Genomic selection in the multi-breed French dairy goat population

Céline Carillier, Helene H. Larroque, Isabelle Palhiere Palhière, Virginie Clément, Rachel Rupp, Christèle Robert-Granié

Do selective sweeps in sheep breeds indicate the genomic sites of breed characteristics?

G.E. Pollott
RVC, Royal College Street, London NW1 0TU, United Kingdom; gpollott@rvc.ac.uk

Most breeds are the result of recent selection for phenotypic characteristics which make that breed unique, often referred to as a selective sweep in natural populations. This process should result in long runs of homozygosity (ROH) around the genomic polymorphisms which determine a breed's key characteristics, particularly if their mode of inheritance is autosomal recessive. Since recombination in each generation has the potential to breakdown ROH, the length of a ROH is indicative of its age; more recent mutations being associated with longer runs. The 67 breeds in the Sheep HapMap dataset, with >20 genotyped animals, were analysed to identify the distribution of ROH within each breed. A ROH was identified when an individual animal had consecutive homozygous SNP genotypes of the majority type, within the breed, at each locus. Missing genotypes were scored as if they were homozygous. Thus a ROH score represents the length, in numbers of SNP, of a continuous run of homozygosity comprising the majority homozygous genotype for the breed at each SNP. The probability of any given score, within a breed, was calculated by 1000 permutations of the whole HapMap dataset drawing 20 animals at random at each permutation. Over 30 breeds were found to have long ROH (>50 SNP; $P<0.05$). For example, the various Texel subgroups were found to have a long ROH on OAR2 between bp positions 116,277,389 and 127,499,743. This contains the Myostatin gene and a mRNA previously identified as being a characteristic of the breed. Interestingly, the Soay breed, a primitive breed from Scotland, was shown to have a long ROH in the same position as that found on OAR2 in the Texel, but comprised a different haplotype. A range of other ROH of interest will be discussed and suggestive sites for breed characteristics presented. This method provides the possibility to identify genomic regions which determine breed characteristics when no candidate gene is suggested by previous studies.

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C. Carillier[1], H. Larroque[1], I. Palhière[1], V. Clément[2], R. Rupp[1] and C. Robert-Granié[1]
[1]Institut National de la Recherche Agronomique (INRA), Station d'amélioration génétique des animaux (UR631), CS 52627, 31326 Castanet-Tolosan Cedex, France, [2]Institut de l'élevage (Idele), CS 52627, 31326 Castanet Tolosan Cedex, France; celine.carillier@toulouse.inra.fr

In French dairy goats, 2,246 females and 872 males from Alpine and Saanen breeds were recently genotyped with the Illumina 50K SNP bead chip, as part of a large genomic project supported by the dairy goat industry stakeholders. The first goal of this study was to investigate linkage disequilibrium (LD) within the population and between the two breeds. The second objective was to examine the effect of adding males, females or males and females in the reference population on the ranking and accuracy of genomic breeding values for young bucks. The level of LD in the multi-breed population (0.14 for 50 kb) was lower than the one found in each breed (0.17) or in literature for cattle (0.18 to 0.30). In addition, the persistence of LD phases between the two breeds decreased rapidly with distance (0.56 for 50 kb). Conventional and genomic evaluations using GBLUP for milk production traits, somatic cell score and type traits were calculated in several multi-breed reference populations (from 67 males to 677 males and 1,985 females). The ranking of animals based on EBV and GEBV were close, with correlations between EBV and GEBV of up to 97%. Rankings were improved by adding animals, males or females only for some traits. Accuracies of genomic predictions were low (from -5% to 38%) because of the small size of the reference population analyzed. For young bucks, average difference between genomic or conventional breeding value accuracies were lower than those reported for other species. Altogether, this first genomic study in Alpine and Saanen goats suggest that the current data is not sufficienct to allow genomic selection to be performed. Other models such as a multiple-trait model, single step genomic BLUP model or models using haplotypes instead of SNP will also be examined in the future.

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