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Design of a SNP parentage assignment panel for French goat breeds

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Knowing pedigrees is essential for selection, conservation and management of animal populations. In French goats, complete and accurate pedigree information is difficult to get because of the increasing use of multiple-sired matings. In the two main French breeds (Alpine and Saanen), only 50% of females involved in the official genetic evaluation have a known sire. In this context, having an efficient way to *a posteriori* identify actual parentage could be profitable both at the breeding scheme and the breeder levels. The objective of this study was to develop a SNP panel to accurately assign paternity in the main French goat breeds. About thirty animals have been genotyped with the GoatSNP50 chip in eight breeds: Alpine, Saanen, Angora, Corsican, Poitevine, Pyrénées, Fossés, Provençale. Four subsets of SNP (64 to 505) were theoretically defined based on call frequency, mendelian incompatibility, Hardy-Weinberg equilibrium test, Minor Allele Frequency and distribution along the genome. Then, the assignment rate of each SNP panel was estimated on Alpine and Saanen data from a QTL detection design, and by using a likelihood based approach. The 505 and 246 SNP panels showed the best results: the average MAF was about 0.42 for all the markers and populations, and the assignment rate was 100%. Before choosing the final panel, an assignment test will be performed in farm conditions (collection of blood samples, multiple-sired matings,...). A selection of SNP located in major genes of interest will be added to those for assignment in order to provide a useful tool to industry.