Detection of QTL for mastitis resistance and related functional traits in Bos taurus and Bos indicus

J. Jardim[1], G. Sahana[2], C. Quirino[1], M. Peixoto[3], G. Santos[3] and M. Lund[2]
[1]University of North Fluminense Darcy Ribeiro (UENF), Laboratory Of Animal Breeding, Avenida Alberto Lamego,2000, sala 54, 28013-602, Brazil, [2]Aarhus University, Quantitative Genetics and Genomics, Blichers Allé 20 building K21, 8830 Tjele, Denmark, [3]Brazilian Agricultural Research Corporation (EMBRAPA), Centro Nacional de Pesquisa em Gado de Leite, Rua Eugênio do Nascimento, 610, 36038-330 Juiz de For a, MG, Brazil; juliagazzoni@mbg.au.dk

The quantitative traits loci (QTL) which are segregating both in Bos taurus and Bos indicus can be mapped precisely if information from both population are joined because they diverged at least one hundred thousand years ago. This study aimed to make genetic associations of milkability traits, udder conformation and udder health in Danish Holstein cattle and to examine if QTL identified in this Bos taurus cattle are segregating in a Bos indicus population, Guzera breed by multi-trait meta-analysis. First we carried out association analysis for milking speed and udder conformation traits (~5,000 deregressed-proof breeding values) in Danish Holstein cattle using imputed whole genome sequence data (~15 million SNPs). Significant QTL regions on 16 chromosomes were identified for udder index trait and 18 genomic regions showed significant association with milking speed in Danish Holstein cattle. Association results for clinical mastitis, milk, fat and protein yields in Danish Holstein cattle were available from previous studies. High-density (770k) genotype data of 25 Guzera sires were used to impute 900 cows genotype with 50k SNP chip. A genome scan for somatic cell count, milk fat and protein yields were carried out in Guzera cattle using imputed HD genotype data. The genomic regions identified in Holstein cattle are being studied in Guzera cattle. Meta-analysis across taurus and indicus populations for individual traits will be carried out using weighted Z-score model. We also plan to do multi-trait meta-analysis within population for closely related trait. The work is in progress. The authors acknowledge FAPEMIG for financing the study, CAPES for granting scholarship and Aarhus University for the support and shared knowledge.

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

T. Tribout[1], M. Barbat[1,2], A. Govignon-Gion[1,3], A. Launay[3], R. Lefebvre[1], A. Barbat[1], M. Boussaha[1], P. Croiseau[1], M.P. Sanchez[1] and S. Fritz[1,2]
[1]GABI, INRA, AgroParisTech, Université Paris-Saclay, Domaine de Vilvert, 78350 Jouy-en-Josas, France, [2]Allice, 149 rue de Bercy, 75012 Paris, France, [3]Idele, 149 rue de Bercy, 75012 Paris, France; thierry.tribout@jouy.inra.fr

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, 17 and 45 significant QTL (-logP>6) were detected in MO, NO and HO breeds, respectively. Among them, 9, 2 and 11 QTL in MO, NO and HO breeds, respectively, were highly significant (-logP>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. Authors acknowledge the financial support from APIS-GENE and the contribution of the 1,000 bull genomes consortium.

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