

Genetic Diversity of Walnut (*Juglans regia* L.) Genotypes Selected from Central Anatolia Region of Turkey with SRAP Markers

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Aim of the study: *Juglans regia* L. with large size, delicious and thin-shelled fruits is the most widely cultivated walnut species worldwide. The genetic material to be used in walnut breeding should be original and the genetic relations among the genotypes should be well elucidated. In present study, efficiency of SRAP method was assessed for walnut genetic diversity studies and the method was used to identify genetic relatedness among walnut genotypes selected from Kayseri region and to determine some biochemical contents of these walnut genotypes.

Material and Methods: The present study was conducted with 50 walnut genotypes known with their superior characteristics (yield and fruit characteristics). Genotypes were selected from central towns (Kocasinan, Melikgazi) and Felahiye, Bunyan, Talas, Hacilar town of the Kayseri province located in Central Anatolia region of Turkey. Some biochemical characters (protein and crude oil content) were investigated. For genetic studies genomic DNA was extracted from young leaf tissues (0.5 g) with CTAB method. Twenty SRAP primer combinations produced clear fragments were used for the study. PCR reaction components, PCR cycling parameters, electrophoresis and gel imaging procedures were performed. A 100 bp standard DNA ladder was used for estimating sizes of fragments. Data of molecular analyses were performed as follows: Bands obtained from SRAP primers were scored based on their scorability. Cluster analysis was performed in accordance with unweighted pair group method with arithmetic averages (UPGMA) method and dendrogram was created with NTSYS pc 2.11 software.

Results: Crude protein contents of the genotypes varied between 14.18-20.82% and crude oil contents varied between 62.21-72.36%. To identify DNA-level genetic diversity in walnut genotypes, 20 SRAP primer combinations were used. A total of 130 bands were obtained and 117 of them were polymorphic. Genetic similarity levels among walnut genotypes varied between 0.62–0.93. In general, all genotypes separated from each other. The genotypes 49 and 50 were the closest ones with a similarity level of 0.93. Quite high polymorphism ratio (90%) of the present study may provide significant outcomes for further breeding studies.

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Keywords: Walnut, *Juglans regia*, SRAP, genetic difference.