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P525 : Cattle

Construction Of A Genetic Map For Detailed Milk Composition QTL Mapping In HF Cattle

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A genetic map was constructed in order to map QTLs for a large amount of very detailed milk composition related phenotypes. Blood samples were collected from 5 large half-sib families of Dutch Holstein Friesian daughters from major breeding sires and from a number of smaller half-sib families.

In order to maximise the putative information content SNPs were selected from previous genotyping experiments in the HF population and from dbSNP. Criteria for inclusion in our panel were that SNPs should a) cover chromosomes on both the genetic map and the physical map fairly even-spaced and equally dense, and b) be heterozygous in the majority of the sires of our population. Over 95% of the selected SNPs could be anchored to chromosomal scaffolds in the 3rd generation bovine genome assembly (BTAU3.1) using BLAT.

We genotyped our families of in total nearly 900 heifers and sires in a whole genome scan with a panel of 1536 SNPs.

Subsequently, genetic maps were constructed for all autosomes using CriMap. The resulting maps showed good coverage. Marker orders were largely in accordance with the physical map. Mean marker density of less than 5 cM and approximately 50% marker heterozygosity over all sires were as envisioned.

This high quality genetic map is currently used within a QTL analysis of the milk composition traits.

Please visit our website <www.milkgenomics.com>.