

observed (H_o) heterozygosity analysis did not revealed differences among populations with an overall value of 0.367 and 0.381, respectively. However, unsupervised admixture assay was able to discriminate seven different populations corresponding with the five historical lines, and the Black Merino and the Serena line. Among the white Merino historical lines, the percentage of individual adscription to their group varied between 100% in the Maesso, Egea, Lopez-Montenegro and Serena, and 50% in Hidalgo and Granda lines. Finally, the F_{st} values between the Black Merino and the rest of the strains varied between 0.089 and 0.123, while between the different strains the values varied between 0.047 and 0.084. In conclusion, we demonstrated the existence of a high level of variability in the Spanish Merino breed, even within the historical genetic lines suggesting a genetic influence of external populations. However, three of the historical lines were highly homogeneous, probably due to the occurrence of a closed mating since its creation. This study, which is the first carried out on the historical lines of Spanish Merino, could help to achieve a better understanding of one of the most important sheep breeds in the world.

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Genomic tools to support breed assignment in small ruminants

Alessio Negro^a, Matteo Cortellari^a, Arianna Bionda^a, Stefano Frattini^a, Stefano Biffani^b, Silverio Grande^c, Paola Crepaldi^a

^aDipartimento di Scienze Agrarie e Ambientali (DISAA), University of Milan, Milano, Italy

^bIstituto di Biologia e Biotecnologia Agraria (IBBA), Consiglio Nazionale delle Ricerche (CNR), Milano, Italy

^cDirezione, Associazione Nazionale della Pastorizia (Asso.Na. Pa.), Roma, Italy

Contact alessio.negro@unimi.it

Animal breed assignment is breed experts' responsibility. They identify the characteristics of different breeds described within the breed standard. Animals' registration to their respective herd-book takes place through verification of the genealogy and/or the correspondence to the breed phenotypic standards. When pedigree information is missing, an animal is assigned to a breed according to phenotypic information only. Today, genomic tools that support the traditional system of breed identification are available. We are presenting the results of the analysis of breeds' assessment with genomic tools of five Italian ovine breeds within 'Conservation, Health and Efficiency Empowerment of Small Ruminant' national project (CHEESR – PSRN 2014–2020). For the purpose of breed assignment, a total of 1122 animals belonging to five different ovine breeds (Comisana, Massese, Fabrianese, Delle Langhe, Gentile di Puglia) were genotyped with the OvineSNP50beadchip. The quality check was performed by Plink

software applying the following thresholds: minor allele frequencies (<0.01), missing genotype (>0.05), missing per individual (>0.05). Furthermore, the individuals' probability of assignment to each K group (Q-values) was analysed with Admixture software and described with JMP software.

The analysis showed high median Q-values for Massese, Comisana, and Delle Langhe sheep, respectively equal to 0.98, 0.95, and 0.95 with an interquartile range (IQR) equal to 0.95–1, 0.91–0.98, and 0.88–0.95. On the other hand, Fabrianese sheep showed more variable values, with a median equal to 0.75 and an IQR equal to 0.61–0.91. Furthermore, Gentile di Puglia breed showed an intermediate median value equal to 0.85 with an IQR equal to 0.69–0.95. Finally, some animals showed low probability of assignment and the lowest values were detected in Fabrianese breed. The results indicate a good agreement of the breed's assignment, in particular for Massese and Comisana breeds, counting about 400 animals for each breed, while in the other breeds, counting 100 animals, also animals with a low probability of assignment were detected. With a properly constructed and updated reference panel containing all Italian ovine breeds or other breeds used in crossbreeding, it will be possible to combine the expert's evaluation with a genomic analysis that allows to discriminate doubtful cases.

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Genomic inbreeding parameters in the autochthonous Reggiana and Modenese cattle breeds

Giuseppina Schiavo^a, Samuele Bovo^a, Anisa Ribani^a, Valerio Joe Utzeri^a, Enrico Mancin^b, Roberto Mantovani^b, Stefania Dall'Olio^a, Luca Fontanesi^a

^aDipartimento di Scienze e Tecnologie Agro-alimentari, University of Bologna, Bologna, Italy

^bDipartimento di Agronomia, Animali, Alimenti, Risorse naturali e Ambiente, University of Padova, Padova, Italy
Contact luca.fontanesi@unibo.it

Reggiana and Modenese are autochthonous dual-purpose cattle breeds reared in the Parmigiano-Reggiano cheese production area. After the setting up of the herd book in the 1960s, inbreeding has been considered in mating plans. Inbreeding is traditionally estimated using pedigree information (FPED). Commercial platforms for high-throughput genotyping allow investigating inbreeding directly using genome information. One of the most effective methods to estimate inbreeding is based on runs of homozygosity (ROH), which can be defined as long homozygous genome regions detected with high density single nucleotide polymorphism (SNP) genotyping tools. The total proportion of