

## Morphological and Molecular Evaluation of Persian Walnut Populations in Northern and Western Regions of Iran

R. Karimi<sup>\*1</sup>, A. Ershadi<sup>2</sup>, A. Ehtesham Nia<sup>3</sup>, M. Sharifani<sup>4</sup>, M. Rasouli<sup>1</sup>, A. Ebrahimi<sup>5</sup>, K. Vahdati<sup>6</sup>

<sup>1</sup> Department of Landscape Engineering, Faculty of Agriculture, Malayer University, Malayer, Iran

<sup>2</sup> Department of Horticultural Science, Faculty of Agriculture, Bu-Ali Sina University, Hamedan, Iran

<sup>3</sup> Department of Horticultural Science, Faculty of Agriculture, Lorestan University, Khorramabad, Iran

<sup>4</sup> Department of Horticulture, Gorgan University of Agricultural Sciences and Natural Resources, Gorgan, Iran

<sup>5</sup> Department of Forestry and Natural Resources, Agriculture College, Purdue University, West Lafayette, USA

<sup>6</sup> Department of Horticulture, College of Aburaihan, University of Tehran, Tehran, Iran

Received: 27 September 2014

Accepted: 10 December 2014

---

### Abstract

In this study, morphological characteristics as well as ten of Simple Sequence Repeat (SSRs) loci were used to analyze the genetic diversity and relationships among 12 natural populations of Persian walnut (*Juglans regia* L.) in northern and western regions of Iran. The results showed that there was a high level of genetic diversity among the walnuts, both in terms of their SSRs loci as well as morphological traits. The nut weight ranged from 11.5 to 17.2 g, kernel weight from 3.2 to 6.3 g, and kernel percentage from 28 to 46.7%. In SSRs analysis, the number of alleles per locus ranged from 6 to 11, with a total of 83 alleles and average of 8.3 alleles and 4.9 effective alleles per locus. The expected heterozygosity (He) varied between 0.70 and 0.87, with an average of 0.79 per locus. The proportion of genetic differences among the walnut populations accounted for 19% of the total variation. The overall gene flow among populations equaled 1.10. The 12 walnut populations were separated into four main groups via the unweighted pair group method (UWPGM) with arithmetic mean cluster analyses based on Nei's unbiased genetic distances.

**Keywords:** Gene flow, Genetic diversity, *Juglans regia*, Microsatellite, Molecular marker

---

### Introduction

The genus *Juglans* includes 21 species, of which the Persian walnut (*Juglans regia* L.) is the most economically important cultivated species in worldwide. Walnut stands are found in Kopet Dag, the low land along the southern shore of the Caspian Sea, and in sporadic locations through the ranges of western and southern regions in Iran (Leslie and McGranahan, 1988). Walnuts were presumably domesticated in Iran and Afghanistan and subsequently introduced to China, Russia and Eastern Europe by ancient tribes (Vahdati 2000, Karimi *et al.*, 2010). The major producers of this species are China, Iran, USA and Turkey (FAO, 2012). Recent research

on the high nutritional value of walnut (Pereira *et al.*, 2008), its beneficial effect on human health derived from its high antioxidant capacity (Anderson *et al.*, 2001), as well as its high  $\omega$ -3 fatty acid concentration (Ros and Mataix, 2006) have resulted in an increased world demand for walnuts (FAO, 2012). Genetics analysis can provide data on a variety of important evolutionary parameters, including genetic variation, the partitioning of variability among populations and the overall levels of inbreeding, selfing versus outcrossing rates. In addition to providing basic evolutionary insights, such analyses are also an important tool for developing effective

---

\*Corresponding author: E-mail: Rouholahkarimi@gmail.com