

P-48 (116)**STUDY OF GENETIC DIVERSITY OF SOME PERSIAN WALNUT GENOTYPES IN KHORASAN RAZAVI PROVINCE WITH ISSR MARKER****Shadi Attar**, Department of Horticultural Science, Ferdowsi University of Mashhad, Mashhad, Iran; sh_at66@yahoo.com (Presenting author)**Prof. Dr. Gholam hossein Davarynejad**, Department of Horticultural Science, Ferdowsi university of Mashhad, 009851 Mashhad, Iran; Davarynej@um.ac.ir**Assist. Prof. Leila Samiee**, Department of Ornamental Plants, Research Center for Plant Sciences, Ferdowsi university of Mashhad, 009851 Mashhad, Iran; leiliasamie@gmail.com**Assoc. Prof. Mohammad Moghaddam**, Department of Horticultural Science, Ferdowsi university of Mashhad, 009851 Mashhad, Iran; Moghaddam75@yahoo.com

Persian walnut (*Juglans regia* L.), belongs to the Juglandaceae family and its natural origin is the mountainous regions of central Asia and especially northern forests of Iran.. Study about the genetic structure of walnut genotypes to identify, select and maintain their genetic resources are important. In order to investigate genetic diversity of some genotypes of Persian walnut in Khorasan Razavi orchards, the ISSR molecular marker is used. With this purpose between 2014 until 2016 about 56 walnut trees from 4 orchard in khorasan Razaviprovince were selected and tagged. Nine primers with high polymorphism and repeatability were selected. After scoring the 1 and 0 numbers was changed to matrix via NTedit software. Genetic similarities samples with the NTSYSpc. Software, was calculated. Dendrogram by cluster analysis with UPGMA method were drawn. The main coordinate's analysis (PCO) was performed using the NTSYS software and grouping samples were evaluated in a two-dimensional plot. Results showed that from 9 primers in total, 118 bands were amplified, that 29 of them were polymorphic. The average amplified fragments for each primer was 9.83. Maximum polymorphism (80%) of the primers was observed in UBC830. In genotypes cluster analysis 10 cluster was formed. ISSR molecular marker somewhat revealed genetic diversity among walnuts genotypes, whereas the genetic diversity was lower than expected. In general by review findings in other parts of the world about walnut genetic diversity and compared with the results of this research, despite the high genetic diversity of walnuts in many areas, but some reports of low genetic diversity of walnuts populations published and unfortunately in recent years this reports has made progress upward. Based on the results of several studying done about the low genetic diversity of walnut, the following factors can be effective in this problem: natural disasters, human impacts such as deforestation, selection and propagation of superior genotypes and sometimes walnuts self-pollination. In this respect there is concern that if this trend of decreasing genetic diversity in the walnut population increased, this invaluable product will be as endangered species, so we should be thinking about remedy.

Keywords: Base pair, Cluster, Local varieties, Primer, Similarity