

GENETIC DIVERSITY OF IRANIAN ASCOCHYTA RABIEI ISOLATES, THE CAUSAL AGENT OF CHICKPEA ASCOCHYTA BLIGHT USING ISSR AND RAPD MARKERS

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A *ascochyta rabiei* is one of the most important foliar diseases of chickpea in the world. In order to study the genetic diversity of Iranian *Ascochyta rabiei* isolates, 27 isolates of the pathogen were isolated from affected chickpea plants from different chickpea growing areas of West of Iran. Phylogenetic analysis pattern for ISSR and RAPD markers grouped isolates into four and three distinct groups, respectively. Both ISSR and RAPD markers showed high level of polymorphism and were found to be effective in determining of genetic diversity in *Ascochyta* blight isolates. The results of cluster analysis by ISSR and RAPD markers showed positive correlation by geographic origins, whereas isolates from "Kurdistan" and "Kermanshah" provinces distinctly grouped in different clusters. Results of present study showed high genetic diversity level in Iranian *Ascochyta rabiei* isolates that might be mediated by gene mutation or chromosomal segment loss and may suggest longer evolutionary period for this fungi from the chickpea growing area in the West of Iran. The results of presented study will be useful for chickpea breeder for effective selection of durable resistance sources.

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