

STRUCTURE and reticulation analysis of genetic diversity in *Prunus scoparia* populations

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Abstract

Almond tree (*Prunus dulcis*, syn. *Prunus amygdalus*, or *Amygdalus communis*) is a small deciduous tree of the genus *Prunus*, in subfamily Prunoideae of Rosaceae. The tree is a native of southwest Asia which grows in Iran and Afghanistan and throughout the Turano-Iranian area.

Iran and Anatolia are the centers of origin for several *Amygdalus* species considered by some as potential subspecies or ecotype (Browicz and Zohary 1996, Kester and Gradziel 1996, Etemadi and Asadi 1999; Ghahreman and Attar 1999), diverged from parental species and adapted to different environmental conditions. The endemic forms occur in Iran either in the form of small, thorny bushes (sub-genus *lycioides*) or of taller, tree-like shrubs which grow in colonies (sub-genus *spartioides* and the colonies of *Amygdalus scoparia* on the southwestern flank of the Zagros) (Zohary 1963, Ladizinsky 1999).

The present study considers genetic diversity analysis of 3 *P. scoparia* populations by using nuclear ISSR markers and tries to reveal genetic distinctness versus admixture of these populations. Three populations studied differed significantly in their molecular characteristics, allele polymorphism and expected heterozygosity and also showed isolation by distance. AMOVA test showed significant genetic difference among 3 populations ($p < 0.01$) and revealed that 48% of total genetic variation is due to among populations variation, while 52% is due to within population variation. This result shows the occurrence of intra as well as inter population

genetic difference in *P. scoparia*. Coalescence analysis of molecular data was performed to obtain different gene trees which were later on retained on species tree. Among different tree topologies produced the best tree with 0 deep coalescence and 0 gene duplication/extinction which shows complete agreement between gene tree and species/population tree was selected. Bayesian model-based clustering showed a good separation of populations at $k = 3$, while reticulation and coalescence analyses revealed horizontal gene transfer and gene exchange among populations.

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