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Selection trace from runs of homozygosity in French dairy sheep

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Runs of homozygosity (ROH) are contiguous homozygous segments of the genome where the haplotypes inherited from each parent are identical. Currently, inbreeding estimated from ROH is considered a powerful approach to distinguish between recent, potentially harmful, from ancient inbreeding, potentially beneficial. Accordingly, inbreeding based on ROH can help to improve the understanding of inbreeding depression. The occurrence of ROH is not randomly distributed across the genome, and islands of ROH across a large number of animals may be the result of selective pressure. The objective of this study is to evaluate whether ROH can be used to explore signatures of selection in French dairy sheep. The data set available included animals from various breeds and subpopulations: Basco-Béarnaise breed (BB); Manech Tête Noire breed (MTN); Manech Tête Rousse breed (MTR); Lacaune Confederation subpopulation (LACCon); and Lacaune Ovitest subpopulation (LACOvi). Animals were genotyped with the Illumina OvineSNP50 BeadChip. After applying filtering criteria, the genomic data included 38,287 autosomal SNPs distributed across 26 chromosomes and 8,700 individuals. One island of ROH was detected on autosome 6 in the same genomic position across animals (between 30 – 40 Mb). Wright's differentiation coefficients for two SNPs within this island of ROH were high (0.67 – 0.68). The linkage disequilibrium between both SNPs was also elevated (0.98). The divergence in allele frequencies in those SNPs grouped BB, MTN and MTR breeds in one cluster, and LACCon and LACOvi subpopulations in another cluster. The closest candidate gene is *NCAPG-LCORL*, which has been reported to be under positive selection and suggested to control height and stature in sheep, as well as growth and feed efficiency in cattle. These findings contribute to the understanding of the effects of selection in shaping the sheep genome.