

Genomic tools to support breed assignment in small ruminants

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Animal breed assignment is breed experts' responsibility. They identify the characteristics of different breeds described within the breed standard. Animals' registration to their respective herdbook 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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