

Euro Virology 2019: Genetic diversity and genome sequencing of some potato virus Y isolates from Egypt- Faiza A Fattouh- Alexandria University

Ariza Faiza A Fattouh

Alexandria University, Egypt

Potato is the second most important food crop in Egypt in terms of yield and cash value. Virus infection is a major factor which affects production and tuber quality. Detection of several different potato viruses has been reported in some studies; yet, few limited studies addressed the genetic characterization of such viruses. PVY is a major virus affecting potato and is of worldwide distribution. The aim of this work is to elucidate more information on PVY genetic diversity in Egypt. Following several surveys for the detection of major viruses affecting potato in different geographic governorates, some PVY isolates were subjected to molecular characterization by means of immunocapture RT-PCR and also full genome sequencing. Multiple recombinant types of PVY were distinguished. At least 3 recombinant strains previously associated with potato tuber necrotic ringspot disease (PTNRD), including a novel recombinant were identified. These discoveries propose the nearness of PTNRD-actuating infection strains tainting potato.

It is privately expended, made or provided for fare to Europe and other Arab nations. Potato is dependent upon contamination by assortment of plant infections, which influence its yield and quality. Potato infection Y (PVY), potato leaf move infection (PLRV), and Alfalfa mosaic infection (AMV) were identified in significant potato-developing territories overviewed. Multiplex-RT-PCR measure was utilized for the identification of those three infections in a single response utilizing three explicit preliminary sets intended to intensify genomic parts of each infection. All three viruses were detected during a single reaction mixture in naturally infected field-grown potatoes. Multiplex RT-PCR improved sensitivity necessary for the first detection of infection. Rate of single, twofold, or triple disease has been recorded in certain areas. Full-length sequencing has been performed for an Egyptian FER segregate of PLRV. Through phylogenetic analysis, it had been shown to occupy an equivalent clade with isolate JokerMV10 from Germany. This is the primary complete nucleotide sequence of an Egyptian isolate of AMV. Genetic biodiversity of devastating potato viruses necessitates continuous monitoring of latest genetic variants of such viruses.

Distinctive potato tests demonstrating mosaic side effects were gathered from a trial station in Giza Governorate, Egypt and were tried utilizing RT-PCR. PVY was enhanced utilizing groundworks spoke to part of the coat protein (CP) quality and 3' untranslated locales (UTR). Phylogenetic tree indicated two principle strain gatherings: Group I refocuses PVYN and PVYNTN secludes, while Group II incorporates PVYO, PVYW and PVYN:O segregates. The Egyptian PVY detach was plainly characterized inside gathering I, and was all the more firmly connected with PVYNTN segregates. Three rationed aminoalkanoic corrosive replacements (V1→I, G7→V

and S8→G) had the option to separate between the two gatherings. As a result, the anticipated CP aminoalkanoic acid was more diverse than the 3'UTR nucleotide sequences (92.6-100% and (97.7-100% identity, respectively). Be that as it may, the personality inside gatherings was around comparative (~97 and ~98%, for CP and 3'UTR, individually). The 3'UTR of the Egyptian seclude demonstrated RNA optional structures not quite the same as those of the 5 PVY strains.

Potato infection Y (PVY) has been accounted for together of the most infections influencing potatoes in Egypt, yet constrained data is out there on PVY strains flowing in potato fields inside the nation. From 2014 to 2016, infection overviews were directed in a few potato-developing governorates of Egypt, and PVY-positive examples were found to speak to at least five unmistakable recombinant PVY strains, including PVYNTN and PVYN-Wi. Entire genome groupings were resolved for four separates speaking to strains PVY-SYR-III (Egypt7), PVY-261-4 (Egypt11), PVYNTNa (Egypt35), and a totally extraordinary recombinant named Egypt24 that joined atomic properties of strains PVY-261-4 and PVY-Wilga156var. At least three recombinants found in Egypt in potato were previously found related to potato tuber necrotic ringspot disease (PTNRD). The distinguishing proof of numerous recombinant sorts of PVY in potato in Egypt, including the novel recombinant Egypt24, proposes a decent nearness of PTNRD-actuating infection strains inside the nation. The potato infection Y (PVY) complex incorporates five non-recombinant strains and a developing number of recombinants. Up to now, the majority of those PVY recombinants were found to be composed of genome segments coming from only two "parental" genomes, PVYO and PVYEu-N, with a little minority including segments from other parents, e.g. PVYC, PVYNA-N, and a portion of the recombinant strain PVY-NE11. Here, extensive examinations of 396 entire genomes of PVY disconnects from 34 nations and a spread of hosts uncovered 28 secludes to be uncommon or novel recombinants. When exposed to an extreme recombination investigation, these 28 PVY disconnects were found to speak to 25 inadequately examined PVY recombinant structures, ten of which had not been perceived already. Nine of the ten novel structures conveyed parental arrangements from PVYNA-N or PVY-NE11 strains recombined with PVYO and PVYEu-N successions, while seven of the new structures contained groupings from three unique guardians. The quantity of known PVY recombinant examples presently remains at thirty-six. These recombinant structures present a test for PVY strain composing, however, may reveal insight into communications among PVY and host opposition qualities.