Using genomes sequences to identify causal variants for milk fatty acids in dairy cattle

Armelle Gion Govignon-Gion, Marie-Pierre Sanchez, Pascal Croiseau, Anne Barbat, Sebastien S. Fritz, Mekki Boussaha, Mickael M. Brochard, Didier Boichard

Using genomes sequences to identify causal variants for milk fatty acids in dairy cattle

Govignon-Gion A.[1,2], Sanchez M.P. [1,2], Croiseau P. [1,2], Barbat A.[1], Fritz S. [1,2,3], Boussaha M. [1,2], Brochard M. [1,2,4], Boichard D. [1,2].

[1]INRA, UMR1313 GABI, F78350, Jouy-en-Josas, [2] AgroParisTech, UMR1313, GABI, F-78352 Jouy-en-Josas, France, [3]Allice, F75012 Paris, [4]Institut de l'Elevage, F75012 Paris.

In the framework of the PhenoFinlait project, milk fatty acids were analyzed by genome wide association study at the whole genome sequence level in three French dairy cattle breeds. Traits were estimated from Mid_Infrared (MIR) spectrometry for cows in first or second parity in Montbeliarde (MO), Normande (NO) and Holstein (HO) cattle breeds. More than 8000 cows were genotyped with the Illumina 50K Beadchip®. These genotypes were subsequently imputed within breed in two steps: a first imputation step was performed from the 50K into the HD beadchip level, using a reference of 522 MO, 546 NO and 776 HO bulls genotyped on the HD chip, and followed by a second imputation step to get into the sequence level, using a multi-breed population of 1147 bulls of the "1000 bull genomes project" as a reference panel. Individual test-day records were first adjusted for environmental effects and then averaged per cow. Analyses were conducted within breeds for 23 fatty acids with GCTA software, which implemented a linear mixed model with a polygenic component (based on a genomic relationship matrix), and a residual. The most significant regions were in agreement with already knows regions for fat components or fatty acid desaturation, e.g. on chromosomes 14 (DGAT1 gene), 19 between 51.3 Mb and 51.4 Mb (FASN) and chromosome 26 around 21 Mb (SCD1). Several additional QTLs were also found on chromosomes 5, 11 (especially in the LGB gene for unsaturated fatty acids), 20 and 27 (AGPAT6). Resolution obtained in the present study was high enough to directly pinpoint to several candidate mutations. The authors acknowledge the financial support from ANR and Apis-Gène, Cniel, FranceAgriMer and FGE, and the contribution of the 1000 bull genomes consortium.

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