

عنوان مقاله:

(TEMPORAL GENETIC STRUCTURE OF IRANIAN POPULATIONS OF BEECH, FAGUS ORIENTALIS (FAGACEAE

محل انتشار:

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نویسندگان:

Parvin Salehi Shanjani - Research Institute of Forests and Rangelands, P. O. Box ۱۳۱۸۵-۱۱۶, Tehran, Iran

Giovanni Giuseppe Vendramin - Institute of Plant Genetic, CNR, Via Madonna del Piano, I-۵۰۰۱۹ Sesto Fiorentino, Firenze, Italy

Mohsen Calagari - Research Institute of Forests and Rangelands, P. O. Box ۱۳۱۸۵-۱۱۶, Tehran, Iran

خلاصه مقاله:

Reforestation with autochthonous species should take into account the preservation of the temporal variability and the geographic structure of genetic diversity in forest species. In order to provide empirical data about the suitability of methods of sampling material, genetic comparison of ۱۰ beech populations (at least ۴۰ trees per population) and their progenies (seeds of ۱۰ mother trees per population, each tree ۷ seeds) were analysed using four highly polymorphic microsatellite loci. The allelic multiplicity was higher in seed samples than adult trees indicating gene flow from adjacent plant populations. The comparison for genetic diversity measures between adult trees and seed generation revealed no significant differences for allelic richness (N_a), effective number of alleles (N_e), and number of rare alleles (N_r), neither observed (H_o) nor expected heterozygosity (H_e). Genetic differentiation in allelic frequencies between adult trees and seeds generation were rather low ($F_{st} = ۰.۰۵۸$). A close genetic relationship between adult trees from seed generation of each population, which revealed by un-weighted pair group method based on arithmetic average (UPGMA) and supported by an analysis of molecular variance (AMOVA), were detected. In this paper some aspects related to seed sampling were discussed.

کلمات کلیدی:

Fagus orientalis, Hyrcanian forests, Genetic diversity, microsatellite, Gene flow, Iran

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