

Multilocus genotype assignment methods among six ovine breeds

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ABSTRACT

One of the most important problems in the rearing of small ruminant breeds, especially if they are at risk of extinction, is the breeding management. Too often in fact we are not able to infer exactly the belonging of two or more similar subjects to a particular breed only on the basis of the morphological traits. On the other hand if we are in presence of a breed at risk of extinction, in which the inbreeding level is high, we could try to perform a crossbreeding with another breed, but how can we choose the appropriate breed? Microsatellites are particularly suitable for this kind of studies because they could be multiplexed and used in an automated sequencer, so we can analyse a relatively high number of loci in a short time. Aim of this work is to test the reliability of a genetic assignment of 5 ovine Italian breeds, namely Pomarancina, Garfagnina Bianca, Appenninica, Massese, and Zerasca (a Mexican breed considered as an out-group), by the use of a small number of microsatellites. Assignment tests are one of the most suitable tools in evaluate breeds like these, where a lack of genealogical information exists. In order to perform the genetic assignment 42 blood samples for each of the mentioned breeds were obtained with single-use Na-Citrate Vacutainer, for a total of 252 head. DNA was isolated from whole blood samples with a "Nucleo Spin Blood®" commercial kit following the manufacturer's procedures. A total of 10 microsatellite loci were analyzed (MCM8, MCM11, OARAE119, FCB4, MAF70, OARCP49, JPM29, HH35, VH72, JPM8). We evaluate three main assignment methods: Bayesian, distance based, and frequencies based. The assignment test was carried on using the GeneClass II and Arlequin software packages. Analyzing the different computational methods we can confirm that Bayesian and frequency-based methods are in general more accurate than distance-based ones (under Infinite Allele Model). Results from log-likelihood are also useful to obtain a visual representation of the genotypic assignment, and also to put in evidence which genotype is closer to the others. Finally, we can suggest that in order to obtain a satisfactory genotypical assignment 10 loci could be adequate, and that the best assignment method results the Bayesian one.