
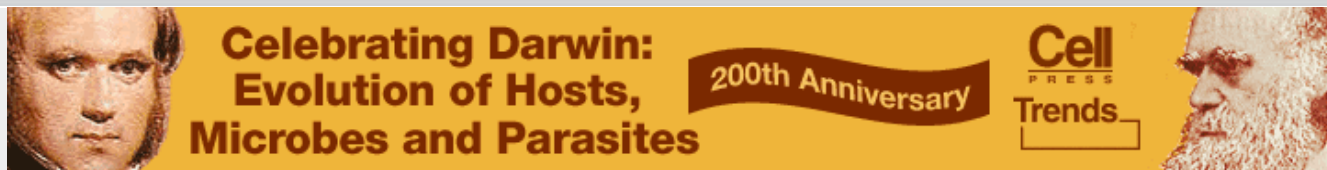



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doi:10.1016/j.scienta.2008.12.012

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Genetic analysis of Tunisian fig (*Ficus carica* L.) cultivars using amplified fragment length polymorphism (AFLP) markers

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Received 23 July 2008; revised 10 December 2008; accepted 11 December 2008. Available online 21 January 2009.

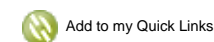
Abstract

Genetic diversity of forty fig cultivars collected from five regions in Tunisia was investigated using amplified fragment length polymorphism (AFLP). A total of 342 reproducible bands amplified with six AFLP primer combinations were obtained. The high percentage of polymorphic bands (%PB) of 97.5 and the resolving power (Rp) collective rate value of 143 were scored. In addition, the polymorphism information content (PIC) values varied from 0.61 to 0.87 with an average of 0.77. Although cluster (UPGMA) and principal components analyses indicate that the cultivars' clustering made independently both from the geographical origin, horticultural classifications and/or from the sex of trees. In addition, the observed variation suggests considerable differentiation among fig cultivars. The present data supports the common origin of the fig cultivars. Analysis of molecular

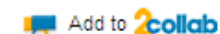
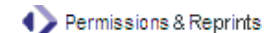
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variance (AMOVA) revealed that average Φ_{ST} value overall loci was 0.026, and the overall distribution pattern of molecular variation indicated that about 97.43% of the total variance was accounted by the within-region variance component. The remaining 2.5% ($P < 0.001$) of the variation was founded among cultivars of the prospected regions. Our results proved that AFLP markers are useful for germplasm discrimination as well as for investigation of fig patterns variation. The information may be useful to define conservation management program.

Keywords: AFLP; *Ficus carica*; Genetic diversity; Tunisia

Article Outline

1. [Introduction](#)
2. [Materials and methods](#)
 - 2.1. [Plant material](#)
 - 2.2. [DNA isolation](#)
 - 2.3. [AFLP analysis](#)
 - 2.4. [Data analysis](#)
3. [Results and discussion](#)
 - 3.1. [AFLP markers and polymorphism](#)
 - 3.2. [Genetic diversity and genotypes relationships](#)
 - 3.3. [Hierarchical partitioning of molecular variation](#)

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