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Genome sequence and detection of *Peach rosette mosaic virus*

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Highlights

- Complete genome presented and analyzed
- Quick and efficient dsRNA protocol described
- Detection protocol that detects both virus RNAs developed

Abstract

Peach rosette mosaic disease was first described in the 1940s affecting peach and plum. It was later determined that peach rosette mosaic virus (PRMV) is the causal agent of the disease. PRMV, a member of the genus *Nepovirus*, infects several perennial crops including stone fruit, grape and blueberry as well as several weed species found in orchards around the world. The molecular characterization of the virus is limited to partial genome sequences making it difficult to develop reliable and sensitive molecular detection tests; the reason that detection is routinely performed using ELISA with antibodies risen against a single virus isolate. Given the potential economic impact of the virus and the modes of transmission which, in addition to nematodes, include seed we studied PRMV in more depth using a modified dsRNA

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