Estimation of LD and haplotype block sizes in European sheep populations

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Detection of QTL influencing somatic cell score in Churra sheep employing the OvineSNP50 BeadChip

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Subclinical mastitis is a major problem for the dairy sheep industry. Somatic cell score (SCS) for milk is generally considered as a good indicator of this complex disease. A previous genome scan performed in a commercial population of Spanish Churra sheep based on the analysis of microsatellite markers, identified a single significant QTL influencing SCS on sheep chromosome (OAR) 20. In the present study we performed a higher density genome-wide analysis in a new commercial population of the same breed using the OvineSNP50 BeadChip. A total of 1696 animals belonging to 16 half-sib families were analysed in this study. Yield Deviations (YD) were considered as the dependent variables in the QTL detection analysis. YD's were calculated, from the raw phenotypic data, as deviations from the population mean and corrected for environmental effects. After a quality control of genotypes, QTL detection was performed using two approaches, based on Linkage Analysis (LA) and combined linkage and linkage disequilibrium analysis (LDLA). Significance thresholds were estimated through permutations and simulations for LA and LDLA respectively. The LA results showed two chromosome-wise significant QTL on ovine chromosomes OAR5 and 25, and one genome-wise significant QTL on OAR20. Segregating families for each of these QTL were identified based on the corresponding within-family analyses. Several chromosome-wise and nine genome-wide significant QTL, on OAR1, 2, 3, 13, 17, 18, 19, 20 and 25, were also identified through LDLA. A preliminary list of positional candidate genes located within the confidence intervals of the most promising QTL regions has been obtained. Additional analyses will be required to help better understand the genetic architecture of these genetic effects. These results were obtained through the EC-funded FP7 Project 3SR-245140 and the Spanish National Project AGL2009-07000.

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Animals from the Sarda (SAW); Lacaune (LAC); Churra (CHU); Scottish Blackface (SBF); Martinique Blackbelly (MBB) and Romane (RMN) breeds were genotyped with the Illumina 50K BeadChip. The resulting data were used: to evaluate the LD decay for increasing distances between SNP; to analyse the LD pattern along the genome and to identify haplotype blocks and their size. LD was measured by r and r^2 statistics for pairs of SNPs from 0 to 1 Mb apart. The average r^2 was calculated for distances between SNPs increasing by 10 Kb steps. The LD pattern along each chromosome was calculated by averaging r^2 in sliding windows of 1 Mb which overlapped 0.5 Mb. The correlations between r at common SNP pairs were calculated to study the level of haplotype sharing between SAW, LAC, SBF and CHU. Correlations between r were calculated both for the whole genome and sliding windows. Haplotype blocks (HB) were estimated using the |D'| based method. No relevant differences in LD decay were observed between breeds, with the highest difference being 0.06 between MBB and CHU. The LD pattern and HB analysis gave similar results. Several sites with an excess of LD were identified, with the most relevant excess LD found on OAR2 and OAR10. In these two sites high r correlations between the four major breeds (SAW, LAC, SBF and CHU) were observed. This result suggests that there is a strong similarity of conserved haplotypes among breeds. These results are obtained by EC-funded FP7 Project 3SR (no. 245140); French SNP data were funded by SHEEPSNPQTL ANR project.

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