IDENTIFICATION OF A PRUNUS VIRUS F-LIKE VIRUS IN SWEET CHERRY

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Introduction

During the last years the broad application of next generation sequencing (NGS) has led to an increase in the number of viruses that are known to infect fruit trees. In the last five years, more than 10 new virus species have thus been identified in stone fruits, belonging in some cases to virus genera previously unknown to infect *Prunus* species. One of these new viral agents, *Prunus virus* F (PrVF) is the first fabavirus reported to infect Prunus fruit trees (1). Here, we report the identification of a virus isolate related to PrVF infecting sweet cherry.

Materials and Methods

In 2014, small interfering RNAs (siRNAs) extracted from a sweet cherry tree known to be infected by *Little cherry virus* 1 (LChV-1) and *Prune dwarf virus* (PDV) were subjected to NGS using the Ion Torrent platform with the PGM system (Ion 318 chip). The siRNA sequencing data generated were analyzed using Geneious and CLC Genomics Workbench 8.0.

Results and Discussion

De novo assembly of siRNAs generated contigs that matched LChV-1 and PDV sequences, as well as some contigs that were similar to already characterized isolates of PrVF. Large fragments of both RNAs of a PrVF-like virus were obtained by itterative mapping of the siRNA reads to the *de novo* contigs. RNA1 concatenated genome fragments (4144 nt) showed 67-68% nt (61% aa) sequence identity to PrVF isolates (Acc. No: KX269865-70). In the case of the RNA2 the contigs obtained (1130 nt concatenated length) were 64-66% (55% in aa) identical with PrVF isolates (Acc. No: KX269871-75). Previous work (1) showed high levels of amino acid identities among PrVF isolates, ranging between 94-98% for RNA1 and 90-97% for RNA2 encoded polyproteins. The current species demarcation criteria for the genus Fabavirus include 75% aa identity for CP and 80% for Pro-Pol. Full genome analysis is underway in order to elucidate whether the identified virus is a divergent variant of PrVF or a novel fabavirus species.

References

1. Villamor et al., 2016. *Archives of Virology* DOI 10.1007/s00705-016-3141-z.