

Accelerate Agrigenomics Breakthroughs

Agrigenomics has undergone dramatic advancements, enabling higher-yielding crops and livestock, greater disease resistance, and improved reproductive health. This progress translates to increased returns on investment and the development of long-term solutions for food production security.

Individual discovery efforts and the work of international research collaborations have facilitated significant breakthroughs in cattle breeding. A pivotal innovation from Illumina was the BovineSNP50 BeadChip, which offers greater accuracy in prediction of individual genetic merit in both dairy and beef cattle.



1970–1990 Observation

Sowing the seeds for genetic breakthroughs.

The Human Genome Research Initiative paves the way for mapping of livestock genomes.

Before 1990, beef and dairy cattle selection relies heavily on pedigree performance test information and progeny testing. Trait-specific expected progeny differences (EPDs) in beef cattle and genetic predictions for dairy cattle are in their infancy. Because limited DNA sequencing data are available for agriculture, the bovine genome is essentially unknown. Early genome research activity is primarily focused on the human genome. Technologies for other species are being developed and applied. The use of restriction fragment length polymorphisms, microsatellites, or STR markers is becoming more widespread and the concept for development of genetic linkage maps for animals and plants slowly emerges.

Several key discoveries advance the field of bovine genomics during this time:

Soller M, et al.¹⁻³ demonstrate the linkage of growth hormone restriction fragment length polymorphisms (RFLPs) with potential phenotypic differences in traits for milk production in Israeli Holstein dairy cattle. This work introduces the concept of detecting linkage between markers and quantitative loci. This finding leads to the discovery of more DNA markers with the potential to transform genetic improvement in livestock through marker-assisted selection and breeding.

The radiation hybrid (RH) panel developed by Womack JE, et al. (1986)⁴ fuels interest in cattle genomics and comparative gene mapping. The RH panel is used to assign enzymes, DNA fragments, and gene sequences to syntenic groups, which are later assigned to chromosomes by Fries R, et al. (1986)⁵ using fluorescence *in situ* hybridization (FISH) cytogenetic tools. This work anchors the bovine physical and genetic linkage maps, which continue to be developed and refined. Fries R, et al. and other collaborators later develop molecular cytogenetic techniques for hybridizing large parts of the bovine genome in yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), and cosmids to specific bovine chromosomes.

1990–2000

Discovery

Exploring the potential of agrigenomics.

Development of physical and genetic linkage maps for cattle occurs, driving research interest and funding.

Interest in linkage associations with animal phenotypes continues to grow, leading to the discovery of markers linked to economically relevant traits. Researchers around the world uncover significant markers for milk volume, protein, and fat content in dairy cattle, catalyzing global interest, research, and funding. Scientists speculate about unmasking additional genetic traits in cattle and how these differences might influence the agricultural industry.

Several key discoveries advance the field of bovine genomics during this time:

Fries R, et al. (1990)⁶ isolate and report the first ubiquitous microsatellites (di-, tri-, and tetranucleotide repeats) in the bovine genome. Many additional microsatellites and RFLPs are discovered as a result of this finding.

Georges M, et al. isolate several dinucleotide repeats to assemble a linkage map for Holstein dairy cattle and apply genomic analysis to livestock improvement.

The United States Department of Agriculture (USDA) Agricultural Research Service (ARS) and Meat Animal Research Center (MARC) publish the first publicly available genetic linkage map for cattle⁷, which is followed by a genetic linkage map developed by researchers in Australia. The original maps are updated and refined by the USDA and others during the 1990s. Research funding from the European Community (EC) is used to develop and merge genetic linkage and physical maps. These maps facilitate identification of quantitative trait loci (QTL), the genes responsible for simple and complex traits involved in meat and milk production in cattle.

2000–2010

Innovation

Cultivating the benefits of genomics.

Illumina introduces the revolutionary BovineSNP50 BeadChip, transforming the dairy and beef industries.

For the first time, accurate and reliable estimates of genetic inheritance are possible. Theoretical evaluations speculate that large numbers of markers evenly distributed across the bovine genome could be used to link phenotype with genotype, predictably estimating the genetic merit of an individual animal. The collection of phenotypic data over the previous decades accelerates the adoption of genomic selection. The BovineSNP50 BeadChip leads to a radical shift from phenotype- to genotype-based breeding.

Several key discoveries advance the field of bovine genomics during this time:

Meuwissen, et al. (2001)⁸ introduce the concept of using genomic selection in agriculture.

Research geneticist Curt Van Tassell develops an algorithm for selecting evenly spaced SNPs that reflect allele frequencies in cattle breeds. Many of these SNPs inform the content of the first BovineSNP50 BeadChip. The reduced representation sequencing method for SNP discovery proposed by Van Tassell is used to generate approximately 62,000 high-quality SNPs that are found on the BovineSNP50 BeadChip⁹ and subsequent Illumina arrays.

The bovine genome sequence is annotated and analyzed¹⁰⁻¹², providing new insights into cattle biology.

Illumina scientists Marylann Munson and Cindy Taylor Lawley lead an organized effort to consolidate SNP genotyping data from around the world, forming the BovineSNP50 Consortium. The SNP content gathered from this consortium is used to develop the BovineSNP50 BeadChip⁹—the first SNP genotyping assay for cattle—in collaboration with the USDA, the University of Missouri, and the University of Alberta. The BovineSNP50 BeadChip is adopted globally by many organizations, including the National Institute for Agricultural Research (INRA), the Centre for Integrative Genetics (CIGENE), the Commonwealth of Scientific and Industrial Research Organization (CSIRO), and others to build an even broader consortium. Researchers, breed associations, and industry leaders begin using the BovineSNP50 BeadChip to combine genotype information with phenotypes, enabling accurate prediction of genetic merit in Holstein, Jersey, and Angus cattle breeds.

2010–2013

Widespread Adoption

Genotype-based breeding is born.

Illumina introduces the BovineLD and BovineHD BeadChips.

Following the introduction of the BovineSNP50 BeadChip, genotyping from sire selection to birth is widely adopted by cattle breeders. Cattle selection intervals and breeding cycles are compressed by leveraging both genomic and reproductive technologies. The BovineSNP50 and subsequent BovineHD and BovineLD BeadChips become industry-leading arrays for cattle screening.

Several key discoveries advance the field of bovine genomics during this time:

In collaboration with several agricultural organizations, Illumina develops the BovineHD BeadChip, a high-density array for genomic selection in cattle. This collaboration involves many prominent agricultural research organizations, including USDA ARS, Pfizer Animal Genetics, the University of Missouri, the National Association of Livestock and Artificial Insemination Cooperatives (UNCEIA), and INRA.

Illumina develops the BovineLD BeadChip¹³—a low-density array for cost-effective genomic selection in beef and dairy cattle—in collaboration with the Department of Primary Industries Victoria, INRA, UNCEIA, and USDA ARS. Illumina BeadChips for bovine genotyping are widely adopted for many cattle breeds and species with large amounts of phenotypic data, statistical predictions of genetic merit, and training populations of animals available. Physical traits in cattle can be evaluated by direct association, as correlated traits, or as haplotypes of many SNPs that account for variation.

Breeding future success through agrigenomics.

Early research and discovery efforts in agriculture lay a strong foundation for modern agrigenomics methods. The BovineSNP50, BovineHD, and subsequent BovineLD+ BeadChips from Illumina revolutionized marker-assisted breeding and selection techniques in agriculture. Today, cattle breeders and farmers are equipped with the accurate genetic information they need to produce commercially viable crops and animals. Through collaboration with the agricultural community, Illumina is committed to developing new solutions for embryonic selection, epigenetics, metagenomics, disease resistance, and more. At Illumina, the innovation in Agrigenomics continues.

To learn more about Illumina technology for genomic selection and how consortia can reduce costs for agricultural researchers, visit www.illumina.com/agrigenomics

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