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► To cite this version:

Didier Boichard, Olivier Bouchez, Aurelien Capitan, Anis Djari, Diane Esquerre, et al.. Large-scale identification of the causative genetic variants influencing traits of economic interest in French dairy breeds. *Plant and Animal Genome*, Jan 2012, San Diego, United States. 2012. <hal-01190277>

HAL Id: hal-01190277

<https://hal.science/hal-01190277v1>

Submitted on 3 Jun 2020

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HAL Authorization

PAG meeting, January 14-18 2012

P0562: Large-Scale Identification of the Causative Genetic Variants Influencing Traits of Economic Interest in French Dairy Breeds

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We recently completed a large-scale QTL mapping project for production traits in the three main dairy breeds used in France, Holstein, Normande and Montbéliarde. More than 3,000 artificial insemination bulls were characterized by the performances of their daughters for 25 production and adaptation traits. All bulls were genotyped with the Illumina Bovine SNP50K BeadChip and whole-genome association studies were done. A total of 305 significant QTL regions were found. Genomic selection methods are already allowing better genetic improvement; however, since of the SNPs present on the whole-genome cattle SNP genotyping microarray, are not in genes and because of the extent of linkage disequilibrium, SNPs associated with economically important traits, are not involved directly in these traits. Until now, the identification of the causative genetic variants involved in the phenotypes of interest remained a difficult task. The identification of these variants, also known as quantitative trait nucleotides (QTNs) involved the mapping of QTLs, the discovery of novel genetic markers in the QTL regions, the fine-mapping of QTLs and then the sequencing of candidate genes. This iterative process was until recently very time-consuming. Novel sequencing technologies offer now new opportunities for the identification of QTNs, with the ability to re-sequence complete genomes, in a relatively cost-effective manner. The aim of our project is to develop a next-generation sequencing-based large-scale approach to identify QTNs influencing milk production in the three main French dairy breeds. Sequence data produced during this project will be part of our contribution to the “1000 bovine genomes” project.