencing the bovine genome took a team of more than 300 researchers from 25 countries six years and \$53 million of funding. L1 Dominette was selected as the reference animal for the project due to her increased genetic

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uniformity which resulted from long-term linebreeding. This level of inbreeding minimized the amount of expected heterozygous haplotypes, making her DNA ‘simpler’ to interpret and the genome sequence easier to assemble.

Throughout the bovine genome project, substantial interest from animal agriculture groups immediately began to leverage preliminary research and the first draft of the bovine sequence into actionable tools and solutions. Parentage verification was an early goal for the application of the bovine reference genome, and by the mid-2000s cattle producers on the cutting edge were utilizing a parentage SNP (single nucleotide polymorphism) panel in place of blood typing for a more robust means of parent verification. In 2009, the cost of SNP genotyping declined to the point it was half the price of microsatellite genotyping, which

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### Sources:

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Rexroad, Caird, et al. “Genome to Phenome: Improving Animal Health, Production, and Well-Being – a New USDA Blueprint for Animal Genome Research 2018–2027.” *Frontiers in Genetics*, vol. 10, 2019, <https://doi.org/10.3389/fgene.2019.00327>.

promoted more academic efforts to identify the SNPs, which could characterize specific breeds and be correlated to the expression of polygenic traits of economic importance. This created an opportunity for cattle genomics consortia and cattle geneticists to work together to develop new methods and genomic products which promoted the adoption of high-throughput genotyping in the cattle industry. Most notably, this time of collaboration resulted in the Bovine HapMap consortium and the design of a new cattle SNP chip — the BovineSNP50. It's important to note that the majority of the genotyping technology used to map the bovine genome was the result of technology developed to map the human genome, as part of the Human Genome Project.

### Effects on agriculture

The accomplishments from sequencing L1 Dominette's DNA have fundamentally improved our understanding of cattle genetics. A tremendous amount of information has been discovered since mapping the bovine genome. Millions of DNA markers have been identified to enhance selection decisions and ultimately the management decisions of individual animals, herds and livestock populations. Human health has also benefited from the sequencing of the bovine genome.

"By comparing the human genome to the genomes of many different species, such as the domestic cattle, we can gain a clearer view of how the human genome works in health and in disease," said Dr. Raynard S. Kington. Dr. Kington served as the Acting Director for the National Institute of Health (NIH) when the bovine breakthrough was publicly published. The NIH's National Human Genome Research Institute and the USDA were two of the primary funders for the bovine sequencing project.

It has been nearly 20 years since L1 Dominette's DNA was

first sequenced and the groundbreaking research was made available to the world. Numerous livestock species have capitalized on the institutional knowledge gained from her DNA and the Bovine Genome Project.

Swine breeding companies actively use genome information to accelerate genetic improvement by 30% and address efforts to mitigate the costly effects of Porcine Reproductive and Respiratory Syndrome. Poultry breeding companies use genome information to accelerate genetic improvement in broilers and layers as well as identifying genetic lines that are more resilient to the negative effects of heat stress. Aquaculture-based breeding systems, which utilize genomic selection, have observed rapid genetic gain by



L1 Dominette 01449

Photo courtesy of USDA Agricultural Research Service Research Geneticist Michael D. MacNeil.

doubling the selection accuracy in a single generation for species such as rainbow trout.

Genomic technology will continue to evolve in its application to food animal production around the globe, ever improving the safety, security and efficiency of agricultural production systems. **HW**

**Editor's Note:** Will Fiske is a technical service scientist for NEOGEN.