Characterization of beet necrotic yellow vein virus in Pakistan

Shawana Ahmad¹ · Asad Ali¹ · Musharaf Ahmad¹ · Najeeb Ullah² · Ume Kalsoom Afridi³ · Nadia Bostan¹ · Rizwana Qureshi¹ · Saleha Tawwab¹ · Ijaz Ahmad¹ · Muhammad Zubair¹

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Beet necrotic yellow vein virus (BNYVV) causes rhizomania disease of sugar beet (*Beta vulgaris* L. ssp. *vulgaris*) and is the most important sugar beet virus affecting both its quality and quantity (Peltier et al. 2008). In 2013–2014, the major sugar beet growing areas of Khyber Pakhtunkhwa province in Pakistan were surveyed for rhizomania. Sugar beet leaf samples showing chlorosis and deformations were collected and tested for BNYVV using polyclonal antibodies (Adgen, UK) in DAS-ELISA (Clark and Adams 1977). BNYVV was detected in four out of 10 samples tested. To confirm the presence of BNYVV, total RNA was extracted from ELISA positive samples with the RNeasy plant minikit (Qiagen, UK) and used in RT-PCR with primers F105 (TGCGAGTAATAAGT AGCCGCCGTCC) and R744 (AATGTGTGCCGTCAC CCGAGCAGC) to amplify the coat protein (CP) gene. A single band of ca. 600 bp was successfully amplified by RT-PCR from the four ELISA positive samples. One amplicon was sequenced (567 nt) in both directions and the consensus sequence was deposited in GenBank as accession number AB908167. Blast analyses showed the highest nucleotide

(98.06%) and amino acid (98.94%) identity of BNYVV-Pak with BNYVV isolate CH6 from China (AB562989). A phylogenetic tree constructed based on CP gene sequences revealed two clades with BNYVV-Pak grouping with Chinese and Iranian isolates. Since BNYVV was previously described in Pakistan (Arif et al. 2015), this is the first report of the molecular characterization of a Pakistani BNYVV isolate.

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✉ Shawana Ahmad
shawanakakakhel@yahoo.com

¹ University of Agriculture Peshawar, Peshawar, Pakistan

² Nuclear Institute for Agriculture and Biology, Faisalabad, Pakistan

³ Kyungpook National University, Daegu, Republic of Korea