

**ABSTRACT**

Ascochyta blight caused by *Ascochyta rabiei* (Pass.) Lab. is one of the most devastating chickpea disease. To determine the genetic and pathogenic diversity of the pathogen, 53 isolates from *Ascochyta rabiei* were collected from eight regions in Lorestan province. The collected samples were cultured on Chickpea Seed Meal Dextrose Agar. For identification of pathogenic diversity, the isolates were divided into seven groups based on molecular methods and SSR markers. From each group one isolate as an indicator was randomly selected and pathogenicity tests conducted using completed randomly design on seven differential chickpea cultivars in greenhouse conditions. Two weeks old seedlings inoculated by spraying spore suspension. After tree weeks diseased isolates were investigated for ascochyta blight using 1-9 scale and based on pattern of ICARDA pathogenicity reaction, two pathotype were identified including pathotypeI from Chegeni, Nourabad, Khorramabad, Kuhdasht regions and pathotypeIII from Alashtar and Azna regions. Genetic diversity from seven sampling regions studied based on using *A. rabiei* specific microsattelite marker. Data in final analysis using SSR five pair selective primers and designing dendrogram tree, isolates with 74% coefficient similarity divided in to 16 groups. Results of precent study can be exploited in improvement of resistance cultivars and developments of quarantine proceedings.

**Key words:** Pathogenicity, Microsattelite, *Ascochyta rabiei*, Genetic diversity



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**Study on genetic and pathogenic diversity  
of *Ascochyta rabiei* isolated from chickpea  
in Lorestan province**

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