

Inter Simple Sequence Repeat Fingerprints for Assess Genetic Diversity of Tunisian Garlic Populations

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Résumé en anglais

Garlic (*Allium sativum* L.) that is cultivated in Tunisia is heterogeneous and unclassified with no registered local cultivars. At present, the level of genetic diversity in Tunisian garlic is almost unknown. Inter Simple Sequence Repeats (ISSR) genetic markers were therefore used to assess the genetic diversity and its distribution in 31 Tunisian garlic accessions with 4 French classified clones used as control. It was the first time that ISSR markers were used to detect diversity in garlic. Seventeen ISSR primers were screened; seven primers detected 73 polymorphic bands. A high level of polymorphic loci (p) was found in Tunisian populations (54%). Nei's total genetic diversity coefficient was 0.45 and 0.34 respectively for Tunisian and French garlic. Genetic distances observed between Tunisian accessions, ranged between 38.4 and 78.1%. Factor analysis of distances' table (AFTD) did not classify accessions on the base of geographical origin or morpho-physiological characters, particularly bolting ability, but confirmed the appurtenance of analyzed accessions to *sativum* botanical subspecies. There was sufficient diversity detected to start a national collection of garlic germplasm which is crucial for the conservation of genetic diversity and its valorization. Keywords: *Allium sativum* L., ISSR markers, genetic diversity, Tunisian garlic populations.

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