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Computational Analyses of Persian Walnut Genetic Data: Notes on Genetic Diversity and Cultivar Phylogeny

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Abstract : Juglans regia L. is an economically important species of edible nuts. Iran is known as a center of origin of genetically rich walnut germplasm and expected to be found a large diversity within Iranian walnut populations. A detailed population genetic of local populations is useful for developing an optimal strategy for in situ conservation and can assist the breeders in crop improvement programs. Different phylogenetic studies have been carried out in this genus, but none has been concerned with genetic changes associated with geographical divergence and the identification of adaptive SNPs. Therefore, we carried out the present study to identify discriminating ITS nucleotides among Juglans species and also reveal association between ITS SNPs and geographical variables. We used different computations approaches like DAPC, CCA, and RDA analyses for the above-mentioned tasks. We also performed population genetics analyses for population effective size changes associated with the species expansion. The results obtained suggest that latitudinal distribution has a more profound effect on the species genetic changes. Similarly, multiple analytical approaches utilized for the identification of both discriminating DNA nucleotides/ SNPs almost produced congruent results. The SNPs with different phylogenetic importance were also identified by using a parsimony approach.

Keywords : Persian walnut, adaptive SNPs, data analyses, genetic diversity

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