Molecular characterization and phylogenetic relationships of a newly discovered Potato virus X (PVX) strain from Peru

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Potato virus X (PVX), a type member of the genus Potexvirus (Alphaflexiviridae) is a widely distributed pathogen, which could cause a significant economic loss, especially in a synergistic co-infection with some potyviruses, such as Potato virus Y. Previously, genomes of several PVX isolates have been sequenced completely. They cluster into two distinct groups (South American and Eurasian). In this study we determined the complete or near complete (99% or more) genomic sequence of 8 PVX isolates from Peru (infected field and greenhouse samples) and characterize their phylogenetic relationships with all other sequenced isolates available.

The strategy of illumina deep sequencing of small RNAs was employed to obtain complete or near complete (99% or more) genome sequences of PVX from symptomatically infected greenhouse (Solanum tuberosum and Datura sp.) and field samples (Solanum tuberosum), collected in Peru. In analysis step, the combination of de-novo short reads assembly (Velvet) and reference reads mapping (MAQ) was used to generate the genome sequences of PVX. Alignment and phylogenetic analyses were performed using MEGA4 and SplitsTree4.12.3 including all complete genome sequences of PVX available from NCBI GenBank database.

Our study shows the utility of small RNAs deep sequencing for successful viral strain differentiation and discovery of new viral strains. Moreover, the discovery of new PVX strain in Peru could indicate existence of higher diversity of this potato pathogen in the region, which would be in agreement with the high diversity of cultivated and wild potatoes present there. A similar pattern may be expected also for other potato pathogens.

Method reference: