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Introgression of wool-shedding genes into the Romane breed sheep

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Wool production in Europe became unprofitable compared to the meat or milk productions. One major reason is that the wool income is lower than the cost of shearing. The Romane breed, a French composite breed between the Berrichon du Cher breed (meat breed) and the Romanov breed (prolific breed), showed little ability to shed. We decided to introgress in the Romane breed the phenotype of wool-shedding of the Martinik Hair breed. Indeed, the Martinik Hair sheep have the ability to annually naturally wool-shed.

The experimental trial of introgression was realized on 4 successive backcrosses from the Martinik Hair (MH) to the Romane breed (RM): F1 (MH*RM), then BC1 (F1*RM), BC2 (BC1*RM) and BC3 (BC2*RM). Two traits were considered: the ability to shed at least a part of the fleece or not, as a binary trait and the extent of shedding as the ratio of wool shed area to total body area. During those backcrosses, animals were measured and selected on their ability to shed at 7 months of age. The BC3 population represents the first generation (G1) of the introgressed population for the wool-shedding phenotype. This introgressed breeding stock (n=150 ewes) was then selected using estimated breeding values based on shedding extension. A high heritability estimate (0.50 ± 0.09) and a large genetic gain (2.2 genetic standard deviations) on wool-shedding were observed after 6 generations of selection, without impairing the production fitness on the Romane sheep. We did not observe a bimodal distribution of wool-shedding extension phenotype, suggesting that not only one mutation is segregating in our population, but more probably a few major genes with large effects due to the large genetic gain observed.

At the G6, 96 animals (9 family sires, 6 to 11 progeny per sire, 10 dams) with extreme phenotypes (total wool shedding or not) including some full-sibs and their dam were selected and genotyped on 50K SNP chip.

This dataset is currently analysed using linkage analysis (LA), linkage disequilibrium (LD) and joint LD-LA mapping using QTLMAP software. The first results showed at least 3 different loci influencing the ability to shed on chromosome OAR3, OAR12 and OAR15. The analysis are in progress to precise those intervals of localization.