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► To cite this version:

Marie-Pierre Sanchez, Armelle Gion, Anne Barbat, Sebastien S. Fritz, Guy Miranda, et al.. Using whole genome sequences to identify candidate mutations of bovine milk fatty acids and proteins in fairy cattle. PAG XXIV - Plant and Animal Genome Conference, Jan 2016, San Diego, United States. pp.P0526, 2016. hal-02793489

HAL Id: hal-02793489

<https://hal.inrae.fr/hal-02793489>

Submitted on 5 Jun 2020

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P0526

Using Whole Genome Sequences to Identify Candidate Mutations of Bovine Milk Fatty Acids and Proteins in Dairy Cattle

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The content in the 6 major proteins and 23 milk fatty acids was analyzed by GWAS at the whole genome sequence level. Phenotypes were estimated from Mid Infrared spectrometry for 116,495 cows in Montbeliarde (MO), Normande (NO) and Holstein (HO) cattle breeds. 3,032 MO, 2,659 NO, and 2,954 HO cows were genotyped with the Illumina 50K Beadchip®. Genotypes were imputed with FImpute software to the HD level using 522 MO, 546 NO, and 776 HO HD genotyped bulls as a reference, and then to the whole genome sequence (27 millions of variants) using 1,147 sequenced bulls from the 1000 bull genomes project (run 4). Individual test-day records were adjusted for environmental effects and averaged per cow. Analyses were conducted within breed with GCTA software, accounting for the population structure through a HD-based genomic relationship matrix.

From 11 to 69 QTL were detected according to traits and breeds. Resolution obtained in the present study was high enough to directly pinpoint strong candidate genes. For fatty acids, remarkable QTL were found on chromosomes 5 (MGST1), 14 (DGAT1) for saturated fat, 17 (BRI3BP) for C4:0, 19 (FASN) for C12:0, or 27 (AGPAT6) for C16:0. For proteins, major QTL were on chromosomes 6 (CSN3) for kappa-casein, 11 (PAEP and GPSM1) for beta-lactoglobulin, 20 (ANKH) for alpha-lactalbumin, 1 (SLC37A1) for kappa-casein, and 2 (ALPL) for alpha-s2 casein.

The authors acknowledge the financial support from ANR, APIS-GENE, Ministry of Agriculture (CASDAR), Cniel, FranceAgriMer and FGE, and the contribution of the 1000 bull genomes consortium.

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