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Using whole genome sequences to identify QTL for udder health and morphology in French dairy cattle

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Genome-wide association studies (GWAS) at the sequence level were performed in Montbéliarde (MO), Normande (NO) and Holstein (HO) breeds for somatic cells counts, clinical mastitis scores, and 9 to 11 udder morphology traits by breed. The number of bulls considered by trait varied from 1,857 to 2,515 in MO breed, from 624 to 2,203 in NO breed, and from 4,959 to 6,321 in HO breed. The considered response variables were the bulls' daughter yield deviations (DYD), derived from the national genetic evaluations. The DYD reliability of all the bulls considered in the analyses exceeded 0.2 (clinical mastitis) or 0.5 (other traits). Genotypes of the bulls for 27,754,235 sequence variants were imputed in 2 steps, using FImpute software: first from 50K level to HD level using 522 MO, 546 NO, and 776 HO HD genotyped bulls as a reference, and then to the sequence level using 1,147 sequenced bulls from the 1,000 bull genomes project.

GWAS were done independently within each breed and for each trait, using GCTA software, accounting for the population structure through a HD-based genomic relationship matrix.

A total of 49, 18 and 47 significant QTL ($-\log P > 6$) were detected in MO, NO and HO breeds, respectively. Among them, 10, 2 and 12 QTL in MO, NO and HO breeds, respectively, were highly significant ($-\log P > 9$). Most of the QTL affected only 1 trait in 1 breed, but locations on chromosomes 4, 6, 17, 19 and 29 showed significant results for 2 to 5 traits within a breed and/or similar traits in 2 breeds.

Multi-markers analyses (BayesC method) were realized on targeted regions around the QTL (from 2 to 9 Mb length) using GS3 software, to reduce the effect of long distance linkage disequilibrium and to narrow the location of the potential causative mutations. Combining these results with functional annotations led us to several good candidate genes, such as RBM19, GC, NPFFR2, RASSF6 and LIFR.

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