Development of a 200 single nucleotide polymorphism panel for parentage assessment for 14 Italian goat breeds

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ABSTRACT

The recent availability of a medium density SNPs chip in goat offers the possibility to develop a useful and less expensive tool for parentage assessment. However, standard approaches of SNP selection for parentage assignment are still ineffective due to a lack of information about markers position. In this study, we describe the identification of a 200 SNPs panel for parentage testing in goat. Data on 350 goats of 14 different Italian breeds genotyped with the Illumina 50K SNP array were provided by the Italian Goat Consortium (IGC).
The 200 SNPs panel was identified by a three-step procedure, as follows: 1) parentage assessment by mendelian errors and genomic parentage to identify true parent-offspring pairs; 2) identification of informative SNPs by canonical discriminant analysis and 3) reduction by mendelian errors and stepwise regression.
The 200 SNPs panel was tested on pairwise comparison of all animals at each locus. Sensitivity, specificity and accuracy of the panel were assessed. The probability of exclusion (Pe) and the probability of a random coincidental match inclusion (Pi) for each breed were estimated.
The panel showed good assessment power, with high sensitivity (0.9429), specificity (1.0) and accuracy (0.99997). Pe values ranged from a minimum of 0.99999981 for Maltese from Sardinia to a maximum of 0.999999999996 for Nicastrese. We further reduced panel size by stepwise regression to 174 SNPs showing the same performance of the 200 SNP panel. The development of tools for parentage assessment could improve breeding management also in species with low genetic information, as goat.

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