Development of a SNP parentage assignment panel in some North-Eastern Spanish meat sheep breeds

J.H. Calvo[1,2], M. Serrano[3], F. Tortereau[4], P. Sarto[2], M.A. Jiménez[3], J. Folch[2], J.L. Alabart[2], S. Fabre[4] and B. Lahoz[2]
[1]ARAID, Av. de Ranillas 1-D, 50018 Zaragoza, Spain, [2]CITA-IA2, Producción y Sanidad animal, Av. Montañana 930, 50059 Zaragoza, Spain, [3]INIA, Mejora Genética Animal, Ctra. La Coruña km 7.5, 28040 Madrid, Spain, [4]Université de Toulouse, INRA, ENVT, 4GenPhySE, Chemin de Borde Rouge, 31326 Castanet-Tolosan, France; jhcalvo@aragon.es

Accurate pedigree information is an essential tool in genetic breeding programs to ensure the highest rate of genetic gain and allows management of inbreeding. However, the proportion of known sires can be very low in Spanish meat sheep populations, particularly in breeds reared in high mountain areas as in the Pyrenees. Single nucleotide polymorphisms (SNPs) are now the DNA markers of choice for parentage assignment. The objective of this study was to develop a SNP assay to use in some North-Eastern Spanish meat sheep populations for accurate pedigree assignment. Nine sheep breeds were sampled: Rasa aragonesa (n=38), Navarra (n=39), Ansotana (n=41), Xisqueta (n=41), Churra Tensina (n=38), Maellana (39), Roya bilbilitana (n=24), Ojinegra (n=36) and Cartera (n=39). We used SNP genotypes from the Illumina OvineSNP50 BeadChip array. Firstly, we selected the 249 SNPs published from the French panel for parentage assignment due to the high values of the Minor Allele Frequency (MAF) reported in the South-West European breeds. In total, 159 SNPs in Hardy-Weinberg equilibrium, displaying a MAF>0.3 and a call rate>0.97 in all the nine populations, and not associated with Mendelian errors in verified family trios or duos were selected. The average MAF was 0.43, ranging from 0.41 (Churra Tensina) to 0.44 (Xisqueta and Navarra). The probability (PI) that two randomly selected individuals having identical genotypes within breed was very low: it reached its lowest and highest value in the Cartera (8.81×10^{-67}) and the Roya bilbilitana populations (2.29×10^{-64}), respectively. The exclusion probabilities of either one or the two randomly selected parent(s) were close to 1 in all populations. The parentage assignment procedure was tested using KASP technology for genotyping in a final panel of 192 SNPs that included 159 SNPs for parentage assignment and 33 functional SNPs (*PrnP*, *BMP15*, *MTNR1A*…).

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