

Assessing genetic diversity and phylogenetic relationship of sixteen Mediterranean chicken breeds

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P-18. Genetic diversity and relationship among 16 Mediterranean chicken populations from five different countries were assessed by sequencing mitochondrial DNA and genotyping 27 microsatellite markers. In addition, six commercial populations were used as reference. A 506 bp fragment of the mtDNA control region was sequenced in 160 DNA individual samples. Twenty-five variable sites were observed. As a result, 21 haplotypes were identified and assigned to three clades. Haplotype E1, which might have its roots in the Indian subcontinent, was most frequent. Other sequences were included in the haplogroups A and B. For the microsatellite analysis, 465 individual blood samples were randomly collected from the 16 local breeds. A total of 242 alleles was found with a mean number of 8.96 alleles per locus. In some populations reduced heterozygosity was observed. This points to the need for appropriate measures to be taken in order to prevent negative effects of inbreeding. Structure analysis exhibited extensive genetic admixture in many of the studied populations. The study revealed that Mediterranean chicken populations, which may originate from three maternal lineages, retain moderate levels of genetic diversity.