

The Role of Iran (Persia) in Apple (*Malus* × *domestica* Borkh.) Domestication, Evolution and Migration via the Silk Trade Route

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Abstract

To shed light on the role of Iran in apple evolution and domestication, the relationships among a collection of 159 apple accessions including indigenous Iranian apple cultivars and landraces, selected wild species, and old apple scion and rootstock cultivars from different parts of the world were investigated. The accessions were assigned into six arbitrary populations for the purpose of generating information on genetic parameters and these were screened with nine simple sequence repeat (SSR) loci selected from previous studies in apple. The SSR allelic data were then used to determine the population structure using STRUCTURE 2.2 software and genetic relationships based on a phenogram constructed using POPGENE 1.32 software. The results showed good agreement between the population structure data and the phenogram, and demonstrated that Iranian cultivars and landraces have a closer genetic affinity with *Malus sieversii* from Central Asia (east of Iran) and *M. orientalis* native to Turkey and Russia, than with other *Malus* species. Also, old apple scion and rootstock cultivars were closely related to one another and grouped between *M. sieversii*/*M. orientalis* and the rest of the wild *Malus* species. The closer genetic and geographic affinity of the Iranian germplasm with *M. sieversii* and *M. orientalis*, together with their location on the Silk Trade Route, suggests that Iran could be one of the major hubs in apple domestication and transfer from Central Asia to the West via the Silk Trade Route. We propose that Iran could be a main center of diversity for domestic apples.

INTRODUCTION

The cultivated apple (*Malus* × *domestica* Borkh.) is not a simple taxonomic group and includes all the cultivated types in the genus *Malus* Mill. The current, most widely accepted theory, based mainly on morphological and molecular evidence, points to series *Malus* (Dunemann et al., 1994) and specifically to *M. sieversii* (Ledeb.) Roem. from Central Asia as the most likely maternal ancestor (Harris et al., 2002). However, based on chloroplast diversity data, Coart et al. (2006) suggested that *M. sylvestris* could be a main

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