



Non-Confidential Description - 3930

“Genomic Regions with Epigenetic Variation that Contribute to Phenotypic Differences in Cattle”

Field of the Invention:

Single-Nucleotide Polymorphisms (SNPs), DNA Methylation, Milk, Fat and Protein Yields, Dairy Cattle Phenotypic Variation

Inventors:

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Background

The combined effects of genetic selection and dairy management have resulted in a doubling of milk yields in the last five decades. However, understanding of how genetic selection alters milk production and other physiological traits remains elusive. In recent years, scientists have recognized that there are genetic mechanisms beyond nucleic acid sequences that can alter an organism’s phenotypes, which are broadly termed epigenetic effects. While significant research efforts have been directed at studying the association of DNA sequence variations, little is known about the influence of epigenetic variation on yield. Methylation of DNA is one such mechanism. By identifying differentially methylated regions (DMRs), one can identify putative regions of epigenetic variation.

Invention Description

The subject invention covers a method of detecting epigenetic markers to identify physiological traits in the animal family, *Bovidae*. The inventors developed this method of utilizing methylation levels of DNA as epigenetic biomarkers to determine extreme high milk, fat and protein yields. Through extensive analysis of genomic DNA extracted from cows (*Bos Taurus*) of well-managed herds, the inventor identified a limited number of high milk-yielding DMRs. This research demonstrates that DMRs are an important cause of phenotypic differences between high producing cows and the control cows.

Status of the Invention

The invention covers kits utilizing customized DNA methylation chips and other DNA methylation detection methods that would be used to screen existing cows for traditional breeding and selection practices. The invention facilitates more accurate selection in cattle breeding programs, which would result in savings in herd management and generate increased earnings from production yield improvements. It can be used to identify whether herd management practices are optimized for milk production. The invention also enables more precision genetic engineering by accelerating the rate of identifying genomic regions contributing to variation in phenotypic traits, including but not limited to milk production, disease resistance, fertility and body composition.

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