

Discovery of known and novel viruses in wild and cultivated blueberry in Florida through viral metagenomic approaches

ABSTRACT

Southern highbush blueberry (interspecific hybrids of *Vaccinium corymbosum* L.) is cultivated near wild *V. corymbosum* as well as closely related species in Florida, USA. The expansion of blueberry cultivation into new areas in Florida and deployment of new cultivars containing viruses can potentially increase the diversity of viruses in wild and cultivated *V. corymbosum*. In this study, viral diversity in wild and cultivated blueberries (*V. corymbosum*) is described using a metagenomic approach. RNA viromes from *V. corymbosum* plants collected from six locations (two cultivated and four wild) in North Central Florida were generated by high throughput sequencing (HTS) and analyzed using a bioinformatic analysis pipeline. De novo assembled contigs obtained from viromes of both commercial and wild sites produced sequences with similarities to plant virus species from a diverse range of families (Amalgaviridae, Caulimoviridae, Endornaviridae, Ophioviridae, Phenuiviridae, and Virgaviridae). In addition, this study has enabled the identification of blueberry latent virus (BILV) and blueberry mosaic associated ophiovirus (BLMaV) for the first time in Florida, as well as a tentative novel tepovirus (blueberry virus T) (BIVT) in blueberry. To the best of our knowledge, this is the first study that compares viral diversity in wild and cultivated blueberry using a metagenomic approach.

Keyword: Metagenomics; Viromes; Blueberry; Florida