

Table S1. Assembly parameters for SPAdes.

Sample	K-mers Used	Minimum Input Read Length
13365	21,33,55 / 21,33,55,89,93,97 *	100 bp
13392	21,33,55,77,89,93,97,107,117,127	130 bp
13394	21,33,55,77,89,93,97,107,117,127	130 bp
13395	21,33,55,77,89,93,97,107,117,127	130 bp
13396	21,33,55,77,89,93,97,107,117,127	130 bp
13399	21,33,55,77,89,93,97,107,117,127	100 bp
13402	21,33,55,77,89,93,97,107,117,127	130 bp
13421	21,33,55,77,89,93,97,107,117,127	130 bp
13430	21,33,55,77,89,93,97,107,117,127	130 bp
13438	21,33,55,77,89,93,97,107,117,127	130 bp
13442	21,33,55,77,89,93,97,107,117,127	130 bp
GF	21,33,55,77 / 21,33,55,77,89,93,97,107,117,127 *	100 bp
HR	21,33,55,77 / 21,33,55,77,89,93,97,107,117,127 *	100 bp
PI-1	21,33,55,77 / 21,33,55,77,89,93,97,107,117,127 *	100 bp
PI-2	21,33,55,77 / 21,33,55,77,89,93,97,107,117,127 *	100 bp

* Assembly was done twice, and any incomplete virus contigs from the first run were used as trusted contigs for the second run.

Table S2. Gene-specific primers used in rapid amplification of cDNA ends (RACE) and reverse transcription (RT)-PCR.

Primer Sequence (5' to 3')	Target Isolate	Usage
TATGACCTAGAAGAAATGCTCAGAC	PtBV-13365, L Segment	5'-RACE First PCR
CCAGCATTGAGAGCACATGGATAC	PtBV-13365, L Segment	5'-RACE Nested PCR
TGTCTTAGTGAATCTTGCATGTATAG	PtBV-13365, L Segment	5'-RACE Sequencing
TGAAGATGACAAAATTGTCAGGAGTGG	PtBV-13365, L Segment	3'-RACE First PCR
AATGAAGTTTCTTCCTCACTAGC	PtBV-13365, L Segment	3'-RACE Nested PCR
TTTCTAATAATCCTTCAGTTTTGC	PtBV-13365, L Segment	3'-RACE Sequencing
CTGTCTTCTATTTTATTTGGATCCAC	PtBV-13365, M Segment	5'-RACE First PCR
TGCAGTTGGGCAAACCCATAC	PtBV-13365, M Segment	5'-RACE Nested PCR
ATATTTGTTTGCCATTGTCC	PtBV-13365, M Segment	5'-RACE Sequencing
TCTCCACTACTCAAAACAACCTGA-TAAGG	PtBV-13365, M Segment	3'-RACE First PCR
TTCTGAAATAGAACAATCACCTG	PtBV-13365, M Segment	3'-RACE Nested PCR
CCTTTCAAAACACATTGCTC	PtBV-13365, M Segment	3'-RACE Sequencing
AAGAATATCTGAAGATGA-TAATGGTTCATATCC	PtBV-13365, S Segment	5'-RACE First PCR
TTTAATTGGAGAACCAGATATATCC	PtBV-13365, S Segment	5'-RACE Nested PCR
ATACATGGCAATGAAATAAATTG	PtBV-13365, S Segment	5'-RACE Sequencing
CATTGTTCAAAAATGTTGTTACAG	PtBV-13365, S Segment	3'-RACE First PCR
TAGTGCAAAGCTTTCAGATTCCAAACC	PtBV-13365, S Segment	3'-RACE Nested PCR
TTTCTTTCTATTTCTGATGATAGAGC	PtBV-13365, S Segment	3'-RACE Sequencing
TTGTGGAAAAGTTAACTCGCAC	PtPV	5'-RACE First PCR
GAGGCAAACCACCCAGTCAG	PtPV	5'-RACE Nested PCR
CAAGGAAAGGGAAGGATCTC	PtPV	5'-RACE Sequencing
AAGCCGCGTACGTATTGATCC	PtPV	3'-RACE First PCR
CCAGTTTATCTGGTGGTAGCTTGAG	PtPV	3'-RACE Nested PCR
TTCTTTGAGAACCAAGAATGAG	PtPV	3'-RACE Sequencing
GTGTATTCCATGCATCTGGC	PtAEV	5'-RACE cDNA Synthesis (Coding Strand)
TAACGCATTAAGTGGTTGCC	PtAEV	5'-RACE First PCR (Coding Strand)
ATTGCGCATCGTGTCATAAG	PtAEV	5'-RACE Nested PCR (Coding Strand)
TACTCACCATGTGGACTGAC	PtAEV	5'-RACE Sequencing (Coding Strand)
AAAGCAAAACAGTGAGTGGC	PtAEV	5'-RACE cDNA Synthesis (Complementary Strand)
GTTTCTTGTGTTGGGTGACG	PtAEV	5'-RACE First PCR (Complementary Strand)
AAGGTTGAGGTGACTAACG	PtAEV	5'-RACE Nested PCR (Complementary Strand)
GATTGAACGGGTTGGAATGG	PtAEV	5'-RACE Sequencing (Complementary Strand)
AGTCAGCGATATTGCGCTCC	PtAV-13365	5'-RACE cDNA Synthesis (Coding Strand)
GCGGTGTACTTGTCACCGAC	PtAV-13365	5'-RACE First PCR (Coding Strand)
CTCAACCAGATCCTTCGGTTCG	PtAV-13365	5'-RACE Nested PCR (Coding Strand)
AGATAACGGAAGACCTTCTG	PtAV-13365	5'-RACE Sequencing (Coding Strand)

AGATGGAATCGTAGCATACCCAATG	PtAV-13365	5'-RACE cDNA Synthesis (Complementary Strand)
CTCTACGGTGACTACTCTTTATTACG	PtAV-13365	5'-RACE First PCR (Complementary Strand)
TGATATACTTGCGTGGTGTG	PtAV-13365	5'-RACE Nested PCR (Complementary Strand)
TCTGAGGACAGCATCGCAGC	PtAV-13365	5'-RACE Sequencing (Complementary Strand)
ATCTCGTCAAAGTCGGGC	PtAV-13438-2	5'-RACE cDNA Synthesis (Coding Strand)
CCTTTCCTCCTTGACAGTTG	PtAV-13438-2	5'-RACE First PCR (Coding Strand)
AGATGAAGGTTGTGACGGTC	PtAV-13438-2	5'-RACE Nested PCR (Coding Strand)
TCATAGGTGATCCCTTGAGC	PtAV-13438-2	5'-RACE Sequencing (Coding Strand)
CACGGGAATCACCATTCTG	PtAV-13438-2	5'-RACE cDNA Synthesis (Complementary Strand)
GCAGGCAATAAGGATCTTTTCG	PtAV-13438-2	5'-RACE First PCR (Complementary Strand)
AGTTTGGAACGACATCATC	PtAV-13438-2	5'-RACE Nested PCR (Complementary Strand)
CTTTTGACCTCCTGGGAGAC	PtAV-13438-2	5'-RACE Sequencing (Complementary Strand)
AGGGTAATTAGCCGCATCACG	PtTV-13365	5'-RACE cDNA Synthesis (Coding Strand)
CCTCATGAACACAAATCGCATCATG	PtTV-13365	5'-RACE First PCR (Coding Strand)
AGTGTTGCTGACAGTACATC	PtTV-13365	5'-RACE Nested PCR (Coding Strand)
GGCAGCAGTCATCGGCTG	PtTV-13365	5'-RACE Sequencing (Coding Strand)
TTTCGCACAAACGTTGACATCTG	PtTV-13365	5'-RACE cDNA Synthesis (Complementary Strand)
TTGTATACTTGGAACCATCGGACC	PtTV-13365	5'-RACE First PCR (Complementary Strand)
GACTGGTCAATTAAACGAGTG	PtTV-13365	5'-RACE Nested PCR (Complementary Strand)
GTGGAGAAGGCTCGGTTTGC	PtTV-13365	5'-RACE Sequencing (Complementary Strand)
GCACCGGATCAATCAACC	PtTV-13421-2	5'-RACE cDNA Synthesis (Coding Strand)
TGAAACAGAATCGCAGCATG	PtTV-13421-2	5'-RACE First PCR (Coding Strand)
GTA CTGCTGTTCAAACCG	PtTV-13421-2	5'-RACE Nested PCR (Coding Strand)
GAACAGTGAGTATGCCAGAG	PtTV-13421-2	5'-RACE Sequencing (Coding Strand)
CACGGGAATCACCATTCTG	PtTV-13421-2	5'-RACE cDNA Synthesis (Complementary Strand)
GCAGGCAATAAGGATCTTTTCG	PtTV-13421-2	5'-RACE First PCR (Complementary Strand)
AGTTTGGAACGACATCATC	PtTV-13421-2	5'-RACE Nested PCR (Complementary Strand)
CTTTTGACCTCCTGGGAGAC	PtTV-13421-2	5'-RACE Sequencing (Complementary Strand)

AGCAGTGAATACAAAGTCTTTGG	PtBV Nucleocapsid Gene	RT-PCR (653 bp Amplicon) Forward Primer and Sequencing
GAGGCACAATTTTCACTTCAAC	PtBV Nucleocapsid Gene	RT-PCR (653 bp Amplicon) Reverse Primer and Sequencing
TAAACAGTTGGTTGAGCAGC	PtAEV Glycotransferase Domain	RT-PCR (305 bp Amplicon) Forward Prime and Sequencing
GACAAGTATGTGCACAGTGG	PtAEV Glycotransferase Domain	RT-PCR (305 bp Amplicon) Reverse Primer and Sequencing
GGTATGATACCTAGTGTTCTCT	PtAV1 ORF2	RT-PCR (432 bp Amplicon) Forward Prime and Sequencing
CGCTAAAAACTTTGGCTTACG	PtAV1 ORF2	RT-PCR (432 bp Amplicon) Reverse Primer and Sequencing
CTATATCACATGCGCTCTCCG	PtAV1 ORF2 Amplicon of PtAV-13395-1	Sequencing (Forward)
TAAGATCTTGCTTGTGCCCTG	PtAV1 ORF2 Amplicon of PtAV-13395-1	Sequencing (Reverse)
ATACATTACATGCGCATTACA	PtAV1 ORF2 Amplicon of PtAV-13395-2	Sequencing (Forward)
CAAAATCTTGCTCGTGCCCAA	PtAV1 ORF2 Amplicon of PtAV-13395-2	Sequencing (Reverse)
GGAGGTAATTCTGAACGATGC	PtAV2 (PtAV-13438-2) ORF2	RT-PCR (496 bp Amplicon) Forward Primer and Sequencing
AGGGAATATCATGCCTCCTG	PtAV2 (PtAV-13438-2) ORF2	RT-PCR (496 bp Amplicon) Reverse Primer and Sequencing
CACGTACGCTCCATAGTG	PtPV Capsid Gene	RT-PCR (646 bp Amplicon) Forward Primer and Sequencing
CCCTGGTTCCTCGTCTAC	PtPV Capsid Gene	RT-PCR (646 bp Amplicon) Reverse Primer and Sequencing
GATGGACTACGGAGCAGAAC	PtTV (Excluding PtTV-13421-2) ORF2	RT-PCR (662 bp Amplicon) Forward Primer and Sequencing
ACATCATGAACGTGCCYACTATT	PtTV (Excluding PtTV-13421-2) ORF2	RT-PCR (662 bp Amplicon) Reverse Primer and Sequencing
GATGGACTATGGAGCCGATC	PtTV-13421-2 ORF2	RT-PCR (662 bp Amplicon) Forward Primer and Sequencing
ACATCAAAAATGTGCTCACAACC	PtTV-13421-2 ORF2	RT-PCR (662 bp Amplicon) Reverse Primer and Sequencing

Table S3. Sources of orthotospovirus and Dugbe virus sequences.

Genus	Virus	Abbreviation	GenBank Accession Number		
			L	M	S
<i>Orthotospovirus</i>	Alstroemeria necrotic streak virus	ANSV	MG696851	MG696852 MK275259 (NSm) (GP)	MG696853
<i>Orthotospovirus</i>	Alstroemeria yellow spot virus	AYSV	MF469033	MF469034	MF469035
<i>Orthotospovirus</i>	Barleria chlorosis-associated virus	BCaV	MW251496	MW251497	MW251498
<i>Orthotospovirus</i>	Bean necrotic mosaic virus	BeNMV	JF417980	JN587269	JN587268
<i>Orthotospovirus</i>	Calla lily chlorotic spot virus	CCSV	FJ822962	DQ256125	DQ256123
<i>Orthotospovirus</i>	Capsicum chlorosis virus	CaCV	DQ256124	FJ822961	AY867502
<i>Orthotospovirus</i>	Chilli yellow ringspot virus	CYRSV	MH779497	MH779496	MH779495
<i>Orthotospovirus</i>	Chrysanthemum stem necrosis virus	CSNV	KM114546	KM114547	KM114548
<i>Orthotospovirus</i>	Groundnut chlorotic fan-spot virus	GCFSV	KP146140	U42555	U27809
<i>Orthotospovirus</i>	Groundnut ringspot virus	GRSV	MH742956	KP146141	AF080526
<i>Orthotospovirus</i>	Groundnut bud necrosis virus	GBNV	AF025538	AB061773	AB038343
<i>Orthotospovirus</i>	Hippeastrum chlorotic spot virus	HCRV	HG763861	MH742957	MH742958
<i>Orthotospovirus</i>	Impatiens necrotic spot virus	INSV	X93218	JX833565	JX833564
<i>Orthotospovirus</i>	Iris yellow spot virus	IYSV	FJ623474	M74904	X66972
<i>Orthotospovirus</i>	Melon severe mosaic virus	MSMV	KX698424	AF214014	AF001387
<i>Orthotospovirus</i>	Melon yellow spot virus	MYSV	AB061774	KX698423	KX698422
<i>Orthotospovirus</i>	Mulberry vein banding virus	MVBaV	KM819698	KM819699	KM819701
<i>Orthotospovirus</i>	Pepper chlorotic spot virus	PCSV	KX247379	KX247378	KX247377
<i>Orthotospovirus</i>	Polygonum ringspot virus	PolRSV	KJ541746	KJ541745	KJ541744
<i>Orthotospovirus</i>	Scadoxus chlorotic ringspot virus	ScCRV	MW080808	MW080809	MW080810
<i>Orthotospovirus</i>	Soybean vein necrosis virus	SVNV	HQ728385	HQ728386	HQ728387
<i>Orthotospovirus</i>	Tomato chlorotic spot virus	TCSV	MH742959	MH742960	MH742961
<i>Orthotospovirus</i>	Tomato necrotic ringspot virus	TNRV	MW256413	MW256414	MW256415
<i>Orthotospovirus</i>	Tomato necrotic spot associated virus	TNSaV	KT984754	KT984753	KM355773
<i>Orthotospovirus</i>	Tomato spotted wilt virus	TSWV	KT717691	KT717692	KT717693
<i>Orthotospovirus</i>	Tomato yellow ring virus	TYRV	JN560178	JN560177	AY686718
<i>Orthotospovirus</i>	Tomato zonate spot virus	TZSV	EF552435	EF552434	EF552433
<i>Orthotospovirus</i>	Watermelon bud necrosis virus	WBNV	GU735408	GU584185	GU584184
<i>Orthotospovirus</i>	Watermelon silver mottle virus	WSMoV	AF133128	U75379	U78734
<i>Orthotospovirus</i>	Zucchini lethal chlorosis virus	ZLCV	KU641378	KU641379	KU641380
<i>Orthonairovirus</i>	Dugbe virus	DUGV	U15018		

NSm: non-structural protein, M segment; GP: glycoprotein precursor.

Table S4. Sources of endornavirus and grapevine leafroll-associated virus 1 sequences.

Genus	Virus	Abbreviation	GenBank Accession
			Number
<i>Alphaendornavirus</i>	Agaricus bisporus endornavirus 1	AbEV1	KY357509
<i>Alphaendornavirus</i>	Basella alba endornavirus 1	BaEV1	AB844264
<i>Alphaendornavirus</i>	Bell pepper endornavirus	BPEV	KX977569
<i>Alphaendornavirus</i>	Cluster bean endornavirus 1	CBEV1	MG764084
<i>Alphaendornavirus</i>	Cucumis melo endornavirus	CmEV	KT727022
<i>Alphaendornavirus</i>	Erysiphe cichoracearum endornavirus	EcEV	KT388110
<i>Alphaendornavirus</i>	Grapevine endophyte endornavirus	GEEV	JX678977
<i>Alphaendornavirus</i>	Helianthus annuus endornavirus	HaEV	MF362666
<i>Alphaendornavirus</i>	Helicobasidium mompa endornavirus 1	HmEV1	AB218287
<i>Alphaendornavirus</i>	Hordeum vulgare endornavirus	HvEV	KT721705
<i>Alphaendornavirus</i>	Hot pepper endornavirus	HPEV	KR080326
<i>Alphaendornavirus</i>	Lagenaria siceraria endornavirus	LsEV	KF562072
<i>Alphaendornavirus</i>	Oryza rufipogon endornavirus	OrEV	AB014344
<i>Alphaendornavirus</i>	Oryza sativa endornavirus	OsEV	D32136
<i>Alphaendornavirus</i>	Persea americana endornavirus 1	PaEV1	JN880414
<i>Alphaendornavirus</i>	Phaseolus vulgaris endornavirus 1	PvEV1	KT456287
<i>Alphaendornavirus</i>	Phaseolus vulgaris endornavirus 2	PvEV2	KT456288
<i>Alphaendornavirus</i>	Phaseolus vulgaris endornavirus 3	PvEV3	MG242064
<i>Alphaendornavirus</i>	Phytophthora endornavirus 1	PEV1	AJ877914
<i>Alphaendornavirus</i>	Rhizoctonia cerealis endornavirus 1	RcEV1	KF311065
<i>Alphaendornavirus</i>	Rhizoctonia solani endornavirus 2	RsEV2	KT823701
<i>Alphaendornavirus</i>	Vicia faba endornavirus	VfEV	AJ000929
<i>Alphaendornavirus</i>	Winged bean endornavirus 1	WBEV1	LC144945
<i>Alphaendornavirus</i>	Yerba mate endornavirus	YmEV	KJ634409
<i>Betaendornavirus</i>	Tuber aestivum endornavirus	TaEV	HQ380014
<i>Ampelovirus</i>	Grapevine leafroll-associated virus 1	GLRaV1	JQ023131

Table S5. Sources of amalgavirus, *Zygosaccharomyces bailii* virus Z and Amasya cherry disease associated chrysovirus sequences.

Genus	Virus	Abbreviation	GenBank Accession Number
<i>Amalgavirus</i>	Allium cepa amalgavirus 1	AcAV1	BK010347
<i>Amalgavirus</i>	Allium cepa amalgavirus 2	AcAV2	BK010348
<i>Amalgavirus</i>	Blueberry latent virus	BBLV	HM029246
<i>Amalgavirus</i>	Rhododendron virus A	RhVA	HQ128706
<i>Amalgavirus</i>	Southern tomato virus	STV	EF442780
<i>Amalgavirus</i>	Spinach amalgavirus 1	SpAV1	KY695011
<i>Amalgavirus</i>	Vicia cryptic virus M	VCVM	EU371896
<i>Amalgavirus</i>	Zoostera marina amalgavirus 1	ZmAV1	KY783316
<i>Amalgavirus</i>	Zoostera marina amalgavirus 2	ZmAV2	KY783317
<i>Zybavirus</i>	<i>Zygosaccharomyces bailii</i> virus Z	ZbV-Z	KU200450
<i>Alphachrysovirus</i>	Amasya cherry disease associated chrysovirus	ACDACV	AJ781166

Table S6. Sources of totivirus and Amasya cherry disease associated chrysovirus sequences.

Genus	Virus	Abbreviation	GenBank Accession Number
<i>Totivirus</i>	<i>Pterostylis sanguinea</i> totivirus A	PtSTVA	KU291927
<i>Totivirus</i>	<i>Saccharomyces cerevisiae</i> virus L-A	ScVLA	J04692
<i>Totivirus</i>	<i>Saccharomyces cerevisiae</i> virus LBCLa	ScVLBC	U01060
<i>Totivirus</i>	<i>Scheffersomyces segobiensis</i> virus L	SsV1	KC610514
<i>Totivirus</i>	<i>Tuber aestivum</i> virus 1	TaV1	HQ158596
<i>Totivirus</i>	<i>Ustilago maydis</i> virus H1	UmVH1	U01059
<i>Totivirus</i>	<i>Xanthophyllomyces dendrorhous</i> virus L1A	XdVL1A	JN997472
<i>Totivirus</i>	<i>Xanthophyllomyces dendrorhous</i> virus L1B	XdVL1B	JN997473
<i>Alphachrysovirus</i>	Amasya cherry disease associated chrysovirus	ACDACV	AJ781166

Table S7. Sources of polerovirus and enamovirus sequences.

Genus	Virus	Abbreviation	GenBank Accession Number
<i>Polerovirus</i>	Beet chlorosis virus	BChV	AF352024
<i>Polerovirus</i>	Beet mild yellowing virus	BMVYV	X83110
<i>Polerovirus</i>	Beet western yellows virus	BWYV	AF473561
<i>Polerovirus</i>	Carrot red leaf virus	CtRLV	AY695933
<i>Polerovirus</i>	Cereal yellow dwarf virus RPS	CYDV-RPS	AF235168
<i>Polerovirus</i>	Cereal yellow dwarf virus RPV	CYDV-RPV	L25299
<i>Polerovirus</i>	Chickpea chlorotic stunt virus	CpCSV	AY956384
<i>Polerovirus</i>	Cotton leafroll dwarf virus	CLDV	GU167940
<i>Polerovirus</i>	Cucurbit aphid-borne yellows virus	CAbYV	X76931
<i>Polerovirus</i>	Faba bean polerovirus 1	FBPV1	MH464873
<i>Polerovirus</i>	Maize yellow dwarf virus RMV	MYDVRMV	KC921392
<i>Polerovirus</i>	Maize yellow mosaic virus	MaYMV	KU248489
<i>Polerovirus</i>	Melon aphid-borne yellows virus	MABYV	EU000534
<i>Polerovirus</i>	Pepo aphid-borne yellows virus	PABYV	KU315177
<i>Polerovirus</i>	Pepper vein yellows virus 1	PeVYV-1	AB594828
<i>Polerovirus</i>	Pepper vein yellows virus 2	PeVYV-2	HM439608
<i>Polerovirus</i>	Pepper vein yellows virus 3	PeVYV-3	KP326573
<i>Polerovirus</i>	Pepper vein yellows virus 4	PeVYV-4	KU999109
<i>Polerovirus</i>	Pepper vein yellows virus 5	PeVYV-5	KY523072
<i>Polerovirus</i>	Pepper vein yellows virus 6	PeVYV-6	LT559483
<i>Polerovirus</i>	Potato leafroll virus	PLRV	D00530
<i>Polerovirus</i>	Pumpkin polerovirus	PuPV	MG800833
<i>Polerovirus</i>	Suakwa aphid-borne yellows virus	SAbYV	JQ700308
<i>Polerovirus</i>	Sugarcane yellow leaf virus	ScYLV	AF157029
<i>Polerovirus</i>	Tobacco vein distorting virus	TVDV	EF529624
<i>Polerovirus</i>	Turnip yellows virus	TuYV	X13063
<i>Enamovirus</i>	Alfalfa enamovirus 1	AEV1	KU297983
<i>Enamovirus</i>	Citrus vein enation virus	CVEV	HF679486
<i>Enamovirus</i>	Grapevine enamovirus 1	GEV1	KX645875
<i>Enamovirus</i>	Pea enation mosaic virus 1	PEMV1	HM439775

Table S8. Numbers of paired reads before and after trimming.

Sample	Raw Data	Assembly*	Mapping**
13365***	27,654,877 27,099,376	19,020,569 17,616,117	22,338,523 22,056,390
	28,022,954	22,763,158	24,106,815
13392	28,337,237	12,522,368	13,524,332
13394	24,458,259	10,070,330	11,569,876
13395	20,649,715	7,922,337	9,044,726
13396	24,316,593	11,199,377	12,221,386
13399	28,257,471	11,741,532	12,647,860
13402	20,913,028	8,931,944	N/A
13421	24,638,458	10,813,580	11,905,838
13430	28,686,506	11,388,182	12,791,672
13438	23,698,290	10,320,423	11,623,667
13442	21,592,081	8,567,868	9,754,992
GF	2,430,909	937,766	1,006,729
HR	3,010,297	1,037,906	1,134,158
PI-1	1,172,786	959,962	N/A
PI-2	3,344,246	2,718,254	N/A

* Trimmed to 100 bp or 130 bp, see Table S2. ** Trimmed to 30 bp. *** This sample was sequenced using three lanes of a flow cell and thus contains three datasets. N/A Not applicable as the process was not performed.

Table S9. Substitution models used in reconstructing maximum likelihood trees in Figures 3 to 7.

Figure	Nucleotide Substitution Models
3	RdRp: GTR+F+R5, GP: GTR+F+R5, NSm: GTR+F+G4, NSs: TPM3u+F+I+G4, N: GTR+F+I+G4
4	GTR+F+R5
5	TVM+F+R3
6	GTR+F+G4
7	Four conserved regions from 5' to 3': TIM2e+R4, SYM+I+G4, TIM2e+I+G4, TIM2e+R3

RdRp: RNA dependent RNA polymerase; GP: glycoprotein precursor; NSm: non-structural protein, M segment; NSs: non-structural protein, S segment; N: nucleocapsid protein.

Table S10. Closest matches of each Pterostylis blotch virus protein from BLASTP searches of the NCBI non-redundant protein sequence database.

Virus Protein	Isolate	Virus Name of the Closest Hit	GenBank Accession Number of the Closest Hit	E-value	Query Coverage (%)	Pairwise Identity (%)
RdRp	PtBV-13365	Barleria chlorosis-associated virus	QVY47424.1	0.0	99	50.8
	PtBV-GF	Barleria chlorosis-associated virus	QVY47424.1	0.0	99	50.9
	PtBV-HR	Barleria chlorosis-associated virus	QVY47424.1	0.0	99	50.7
	PtBV-13399	Barleria chlorosis-associated virus	QVY47419.1	0.0	99	50.7
NSm	PtBV-13365	groundnut ringspot virus	AAM47012.1	5.E-93	84	50.2
	PtBV-GF	groundnut ringspot virus	AAM47012.1	4.E-93	84	50.2
	PtBV-HR	groundnut ringspot virus	AAM47012.1	2.E-93	84	50.6
	PtBV-13399	groundnut ringspot virus	QBC75818.1	1.E-91	79	51.6
GP	PtBV-13365	Barleria chlorosis-associated virus	QVY47426.1	0.0	94	44.3
	PtBV-GF	Barleria chlorosis-associated virus	QVY47426.1	0.0	94	44.2
	PtBV-HR	Barleria chlorosis-associated virus	QVY47426.1	0.0	94	44.1
	PtBV-13399	Barleria chlorosis-associated virus	QVY47426.1	0.0	94	44.4
NSs	PtBV-13365	tomato chlorotic spot virus	QBC75815.1	2.E-15	93	21.1
	PtBV-GF	groundnut ringspot virus	AYA95028.1	2.E-16	96	23.7
	PtBV-HR	groundnut ringspot virus	AYA95028.1	2.E-16	96	23.7
	PtBV-13399	impatiens necrotic spot virus	QAU55706.1	1.E-12	93	23.1
N	PtBV-13365	bean necrotic mosaic virus	YP_006468900.1	6.E-45	96	39.7
	PtBV-GF	bean necrotic mosaic virus	YP_006468900.1	6.E-45	96	39.7
	PtBV-HR	bean necrotic mosaic virus	YP_006468900.1	6.E-45	96	39.7
	PtBV-13399	bean necrotic mosaic virus	YP_006468900.1	3.E-44	96	39.3

RdRp: RNA dependent RNA polymerase; GP: glycoprotein precursor; NSm: non-structural protein, M segment; NSs: non-structural protein, S segment; N: nucleocapsid protein.

Table S11. Pairwise sequence identities (%) of the orthotospoviruses identified in this study.

Gene/Protein		PtBV-13365	PtBV-GF	PtBV-HR	PtBV-13399
RdRp	PtBV-13365		99.5	99.4	97.8
NSm			99.7	98.2	97.9
GP			99.7	99.3	98.9
NSs			98.2	98.2	93.4
N			100.0	100.0	99.6
RdRp	PtBV-GF	98.10		99.7	97.8
NSm		99.18		98.5	97.6
GP		99.22		99.3	98.9
NSs		98.30		100.0	94.0
N		98.37		100.0	99.6
RdRp	PtBV-HR	98.2	99.1		97.7
NSm		98.3	98.5		96.6
GP		98.0	98.1		98.5
NSs		98.0	99.0		94.0
N		97.8	98.9		99.6
RdRp	PtBV-13399	90.1	90.2	90.2	
NSm		96.1	95.7	95.6	
GP		96.6	96.7	96.5	
NSs		91.4	91.7	91.4	
N		92.0	93.1	92.5	

Nucleic acid identities (in black font) are shown in the bottom left half of the table while amino acid identities (in red font) are shown in the top right half. RdRp: RNA dependent RNA polymerase; GP: glycoprotein precursor; NSm: non-structural protein, M segment; NSs: non-structural protein, S segment; N: nucleocapsid protein.

Table S12. Pairwise sequence identities (%) of the amalgaviruses identified in this study.

	PtAV- 13365	PtAV- 13392	PtAV- 13394	PtAV- 13395- 1	PtAV- 13395- 2	PtAV- 13396	PtAV- 13421	PtAV- 13430	PtAV- 13438- 1	PtAV- 13438- 2	PtAV- 13442
PtAV-13365		88.7 90.3	89.1 90.1	89.2 90.2	96.5 96.5	96.8 96.8	99.3 99.2	88.7 90.2	99.5 99.5	40.6 46.7	96.9 96.9
PtAV-13392	85.1 86.5		92.5 93.1	92.6 93.2	88.9 90.5	88.9 90.5	89.0 90.8	99.5 99.5	88.9 90.5	41.0 46.8	88.9 90.4
PtAV-13394	85.5 86.7	89.5 90.2		99.9 99.9	89.4 90.4	89.5 90.4	89.4 90.6	92.7 93.3	89.2 90.4	41.2 47.4	89.3 90.1
PtAV-13395- 1	85.8 87.2	89.5 90.3	99.2 99.3		89.4 90.4	89.5 90.4	89.5 90.8	92.8 93.5	89.3 90.5	41.2 47.4	89.4 90.2
PtAV-13395- 2	94.6 94.8	84.9 86.5	85.9 87.0	86.1 87.4		99.7 99.7	96.8 96.8	88.9 90.5	96.8 96.8	40.8 46.9	99.3 99.2
PtAV-13396	94.7 94.9	85.0 86.5	86.0 87.0	86.1 87.2	99.6 99.7		97.1 97.0	88.9 90.5	97.1 97.0	40.8 46.9	99.6 99.5
PtAV-13421	99.1 99.0	85.1 86.5	85.3 86.5	85.6 87.0	94.8 95.0	95.0 95.0		89.0 90.8	99.6 99.5	40.8 46.9	97.0 96.9
PtAV-13430	85.1 86.4	99.4 99.3	89.5 90.2	89.5 90.2	85.0 86.5	85.0 86.4	85.0 86.4		88.9 90.5	41.0 46.9	88.9 90.4
PtAV-13438- 1	99.3 99.2	84.9 86.4	85.3 86.6	85.7 87.1	94.7 95.0	94.8 95.0	99.3 99.4	84.9 86.3		40.7 46.8	97.2 97.2
PtAV-13438- 2	48.2 50.8	49.3 52.2	48.7 51.9	48.8 52.1	47.8 50.6	47.8 50.7	48.2 50.9	49.3 52.2	48.1 50.9		40.7 46.8
PtAV-13442	94.8 95.0	85.0 86.5	86.2 87.2	86.4 87.5	98.7 99.0	98.9 99.1	95.0 95.1	85.0 86.5	94.9 95.2	47.9 50.6	

Nucleic acid identities (in black font) of the coding region (the genome sequence excluding the 5' and 3' untranslated regions) and ORF2 are shown in the bottom left half of the table while amino acid identities (in red font) of the predicted ORF1–ORF2 fusion protein and the ORF2 product are shown in the top right half. In each cell, the value on the top is the pairwise identity of the coding region/fusion protein while the one at the bottom is the pairwise identity ORF2 or its product.

Table S13. Closest matches of the predicted Pterostylis amalgavirus fusion protein and ORF2 product from BLASTP searches of the NCBI non-redundant protein sequence database.

Virus Protein	Isolate	Virus Name of the Closest Hit	GenBank Accession Number of the Closest Hit	E-value	Query Coverage (%)	Pairwise Identity (%)
ORF1– ORF2 Fusion Protein	PtAV-13365	Festuca pratensis amalgavirus 3	DAB41731.1	0.0	95	45.7
	PtAV-13392	Festuca pratensis amalgavirus 3	DAB41731.1	0.0	95	46.4
	PtAV-13394	Camellia totivirus A *	QED42799.1	0.0	96	47.9
	PtAV-13395-1	Camellia totivirus A *	QED42799.1	0.0	96	47.9
	PtAV-13395-2	Festuca pratensis amalgavirus 3	DAB41731.1	0.0	94	46.1
	PtAV-13396	Festuca pratensis amalgavirus 3	DAB41731.1	0.0	95	45.8
	PtAV-13421	Festuca pratensis amalgavirus 3	DAB41731.1	0.0	95	46.0
	PtAV-13430	Festuca pratensis amalgavirus 3	DAB41731.1	0.0	95	46.3
	PtAV-13438-1	Festuca pratensis amalgavirus 3	DAB41731.1	0.0	95	45.8
	PtAV-13438-2	Gevuina avellana amalgavirus 1	DAB41733.1	0.0	99	53.5
	PtAV-13442	Festuca pratensis amalgavirus 3	DAB41731.1	0.0	95	45.7
Product of ORF2	PtAV-13365	Zostera marina amalgavirus 2	YP_009362304.1	0.0	92	56.6
	PtAV-13392	Camellia totivirus A *	QED42799.1	0.0	98	53.7
	PtAV-13394	Camellia totivirus A *	QED42799.1	0.0	95	54.7
	PtAV-13395-1	Camellia totivirus A *	QED42799.1	0.0	95	54.7
	PtAV-13395-2	Zostera marina amalgavirus 2	YP_009362304.1	0.0	93	56.7
	PtAV-13396	Zostera marina amalgavirus 2	YP_009362304.1	0.0	93	56.7
	PtAV-13421	Zostera marina amalgavirus 2	YP_009362304.1	0.0	92	56.7
	PtAV-13430	Camellia totivirus A *	QED42799.1	0.0	98	53.7
	PtAV-13438-1	Zostera marina amalgavirus 2	YP_009362304.1	0.0	92	56.7
	PtAV-13438-2	Gevuina avellana amalgavirus 1	DAB41733.1	0.0	99	59.0
	PtAV-13442	Zostera marina amalgavirus 2	YP_009362304.1	0.0	93	56.5

* Homology search suggested the virus should be classified as an amalgavirus rather than a totivirus

Table S14. Pairwise sequence identities (%) of the totiviruses identified in this study.

	Pt-TV-13365	Pt-TV-13421-1	Pt-TV-13421-2	Pt-TV-GF	Pt-TV-HR
Pt-TV-13365		95.0	66.4	94.9	94.9
Pt-TV-13421-1	80.6		66.4	97.7	97.7
Pt-TV-13421-2	64.4	64.4		66.5	66.3
Pt-TV-GF	80.8	86.3	64.1		99.4
Pt-TV-HR	80.4	86.2	63.9	98.0	

Nucleic acid identities (in black font) of the coding regions (the genome excluding the 5' and 3' untranslated regions) are shown in the bottom left half of the table while amino acid identities (in red font) of the ORF1–ORF2 fusion protein are shown in the top right half.

Table S15. Closest matches of the predicted Pterostylis totivirus fusion protein and ORF2 product from BLASTP searches of the NCBI non-redundant protein sequence database.

Virus Protein	Isolate	Virus Name of the Closest Hit	GenBank Accession Number of the Closest Hit	E-value	Query Coverage (%)	Pairwise Identity (%)
ORF1–ORF2 Fusion Protein	PtTV-13365	maize-associated totivirus 3	AUH27273.1	0.0	99	43.5
	PtTV-13421-1	maize-associated totivirus 3	AUH27273.1	0.0	99	43.8
	PtTV-13421-2	maize-associated totivirus 3	AUH27273.1	0.0	99	43.5
	PtTV-GF	maize-associated totivirus 3	AUH27273.1	0.0	99	43.5
	PtTV-HR	maize-associated totivirus 3	AUH27273.1	0.0	99	43.5
Product of ORF2	PtTV-13365	Pterostylis sanguinea totivirus A	AOX47551.1	0.0	91	69.9
	PtTV-13421-1	Pterostylis sanguinea totivirus A	AOX47551.1	0.0	91	69.8
	PtTV-13421-2	Pterostylis sanguinea totivirus A	AOX47551.1	0.0	91	68.6
	PtTV-GF	Pterostylis sanguinea totivirus A	AOX47551.1	0.0	91	69.7
	PtTV-HR	Pterostylis sanguinea totivirus A	AOX47551.1	0.0	91	69.7

Table S16. Closest matches of the predicted Pterostylis polerovirus proteins from BLASTP searches of the NCBI non-redundant protein sequence database.

Virus Protein	Virus Name of the Closest Hit	GenBank Accession Number of the Closest Hit	E-value	Query Coverage (%)	Pairwise Identity (%)
P0	cereal yellow dwarf virus RPS	QGT40983.1	3E-08	78	29.4
P1	tobacco yellow virus	QIZ03428.1	4E-126	99	38.4
P2 *	potato leafroll virus	AAL77939.1	0.0	89	67.2
P1–P2	potato leafroll virus	ARS33717.1	0.0	99	51.1
P3a	beet mild yellowing virus	QYA72330.1	4E-14	97	68.9
P3	cereal yellow dwarf virus RPV	QDM54317.1	5E-78	99	68.1
P4	potato leafroll virus	ABY49849.1	6E-39	98	64.6
P3–P5	Brassica yellows virus	BBG75785.1	0.0	90	55.4

* Product of ORF2

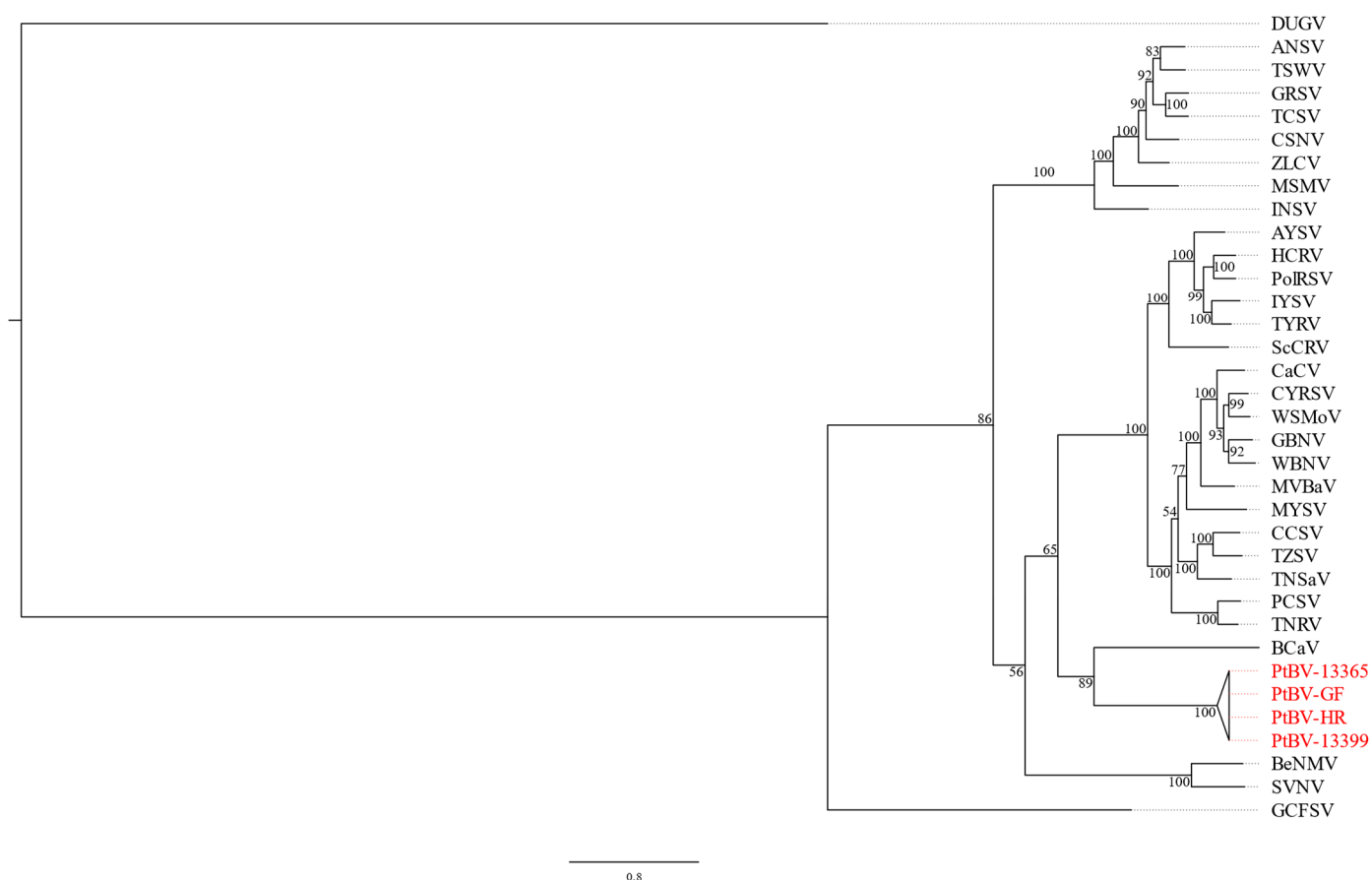


Figure S1. Maximum likelihood phylogenetic tree based on RNA dependent RNA polymerase gene rooted to Dugbe virus (DUGV). The nucleotide substitution model used was GTR+F+R4. The acronyms in red font correspond to Pterostylis blotch virus (PtBV) sequences. The other virus acronyms are defined in Table S3. The numbers next to the branches are non-parametric bootstrap values based on 1000 replicates.

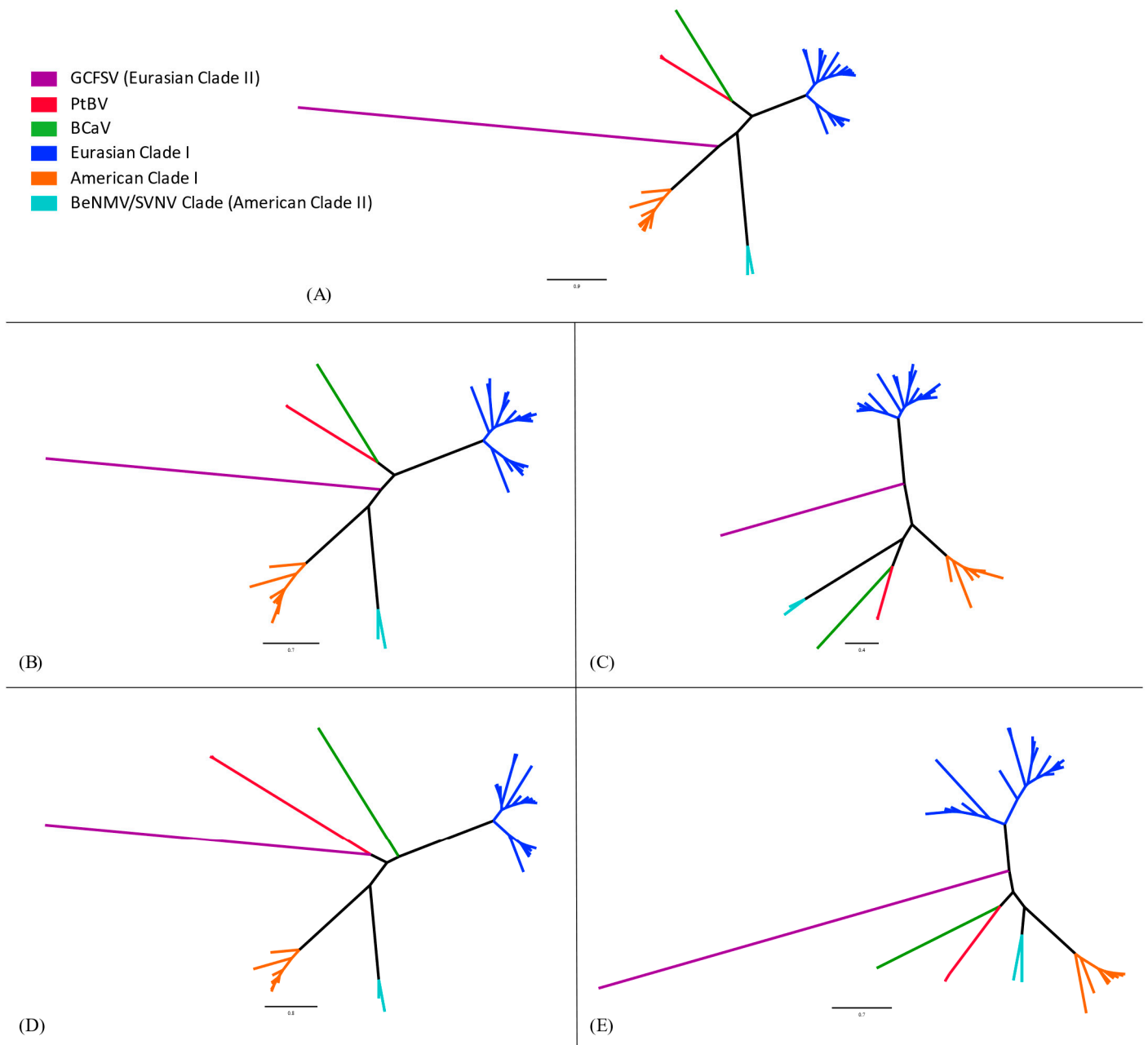


Figure S2. Maximum likelihood phylogenetic gene trees of orthotospoviruses. (A) RNA dependent RNA polymerase; substitution model: GTR+F+R6. (B) Non-structural protein, M segment; substitution model: GTR+F+R5. (C) Glycoprotein precursor; substitution model: GTR+F+G4. (D) Non-structural protein, S segment; substitution model: TPM3+F+I+G4. (E) Nucleocapsid protein; substitution model: GTR+F+I+G4. GCFSV, groundnut chlorotic fan-spot virus; PtBV, Pterostylis blotch virus; BCaV, Barleria chlorosis-associated virus; BeNMV, bean necrotic mosaic virus; SVNV, soybean vein necrosis virus.

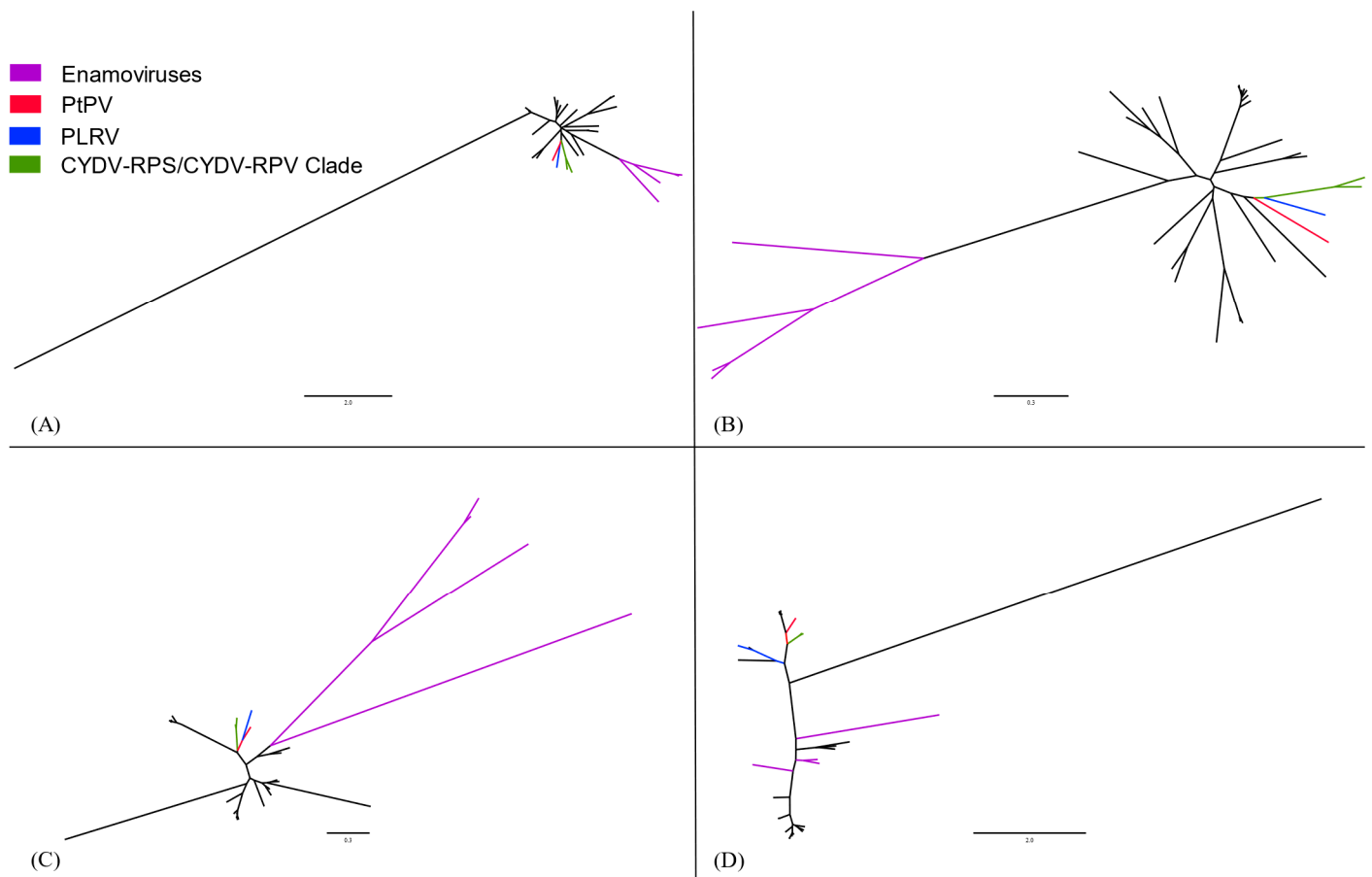


Figure S3. Maximum likelihood phylogenetic gene trees of poleroviruses and enamoviruses. (A) Conserved domain of serine proteinase; substitution model: TIM2e+R4. (B) Conserved domain of RNA dependent RNA polymerase; substitution model: SYM+I+G4. (C) Conserved domain of major capsid protein; substitution model: TIM2e+G4. (D) Conserved domain of minor capsid protein; substitution model: TIM2e+G4. PtPV, Pterostylis polerovirus; PLRV, potato leafroll virus; CYDV, cereal yellow dwarf virus.