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Chloroplast DNA Diversity of Tunisian Barley Landraces as Revealed by cpSSRs Molecular Markers and Implication for Conservation Strategies

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Abstract

In Tunisia, barley local landraces are still cropped for human and animal consumption in some subsistence farming systems under marginal and stressed conditions. These high-value genetic resources present a potential source of resistance genes to biotic and abiotic stresses useful for both national and international breeders. Actually, they are represented by threatened small populations, which face a high risk of genetic erosion and progressive substitution by modern varieties. In this study, the genetic diversity of 60 Tunisian barley landraces was assessed using six chloroplast microsatellites. All loci were found polymorphic, with 2 or 3 alleles per locus. Thirteen alleles were detected across the studied sample, which were combined into 8 haplotypes, giving a haplotype diversity (Hd) of 0.847. High punctual and haplotype genetic diversity was observed for Tunisian barley landraces when compared to other germplasms from other regions of the world. The genetic structure analysis revealed two major clusters of Tunisian barley landraces, which confirms their multiorigin. This result was corroborated by the median-joining network showing the genetic relationships among the eight detected haplotypes. The AMOVA analysis revealed that 83% of the genetic variation is between populations, which requires the in situ and ex situ conservation of plant material for all Tunisian populations of barley landraces. Information on genetic variation within the chloroplast genome is of great interest to ensure an efficient conservation strategy that takes into account the preservation of the various maternal lineages of Tunisian barley.

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Biography

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