

DISEASE NOTE

VIRULENCE AND GENETIC VARIABILITY OF *NEOCOSMOSPORA VASINFECTA* CAUSING ROOT ROT IN CHICKPEA

H. Ali, K. Pervaiz Akhtar, T. Mahmud Shah and N. Iqbal

Nuclear Institute for Agriculture and Biology, Jhang Road, Faisalabad, Pakistan

Since chickpea (*Cicer arietinum*) root rot caused by *Neocosmospora vasinfecta* is widespread in Khushab, Jhang and Layyah, three regions of the Pujab province (Ali *et al.*, 2011), a study was conducted to assess the virulence and genetic diversity of a number of fungal isolates which, upon isolation on chickpea seed meal agar, yielded white cottony colonies within 7-10 days at 25°C. Virulence assays of seven such isolates were carried out in pots in a glasshouse and a growth-room using the susceptible genotypes JG62 and Aug424, as described by Sharma *et al.* (2005) and Infantino *et al.* (2006). All tested isolates were virulent on both genotypes with variable reaction from least to highly aggressive. Four out of five isolates from Khushab and the only isolate from Layyah were aggressive. For genetic diversity analysis, eight RAPD and nine URP markers (Kang *et al.*, 2002) were used. Analysis showed that the seven *N. vasinfecta* isolates fall into three distinct clades, with URP markers allowing a better definition of genetic variability than RAPD. Virulence and genetic diversity tests proved that the seven isolates fall into three distinct groups. Cluster analysis was performed based on the un-weighted pair group method with arithmetic means (UPGMA) using the Genstat software (10th Edition). No overlap between genetic and virulence groups was detected, nor a correlation was found between these two variables and the geographical origin of the isolates. This preliminary study will form the basis for a comprehensive future work on more isolates and may lead to identify *N. vasinfecta*-resistant genotypes, potentially forming part of an efficient strategy to manage chickpea root rot.

Ali H., Akhtar K.P., Shah T.M., Amjad A., 2011. First report of *Neocosmospora vasinfecta* causing root rot disease of chickpea in Pakistan. *Journal of Plant Pathology* **93**:79.

Infantino A., Kharrat M., Riccioni L., Coyne C.J., McPhee K. E., Niklaus J., Grünwald N.J., 2006. Screening techniques and sources of resistance to root diseases in cool season food Legumes. *Euphytica* **147**:201-221.

Kang H.W., Park D.S., Park Y.J., You C.H., Lee B.M., Eun M.Y., Go S.J., 2002. Fingerprinting of diverse genomes using PCR with universal rice primers generated from repetitive sequence of Korean weedy rice. *Molecules and Cells* **13**:281-7.

Corresponding author: H. Ali
Fax: +92419201776
E-mail: hinali991@hotmail.com

Received May 11, 2014
Accepted August 22, 2014

DISEASE NOTE

POWDERY MILDEW CAUSED BY *GOLOVINOMYCES CICHORACEARUM* ON *SYMPHYOTRICHUM SUBULATUM* var. *SQUAMATUM* IN IRAN

H.A. Mirhosseini, V. Babaeizad, L. Hashemi and E. Basavand

Department of Plant Protection, Sari Agricultural Sciences and Natural Resources University, P.O.BOX 578, Mazandaran, Sari, Iran

Symphiotrichum subulatum var. *squamatum* (Spreng.) S.D. Sundb. (Syn: *Conyzanthus squamatus*) is one of the weeds which occurs in many regions of south Caspian Sea, especially around rice fields and along road sides, where more water is available. In June 2014, a powdery mildew was observed on *C. squamatus* in Guilan and Mazandaran provinces. Symptoms first appeared as small, nearly circular white spots that enlarged and coalesced over time. As the disease progressed, a white mycelium covered the entire plant. Conidiophores were erect 80-146.5 × 10-14 µm in size and bore 2-4 immature conidia in short chains with sinuate edge-line, measuring 21-43 × 17-24 µm. Conidia were hyaline and cylindrical and lacked distinct fibrosin bodies. Long, unbranched germ tubes grew from the ends of conidia. These morphological characteristics suggested that the powdery mildew fungus is *Golovinomyces cichoracearum* (anamorph *Euoidium* sp.) (Braun, 1987). Chasmothecia were not observed in the collected samples. To confirm the morphological identification, the ITS-rDNA region was amplified using the primer pair ITS4/ITS5 (White *et al.*, 1990) and sequenced (GenBank accession No. KM434159). Blast analysis of the 563 bp amplicon showed 99% similarity with *G. cichoracearum* (EU233820). Pathogenicity was ascertained on healthy potted host plants, inoculated by touching them with mildew-infected leaves. Non-inoculated plant served as controls. After 5-7 days, a fungus developed on inoculated plants with a morphology matching that of the original pathogen. Non-inoculated control plants did not develop powdery mildew symptoms. To our knowledge, this is the first report of *G. cichoracearum*-induced powdery mildew on *C. squamatus* in Iran, whereas a powdery mildew caused by *Oidium* sp. had previously been recorded on this plant (Aeenfar, 2006).

Aeenfar H., 2006. Identification of powdery mildew fungi (Erysiphaceae) and their hosts in Mashhad and Mashhad vicinity. MSc Thesis. Tehran Payam Noor University, Iran.

Braun U., 1987. A Monograph of the *Erysiphales* (Powdery Mildews). Cramer J., Berlin-Stuttgart, Germany.

White T.J., Bruns T., Lee S., Taylor J.W., 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis M.A., Gelfand D.H., Sninsky J.J., White T.J. (eds). PCR Protocols: A Guide to Methods and Applications, pp. 315-322. Academic Press, San Diego, CA, USA.

Corresponding author: H.A. Miroseini
Fax: +98.1133822567
E-mail: alimirhosseini@yahoo.com

Received November 20, 2014
Accepted February 3, 2015