

An assessment of genetic variability and relationships among wild-grown blackthorn (*Prunus spinosa* L.) plants based on RAPD markers

Y. Erturk¹, S. Ercisli², D. Maghradze³, E. Orhan² and G. Agar⁴

¹Hamza Polat Vocational School, Ataturk University, Ispir-Erzurum, Turkey
²Department of Horticulture, Faculty of Agriculture, Ataturk University, Erzurum, Turkey
³Department of Genetics and Breeding, Institute of Horticulture and Vine Making, Tbilisi, Georgia
⁴Department of Biology, Faculty of Arts and Science, Ataturk University, Erzurum, Turkey

Corresponding author: S. Ercisli E-mail: sercisli@hotmail.com

Genet. Mol. Res. 8 (4): 1238-1244 (2009) Received June 2, 2009 Accepted July 25, 2009 Published October 13, 2009

ABSTRACT. *Prunus spinosa*, blackthorn, exists as wild populations that inhabit uncultivated uplands of Coruh Valley in the northeastern part of Turkey; the fruit is used to make preserves. We examined genetic diversity in wild-grown *Prunus spinosa*; 16 individual plants from wild populations of Coruh Valley were sampled and subjected to RAPD (random amplified polymorphic DNA) analysis. We tested 51 random decamer primers; 15 of them gave reproducible polymorphic patterns. These 15 primers produced 226 bands, of which 65% were polymorphic. A UPGMA dendrogram clearly divided the genotypes into four groups; we concluded that RAPD analysis can be used for examining genetic relatedness among blackthorn genotypes.

Key words: Blackthorn; Genetic diversity; *Prunus spinosa*; Random amplified polymorphic DNA

©FUNPEC-RP www.funpecrp.com.br

Genetics and Molecular Research 8 (4): 1238-1244 (2009)