Exploring host – pathogen co-evolution rate in natural and agricultural ecosystems: A case study from *Cicer* spp. – *Ascochyta rabiei* pathosystem

Talap Talapov1, Olcay Dedecan 1, Dürdane Mart2, Aladdin Hamwieh3, Lars G. Kamphuis4, Canan Can1

*E-mail of corresponding author* [*ayselcan1938@gmail.com*](mailto:ayselcan1938@gmail.com)*,* [*can@gantep.edu.tr*](mailto:can@gantep.edu.tr)

1 Department of Biology, Gaziantep University, Gaziantep, TR

2 Eastern Mediterranean Agricultural Research Institute, Adana, TR

3 International Center for Agricultural Research in the Dry Areas: Cairo, EG

4 Centre for Crop and Disease Management, Curtin University,AU

*Ascochyta rabiei* causal agent of the Ascochyta blight disease of *Cicer arietinum* limits chickpea cultivation worldwide. Southeastern Anatolia region of Türkiye takes place within the Fertile Crescent where chickpeas were first cultivated in human history and that it is considered to be the origin center of both the host and the pathogen (Abbo et al., 2003).

Field studies conducted by our group for the last 10 years, *D. rabiei* isolates were obtained from annual (*C. reticulatum, C. pinnatifidum, C. bijugum, C. turcicum*), perennial (*C. anatolicum*, *C. isauricum*) and cultivated *Cicer* species (Nalçacı et al., 2021; Talapov et al., 2023). Structure of *A. rabiei* populations from the wild *Cicer* species revealed by mating type and pathogenicity exhibit ecotype difference when compared to that of *C. arietinum*, indicating that host adaptation of the wild *A. rabiei* population is driven differentially since there is no selection pressure in natural ecosystems. Consequently, the co-evolution rate of the wild and cultivated pathosystems differs from each other. Comparison of wild and cultivated pathosystems is important to reveal *A. rabiei* - *Cicer* spp. co-evolution rate and to predict the evolution of the agent under different ecological conditions. Comparative analysis of *A. rabiei* genomes obtained from perennial and annual *Cicer* spp., definition of population structures, and presentation of effector gene repertoire will contribute to its development as a model system to study. Understanding the mechanism by which wild species tolerate *A. rabiei* will enable the development of innovative methods to combat the pathogen in agricultural systems.

*Abbo et al., ‘Evolution of cultivated chickpea: four bottlenecks limit diversity and constrain adaptation’, Functional Plant Biology,Vol. 30, no. 10, 2003, p. 1081.*

*Nalçacı et al., ‘Epiphytotics of chickpea Ascochyta blight in Turkey as influenced by climatic factors’.Journal of Plant Diseases and Protection, Vol. 128, 2021, p.1121*

*Talapov et al., ‘First Report of Ascochyta rabiei Infections on Endemic Turkish Populations of Cicer bijugum and C. turcicum’.Plant Disease, Vol.107, no. 12, 2023, p.4020.*