ORIGINAL ARTICLE



Assessment of genetic diversity of thirty Tunisian fig (*Ficus carica* L.) accessions using pomological traits and SSR markers

Awatef Essid¹ · Fateh Aljane¹ · Mohamed Hichem Neily¹ · Ali Ferchichi² · José Ignacio Hormaza³

Received: 13 July 2020 / Accepted: 30 November 2020 © The Author(s), under exclusive licence to Springer Nature B.V. part of Springer Nature 2021

Abstract

Sixteen pomological traits were employed to characterize the diversity of 30 fig accessions collected mainly from Southeastern Tunisia and maintained at CFPA 'El Gordhab', Tataouine, in Southeastern Tunisia. Additionally, 13 simple sequence repeat (SSR) loci were analyzed to detect the genetic diversity of the 30 fig accessions. In this study, qualitative data (fruit shape, fruit external color, fruit internal color, abscission of the stalk from the twig, skin peeling, fruit skin firmness) showed morphological variation within accessions. A highly significant difference (p < .01) among accessions was revealed for all the quantitative traits. The first three components (PC1, PC2, and PC3) of PCA accounted for 52.99% of the total variability. PC1, PC2, and PC3 accounted respectively for 28.02, 13.05, and 11.91% of the total variance. The most discriminating morphological parameters were fruit length and diameter, stalk length and diameter, neck length and diameter, stalk and flesh thickness, fruit shape, skin peeling, and skin firmness. Concerning the molecular results, 40 alleles were revealed. The number of alleles ranged between 2 to 6 with a mean of 3.08 alleles per locus. The observed heterozygosity (Ho) ranged from 0.03 (LMFC21, LMFC23, and LMFC32) to 0.83 (LMFC30) with an average of 0.43. The expected heterozygosity (He) varied from 0.03 (LMFC21, LMFC 23 and LMFC32) to 0.74 (LMFC30) with an average of 0.37. UPMGA cluster analysis and PCA grouped the accessions in 6 groups. Our results showed that the SSR markers used detected low genetic diversity within the accessions studied.

Keywords Ficus carica L. · Tunisia · Genetic diversity · Pomological traits · SSRs markers

Introduction

The fig (*Ficus carica* L.) which belongs to the family Moraceae [1], is largely distributed along the Mediterranean basin, east, and western Asia [2]. Whether fresh or dried, fig fruits are particularly nutritive: rich in fiber, minerals, proteins, sugars, organic acids, and antioxidant compounds [3–5]. Moreover, they have been valued for their medicinal potential, and health-promoting features [6–11].

Awatef Essid awatef.essid@gmail.com

Published online: 03 January 2021

- Laboratoire d'Aridoculture et Cultures Oasiennes, Institut des Régions Arides de Médenine (IRA), Médenine 4119. Université de Gabès, Gabès, Tunisia
- Institut National Agronomique de Tunisie, 43 Avenue Charles Nicolle, 1082 Cité Mahrajène, Tunis, Tunisia
- Instituto de Hortofruticultura Subtropical y Mediterránea "La Mayora", Consejo Superior de Investigaciones Científicas (IHSM-CSIC), 29750 Algarrobo-Costa, Málaga, Spain

The fig is a gynodioecious species with male trees (caprifigs) that produce syconia with separate male and female flowers and female trees that produce syconia with only female flowers. Three types of female figs are cultivated: the common-type that produces parthenocarpic fruits without pollination and can produce one (unifera varieties) or two (bifera varieties) crops, the Smyrna-type that requires pollination from caprifigs, and the San Pedro-type that produces a first parthenocarpic crop (breba) and a second crop (fig) after pollination from caprifigs.

Extensive studies addressing the agro-morphological characterization of fig cultivars have been reported in several countries, mainly Turkey [12–16], Italy [17], Greece [18], Morocco [19–21], Algeria [22, 23], Spain [24, 25] and Tunisia [26–34].

Since such characterization is known to be expensive and often ineffective in differentiating genotypes due to the great influence of the environmental conditions [35] molecular characterization of fig cultivars has been carried out using different molecular markers [17, 18, 35, 36].

