

Genetic Diversity Analysis in Ecological Populations of Persian Walnut

Authors : Masoud Sheidai, Fahimeh Koozdar, Hashem Sharifi

Abstract : *Juglans regia* (L.) commonly known as Persian walnut of the genus *Juglans* L. (Juglandaceae) is one of the most important cultivated plant species due to its high-quality wood and edible nuts. The genetic diversity analysis is essential for conservation and management of tree species. Persian walnut is native from South-Eastern Europe to North-Western China through Tibet, Nepal, Northern India, Pakistan, and Iran. The species like Persian walnut, which has a wide range of geographical distribution, should harbor extensive genetic variability to adapt to environmental fluctuations they face. We aimed to study the population genetic structure of seven Persian walnut populations including three wild and four cultivated populations by using ISSR (Inter simple sequence repeats) and SRAP (Sequence related amplified polymorphism) molecular markers. We also aimed to compare the genetic variability revealed by ISSR neutral multilocus marker and rDNA ITS sequences. The studied populations differed in morphological features as the samples in each population were clustered together and were separate from the other populations. Three wild populations studied were placed close to each other. The mantel test after 5000 times permutation performed between geographical distance and morphological distance in Persian walnut populations produced significant correlation ($r = 0.48$, $P = 0.002$). Therefore, as the populations become farther apart, they become more divergent in morphological features. ISSR analysis produced 47 bands/ loci, while we obtained 15 SRAP bands. G_{st} and other differentiation statistics determined for these loci revealed that most of the ISSR and SRAP loci have very good discrimination power and can differentiate the studied populations. AMOVA performed for these loci produced a significant difference (< 0.05) supporting the above-said result. AMOVA produced significant genetic difference based on ISSR data among the studied populations ($\Phi_{iPT} = 0.52$, $P = 0.001$). AMOVA revealed that 53% of the total variability is due to among population genetic difference, while 47% is due to within population genetic variability. The results showed that both multilocus molecular markers and ITS sequences can differentiate Persian walnut populations. The studied populations differed genetically and showed isolation by distance (IBD). ITS sequence based MP and Bayesian phylogenetic trees revealed that Iranian walnut cultivars form a distinct clade separated from the cultivars studied from elsewhere. Almost all clades obtained have high bootstrap value. The results indicated that a combination of multilocus and sequencing molecular markers can be used in genetic differentiation of Persian walnut.

Keywords : genetic diversity, population, molecular markers, genetic difference

Conference Title : ICEG 2018 : International Conference on Ecological Genetics

Conference Location : Rome, Italy

Conference Dates : November 12-13, 2018