

Determination of Genetic Relationship among Local wheat landraces, Azerbaijan Originated wheat cultivars and Some Wild Wheat Genotypes by using ISSR

Merve NAZLI¹, Mikail AKBULUT¹, Ramiz T. ALIYEV²

¹Department of Biology, Faculty of Science, Erciyes University, Turkey

² Genetic Resources Institute, Azerbaijan National Academy of Sciences, 155 Azadliq Ave,
Baku, Azerbaijan
akbulut@erciyes.edu.tr

Aim of the study: In this study, we aimed to determine genetic relationships between local wheat landraces grown in Turkey and some wild wheat genotypes and Azerbaijani wheat cultivars.

Material and Methods: In this study, genetic diversity among 160 wheat genotypes including 133 local bread wheat landraces originated from different regions of Turkey, some wild wheat genotypes and Azerbaijani wheat accessions were used. They were supplied from “Ankara Field Crops Central Research Institute” and “Azerbaijan National Academy of Genetic Resources Institute” Total DNA was extracted from 300 mg fresh leaf tissue of wheat seedlings. Ten ISSR primers were used to detect the genetic polymorphism among the wheat accessions. DNA bands in the gel photographs were visually scored as present (1) or absent (0) and the data were analyzed using the Numerical Taxonomy Multivariate Analysis System (NTSYS-pc) version 2.1 software package (Rohlf, 2000). To determine genetic relationships, a genetic similarity (GS) matrix was created based on simple matching coefficients and the GS matrix was used to construct a dendrogram using the unweighted pair group method arithmetic average (UPGMA). By using dissimilarity matrix, neighbor-joining (NJ) dendrogram was also generated. Principal component analysis was conducted to determine genetic relationship among the barley genotypes. The partitioning of molecular variance among groups and within population was calculated by the AMOVA in ARLEQUIN ver. 3.0 software (Univ. of Geneva, Geneva, Switzerland) (Excoffier et al 2005).

Results: In this study, 10 Inter Simple Sequence Repeat (ISSR) primers were used to determine the diversity in 160 wheat samples containing wild diploid, tetraploid, hexaploid local, and some hexaploid wheat genotypes from Azerbaijan. As a result of the clustering analysis using UPGMA method, it was determined that wheat genotypes are mainly grouped on species basis and Azerbaijan hexaploid wheat samples were also grouped separately. Similar results were obtained with the principal component analysis (PC). With the Molecular Variance Analysis (AMOVA), 25.37%, 13.96% and 60.67% variation rates were detected between groups, among the populations within the group and within populations, respectively. The intra-population diversity was statistically significant ($p < 0.001$). Considering all the wheat sample studied, the level of genetic diversity was found to be considerably high (91.6 %). Given the rate of polymorphism obtained, the ISSR markers were found to be useful in investigating the genetic diversity of wheat genotypes.

Acknowledgements: This study was supported by Erciyes University research fund with the code of FYL-2015-5956

Keywords: *Triticum aestivum*, wheat, Genetic diversity, ISSR, UPGMA.