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Probing Potato's Response to Potato virus Y infection

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Potato virus Y (PVY) continues to be a constraint to the potato industry globally due to its effects on tuber quality and yield. With the emergence of new strains of PVY, developing new management strategies for PVY-related disease is of utmost importance. Investigating genetic sources to develop potato varieties with multiple disease resistance is one such strategy that could be cost effective and sustainable. One of the main objectives of the Tri-State (ID, OR & WA) potato breeding and variety development program is to develop new russet varieties with increased resistance to PVY. Two of the new clones, Payette Russet and POR06V12-3 (to be released as Castle Russet) are resistant to all strains of PVY and possess good processing quality. Identifying the difference in host response at the molecular level in these new clones compared to older varieties such as Russet Burbank (sensitive to PVY) will provide valuable information about the nature of this resistance. Gaining insights into the underlying molecular pathways that differ between resistant and sensitive cultivars could provide molecular markers that could be used for rapid screening for virus resistance.

Many strains of PVY have been reported around the world; among them PVY-O, PVY-N, PVY-NTN are major strains identified in the Northwest. Prevalence of these strains is constantly changing. Also each of these PVY strains has different effects on the same cultivar (Figure 1).

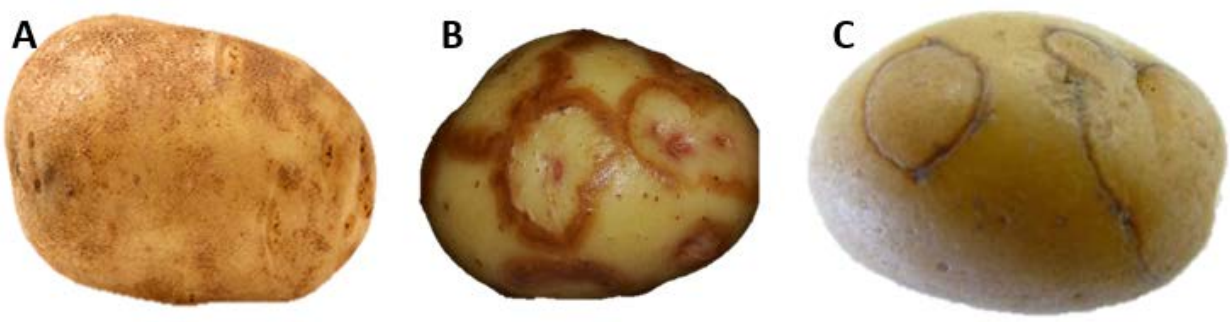

Figure 1: Potato tubers infected with (A) PVY-O, (B) PVY-NTN and (C) PVY-N Wilga strains. Photo courtesy: www.potatovirus.com

Currently, N-Wilga appears to be the predominant strain in the region. One of the ways, plants respond to virus infection is by targeted degradation of the invading viral RNA molecules (the genome of PVY is composed of RNA) – resulting in small (17 to 24 nucleotides) RNA pieces. An undesirable outcome of this response is that these virus-derived small interfering RNAs (vsiRNAs) in turn could suppress some of the plant's gene expression through a phenomenon called RNA interference, thus leading to changes in the plant's gene expression. Different strains of PVY mentioned earlier are slightly different in their genetic make-up, and could lead to differences in siRNA profiles derived from each upon infection. In our recent study, we used the vsiRNA profiles of three PVY strains (PVY-O, PVY-N, PVY-NTN) infecting the potato cv. Russet Burbank. Our results showed that infection of potato by each of these three strains resulted in different siRNA profiles. To understand this strain-specific accumulation of vsiRNAs, we mapped the vsiRNA obtained from each strain to the PVY genome. Most of the siRNAs generated from PVY-N strain were found to be originated from the Hc-Pro region of the viral genome, however, the CI gene of the virus generated the highest number of siRNAs in both PVY-O and PVY-NTN strains.

Furthermore, to identify the unique siRNAs generated from infection by each strain, we mapped the vsiRNAs to the host genome. Approximately 40,000 potential vsiRNA targets in potato transcriptome were identified with strains PVY-N and PVY-O, and the number of target genes was higher i.e. about 60,000 targets were identified in the host transcriptome with vsiRNA derived from PVY-NTN strain. These data were filtered further to identify the unique target genes with respect to each PVY strain, which varied from 17,500 to 22,000 depending on the PVY strain. Pathway analysis using the Kyoto Encyclopedia of Genes and Genomes (KEGG) database, showed that genes involved in plant hormone signaling pathway and plant-pathogen interactions were targeted by the vsiRNA derived from all three PVY strains. This study provided us with a better understanding PVY pathogenicity, which in future could be used to develop improved approaches to mitigate the effects of PVY.

Evolution of new strains of PVY-Wilga through recombination of older PVY strains is posing new challenges to the sustainable potato production. With the support from the Northwest Potato Research Consortium, we are investigating the gene expression profiles of resistant (POR06V12-3) and susceptible (Russet Burbank) potato clones in response to different strains of PVY using High Throughput Sequencing technology.

Proceedings of the 2017 WA/OR Potato Conference Available

Every year since 1962 there has been a Proceedings from the Washington, and now Washington/Oregon, Potato Conference. It is typically released in June, giving authors time to compose articles after the conference. The 2017 Proceedings was recently completed and is posted on the front of the Northwest Potato Research Consortium website, http://www.nwpotatoresearch.com/. In the coming weeks each article will be entered into the research library so that they are fully searchable.