



First report of Sweet potato virus C infecting sweet potato in Israel

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Received: 25 Apr 2013. **Published:** 20 Sep 2013. **Keywords:** *Ipomoea batatas*, sweet potato virus disease, viral synergism

In October 2011 sweet potato (*Ipomoea batatas*) mother plants (mainly cv. Georgia Jet) in Israel suffered an epidemic of sweet potato virus disease (SPVD). The plants were of poor appearance, grew feebly and showed strong leaf malformation, mosaic, purpling, chlorosis, cupping, vein yellowing and occasional feathery mottle symptoms (Figs. 1-3). SPVD is the result of synergism between *Sweet potato chlorotic stunt virus* (SPCSV, genus *Crinivirus*) and either *Sweet potato feathery mottle virus* (SPFMV, genus *Potyvirus*) or *Sweet potato mild mottle virus* (genus *Ipomovirus*) (Tairo *et al.*, 2005; Clark *et al.*, 2012). RNA extraction was performed on leaves from symptom-bearing plants using Tri-Reagent (Molecular Research Center, Cincinnati, OH, USA). First strand cDNA synthesis was performed with a RevertAid cDNA synthesis kit (Fermentas, Thermo Scientific Molecular Biology, Waltham, MA, USA). Potyvirus-degenerate primers corresponding to the cylindrical inclusion protein gene were used in PCR (Ha *et al.*, 2008). A distinct ~700 bp amplicon was obtained from five symptom-bearing plants. The amplicon was cloned and sequenced and was shown to correspond to the *Sweet potato virus C* (SPVC) Bungo isolate (Yamasaki *et al.*, 2010). The entire nucleotide sequence (10,828 nts excluding the 3'-terminal poly (A) tail) of the Israeli SPVC isolate was determined using overlapping primers from the Bungo strain (Yamasaki *et al.*, 2010) and deposited in GenBank (Accession no. JX489166). The Israeli strain had 98% identity to the Bungo strain at the nucleotide level and 99% at the amino acid level. SPVC is a distant variant of SPFMV (Tairo *et al.*, 2005) that has been known for many years in Israel based on symptom appearance and immunological tests (Cohen *et al.*, 1988).

No other potyvirus was found by RT-PCR in the SPVD-affected mother plants. SPVD was transmitted by graft inoculation from the SPVD-plants to virus-indexed sweet potato cv. Derby and to SPCSV-infected sweet potato cv. Georgia Jet. Inoculations were confirmed by symptoms and RT-PCR. SPVC was transmitted by mechanical inoculation to *Nicotiana benthamiana* with strong mosaic symptoms. Field samples obtained from March to June 2012 were screened by RT-PCR using the degenerate potyvirus primers described above and new SPVC-specific primers (forward 5'-CAAATCAACAGGTTTGCCTTTTAT-3' and reverse

5'-AGTTCATCGACTTCATTGTAACCTG-3'). PCR conditions were as in Ha *et al.* (2008), but with an annealing temperature of 56°C, which generated the expected 520 bp fragment. Of 170 field samples (each composed of 25 leaf samples) collected from all four major sweet potato growing areas in Israel, 46 (27%) were SPVC-infected. To our knowledge this is the first report of SPVC in Israel.

Acknowledgements

Contribution from the Agricultural Research Organization, Volcani Center, Bet Dagan, Israel, No. 512/12. Photo credits – Dani Shavit.

References

- Clark CA, Davis JA, Abad JA, Cuellar WJ, Fuentes S, Kreuze JF, Gibson RW, Mukasa SB, Tugume AK, Tairo FD, Valkonen JPT, 2012. Sweetpotato viruses: 15 years of progress on understanding and managing complex diseases. *Plant Disease* **96**,168-185. [<http://dx.doi.org/10.1094/PDIS-07-11-0550>]
- Cohen J, Salomon R, Loebenstein G, 1988. An improved method for purification of sweet potato feathery mottle virus directly from sweet potato. *Phytopathology* **78**, 809-811. [<http://dx.doi.org/10.1094/Phyto-78-809>]
- Ha C, Coombs S, Revill PA, Harding RM, Vu M, Dale JL, 2008. Design and application of two novel degenerate primer pairs for the detection and complete genomic characterization of potyviruses. *Archives of Virology* **153**, 25-36. [<http://dx.doi.org/10.1007/s00705-007-1053-7>]
- Tairo F, Mukasa SB, Jones RAC, Kullaya A, Rubaihayo PR, Valkonen JPT, 2005. Unravelling the genetic diversity of the three main viruses involved in Sweet Potato Virus Disease (SPVD), and its practical implications. *Molecular Plant Pathology* **6**, 199-211. [<http://dx.doi.org/10.1111/j.1364-3703.2005.00267.x>]
- Yamasaki S, Sakai J, Fuji S, Kamisoyama S, Emoto K, Ohshima K, Hanada K, 2010. Comparisons among isolates of *Sweet potato feathery mottle virus* using complete genomic RNA sequences. *Archives of Virology* **155**, 795-800. [<http://dx.doi.org/10.1007/s00705-010-0633-0>]



Figure 1



Figure 2



Figure 3

To cite this report: Prakash S, Tam Y, Zeidan M, Abu-Ras A, Gaba V, 2013. First report of *Sweet potato virus C* infecting sweet potato in Israel. *New Disease Reports* **28**, 4. [<http://dx.doi.org/10.5197/j.2044-0588.2013.028.004>]

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