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Electronic Supplementary Material

The Distribution of Different Clades of Seneca Valley Viruses in Guangdong Province, China

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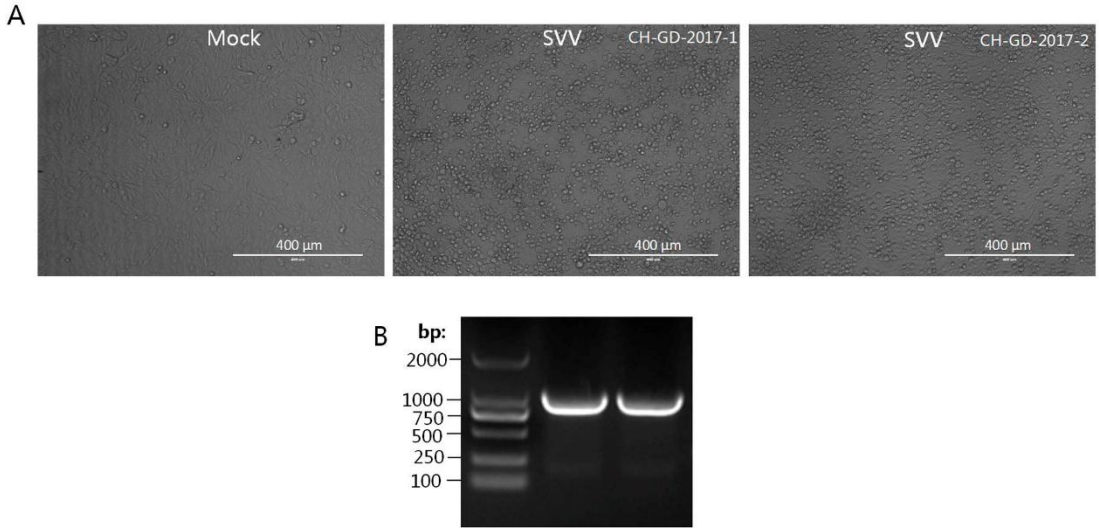
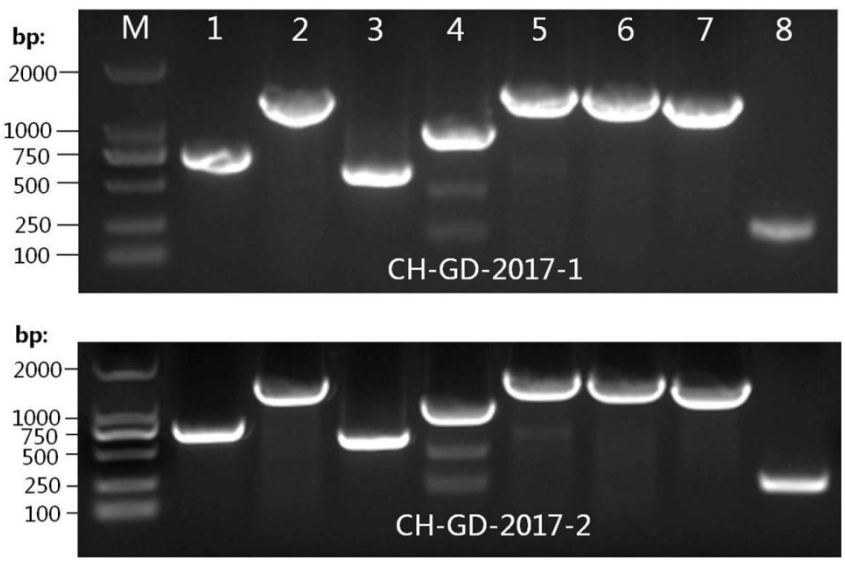
Supplementary Table S1. The primers used in this study.

Gene	Primers(5′→3′)	Fragment length
SVV-detection-VP1	Forward: TCGGTTTATTCTGCTGATGGCTGG Reverse: GTTGGTCTCGACGTCGCCTGAT	975 bp
SVV-1	Forward: TTGAAAGGGGGGGCTGGGCCC Reverse: CGATCTTGACTTTTGTTCCGGTTAC	743 bp
SVV-2	Forward: GATACAGCCTCTGGCACCTTT Reverse: GGGTACGCACATTCCCGTA	1372 bp
SVV-3	Forward: CACCCAGAGAAAATTCGCTTA Reverse: CAGGTGGTAGAGTAATTTTGGTCA	603 bp
SVV-4	Forward: TCGGTTTATTCTGCTGATGGCTGG Reverse: GTTGGTCTCGACGTCGCCTGAT	975 bp
SVV-5	Forward: GGGGACCATTTACGCCTTTA Reverse: GTCGACCAACTCTAGGAGATTGAA	1462 bp
SVV-6	Forward: CTGTCACCATTGCTGATCCTTCT Reverse: CCTCATCTAGGTCAACATCCTTGTT	1422 bp
SVV-7	Forward: CTAAATTGAGAAAGACGACCGCA Reverse: TGCAGGTACTCGTGACTCGGTAC	1309 bp
SVV-8	Forward: GGAACACTACTCGAGAAGCT Reverse: TTCCCTTTTCTGTTCCGAC	223 bp



Supplementary Figure S1. Identification of two SVV strains from Guangdong Province in 2017. A. BHK-21 cells were mock-infected or infected with CH-GD-2017-1 and SVV CH-GD-2017-2. The CPE was observed at 12 hours postinfection. B. Amplification of *VP1* genes from CH-GD-2017-1 and SVV CH-GD-2017-2 isolated from the virus-infected BHK-21 cell cultures.



Supplementary Figure S2. Amplification of different regions of viral genomes of CH-GD-2017-1 and SVV CH-GD-2017-2. M represented DNA ladder. Lanes 1¬8 represented the eight fragments amplified by the eight pairs of primers listed in Supplementary Table S1.