

SEQUENCING OF THREE ISOLATES AND PREVALENCE OF POTATO VIRUS Y IN TOBACCO FIELDS OF GOLESTAN PROVINCE, AND PHYLOGENETIC COMPARISON OF THE IRANIAN AND WORLD ISOLATES OF THE VIRUS *

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Abstract

To determine the prevalence of *Potato virus Y* (PVY) in tobacco fields of Golestan province, a total of 182 samples showing virus type symptoms PVY infection in collected samples was assessed using a polyclonal antiserum in DAS-ELISA test. Of all collected samples 90 were infected by PVY. Viral RNA was extracted using RNX-Plus kit. The extracted RNA was reverse transcribed using oligo dT primer to create the respective cDNA, which was amplified by PCR using a PVY-specific primer pair designed on CP region. After verification on 1% agarose gel in electrophoresis, the expected band of ~1000 bp size was amplified. PCR products were directly sequenced and the sequences of about 850 nucleotides were aligned with 30 sequences of the GenBank. Multiple alignment and phylogenetic analyses were performed by ClustalX and BLAST programs in BioEdit software and phylogenetic dendrogram was produced using maximum parsimony method. The results showed that all PVY sequences can be placed into 4 groups. Aliabad and Fazelabad isolates were grouped with isolates from Italy, Spain and Boushehr, while Minoodasht isolate was grouped with isolates from the Netherlands, United Kingdom and Taiwan.

Keywords: Tobacco, potato virus Y, DAS-ELISA, CP, Phylogenetic analysis.

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