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Genetic variability of three local cattle breeds (Calvana, Pontremolese, Garfagnina) by STR analysis

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ABSTRACT

The dramatic size contraction of local cattle breeds due to replacement with cosmopolite improved breeds highlights the need for native genetic resources conservation. In 1985, the Anagraphic Register of local cattle breeds and small-size ethnic groups was established by the Italian Ministry of Agriculture and Forestry. Calvana, Pontremolese and Garfagnina are among the included breeds. They are all native from Tuscany. Present breeding area covers the provinces of Firenze, Prato, Pistoia and Siena for the Calvana breed (around 280 heads), while it is restricted to the province of Lucca for both Garfagnina (around 180 heads) and Pontremolese. This latter breed consists, nowadays, of less than 40 heads, while being around 15000 in 1940s.

The characterization of the genetic structure and variability via molecular markers could provide useful information for breed management and conservation. In the present study, a total of 149 animals, evenly distributed among the three breeds, were genetically characterized by using 22 STR markers located on 13 different chromosomes. Among these, ten (BM1818, BM1824, ETH10, ETH152, ETH3, HEL9, ILST006, INRA63, TGLA126, TGLA227) belonged to the panel of 30 microsatellites recommended by the ISAG-FAO Working Group on domestic animal diversity. Mean number of alleles per locus in the total sample was 9.9, ranging from 5 (ETH10) to 14 (BMS690, HEL9, ETH152). Within population mean number of alleles did not vary among the three population samples (range, 6.4 to 6.8).

On the other hand, almost all loci showed several low frequency alleles "private" to one breed only. Mean locus heterozygosity in the total sample was 0.426. All loci showed a significant excess of homozygous genotypes in all the three breeds. Only the HEL9 locus (BTA8) was characterized, in all breeds, by a significant excess of heterozygous genotypes. Average F_{IS} over all loci was 0.287 for Garfagnina, 0.378 for Calvana, and 0.479 for Pontremolese. Significant pair-wise linkage disequilibrium (or gametic imbalance, for unlinked loci) was observed for all breeds. In particular, more than 40% of all possible pair-wise comparisons were in linkage disequilibrium in the Pontremolese breed. A breed assignment test based on a log-likelihood approach allowed the correct allocation of 100% of individuals to their true breed of origin.