



Genetic diversity analysis in Tunisian perennial ryegrass germplasm as estimated by RAPD, ISSR, and morpho-agronomical markers

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ABSTRACT. Tunisia is rich in diverse forage and pasture species including perennial ryegrass. In order to enhance forage production and improve agronomic performance of this local germplasm, a molecular analysis was undertaken. Random amplified polymorphic DNA (RAPD), inter simple sequence repeats (ISSR) and morpho-agronomical traits markers were used for genetic diversity estimation of ryegrass germplasm after screening 20 spontaneous accessions, including a local and an introduced cultivars. Same mean polymorphism information content values were obtained (0.37) for RAPD and ISSR suggesting that both marker systems were equally effective in determining polymorphisms. The average pairwise genetic distance values were 0.57 (morpho-agronomical traits), 0.68 (RAPD), and 0.51 (ISSR) markers data sets. A higher Shannon diversity index was obtained with ISSR marker (0.57) than for RAPD (0.54) and morpho-agronomical traits (0.36). The Mantel test based on genetic distances of a combination of molecular markers and morpho-agronomical data exhibited

a significant correlation between RAPD and ISSR data, suggesting that the use of a combination of molecular techniques was a highly efficient method of estimating genetic variability levels among Tunisian ryegrass germplasm. In summary, results showed that combining molecular and morpho-agronomical markers is an efficient way in assessing the genetic variability among Tunisian ryegrass genotypes. In addition, the combined analysis provided an exhaustive coverage for the analyzed diversity and helped us to identify suitable accessions showed by Beja and Jendouba localities, which present large similarities with cultivated forms and can be exploited for designing breeding programmes, conservation of germplasm and management of ryegrass genetic resources.

Key words: Genetic diversity; Germplasm; ISSR; Morpho-agronomy; Perennial ryegrass; RAPD