

Supplementary file 1. Matches to sequences in the Genbank database.

This supplementary file provides a number of the sequences obtained from seed lots and an analysis of likely associations of the isolates. Generally the longest available sequences were selected for this file and analysis.

Methods

The GenBank non-redundant nucleotide sequence database was searched for matches to the sequences by using the BLASTN (BLAST nucleotide) program. Dendrograms generated by the minimum evolution method, as implemented in BLASTN suite of programs, were used along with the BLASTN search results to find the closest matching sequences in the database and to identify clusters of isolates to which the seed isolates were likely to belong. Alignments were made using the MAFFT programs and the FFT-NS-i method, with a gap opening parameter of 1.

Isolates from seed lots were named using the following convention: viroid species, host, location, submission reference number and first initial of testing laboratory.

Host: Ca= Capsicum; To = Tomato,

Region: Eu = Europe; EA – east Asia; NK = region not known; ME = middle east; As = Asia; SAm = South America; SAs – South Asia

Lab: C=CHS; E = EAMI

References to methods

- Altschul, G.F.; Gish, W.; Miller, W.; Myers, E.W.; Lipman, D.J. Basic local alignment search tool. *J. Mol. Biol.* **1990**, *215*, 403–410.
- blastn suite. National Center for Biotechnology Information. Available online: <https://blast.ncbi.nlm.nih.gov/Blast.cgi> (accessed on 30 November 2018).
- Katoh, K.; Standley, D.M. MAFFT Multiple Sequence Alignment Software Version 7: Improvements in Performance and Usability. *Mol. Biol. Evol.* **2013**, *30*, 772–80.
- MAFFT alignment implementation: <https://mafft.cbrc.jp/alignment/server/>

Table S1. Matches to sequences in the Genbank non-redundant database.

CLVd
CLVdCaEA1302154C, CLVdToME1155E, CLVdToME1273E are closest to the sequences of a cluster of isolates that includes Rutgers 3 (JF742635.1), Prayong-16 (KC143294.1) and Chaipayong-16 (KM214217.1); BLAST searches indicated 98-99% identity and 100% coverage. CLVdToAs1385E is closest to the sequences of a cluster of isolates that includes CM10-6c1 (JF446929.1) and NC17 (AM698094.1); BLAST searches indicated 98-99% identity and 100% coverage. CLVdToNK1285E is closest to sequences of a cluster that includes PQ-49 (DQ923058) and MC-M-11 (AM698095) with 99% identity and 100% coverage.
PSTVd
PSTVdCaSAm1302191C is closest to the sequences of a cluster of isolates that includes PSTVd SJ1PL (KC707563); BLAST searches indicated 100% identity and 100% coverage. PSTVdToSAm130212C is closest to the sequences of the cluster of isolates that includes the isolates UK (AJ583449) and Naaldwijk isolate (X17268) and appears to fall within this cluster; BLAST searches indicated 98-99% identity and 98% coverage. PSTVdToSAm130211C is closest to this same cluster of isolates, but appears to fall outside the cluster; BLAST searches indicated 96% identity and 99% coverage. PSTVdToEA130225C is closest to the sequences of isolates DN12 (KR611353) and VNIKH-08-94B (JQ889846), with searches indicating 96% identity and 100% coverage. PSTVdToSAs27617C is closest to the sequences of the cluster isolates that includes ODN (KR611362) and WS_Bor-10-232m (JQ889848); BLAST indicated with 98% identity and 99% coverage. PSTVdToEA1291E is closest to the sequences of isolates Dasongping01 (KX159281) and 6131669 (KY936882); BLAST indicated 94% identity and 100% coverage.
PCFVd

PCFVdToNK567E, PCFVdCaEu27662C and PCFVdToAs1393E are closest to sequences of a cluster of isolates represented in the database that includes the isolates NK-12c2 (JF446898) and Somjit-20 (KM214229); BLAST searches indicated 98-99% identity and 100% coverage.

TASVd

TASVdToAs1433E and TASVdToNK1435E are closest to the sequences of a cluster of isolates that includes the isolates 5458774 (KX579067) and an unnamed Tunisian isolate(DQ144506); BLAST searches indicated 94-99% identity and 100% coverage.

TCDVd

TCDVdToAf130222C and TCDVdToAf130227C are closest to the sequences of a cluster of isolates that includes GBVdC_TCDVd02 (KU714937) and an unnamed isolate from petunia in the UK (EF582393); BLAST searches indicated up to 99% identity and 96% coverage.

Figure S1. Alignment of CLVd sequences. The alignment shows there are extensive stretches of matching sequence.

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Sequences

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