



Study of genetic diversity in Tunisian local cattle populations using ISSR markers

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1 ABSTRACT

The inter-simple DNA sequence repeat (ISSR) method was used to study genetic diversity in three local cattle from the north, northeast and north west of Tunisia. Twenty samples were analysed using three ISSR primers. In total, 22 bands were amplified of which 15 are polymorphic (68.18%). The total genetic diversity (Ht), genetic diversity within populations (Hs), coefficient of gene differentiation (Gst) and gene flow (Nm) were 0.2706, 0.01314, 0.8841 and 0.0656. To better visualize the structure of the population, a UPGMA dendrogram constructed from the genetic distances of NEI shows that the populations of North (Bizerte) and Northeast (Nabeul) are genetically closest while that of Northwest (Jendouba and Siliana) is the furthest from the two others.