



Complete genome characterization and population dynamics of potato virus Y-NTN strain from India

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Abstract Potato virus Y (PVY) is a major threat to potato cultivation worldwide. PVY exists as biologically and genetically distinct strains and causes varying degrees of pathogenicity and a wide range of symptoms in potato. Knowledge of the nature of PVY strains is essential for breeding PVY resistant cultivars that are durable against a wide range of strains. We report the complete genome of a PVY potato isolate (JK12) characterised from the potato production areas of Jammu and Kashmir, India. Nucleotide sequence comparisons and phylogenetic analysis with known PVY strains revealed that the isolate belongs to the NTN strain of PVY. At the whole genome sequence level, the JK12 isolate shared the highest identity (99.42%) with PVY-NTN strains reported from Germany, followed by those from United Kingdom (99.34%) and Japan (99.33%). Recombination detection analysis identified two recombination break points and JK12 appeared to have originated from a recombination event between a PVY-N strain from Belgium as a major parent and a PVY-O strain from China as the minor parent. Our results suggest possible mutation and recombination could be the basis for the evolution and

the subsequent establishment of NTN in this region. Furthermore, a global evolutionary lineage analysis of all the known PVY strains showed relatively low nucleotide diversity among the PVY-NTN strains. Neutrality tests showed that all the genotypes of PVY are undergoing purifying selection suggesting population expansion of PVY. This is the first report of complete genomic characterization of an NTN strain of PVY isolated from commercial potato fields in India. The implications of the emergence of this strain in the Indian context are discussed.

Keywords Potato virus Y · PVY-NTN strain · Genome analysis · Recombination · Virus evolution

Introduction

Potato virus Y (PVY) is a major pathogen of potatoes worldwide, resulting in yield losses of up to 80% [40]. PVY is a type member of the genus *Potyvirus* in the family *Potyviridae* [27, 43]. PVY has a wide host range and infects plants belonging to nine different families including the family *Solanaceae* and the prominent susceptible hosts include pepper, potato, tobacco and tomato [27, 34]. PVY is transmitted through vegetative propagation of infected material and by several species of aphids in a non-persistent manner [10].

The genome of PVY is characterized by a single-stranded, positive-sense RNA of approximately 9.7 kb in length [47]. PVY genome has a single large open reading frame (ORF), which encodes a single polyprotein, flanked by 5' and 3' untranslated regions (UTRs). Three viral proteases are involved in cleaving the expressed polyprotein into 10 products [3]. P1 is the first coded protein from the 5' end and is the most variable protein among all the PVY-coded

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