

Molecular Evolution and Phylogenetic Study of the *atpB-rbcL* Spacer of Chloroplast DNA in Ficus Genus (Moraceae Family)

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University Campus El Manar 2092, Tunis, Tunisia

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Abstract

Non coding region of chloroplast DNA of *Ficus* genus were examined to elucidate molecular evolution of palstome genome. *Material and Methods:* Herein, 123 sequences of *atpB-rbcL* intergenic spacer of 73 *Ficus* species were used and thirty-two represent *Ficus carica*. *Main Results:* The base pair length for the *atpB-rbcL* spacer is 810 bp of the *Ficus* genus and with an average of 873.2 bp for the *Ficus carica* species. The relatively high A+T values (66.8% (*F. carica*)–68.7% (*Ficus* genus)) of *atpB-rbcL* intergenic spacer may explain the high proportion of the identified transversions (ti/tv=0.349 (*Ficus carica*) and ti/tv=0.577 (*Ficus* genus)). The observed variation patterns provide evidence that *Ficus* species have been undergoing rapid expansion of the all sequences of *atpB-rbcL* intergenic spacer (Fu and Li's statistical tests (D*:-3.06007*; P < 0.05, F*:-3.29443**; P < 0.02) and (D*:-5.81985** (P < 0.02), F*:-5.28101** ; P < 0.02) for *Ficus carica* and *Ficus* genus respectively) and positive selection without a hitchhiking effect. We notice also, that the *Ficus carica* species is among the oldest species of the genus that can be considered among the ancestral species.

Keywords: chloroplast DNA, *atpB-rbcL* intergenic spacer, *Ficus carica* L. *Ficus* genus, Tunisia

Research highlight: this work could be appropriate for creating a strategic conservation program, benefitting future breeding programs.

VII 
International
Symposium
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ISHS 中国·北京
14th-20th August, 2023
Weiyuan, Sichuan, China

CERTIFICATE OF ATTENDANCE

PRESENTED TO

Dr. Ghada Baraket, University of Tunis El Manar, Tunisia

For attending and delivering an oral presentation at the VII International Symposium on Fig,
held from August 15 to 18, 2023, in Weiyuan County, Sichuan Province, China

Presentation title: Molecular Evolution and phylogenetic study of the atpB-rbcL spacer of chloroplast DNA in Ficus
Genus (Moraceae Family)

On behalf of the Organizing Committee

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