

Mating Type, Pathotype and RAPDs Analysis in *Didymella rabiei*, the Agent of *Ascochyta* Blight of Chickpea

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Eleven pathotype groups (A-K), including five not previously reported, of *Didymella rabiei* (anamorph *Ascochyta rabiei*), representing isolates of the pathogen from *Ascochyta* blight-affected chickpeas mainly from India, Pakistan, Spain and the USA, were characterized using 44 single-spore isolates tested against seven differential chickpea lines. Of 48 isolates tested for mating type, 58% belonged to MAT 1-1 and 42% to MAT 1-2. Thirty-nine *D. rabiei* isolates, as well as two isolates of *Ascochyta pisi* and six isolates of unrelated fungi, were analyzed using Randomly Amplified Polymorphic DNAs (RAPDs) employing five primers (P2 at 40°C, and OPA3, OPC1, OPC11 and OPC20 at 35°C). Computer cluster analysis (UPGMA / NTSYS-PC) detected a relatively low level of polymorphism among all the *D. rabiei* isolates, although at *ca* 7% dissimilarity, *ca* 10 RAPD groups [I-X] were demarcated, as well as subclustering within the larger groups. By the same criteria, the maximum dissimilarity for the whole population of *D. rabiei* isolates was *ca* 13%. No correlation was found between different RAPD groups, pathotype, or mating type of *D. rabiei*, although some evidence of clustering based on geographic origin was detected. The use of RAPDs enabled us to identify specific DNA fragments that may have a potential use as genetic markers in sexual crosses, but none which could be used as virulence markers.

KEY WORDS: *Ascochyta rabiei*; teleomorphic stage; genetic diversity; *Cicer arietinum*.

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