



Genetic characterization of pea (*Pisum sativum*) germplasm from Turkey using morphological and SSR markers

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ABSTRACT. The need for the conservation of plant genetic resources has been widely accepted. Germplasm characterization and evaluation yield information for more efficient utilization of these valuable resources. The aim of the present study was to characterize the pea germplasm conserved at the Aegean Agricultural Research Institute of Turkey using morphological and simple sequence repeat (SSR)-based molecular approaches. Genetic characterization of 30 pea genotypes collected from different regions of Turkey and 10 commercial pea cultivars was performed using the criteria of the International Union for the Protection of New Varieties of Plants (UPOV) (TG 7/9 *Pisum sativum*), and with 10 SSR markers. We originally tested 15 SSR markers; 10 of these markers were selected on the basis of high polymorphism information content in the molecular assays. Sixty-one alleles were detected at the 10 loci. The number of alleles per SSR locus ranged from 3 (PVSBE2) to 12 (AB53), with a mean of 6.1 alleles. The most informative loci were AB53 (12 alleles), AA355 (9 alleles), AD270 (8 alleles), A9 (7 alleles), AD61 (7 alleles), and AB25 (6 alleles). The UPGMA dendrogram defined by

SSR markers revealed genetic relatedness of the pea genotypes. These findings can be used to guide future breeding studies and germplasm management of these pea genotypes.

Key words: Pea; *Pisum sativum*; Simple sequence repeat; Morphology; Genetic characterization