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Genetic Diversity of Quercus Persica Healthy Stands in Zagros Forest

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Abstract

This project was conducted in Zagros forests of Ilam province in the west of Iran, where Quercus persica is native to the region and they have been extending naturally in the tropical regions. The main concern of this project was to address the Oak decline of Zagros forests of Iran. Several theories have been proposed to pinpoint this challenge of which genetic erosion could be mentioned. A site showing a range of symptoms of Oak decline was inspected phenotypically where, mortality of the oak trees was noticeable. We selected seventy individual stands of Q. persica (from across 50000 ha) after the general sampling and analysis randomly divided in four groups to answer the following research questions. How much is the level of genetic diversity of the Ilam Oak forests? Are there any genetic differences between the studied phenotypes? Do the phenotypically healthy stands fall into the special genetic category? The genetic diversity was evaluated using SSR marker and UPGMA method. The results show a high genetic diversity among stands of various phenotypes. Twenty-seven polymorphic loci (87.10 %) were found in in the first group, 26 (83.87 %) in the second group, 24 (77.42 %) in the third group, and 30 (96.77 %) in the fourth group. The percentage of polymorphic loci and Shannon index within and among the groups showed that the fourth group had the highest number of polymorphic loci (30) and percentage of polymorphic loci (96.77). Positive values of heterozygosity (Ht) across the entire stands provides invaluable genetic resources to help improve the suitability of the oak forest.

Keywords: Ecosystem degradation, oak Decline, Quercus persica, Zagros forests

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