

reads in the interacting transcriptomes. About 10% of unigenes were from the pathogen. There were 132 induced unigenes of isolate AR19 in the first 12 hpi, nine of them were highly expressed during 24 to 96 hpi, and 42 of them were consistently expressed up to 96 hpi. There were 178 induced unigenes of isolate AR628, six of them were highly expressed during 24 to 96 hpi, and 69 of them were consistently expressed up to 96 hpi. Analysis showed a strong induction for the expression of pathogen genes that belonged to different functional categories. The functions of these induced genes and their roles in pathogenesis remain to be investigated.

Characterization of *Ascochyta rabiei* for population structure, mating type and pathogenic variability from Pakistan and United States. H. ALI¹, S.S. ALAM¹, R.N. ATTANAYAKE², M. RAHMAN³ and W. CHEN². ¹Nuclear Institute for Agriculture and Biology, Faisalabad, Pakistan. ²USDA-ARS, Washington State University, Pullman, Washington, USA. ³National Institute for Biotechnology and Genetic Engineering, Faisalabad, Pakistan. *E-mail: hinali991@hotmail.com

Chickpea production is greatly hampered by blight causing fungal pathogen *Ascochyta rabiei* (AR) in chickpea growing regions of the world. Genetic variability and mating type frequency of thirty two AR isolates from six geographical regions of Pakistan were compared with a US-AR population. Pakistani AR (PAR) population had an apparent skewed (3 Mat1-2: 1 Mat1-1) distribution, although Chi-square tests showed non-significant deviation from equal distribution due to small sample sizes and the US-population showed a 1:1 distribution. The results showed that sexual reproduction is rare in PAR due to either unavailability of both mating types or lack of conducive environment but statistical analysis showed panmixia which may be due to past recombinational events. Genetic variation at six microsatellite loci was assessed and each isolate was assigned to a microsatellite haplotype. Population structure using Bayesian analyses differentiated isolates into three distinct clusters, two clusters of PAR and one of the US isolates. However, few isolates from US shared same genetic background with one cluster of the PAR isolates, providing a link of inter-continental migration of the pathogen due to import of seeds. Additionally, the two clusters of Pak-isolates are not strictly linked to the geographic locations in Pakistan, suggesting frequent gene flow of AR among different locations. Pathogenic variability of nineteen PAR collected from two different provinces was assessed. The results based on the reaction of isolates with differential lines showed that aggressive and highly aggressive pathotypes II and III respectively are prevalent in Pakistan as compared to least aggressive pathotype I. It is interesting to note that highly aggressive pathotypes III and IV have only been

reported from Syria and Pakistan where we assume less frequency of sexual reproduction due to predominance of one mating type, in contrast to other countries where both mating types are present in equal ratio hence, this issue needs further investigations.

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Effects of temperature on virulence of *Didymella rabiei* pathotypes affecting chickpea. S. AHMED* and M. IMTIAZ. International Center for Agricultural Research in the Dry Areas (ICARDA), Aleppo, Syria. *E-mail: s.a.kemal@cgiar.org

Chickpea (*Cicer aritenum*) is one of the most important food legumes grown around the world in more than 50 countries. The yield gap of chickpea is high due to abiotic and biotic constraints where *Ascochyta* blight (*Didymella rabiei*) causes yield instability in different regions. High yielding chickpea varieties were developed and released in many countries; however some varieties were taken out of production due to susceptibility to new virulent pathotypes of the pathogen. Knowledge of the interactions of *Didymella-Cicer* with the environment has practical significance because the environment may alter the performance of cultivars and pathogen populations in the field. Little is known on how temperature may affect the virulence of different pathotypes of *D. rabiei*. The effects of temperature (10, 15, 20 and 25°C) on the virulence of four Pathotypes (P-I, P-II, P-III and P-IV) were studied using six chickpea genotypes (Ghab-1, Ghab-2, Ghab-3, Ghab-4, Ghab-5 and ICC-12004) with varying levels of blight resistance under controlled conditions. The results showed that the interactions of temperature with pathotypes as measured by virulence index were statistically significant but without changes in the ranking of the pathotype virulence on the host genotypes. The mean virulence index of the four pathotypes ranged from 3.3 in P-I to 7.2 in P-IV. P-4 showed high mean virulence index under all temperature regimes followed by P-3 compared with the other two. The least virulent P-1 among the tested pathotypes showed high average virulence index at 10°C on the test genotypes. Similar results were obtained for the chickpea genotypes where significant genotype-temperature interactions were detected but no changes in the ranking of resistance to *Ascochyta* blight. Except for Ghab-1, which is the most susceptible genotype, the remaining genotypes showed high disease severity at temperature 10 and 15°C. This study showed that *D. rabiei* population has developed pathotypes that can cause disease epidemics irrespective of temperature regimes in Syria and there is a need to further investigate the response of pathogen populations to temperature from similar Mediterranean environments.