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STRUCTURE OF GENETIC DIVERSITY OF WILD AND CULTIVATED FIG TREE IN TUNISIA BY THE COMBINED ANALYZES OF SCOT AND RGAP MOLECULAR MARKERS

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The measurement of genetic diversity within and between populations is crucial to guide research methods conservation of plants and their sustainable use for genetic improvement. This work is devoted to a combined analysis of data from the two typing systems for a more complete understanding of the diversity available in the wild and cultivated Tunisian fig tree for better exploitation in the conservation and the definition of selection and conservation strategies. 12 SCoT primers and 5 RGA primers were used on 62 Tunisian fig trees. Results and conclusion: These primers revealed 139 SCoT-RGA markers (86.88%) that were found to be polymorphic. The diversity parameters showed the efficiency of the SCoT-RGA primers and the high level of polymorphism detected in the two compartments of fig trees studied. A high number of effective migrants was detected (Nm = 5.27) reflecting the significant gene flow recorded between cultivated and wild fig trees. Indeed, the value of Gst recorded is 0.087 and AMOVA revealed significant differences in the distribution of perceived genetic diversity rather within groups (87%) than between groups (13%) of fig trees studied. The combined dendrograms display three main groups asserting the topology of the dendrogram obtained by the SCoT markers. The results suggest that SCoT markers can be used as reliable and informative markers to detect levels of polymorphism and draw up the genetic links in the species Ficus carica L.

Keywords: Cultivated, Fig. SCoT-RGA, Tunisian, wild.















ATTESTATION DE PARTICIPATION

Délivrée à

Sahar HAFFAR

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Pr. Besma BEL HADJ JRAD













