

Supplementary file 2. Isolates with identical sequences obtained from different seed lots.

This supplementary file provides alignments of viroid sequences obtained from different seed lots which were identified as being 100% identical to each other or nearly identical.

Methods

All sequences of the same viroid species were aligned and compared using MEGA7 to identify identical sequences. Sequences of any length were selected as long as they were of sufficient quality for analysis. Multiple alignments were made using the MUSCLE program running with the default parameters. The evolutionary distances were computed in MEGA7 using default parameters. To confirm and visualise the extent of the sequence similarity, identical isolates were re-aligned using CLUSTAL OMEGA. The GenBank non-redundant nucleotide sequence database was searched for matches to the sequences by using the blastn (BLAST nucleotide) program. All the BLASTN matches reported in this document covered 100% of the query sequences, excluding any unresolved nucleotide positions ('N').

References

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- Blast searches of GenBank: <https://blast.ncbi.nlm.nih.gov/Blast.cgi>
- CLUSTAL OMEGA: <https://www.ebi.ac.uk/Tools/msa/clustalo/>
- MAFFT alignments: <https://mafft.cbrc.jp/alignment/server/>

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: Af = Africa; As = Asia; Eu = Europe; EA – east Asia; ME = middle east; NAm = North America;

NK = region not known; SAm = South America; SAs – South Asia

Lab: C=CHS; E = EAMI

Figure S6. Identical PSTVd sequences obtained from different seed lots. PSTVdToNK12/744E, PSTVdCaNam14/675E, PSTVdCaNam14/627E and PSTVdCaNam15/1046E are identical; they have 100% nucleotide identity to the Chinese Potato spindle tuber viroid isolate ODN (KR611362) and others.

PSTVdToNK12/744E	CTGGAGCGAACTGGCAATAAGGACGGTGGGGAGTGCCAGCGGCCGACAGGAGTAATTCC	60
PSTVdCaNam14/675E	CTGGAGCGAACTGGCAATAAGGACGGTGGGGAGTGCCAGCGGCCGACAGGAGTAATTCC	60
PSTVdCaNam14/627E	CTGGAGCGAACTGGCAATAAGGACGGTGGGGAGTGCCAGCGGCCGACAGGAGTAATTCC	60
PSTVdCaNam15/1046E	CTGGAGCGAACTGGCAATAAGGACGGTGGGGAGTGCCAGCGGCCGACAGGAGTAATTCC	60

PSTVdToNK12/744E	CGCCGAAACAGGGTTTTACCCCTTCCTTTCTTCGGGTGTCCTTCCTCGCGCCCGCAGGTC	120
PSTVdCaNam14/675E	CGCCGAAACAGGGTTTTACCCCTTCCTTTCTTCGGGTGTCCTTCCTCGCGCCCGCAGGTC	120
PSTVdCaNam14/627E	CGCCGAAACAGGGTTTTACCCCTTCCTTTCTTCGGGTGTCCTTCCTCGCGCCCGCAGGTC	120
PSTVdCaNam15/1046E	CGCCGAAACAGGGTTTTACCCCTTCCTTTCTTCGGGTGTCCTTCCTCGCGCCCGCAGGTC	120

PSTVdToNK12/744E	CACCCCTCGCCCCCTTTGCGCTGTCGCTTCGGCTAC-	156
PSTVdCaNam14/675E	CACCCCTCGCCCCCTTTGCGCTGTCGCTTCGGCTACT	157
PSTVdCaNam14/627E	CACCCCTCGCCCCCTTTGCGCTGTCGCTTCGGCTACT	157
PSTVdCaNam15/1046E	CACCCCTCGCCCCCTTTGCGCTGTCGCTTCGGCTACT	157

Figure S7. PSTVd sequences obtained from different seed lots. PSTVdToNK13/567E, PSTVdCaEu13/102E, PSTVdToNK12/868E and PSTVdToNK13/020E are identical and were found to have 98% nucleotide identity to the Polish experimental isolate Potato spindle tuber viroid isolate S7 (AY492081).

PSTVdToEu13/101bE	-----GGGTAGTGCCAGCGGCCGACAGGAGTAATTCC	32
PSTVdToNK12/868E	CTGGAGTGAACTGGCAAAAAAGGACGGTGGGGAGTGCCAGCGGCCGACAGGAGTAATTCC	60
PSTVdToNK13/567E	CTGGAGCGAACTGGCAAAAAAGGACGGTGGGGAGTGCCAGCGGCCGACAGGAGTAATTCC	60
PSTVdCaEu13/102E	CTGGAGCGAACTGGCAAAAAAGGACGGTGGGGAGTGCCAGCGGCCGACAGGAGTAATTCC	60
PSTVdToNK13/020E	CTGGAGCGAACTGGCAAAAAAGGACGGTGGGGAGTGCCAGCGGCCGACAGGAGTAATTCC	60
	*** *****	
PSTVdToEu13/101bE	CTGCTGAAACAGGGTTTTACCCCTTCCTTTCTTCAGGTTTCCTTCCTCGCGCCCGCAGGT	92
PSTVdToNK12/868E	CTGCTGAAACAGGGTTTTACCCCTTCCTTTCTTCAGGTTTCCTTCCTCGCGCCCGCAGGT	120
PSTVdToNK13/567E	CTGCTGAAACAGGGTTTTACCCCTTCCTTTCTTCAGGTTTCCTTCCTCGCGCCCGCAGGT	120
PSTVdCaEu13/102E	CTGCTGAAACAGGGTTTTACCCCTTCCTTTCTTCAGGTTTCCTTCCTCGCGCCCGCAGGT	120
PSTVdToNK13/020E	CTGCTGAAACAGGGTTTTACCCCTTCCTTTCTTCAGGTTTCCTTCCTCGCGCCCGCAGGT	120

PSTVdToEu13/101bE	CCACCCCTCGCCCCCTTTGCGCTGTCGCTTCGGCTACTACCCGGTGGATACAACCTGAAGC	152
PSTVdToNK12/868E	CCACCCCTCGCCCCCTTTGCGCTGTCGCTTCGGCTACT-----	158
PSTVdToNK13/567E	CCACCCCTCGCCCCCTTTGCGCTGTCGCTTCGGCTACT-----	158
PSTVdCaEu13/102E	CCACCCCTCGCCCCCTTTGCGCTGTCGCTTCGGCTACT-----	158
PSTVdToNK13/020E	CCACCCCTCGCCCCCTTTGCGCTGTCGCTTCGGCTACT-----	158

PSTVdToEu13/101bE	T	153
PSTVdToNK12/868E	-	158
PSTVdToNK13/567E	-	158
PSTVdCaEu13/102E	-	158
PSTVdToNK13/020E	-	158

Figure S8. Identical and nearly identical PSTVd sequences obtained from different seed lots. PSTVdToNK1713172C, PSTVdCaNA14/836E and PSTVdCaAf13/124E are identical and were found to have 100% nucleotide identity to the Chinese Potato spindle tuber viroid isolate ODN (KR611362.1) and others.

PSTVdTo1713172C	-----CTGGAGCGAACTGGCAATAAGGACGGTGGGGAGTGCCCAGCGGCCG	46
PSTVdCaNA14/836E	-----CTGGAGCGAACTGGCAATAAGGACGGTGGGGAGTGCCCAGCGGCCG	46
PSTVdCaAf13/124E	-----CTGGAGCGAACTGGCAATAAGGACGGTGGGGAGTGCCCAGCGGCCG	46
PSTVdToME27642C	-----CTGGAGCGAACTGGCAACAAGGACGGTGGGGAGTGCCCAGCGGCCG	46
PSTVdCaSA1302191C	-----GGGGAAACCTGGAGCGAACTGGCAATAAG-GCGGTGGGGAGTGCCCAGCGGCCG	53
PSTVdToEAs13/161E	ATCCCCGGGGAAACCTGGAGCGAACTGGCAATAAGGACGGTGGGGAGTGCCCAGCGGCCG	60

PSTVdToNK1713172C	ACAGGAGTAATTCCCGCCGAAACAGGGTTTTACCCCTTCCTTTCTTCGGGTGTCCTTCCT	106
PSTVdCaNA14/836E	ACAGGAGTAATTCCCGCCGAAACAGGGTTTTACCCCTTCCTTTCTTCGGGTGTCCTTCCT	106
PSTVdCaAf13/124E	ACAGGAGTAATTCCCGCCGAAACAGGGTTTTACCCCTTCCTTTCTTCGGGTGTCCTTCCT	106
PSTVdToME27642C	ACAGGAGTAATTCCCGCCGAAACAGGGTTTTACCCCTTCCTTTCTTCGGGTGTCCTTCCT	106
PSTVdCaSA1302191C	ACAGGAGTAATTCCCGCCGAAACAGGGTTTTACCCCTTCCTTTCTTCGGGTGTCCTTCCT	113
PSTVdToEAs13/161E	ACAGGAGTAATTCCCGCCGAAACAGGGTTTTACCCCTTCCTTTCTTCGGGTGTCCTTCCT	120

PSTVdToNK1713172C	CGCGCCCGCAGGACCACCCCTCGCCCCCTTTGCGCTGTCGCTTCGGCTACT-----	157
PSTVdCaNA14/836E	CGCGCCCGCAGGACCACCCCTCGCCCCCTTTGCGCTGTCGCTTCGGCTACT-----	157
PSTVdCaAf13/124E	CGCGCCCGCAGGACCACCCCTCGCCCCCTTTGCGCTGTCGCTTCGGCTACT-----	157
PSTVdToME27642C	CGCGCCCGCAGGACCACCCCTCGCCCCCTTTGCGCTGTCGCTTCGGTTACT-----	157
PSTVdCaSA1302191C	CGCGCCCGCAGGACCACCCCTCGCCC-CTTTGCGCTGTCGCTTCGGCTACTACCCGGTGG	172
PSTVdToEAs13/161E	CGCGCCCGCAGGACCACCCCTCGCCCCCTTTGCGCTGTCGCTTCGGCTACTACCCGGTGG	180

PSTVdToNK1713172C	-----	157
PSTVdCaNA14/836E	-----	157
PSTVdCaAf13/124E	-----	157
PSTVdToME27642C	-----	157
PSTVdCaSA1302191C	AAACAACCTGAAGCTCCCGAGAACCGCTTTTTCTCTATCTT-CCTTGCTTCGGGGCGAGGG	231
PSTVdToEAs13/161E	AAACAACCTGAAGCTCCCGAGAACCGCTTTTTCTCTATCTTTCTTGCTTCGGGGCGAGGG	240
PSTVdToNK1713172C	-----	157
PSTVdCaNA14/836E	-----	157
PSTVdCaAf13/124E	-----	157
PSTVdToME27642C	-----	157
PSTVdCaSA1302191C	TGTTTAGCCCTTGGAACCGCAGTTGGTTCCCT-----	262
PSTVdToEAs13/161E	TGTTTAGCCCTTGGAACCGCAGTTGGTTCCCTCGGAATAAAGGCGGCTCGGAGGAGCGCTTCAGGG	300
PSTVdToNK1713172C	-----	157
PSTVdCaNA14/836E	-----	157
PSTVdCaAf13/124E	-----	157
PSTVdToME27642C	-----	157
PSTVdCaSA1302191C	-----	262
PSTVdToEAs13/161E	ACACCTGACCTCCTGAGCAGAAAAGAAAAAGAGGCGGCTCGGAGGAGCGCTTCAGGG	359

Figure S9. Identical and nearly identical PSTVd isolates obtained from different seed lots. PSTVdToNK12/820E, PSTVdToNK13/1051E, PSTVdToAs13/1070E, PSTVdToNK13/1100E, PSTVdToNK13/1104E and PSTVdToNAm13/1206E are identical and were found to have 100% nucleotide identity to the Australian Potato spindle tuber viroid isolate CVNBC36 (KP454054) and others.

PSTVdTOEu13/967E	CTGGAGCGAACTGGCAAAAGGCGCGGTGGGGAGTGCCTCGCGGCCGACAGGAGTAATTCC	60
PSTVdToNK13/1046E	CTGGAGCGAACTGGCAAAAGGCGCGGTGGGGAGTGCCTCGCGGCCGACAGGAGTAATTCC	60
PSTVdToEu27648C	-----CAAAAGGCGCGGTGGGAAGTGCCTCGCGGCCGACAGGAGTAATTCC	46
PSTVdToNK12/820E	CTGGAGCGAACTGGCAAAAGGCGCGGTGGGGAGTGCCTCGCGGCCGACAGGAGTAATTCC	60
PSTVdToNK13/1051E	CTGGAGCGAACTGGCAAAAGGCGCGGTGGGGAGTGCCTCGCGGCCGACAGGAGTAATTCC	60
PSTVdToAs13/1070E	CTGGAGCGAACTGGCAAAAGGCGCGGTGGGGAGTGCCTCGCGGCCGACAGGAGTAATTCC	60
PSTVdToNK13/1100E	CTGGAGCGAACTGGCAAAAGGCGCGGTGGGGAGTGCCTCGCGGCCGACAGGAGTAATTCC	60
PSTVdToNK13/1104E	CTGGAGCGAACTGGCAAAAGGCGCGGTGGGGAGTGCCTCGCGGCCGACAGGAGTAATTCC	60
PSTVdToNAm13/1206E	CTGGAGCGAACTGGCAAAAGGCGCGGTGGGGAGTGCCTCGCGGCCGACAGGAGTAATTCC	60

PSTVdTOEu13/967E	TGCCGAAACAGGGTTTTACCCCTTCCTTTCTTCAGGTTTCCTTCCTCGCGCCCGCAGGAT	120
PSTVdToNK13/1046E	TGCCGAAACAGGGTTTTACCCCTTCCTTTCTTCAGGTTTCCTTCCTCGCGCCCGCAGGAT	120
PSTVdToEu27648C	TGCCGAAACAGGGTTTTACCCCTTCCTTTCTTCAGGTTTCCTTCCTCGCGCCCGCAGGAT	106
PSTVdToNK12/820E	TGCCGAAACAGGGTTTTACCCCTTCCTTTCTTCAGGTTTCCTTCCTCGCGCCCGCAGGAT	120
PSTVdToNK13/1051E	TGCCGAAACAGGGTTTTACCCCTTCCTTTCTTCAGGTTTCCTTCCTCGCGCCCGCAGGAT	120
PSTVdToAs13/1070E	TGCCGAAACAGGGTTTTACCCCTTCCTTTCTTCAGGTTTCCTTCCTCGCGCCCGCAGGAT	120
PSTVdToNK13/1100E	TGCCGAAACAGGGTTTTACCCCTTCCTTTCTTCAGGTTTCCTTCCTCGCGCCCGCAGGAT	120
PSTVdToNK13/1104E	TGCCGAAACAGGGTTTTACCCCTTCCTTTCTTCAGGTTTCCTTCCTCGCGCCCGCAGGAT	120
PSTVdToNAm13/1206E	TGCCGAAACAGGGTTTTACCCCTTCCTTTCTTCAGGTTTCCTTCCTCGCGCCCGCAGGAT	120

PSTVdTOEu13/967E	CCACCCCTCGCCCCCTTGCCTGTGCTCGCTTTCGCTACT	155
PSTVdToNK13/1046E	CACCCCTCGCCCCCTTGGACTGTGCTTTCGCTACT	156
PSTVdToEu27648C	CACCCCTCGCCCCCTTGCCTGTGCTCGCTTTCGCTACT	142
PSTVdToNK12/820E	CACCCCTCGCCCCCTTGCCTGTGCTCGCTTTCGCTACT	156
PSTVdToNK13/1051E	CACCCCTCGCCCCCTTGCCTGTGCTCGCTTTCGCTACT	156
PSTVdToAs13/1070E	CACCCCTCGCCCCCTTGCCTGTGCTCGCTTTCGCTACT	156
PSTVdToNK13/1100E	CACCCCTCGCCCCCTTGCCTGTGCTCGCTTTCGCTACT	156
PSTVdToNK13/1104E	CACCCCTCGCCCCCTTGCCTGTGCTCGCTTTCGCTACT	156
PSTVdToNAm13/1206E	CACCCCTCGCCCCCTTGCCTGTGCTCGCTTTCGCTACT	156

Figure S10. Identical TCDVd sequences from different seed lots. TCDVdToAf130227C and TCDVdToMEMC27642C are identical and were found to have 100% nucleotide identity with UK isolate Tomato chlorotic dwarf viroid (EF582393).

TCDVdToAf	-----GGGGAAACCTGGAGCGAACTGGCAAAAGGCGGCAGGGAGCTTGTGGAAGGCGAA	54
TCDVdToMEMC27642C	ATCCCCGGGGAAACCTGGAGCGAACTGGCAAAAGGCGGCAGGGAGCTTGTGGAAGGCGAA	60

TCDVdToAf	ACAGGAGTAATCCCAGAGAGAAACAGGGTTTTACCCCTTCCTTTCTGATTCGGTTTCCTTC	114
TCDVdToMEMC27642C	ACAGGAGTAATCCCAGAGAGAAACAGGGTTTTACCCCTTCCTTTCTGATTCGGTTTCCTTC	120

TCDVdToAf	CTTTGCGCGCCACTCGACCCCTCGCCCCCTTGCCTGTGCTTCGGCAACTACCCGGTGG	174
TCDVdToMEMC27642C	CTTTGCGCGCCACTCGACCCCTCGCCCCCTTGCCTGTGCTTCGGCAACTACCCGGTGG	180

TCDVdToAf	AAACAACCTGAAGCTCCCGAGAACCGCTTTTTCTCTATCTTGCTGCTACCGGGGCGAGGGT	234
TCDVdToMEMC27642C	AAACAACCTGAAGCTCCCGAGAACCGCTTTTTCTCTATCTTGCTGCTACCGGGGCGAGGGT	240

TCDVdToAf	GTTTAGCCCTTGGAACCGCAGTTGGTTCCTCGGAACCTAACTCGTGGTTCCTGTGGTTCA	294
TCDVdToMEMC27642C	GTTTAGCCCTTGGAACCGCAGTTGGTTCCTCGGAACCTAACTCGTGGTTCCTGTGGTTCA	300

TCDVdToAf	CACCTGACCTCCTGTGCAGAAAAGAAAAAGATAGGCGGCTCGGAGGAGCGCTTCAGGAT	354
TCDVdToMEMC27642C	CACCTGACCTCCTGTGCAGAAAAGAAAAAGATAGGCGGCTCGGAGGAGCGCTTCAGGAT	358

TCDVdToAf	AGGCCATGT	363
TCDVdToMEMC27642C	-----	358

Figure S11. Distinct CLVd sequences obtained from different seed lots. No CLVd seed isolates were identical. CLVdCaEu16169C and CLVdCaEA1302154C had one nucleotide difference between the overlapping sequences. CLVdCaEu16169C had 98% nucleotide identity to Thailand isolate Columnnea latent viroid clone Prayong-16 (KC143294). CLVdCaEA1302154C had 99% nucleotide identity to Thailand isolate Columnnea latent viroid clone Prayong-16 (KC143294) and others.

CLVdCaEu16169C	-----	0
CLVdCaEA1302154C	CGGAAC TAAACTCGTGGTTCCTGTGGTTCACACCTGACCCCTGCAGCCATGCAAAGAAAAA	60
CLVdCaEu16169C	-----	0
CLVdCaEA1302154C	AAGAACGGGAGGAAGAGCGCAAGAGCGGTCTCAGGAGCCCCTGGGGCAACTCAGACCGAG	120
CLVdCaEu16169C	-----TTCAGACAGGAGTAATACCAGCTGAAACAGG	31
CLVdCaEA1302154C	CGGGGTCTTGACCAGTGGCGAGCGCCCTGTTTCAGACAGGAGTAATCCCAGCTGAAACAGG *****	180
CLVdCaEu16169C	GTTTTCACCCCTTCCTTTCTTCTGGTTCCTTCCTCTGCTTCAGCGGCCTCGCCCGGAGTC	91
CLVdCaEA1302154C	GTTTTCACCCCTTCCTTTCTTCTGGTTCCTTCCTCTGCTTCAGCGGCCTCGCCCGGAGTC *****	240
CLVdCaEu16169C	TTGACCAGCGCAGGTTCTGACGCGACCGGTGGCATCACCGAGTTCGCTCAAGCCTCAACC	151
CLVdCaEA1302154C	TTGACCAGCGCAGGTTCTGACGCGACCGGTGGCATCACCGAGTTCGCTCAAGCCTCAACC *****	300
CLVdCaEu16169C	TCCTTTTCTTCTATTCTAGCTTGGTCTCCGGGCGAGGGTGTTTAGCCCTTGGAACCGCAG	211
CLVdCaEA1302154C	TCCTTTTCTTCTATTCTAGCTTGGTCTCCGGGCGAGGGTGTTTAGCCCTTGGAACCGCAG *****	360
CLVdCaEu16169C	TTGGTTCCTCGGAAC TAAACTCGTGGTTCCTGTGGTTCACACCTGACCCCTGCAGCCATGC	271
CLVdCaEA1302154C	TTGGTTCCT----- *****	369
CLVdCaEu16169C	AAAGAAAAAAGAACGGGAGGAAGAGCGCAAGAGCGGTCTCAGGAGCCCC	322
CLVdCaEA1302154C	-----	3

Figure S12. Distinct CLVd sequences. CLVdToAs13/1073E and CLVdToAs13/1076E were most closely related and had four nucleotide differences between the overlapping sequences. CLVdToAs13/1073E had 99% nucleotide identity to Thailand isolate CLVd isolate CM10-6c1 (JF446929). CLVdToAs13/1076E had 98% nucleotide identity to Thailand isolate CLVd isolate CM10-6c1 (JF446929).

CLVdToAs13/1073E	CGGAAC TAAACTCGTGGTTCCTGTGGTTCACACCTGACCCCTGCAGCCATGCAAAGAAAAA	60
CLVdToAs13/1076E	CGGAAC TAAACTCGTGGTTCCTGTGGTTCACACCTGACCCCTGCAGCCATGCAAAGAAAAA *****	60
CLVdToAs13/1073E	AAGAACGGGAGGAAGAGCGCAAGAGCGGTCTCAGGAGCCCCGGGGCAACTCAGACCGAGC	120
CLVdToAs13/1076E	AAGATTGGGAGGAGAGCGCAAGAGCGGTCTCAGGAGCCCCGGGGCAACTCAGACCGAGC ****	120
CLVdToAs13/1073E	GGGGATCGCGACCGAGGGCGGAAGCCTGCTTCAGACAGGAGTAATCCCCGCTGAAACAG	180
CLVdToAs13/1076E	GGGGATCGCGACCGAGGGCGGAAGCCTGCTTCAGACAGGAGTANNNNNNNNNNNNNNN *****	180
CLVdToAs13/1073E	GGTTTTACCCCTTCCTTTCTTCGGGTTTCCTTCCTCTGCTTGCGGCCTCGCCCGGAGTCT	240
CLVdToAs13/1076E	NNNNNN--NNNNNNNNNNNNNNNNNNNNNTTCCTCTGCTTGCGGCCTCGCCCGGAGTCT *****	238
CLVdToAs13/1073E	TCGAATCCAGCGCAGGTTCTGACGCGACCGGTGGCATCACCGAGTTGCTCAAGCCTCAAC	300
CLVdToAs13/1076E	TCGAATCCAGCGCAGGTTCTGACGCGACCGGTGGCATCACCGAGTTGCTCAAGCCTCAAC *****	298
CLVdToAs13/1073E	CTCCTTTTCTCTATTCTACGCTTGGTCTCCGGGCGAGGGTGTTTAGCCCTTGGAACCGC	360
CLVdToAs13/1076E	CTCCTTTTCTCTATTCTACGCTTGGTCTCCGGGCGAGGGTGTTTAGCCCTTGGAACCGC *****	358
CLVdToAs13/1073E	AGTTGGTTCCT	371
CLVdToAs13/1076E	AGTTGGTTCCT *****	369

Figure S13. Distinct CLVd sequences. CLVdToAs13/1075E and CLVdToAs13/1074E were most closely related and had two nucleotide differences between the overlapping sequences. CLVdToAs13/1074E 98% nucleotide identity to Thailand isolate CLVd isolate CM10-6c1 (JF446929). CLVdToAs13/1075E had 99% nucleotide identity to Thailand isolate CLVd isolate CM10-6c1 (JF446929.1).

CLVdToAs13/1074E	CGGAACATAAACTCGTGGTTCCTGTGGTTCACACCTGACCCCTGCAGCCATGCAAAGAAAAA	60
CLVdToAs13/1075E	CGGAACATAAACTCGTGGTTCCTGTGGTTCACACCTGACCCCTGCAGCCATGCAAAGAAAAA	59

CLVdToAs13/1074E	AAGATTGGGAGGAAGAGCGCAAGAGCGGTCTCAGGAGCCCCGGGGCAACTCAGACCGAGC	120
CLVdToAs13/1075E	AAGAACGGGAGGAAGAGCGCAAGAGCGGTCTCAGGAGCCCCGGGGCAACTCAGACCGAGC	119
**** *		
CLVdToAs13/1074E	GGGGATCGCGGACCGAGGGCGGAAGCCTGCTTCAGACAGGAGTAATCCCCGCTGAAACAG	180
CLVdToAs13/1075E	GGGGATCGCGGACCGAGGGCGGAAGCCTGCTTCAGACAGGAGTAATCCCCGCTGAAACAG	179

CLVdToAs13/1074E	GGTTTTACCCCTTCCTTTCTTCGGGTTTCCTTCCTCTGCTTGCGGCCTCGCCCGGAGTCT	240
CLVdToAs13/1075E	GGTTTTACCCCTTCCTTTCTTCGGGTTTCCTTCCTCTGCTTGCGGCCTCGCCCGGAGTCT	239

CLVdToAs13/1074E	TCGAATCCAGCGCAGGTTCAGCGGACCGGTGGCATCACCGAGTTGCTCAAGCCTCATC	300
CLVdToAs13/1075E	TCGAATCCAGCGCAGGTTCAGCGGACCGGTGGCATCACCGAGTTGCTCAAGCCTCATC	299

CLVdToAs13/1074E	CTCCTTTTCTCTATTCTACGCTTGGTCTCCGGGCGAGGGTGTTAGCCCTTGGAAACCGC	360
CLVdToAs13/1075E	CTCCTTTTCTCTATTCTACGCTTGGTCTCCGGGCGAGGGTGTTAGCCCTTGGAAACCGC	359

CLVdToAs13/1074E	AGTTGGTTCCT	371
CLVdToAs13/1075E	AGTTGGTTCCT	370

Figure S14. Identical PCFVd sequences obtained from different seed lots. The listed PCFVd seed isolates are identical to KC762952 across the available sequence. KC762952 differed from KC762953 (another isolate from the seed detections) by two nucleotides. PCFVdCaME15/707E, PCFVdToME14/0008E and PCFVdToAf14/1068E isolates are identical and have 99% nucleotide identity with isolates KC762952.1 and KC762953.1 previously found in seed tested by Australia.

PCFVdCaNK13/1127E	CCGGATTCTTCTAAGGGTGCCTGTGGTGCCTCCCCGAAGCCCGCTTAGGGAAAAAGAAA	60
PCFVdToNAm13/968E	CCGGATTCTTCTAAGGGTGCCTGTGGTGCCTCCCCGAAGCCCGCTTAGGGAAAAAGAAA	60
PCFVdCaNK13/1192E	CCGGATTCTTCTAAGGGTGCCTGTGGTGCCTCCCCGAAGCCCGCTTAGGGAAAAAGAAA	60
KC762952.1	CCGGATTCTTCTAAGGGTGCCTGTGGTGCCTCCCCGAAGCCCGCTTAGGGAAAAAGAAA	60
KC762953.1	CCGGATTCTTCTAAGGGTGCCTGTGGTGCCTCCCCGAAGCCCGCTTAGGGAAAAAGAAA	60
PCFVdToAf14/1068E	-----	0
PCFVdToME14/0008E	-----	0
PCFVdCaME15/707E	-----	0
PCFVdToNK13/1170E	-----	0
PCFVdToEu13/1252E	-----	0
PCFVdCaNAm14/628E	-----	0
PCFVdToNAm14/675E	-----	0
PCFVdCaEAs14/847E	-----	0
PCFVdCaEAs14/981E	-----	0
PCFVdCaAs14/1107E	-----	0
PCFVdCaEAs14/1154E	-----	0
PCFVdCaNK13/1127E	GGGGAAGCAAGCATCTCCTGTTCAGGGATCCCCGGGGAAACCTGGACAGACCGGGCGGAG	120
PCFVdToNAm13/968E	GGGGAAGCAAGCATCTCCTGTTCAGGGATCCCCGGGGAAACCTGGACAGACCGGGCGGAG	120
PCFVdCaNK13/1192E	GGGGAAGCAAGCATCTCCTGTTCAGGGATCCCCGGGGAAACCTGGACAGACCGGGCGGAG	120
KC762952.1	GGGGAAGCAAGCATCTCCTGTTCAGGGATCCCCGGGGAAACCTGGACAGACCGGGCGGAG	120
KC762953.1	GGGGAAGCAAGCATCTCCTGTTCAGGGATCCCCGGGGAAACCTGGACAGACCGGGCGGAG	120
PCFVdToAf14/1068E	-----CTGGACAGACCGGGCGGAG	19
PCFVdToME14/0008E	-----CTGGACAGACCGGGCGGAG	19
PCFVdCaME15/707E	-----CTGGACAGACCGGGCGGAG	19
PCFVdToNK13/1170E	-----CTGGACAGACCGGGCGGAG	19
PCFVdToEu13/1252E	-----CTGGACAGACCGGGCGGAG	19
PCFVdCaNAm14/628E	-----CTGGACAGACCGGGCGGAG	19

PCFVdToNA14/675E	-----CTGGACAGACCGGGCGGAG	19
PCFVdCaEAs14/847E	-----CTGGACAGACCGGGCGGAG	19
PCFVdCaEAs14/981E	-----CTGGACAGACCGGGCGGAG	19
PCFVdCaAs14/1107E	-----CTGGACAGACCGGGCGGAG	19
PCFVdCaEAs14/1154E	-----CTGGACAGACCGGGCGGAG	19

PCFVdCaNK13/1127E	AAGCGCACGAGCGGGACCGTCTTCTGACAGGAGTAATCCCCGCTGAAACAGGGATTTTC	180
PCFVdToNA13/968E	AAGCGCACGAGCGGGACCGTCTTCTGACAGGAGTAATCCCCGCTGAAACAGGGATTTTC	180
PCFVdCaNK13/1192E	AAGCGCACGAGCGGGACCGTCTTCTGACAGGAGTAATCCCCGCTGAAACAGGGATTTTC	180
KC762952.1	AAGCGCACGAGCGGGACCGTCTTCTGACAGGAGTAATCCCCGCTGAAACAGGGATTTTC	180
KC762953.1	AAGCGCACGAGCGGGACCGTCTTCTGACAGGAGTAATCCCCGCTGAAACAGGGATTTTC	180
PCFVdToAf14/1068E	AAGCGCACGAGCGGGACCGTCTTCTGACAGGAGTAATCCCCGCTGAAACAGGGATTTTC	79
PCFVdToME14/0008E	AAGCGCACGAGCGGGACCGTCTTCTGACAGGAGTAATCCCCGCTGAAACAGGGATTTTC	79
PCFVdCaME15/707E	AAGCGCACGAGCGGGACCGTCTTCTGACAGGAGTAATCCCCGCTGAAACAGGGATTTTC	79
PCFVdToNK13/1170E	AAGCGCACGAGCGGGACCGTCTTCTGACAGGAGTAATCCCCGCTGAAACAGGGATTTTC	79
PCFVdToEu13/1252E	AAGCGCACGAGCGGGACCGTCTTCTGACAGGAGTAATCCCCGCTGAAACAGGGATTTTC	79
PCFVdCaNA14/628E	AAGCGCACGAGCGGGACCGTCTTCTGACAGGAGTAATCCCCGCTGAAACAGGGATTTTC	79
PCFVdToNA14/675E	AAGCGCACGAGCGGGACCGTCTTCTGACAGGAGTAATCCCCGCTGAAACAGGGATTTTC	79
PCFVdCaEAs14/847E	AAGCGCACGAGCGGGACCGTCTTCTGACAGGAGTAATCCCCGCTGAAACAGGGATTTTC	79
PCFVdCaEAs14/981E	AAGCGCACGAGCGGGACCGTCTTCTGACAGGAGTAATCCCCGCTGAAACAGGGATTTTC	79
PCFVdCaAs14/1107E	AAGCGCACGAGCGGGACCGTCTTCTGACAGGAGTAATCCCCGCTGAAACAGGGATTTTC	79
PCFVdCaEAs14/1154E	AAGCGCACGAGCGGGACCGTCTTCTGACAGGAGTAATCCCCGCTGAAACAGGGATTTTC	79
	*****:*** :	

PCFVdCaNK13/1127E	CCTTCCTTTCTTCGGGTTTCCTTCCTCAGTCGACCGGTCCGCGTCGGCCTTCTCGCGCAC	240
PCFVdToNA13/968E	CCTTCCTTTCTTCGGGTTTCCTTCCTCAGTCGACCGGTCCGCGTCGGCCTTCTCGCGCAC	240
PCFVdCaNK13/1192E	CCTTCCTTTCTTCGGGTTTCCTTCCTCAGTCGACCGGTCCGCGTCGGCCTTCTCGCGCAC	240
KC762952.1	CCTTCCTTTCTTCGGGTTTCCTTCCTCAGTCGACCGGTCCGCGTCGGCCTTCTCGCGCAC	240
KC762953.1	CCTTCCTTTCTTCGGGTTTCCTTCCTCAGTCGACCGGTCCGCGTCGGCCTTCTCGCGCAC	240
PCFVdToAf14/1068E	CCTTCCTTTCTTCGGGTTTCCTTCCTCAGTCGACCGGTCCGCGTCGGCCTTCTCGCGCAC	139
PCFVdToME14/0008E	CCTTCCTTTCTTCGGGTTTCCTTCCTCAGTCGACCGGTCCGCGTCGGCCTTCTCGCGCAC	139
PCFVdCaME15/707E	CCTTCCTTTCTTCGGGTTTCCTTCCTCAGTCGACCGGTCCGCGTCGGCCTTCTCGCGCAC	139
PCFVdToNK13/1170E	CCTTCCTTTCTTCGGGTTTCCTTCCTCAGTCGACCGGTCCGCGTCGGCCTTCTCGCGCAC	139
PCFVdToEu13/1252E	CCTTCCTTTCTTCGGGTTTCCTTCCTCAGTCGACCGGTCCGCGTCGGCCTTCTCGCGCAC	139
PCFVdCaNA14/628E	CCTTCCTTTCTTCGGGTTTCCTTCCTCAGTCGACCGGTCCGCGTCGGCCTTCTCGCGCAC	139
PCFVdToNA14/675E	CCTTCCTTTCTTCGGGTTTCCTTCCTCAGTCGACCGGTCCGCGTCGGCCTTCTCGCGCAC	139
PCFVdCaEAs14/847E	CCTTCCTTTCTTCGGGTTTCCTTCCTCAGTCGACCGGTCCGCGTCGGCCTTCTCGCGCAC	139
PCFVdCaEAs14/981E	CCTTCCTTTCTTCGGGTTTCCTTCCTCAGTCGACCGGTCCGCGTCGGCCTTCTCGCGCAC	139
PCFVdCaAs14/1107E	CCTTCCTTTCTTCGGGTTTCCTTCCTCAGTCGACCGGTCCGCGTCGGCCTTCTCGCGCAC	139
PCFVdCaEAs14/1154E	CCTTCCTTTCTTCGGGTTTCCTTCCTCAGTCGACCGGTCCGCGTCGGCCTTCTCGCGCAC	139

PCFVdCaNK13/1127E	TGCTGTCCGGCTACTACCCGGTGGATACAACAGAGAGGTGCTTTTCTTCCACCCGAC	300
PCFVdToNA13/968E	TGCTGTCCGGCTACTACCCGGTGGATACAACAGAGAGGTGCTTTTCTTCCACCCAAC	300
PCFVdCaNK13/1192E	TGCTGTCCGGCTACTACCCGGTGGATACAACAGAGAGGTGCTTTTCTTCCACCCGAC	300
KC762952.1	TGCTGTCCGGCTACTACCCGGTGGATACAACAGAGAGGTGCTTTTCTTCCACCCAAC	300
KC762953.1	TGCTGTCCGGCTACTACCCGGTGGATACAACAGAGAGGTGCTTTTCTTCCACCCGAC	300
PCFVdToAf14/1068E	TGCTGTCCGGCTACT-----	154
PCFVdToME14/0008E	TGCTGTCCGGCTACT-----	154
PCFVdCaME15/707E	TGCTGTCCGGCTACT-----	154
PCFVdToNK13/1170E	TGCTGTCCGGCTACT-----	154
PCFVdToEu13/1252E	TGCTGTCCGGCTACT-----	154
PCFVdCaNA14/628E	TGCTGTCCGGCTACT-----	154
PCFVdToNA14/675E	TGCTGTCCGGCTACT-----	154
PCFVdCaEAs14/847E	TGCTGTCCGGCTACT-----	154
PCFVdCaEAs14/981E	TGCTGTCCGGCTACT-----	154
PCFVdCaAs14/1107E	TGCTGTCCGGCTACT-----	154
PCFVdCaEAs14/1154E	TGCTGTCCGGCTACT-----	154

PCFVdCaNK13/1127E	TTCTACCGACGCGGCCGGGAGTGAAGCTACCCGGGACCCGAGAGGATCT	349
PCFVdToNA13/968E	TTCTACCGACGCGGCCGGGAGTGAAGCTACCCGGGACCCGAGAGGATCT	349
PCFVdCaNK13/1192E	TTCTACCGACGCGGCCGGGAGTGAAGCTACCCGGGACCCGAGAGGATCT	349
KC762952.1	TTCTACCGACGCGGCCGGGAGTGAAGCTACCCGGGACCCGAGAGGATCT	349
KC762953.1	TTCTACCGACGCGGCCGGGAGTGAAGCTACCCGGGACCCGAGAGGATCT	349
PCFVdToAf14/1068E	-----	154
PCFVdToME14/0008E	-----	154
PCFVdCaME15/707E	-----	154
PCFVdToNK13/1170E	-----	154
PCFVdToEu13/1252E	-----	154
PCFVdCaNA14/628E	-----	154
PCFVdToNA14/675E	-----	154
PCFVdCaEAs14/847E	-----	154
PCFVdCaEAs14/981E	-----	154
PCFVdCaAs14/1107E	-----	154
PCFVdCaEAs14/1154E	-----	154

Figure S15. Identical CEVd sequences obtained from different seed lots. CEVdToNK13/042E and CEVdToEu27649 are identical and each has 100% nucleotide identity with Canadian isolate CEVd isolate imp2, (EU877743.1). CEVdToEu13/009E, CEVdToNK13/020E, CEVdToSAm13/008E, CEVdToNK13/45E, CEVdToNK13/019E, CEVdToEu13/046E and CEVdCaEA13/126E are identical and have 99% nucleotide identity with Belgian CEVd isolate GBVdC_CEVd02 (KX084708.1) and Canadian isolate CEVd isolate imp2 (EU877743.1). CEVdToEu13/046E and CEVdCaEA13/126E are identical and have 98% nucleotide identity with Belgian CEVd isolate GBVdC_CEVd02 (KX084708.1).

CEVdToEu27649	-----GCTGCTTCGGTCGCCGCGGATCACTGGCGTC	31
CEVdToEu13/046E	CTGGAGGAAGTCGAGGTCGGGGGGGAACAGCTGCTTCGGTCGCCGCGGATCCCTGGCGTC	60
CEVdCaEA13/126E	CTGGAGGAAGTCGAGGTCGGGGGGGAACAGCTGCTTCGGTCGCCGCGGATCCCTGGCGTC	60
CEVdToNK13/020E	CTGGAGGAAGTCGAGGTCGGGGGGGAACAGCTGCTTCGGTCGCCGCGGATCCCTGGCGTC	60
CEVdToEu13/009E	CTGGAGGAAGTCGAGGTCGGGGGGGAACAGCTGCTTCGGTCGCCGCGGATCCCTGGCGTC	60
CEVdToSAm13/008E	CTGGAGGAAGTCGAGGTCGGGGGGGAACAGCTGCTTCGGTCGCCGCGGATCCCTGGCGTC	60
CEVdToNK13/45E	CTGGAGGAAGTCGAGGTCGGGGGGGAACAGCTGCTTCGGTCGCCGCGGATCCCTGGCGTC	60
CEVdToNK13/019E	CTGGAGGAAGTCGAGGTCGGGGGGGAACAGCTGCTTCGGTCGCCGCGGATCCCTGGCGTC	60
CEVdToNK13/042E	CTGGAGGAAGTCGAGGTCGGGGGGGAACAGCTGCTTCGGTCGCCGCGGATCACTGGCGTC	60

CEVdToEu27649	CAGCGGAGAAACAGGAGCTCGTCTCCTTCCTTTTCGCTGCTGGCTCCACATCCGATCGTCG	91
CEVdToEu13/046E	CAGCGGAGAAACAGGAGCTCGTCTCCTTCCTTTTCGCTGCTGGCTCCACATCCGATCGTCG	120
CEVdCaEA13/126E	CAGCGGAGAAACAGGAGCTCGTCTCCTTCCTTTTCGCTGCTGGCTCCACATCCGATCGTCG	120
CEVdToNK13/020E	CAGCGGAGAAACAGGAGCTCGTCTCCTTCCTTTTCGCTGCTGGCTCCACATCCGATCGTCG	120
CEVdToEu13/009E	CAGCGGAGAAACAGGAGCTCGTCTCCTTCCTTTTCGCTGCTGGCTCCACATCCGATCGTCG	120
CEVdToSAm13/008E	CAGCGGAGAAACAGGAGCTCGTCTCCTTCCTTTTCGCTGCTGGCTCCACATCCGATCGTCG	120
CEVdToNK13/45E	CAGCGGAGAAACAGGAGCTCGTCTCCTTCCTTTTCGCTGCTGGCTCCACATCCGATCGTCG	120
CEVdToNK13/019E	CAGCGGAGAAACAGGAGCTCGTCTCCTTCCTTTTCGCTGCTGGCTCCACATCCGATCGTCG	120
CEVdToNK13/042E	CAGCGGAGAAACAGGAGCTCGTCTCCTTCCTTTTCGCTGCTGGCTCCACATCCGATCGTCG	120

CEVdToEu27649	CTGAAGCGCCACGCCCCCTCGCCCGGAGCTTCTCTCTGGAGACTACCCGGTGGAACAAC	151
CEVdToEu13/046E	CTGAAGCGCCACTCCCCCTCGCCCGGAGCTTCTCTCTGGAGACT-----	164
CEVdCaEA13/126E	CTGAAGCGCCACTCCCCCTCGCCCGGAGCTTCTCTCTGGAGACT-----	164
CEVdToNK13/020E	CTGAAGCGCCACGCCCCCTCGCCCGGAGCTTCTCTCTGGAGACT-----	164
CEVdToEu13/009E	CTGAAGCGCCACGCCCCCTCGCCCGGAGCTTCTCTCTGGAGACT-----	164
CEVdToSAm13/008E	CTGAAGCGCCACGCCCCCTCGCCCGGAGCTTCTCTCTGGAGACT-----	164
CEVdToNK13/45E	CTGAAGCGCCACGCCCCCTCGCCCGGAGCTTCTCTCTGGAGACT-----	164
CEVdToNK13/019E	CTGAAGCGCCACGCCCCCTCGCCCGGAGCTTCTCTCTGGAGACT-----	164
CEVdToNK13/042E	CTGAAGCGCCACGCCCCCTCGCCCGGAGCTTCTCTCTGGAGACT-----	164

CEVdToEu27649	TGAAGCTTCTCTCTGGAGACTACCCGGTGGAACAAC	194
CEVdToEu13/046E	-----	164
CEVdCaEA13/126E	-----	164
CEVdToNK13/020E	-----	164
CEVdToEu13/009E	-----	164
CEVdToSAm13/008E	-----	164
CEVdToNK13/45E	-----	164
CEVdToNK13/019E	-----	164
CEVdToNK13/042E	-----	164