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THE GENETIC VARIABILITY OF THE PODOLICA CATTLE BREEDS: PRELIMINARY RESULTS

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The Podolica cattle breed is autochthonous of the South Italy and characterised by its particular rusticity. This study presents the preliminary results on its genetic variability analysed using DNA STR markers. A total of 20 microsatellite loci were studied in 80 Podolica individuals bred in Gargano area. Allelic frequencies, number of polymorphisms, deviations from Hardy-Weinberg proportions, linkage disequilibria between loci and genetic similarities between animals were calculated. The results showed a high deficiency of heterozygotes, the observed mean of heterozygosis being 0.449, whereas the expected mean was 0.766. Many markers showed also deviations from Hardy-Weinberg proportions and significant linkage disequilibria between loci. However the genetic similarity within the population was low (0.281) and the average number of alleles per locus was high (10), representing a high genetic variability. In order to justify these results we could hypothesize a division of the breed in subpopulations genetically homogeneous, but distant one from each other. This situation probably derived from non-random mating within each herd (consanguinity) and from the lack of exchange of genetic material between the herds. We could therefore explain such a high heterozygotes deficiency and the high genetic variability within the population. The results permit to suggest specific applications to choice the animals that may guarantee the best genetic combination in order to reduce actual problems. A new study with a wide survey and sources of variability, may confirm this hypothesis. In this way we may have the information necessary for the correct management of the reproductive activities and for genomic traceability of meat production.