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Genetic database development for the characterisation of Sicilian sheep population

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The most representative sheep in Sicily are Belicina, Comisana, Pinzirita, Barbaresca and the crossbred derived sheep from all these species. In this study, the allelic frequencies of the Sicilian sheep population were investigated. This is currently the gold standard to determine the genetic identity and/or family even with limited amounts of samples or when the DNA is degraded. The aim of the study was to provide a reference data bank and to evaluate a microsatellite panel for pedigree analysis as suggested by the International Society for Animal Genetics (ISAG).

There are various studies on European sheep, but few datasets have been developed based on the population of Sicilian sheep. The reference database will include allele frequencies at each locus and will determine genetic parameters for Sicilian ovine species selection. Our results indicated that Hardy Weinberg equilibrium was not always maintained. These results could be explained by non-random mating.

This database will be an important addition to aid in relationship, parentage and meat traceability as well as for disease prevention programmes. Parentage identification is potentially important for veterinary police to investigate theft or/and animal substitutions on Sicilian farms, whereas molecular fingerprinting can be useful in controlling livestock breeding.

The standardised panels of allele frequencies represent a molecular fingerprinting tool which can be used to characterise the subjects with very high definition levels and can be useful to control all the livestock. The parentage identification could be important for the veterinary police to investigate theft or animal substitutions in Sicilian farms.

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