Analysis of genetic diversity of Tunisian pistachio (*Pistacia vera* L.) using sequence-related amplified polymorphism (SRAP) markers

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ABSTRACT. Sequence-related amplified polymorphism (SRAP) markers preferentially amplify open reading frames and were used to study the genetic diversity of Tunisian pistachio. In the present study, 43 *Pistacia vera* accessions were screened using seven SRAP primer pairs. A total of 78 markers was revealed (95.12%) with an average polymorphic information content of 0.850. The results suggest that there is strong genetic differentiation, which characterizes the local resources (G_{ST} = 0.307). High gene flow (N_m = 1.127) among groups was explained by the exchange of plant material among regions.

Analysis of molecular variance revealed significant differences within groups and showed that 73.88% of the total genetic diversity occurred within groups, whereas the remaining 26.12% occurred among groups. Bayesian clustering and principal component analysis identified three pools, El Guettar, Pollenizers, and the rest of the pistachios belonging to the Gabès, Kasserine, and Sfax localities. Bayesian analysis revealed that El Guettar and male genotypes were assigned with more than 80% probability. The BayeScan method proposed that locus 59 (F13-R9) could be used in the development of sex-linked SCAR markers from SRAP since it is a commonly detected locus in comparisons involving the Pollenizers group. This is the first application of SRAP markers for the assessment of genetic diversity in Tunisian germplasm of *P. vera*. Such information will be useful to define conservation strategies and improvement programs for this species.

Key words: *Pistacia vera*; Genetic diversity; SRAP markers; Structure analysis