

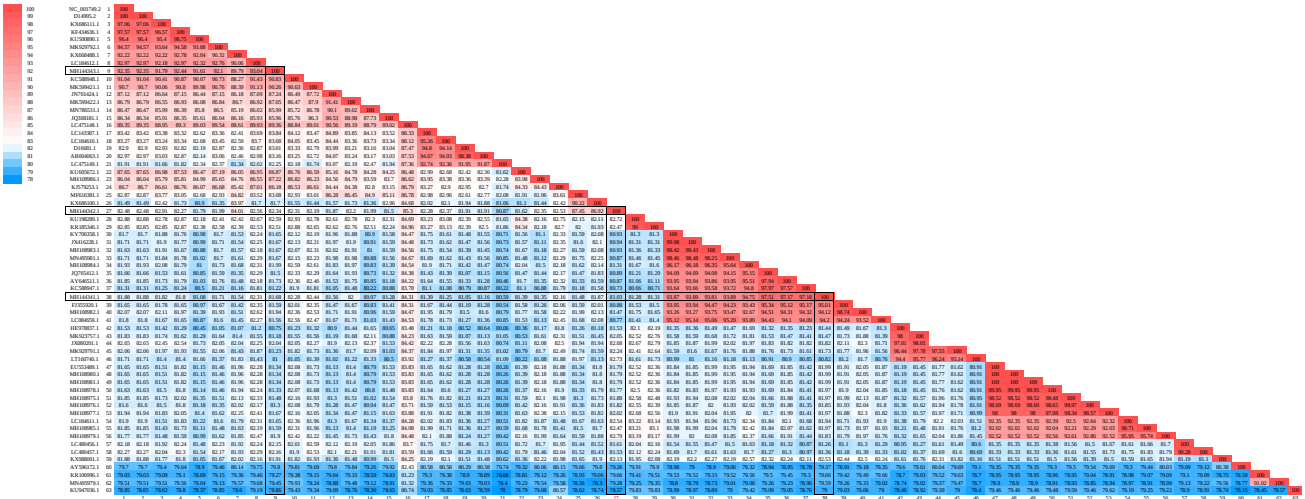
Appendix A Primers used to amplify and detect viral RNAs

Primer Names ¹	Primer sequence (5'-3')
For amplifying the complete ASGV genomes	
ASGV1-1F	CCTTAGAAGTGACAAATCGC
ASGV1-1R	ACTGCTCTTTCCCGACTA
ASGV1-2F	CGAAGTTGTCAATGTGCC
ASGV1-2R	GCTAAAGACCCAAGCCTAC
ASGV1-3F	ATGATGTCACCTTCTGGGC
ASGV1-3R	AATCCTTTGGACCACCGT
ASGV1-5'RACE_GSP1	GCCCATTGGATACCACTAC
ASGV1-5'RACE_GSP2	TCATAACATTTCAGAGGCAACACCAT
ASGV1-5'RACE_GSP3	ACAACCCTGTCAATCTCTGGTATGG
ASGV1-3'RACE_GSP2	TTTGGGGAAAATGAGTTTGAAGAC
ASGV1-3'RACE_GSP3	TTTGATACCCCACCAGTTCATTACA
ASGV2-1F	GCAATCAACAAACTTCCCAG
ASGV2-1R	CCTTCCTTCAACAACCTGAC
ASGV2-2F	ATGACCACTGAAGATGGGC
ASGV2-2R	TATGTGCTGGAAACACGC
ASGV2-3F	ATCAAGCCTCAGATGACG
ASGV2-3R	TCCAGGTTACTCTCCGAAC
ASGV2-5'RACE_GSP1	AGCCCACTGAATACCACTAC
ASGV2-5'RACE_GSP2	CTGGGCTCCTTTGAACTTTATCTC
ASGV2-5'RACE_GSP3	TACGTGTAAGGCATTGATCTCTAAG
ASGV2-3'RACE_GSP2	ATTTGATACCCCTCCGGTTCATTAC
ASGV2-3'RACE_GSP3	GCTTTGTGAACCATTGTGCTGATCTA
ASGV3-1F	TAGAAGTGACCAACCGCT
ASGV3-1R	TGTAAGGTATCCAGGTGGG
ASGV3-2F	CACAATAGGGATAGGGCTG
ASGV3-2R	CTTCATCAATCTCGTCGC
ASGV3-3F	CGGGTCACTGGCAATAAT
ASGV3-3R	CCTCTTGGTCATTCTGTCTG
ASGV3-5'RACE_GSP1	ACTCAGAGGCAACACCATC
ASGV3-5'RACE_GSP2	TGCAACAACCTCTGTCAATTTCTGGG
ASGV3-5'RACE_GSP3	CATCCCTAAAGATTTGATTTTCCCG
ASGV3-3'RACE_GSP2	ACTGAGTTGTTTGCCCTCG
ASGV3-3'RACE_GSP3	CCCTCTCAGCTAGAATTGAA
For detection of viruses	
ASGV-904F	AGAGAGGATTTAGGTCCCT
ASGV-904R	AGAGTGGACAAACTCTAGAC
CTV-F ¹	ATGGATAATACTAGCGGACA
CTV-R	TCAGATGAAGTGGTGTTCAC
CYVCV-F	TACCGCAGCTATCCATTTCC
CYVCV-R	GCAGAAATCCCGAACCCTA

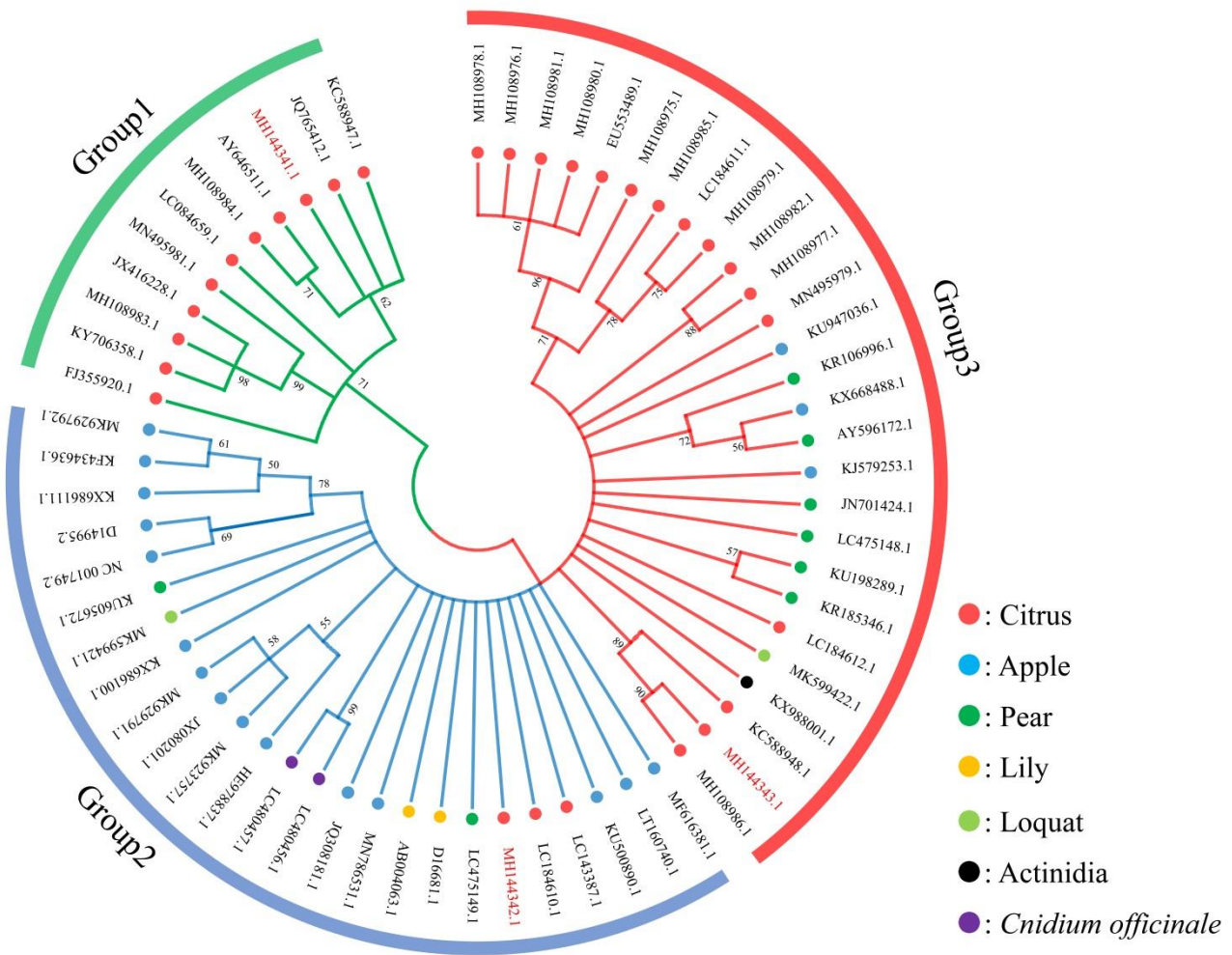
¹ CTV: citrus tristeza virus; CYVCV: citrus yellow vein clearing virus.



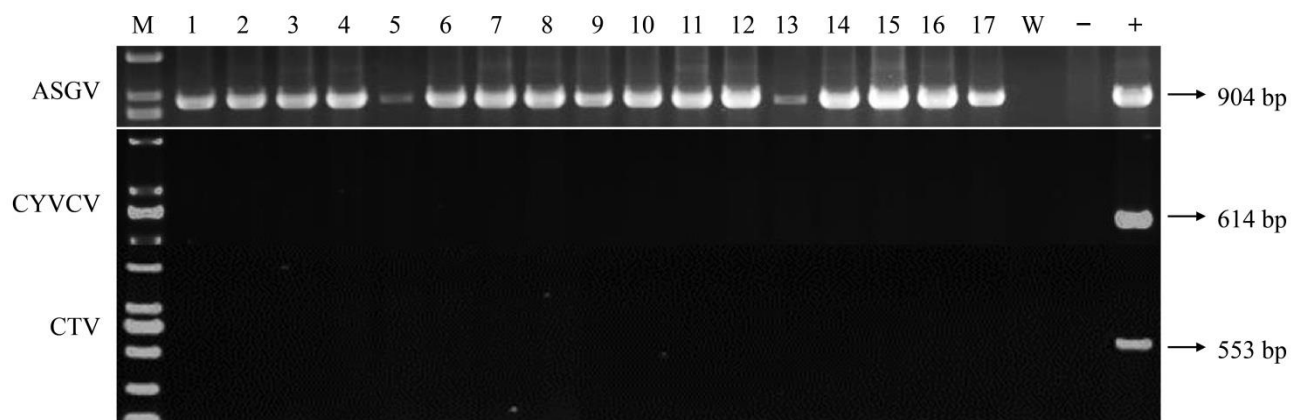
Appendix B Diseased HJY trees (front) showing obvious dwarfing compared to healthy GXY trees (behind).



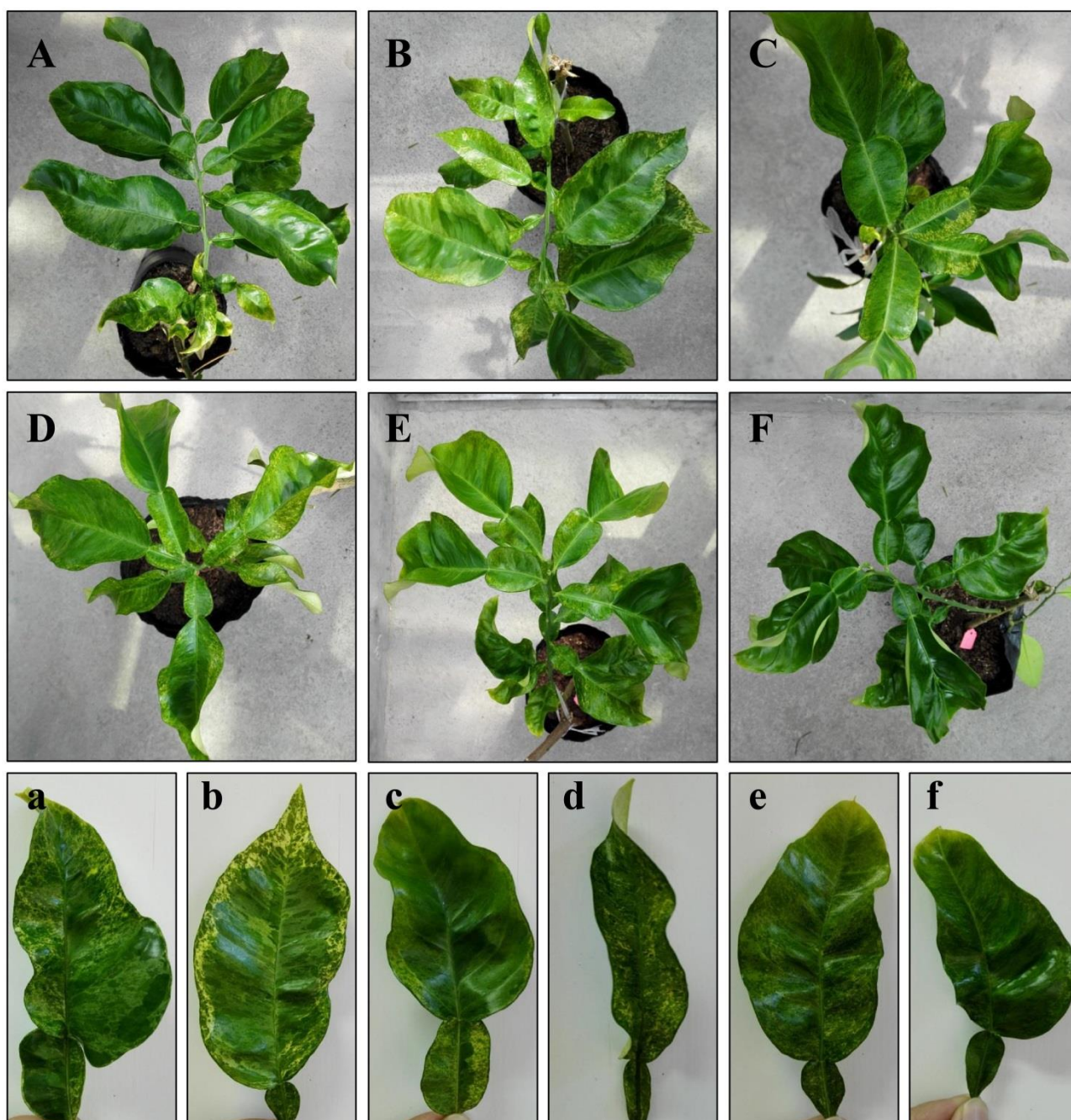
Appendix C Sequence identities based on complete genome sequences of three ASGV variants (this study) and 60 ASGV variants (NCBI).



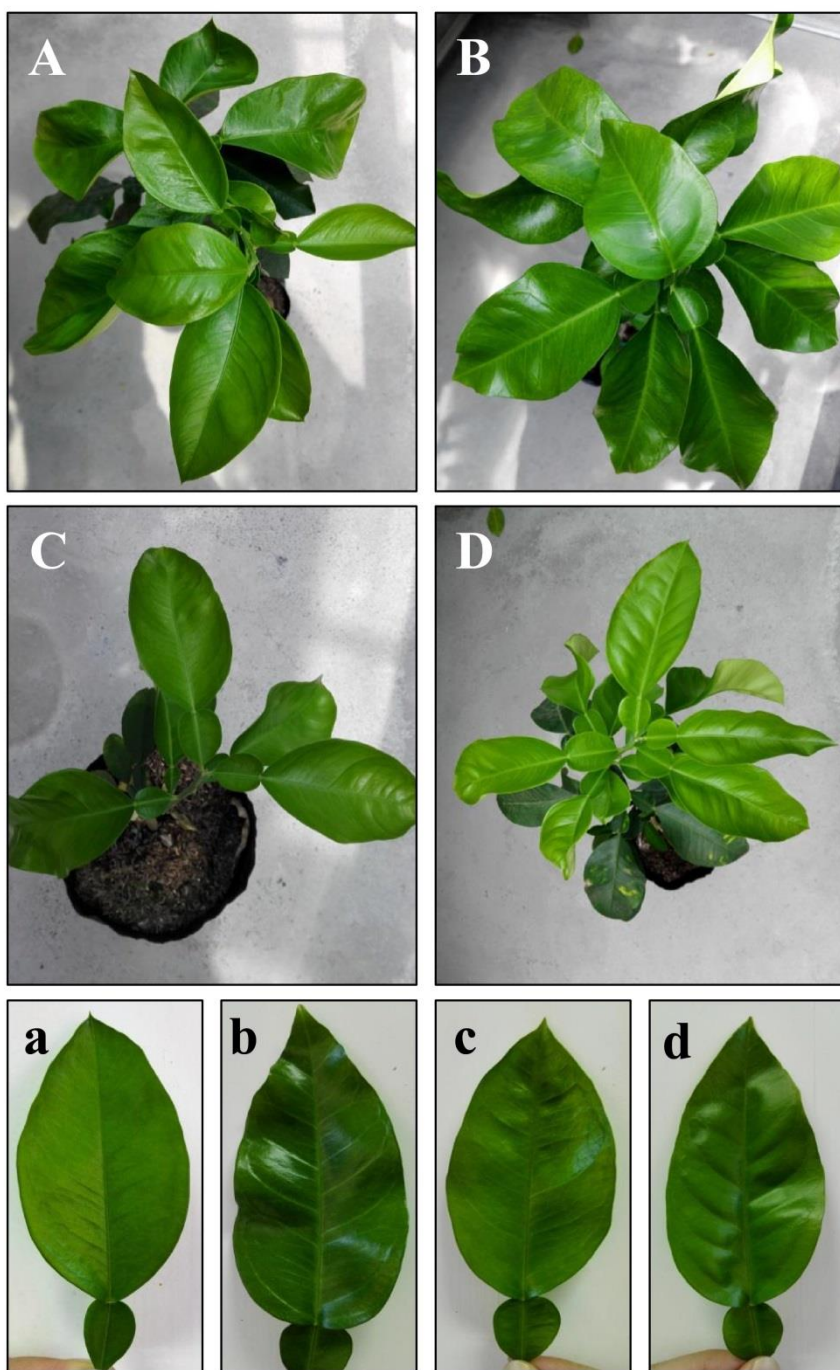
Appendix D Phylogenetic tree based on coat protein amino acid sequences of three ASGV variants (this study) and 60 ASGV variants (NCBI). The tree was constructed by MEGA7 using the maximum likelihood method with 1,000 bootstrap replications. Bootstrap values less than 50 are not shown. Variants used in the tree are indicated by accession number. The red, blue, green, and yellow bars and branches denote four groups of ASGV. Circles with different colors represent different hosts of ASGV (● : Citrus ● : Apple ● : Pear ● : Lily ● : *Cnidium officinale* ● : Actinidia ● : Loquat). Three ASGV variants identified in this study are indicated in bold red font.



Appendix E RT-PCR assay of ASGV, citrus yellow vein clearing virus (CYVCV), and citrus tristeza virus (CTV) in Chandler pummelo (Cp) rootstocks graft-inoculated with buds of diseased Huangjinmiyou pummelo trees using specific primers (Supplementary Table S1). Lane M, DL2000 marker; Lanes 1 to 17: samples 1 to 17; lane W, water control; line -, healthy control; lanes +, positive controls



Appendix F Huangjinmiyou pummelo plants sprouting at 20-24 °C. A, B, C, D, E, F, samples 2, 3, 4, 5, 6, 9; a, b, c, d, e, f, leaves of corresponding plants.



Appendix G Huangjinmiyou pummelo plants sprouting at 30-35 °C. A, B, C, D, samples 13, 15, 16, 17; a, b, c, d, leaves of corresponding plants.