

Supplementary Text and Tables

Text S1. East Asian Passiflora virus (EAPV) genome sequence assembled from RNA-Seq data.

>EAPV sequence from patchouli plant RNA-SEQ data(contig 8097)

CATAGAAACCAACGTCATCATATTTCCAAGCTTTCTTGAATTAGCACTCAGACTTGCAAGCAAGATTTACAA
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TGCTGGGTGCGAAGGTTTGTGTGGATGATTTTAAACAACCAGTTTACAGCTTGAATTTAATTTGTCCATGGACT
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>EAPV CP-patchouli (contig 940)

CTATCGATGCTAGAGGCGATGGAGGAAAAAGGGATAGAGGTAAGGACAAACAGGCAAGAACTCTAGCAAA
CCCTGAAAATCCAAATCCCAGTAATCCAAATAATGATAGCAATTCATCAATTGTGCGTGATAAGGACGTCAA
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GGGATGTTAGTCAAAACATGCACACCCTTTTGGGTGTGAGCTCTATGCAG

Table S1. Primers used for virus identification from infected plants.

Virus	Sequence	Region of genome	Ta for PCR	Amplicon size
TelMV	F=GAGCAACCAAGCAGCAGTTTG R=CAACGAGGGCGGCTGCCTTC	CP	60	432
	F=GATGACAATCAGATGAGCGTC R=ACCATTTCATGATGACGTCAT		52	388
EAPV	F=TGGTGCATTGACAATGGCAC R=GCAGTGTGCCTTTTCGGTATTCTCGC	CP	59	401
	F=GGATTGGACATGAGCAATTGCTC R=CTACCAGCCCCGTATGGAAAC		56	301
BBWV-2	F=GCGCACCATATATTTTGAAGATC R=ACGAGTGGCATACTCGTACAA	RNA-1	52	558
	F=GTGGCAGCTTCCCATACTG R=CAGGGCATGCATGCACTGACTC		59	437
PCaCA	F=GGCGATATTCTCTCCAGTATCCTTAT R=GCCTGATGAACAATGGAACCTCGACATAGG	P protein	56	651
	F=GCAAAGGGTGATGAAGATAGC R=GCTCCTCTAAATGTGCTGGAGTC		52	749
PogACRV2_Pog	F=GCTATGAATGCATACATCCCCTGG R=CAGCAGTAAAACATCCCGAGAC	L	54	525
	F=TGAGAGTGTAGTCGACAACATC R=AACTTCCTCCCTTGGTCATC		52	1767
PogACRV1_Pog	F=GCTGCCTTTATAATGAAGTTGAACGG R=ATCTCGTGGTCCTTAATCAAGTC	RdRp	54	432

Note: For TelMV, a pair of primers were used in the RT-PCR, whereas two pairs of primers were used for each of the other viruses.

Table S2. Primers used for virus identification from inoculated *N. benthamiana* plants.

Virus	Sequence	Region of genome	Ta for PCR	Amplicon size
TelMV	F=GAGCAACCAAGCAGCAGTTTG R=CAACGAGGGCGGCTGCCTTC	CP	60	430
	F=TGGTGCATTGACAATGGCAC R=GCAGTGTGCCTTTTCGGTATTCTCGC		59	401
EAPV	F=GGATTGGACATGAGCAATTGCTC R=CTACCAGCCCCGTATGGAAAC	CP	56	301
	F=GCGCACCATATATTTTGAAGATC R=ACGAGTGGCATACTCGTACAA		52	558
BBWV-2	F=GCGCACCATATATTTTGAAGATC R=ACGAGTGGCATACTCGTACAA	RNA-1	52	558
PogACRV1_Pog	F=GCTGCCTTTATAATGAAGTTGAACGG R=ATCTCGTGGTCCTTAATCAAGTC	RdRp	54	432

Note: Ta (annealing temperature) for PCR reaction.

Table S3. Blast X analysis of viral contigs from each sample.

Sample	Closely related virus	Family	No. of contigs	Length of contigs	% Amino Acid identity	% Query coverage
NX-1	Pogostemen alphacyrhabdovirus 2	<i>Rhabdoviridae</i>	6	874-10029	86.18-100	44-100
	pogostemom alphacytorhabdovirus 1	<i>Rhabdoviridae</i>	5	319-10029	100	33-99
	Telosma mosaic virus	<i>Potyviridae</i>	17	202-546	54.79-98.53	88-100
	Broad bean wilt virus 2	<i>Secoviridae</i>	6	205-1769	89.16-100	97-100
NX-2	Pogostemen alphacyrhabdovirus 2	<i>Rhabdoviridae</i>	10	488-9841	56-99	86.31-100
	pogostemom alphacytorhabdovirus 1	<i>Rhabdoviridae</i>	3	1264-10344	100	57-84
	Telosma mosaic virus	<i>Potyviridae</i>	19	202-476	45.83-98.41	56-100
	Broad bean wilt virus 2	<i>Secoviridae</i>	3	217-5725	93.34-97.81	97-99
NX-3	Pogostemen alphacyrhabdovirus 2	<i>Rhabdoviridae</i>	7	319-7476	82-100	42-100
	pogostemom alphacytorhabdovirus 1	<i>Rhabdoviridae</i>	2	4875-8395	100	28-73
	Telosma mosaic virus	<i>Potyviridae</i>	11	202-330	59.72-96.19	96-99
	Broad bean wilt virus 2	<i>Secoviridae</i>	9	200-5776	68.09-100	51-100
PX-1	Patchouli chlorosis-associated cytorhabdovirus	<i>Rhabdoviridae</i>	2	3573-8859	82.19-90.12	34-70
	Telosma mosaic virus	<i>Potyviridae</i>	22	201-770	59.05-100	82-100
	East Asian Passiflora virus	<i>Potyviridae</i>	34	202-2199	56.9-98.11	60-100
	Broad bean wilt virus 2	<i>Secoviridae</i>	2	764-1013	93.04-97.64	80-99
PX-2	Patchouli chlorosis-associated cytorhabdovirus	<i>Rhabdoviridae</i>	2	642-8865	79.27-82.19	70-76
	Telosma mosaic virus	<i>Potyviridae</i>	24	201-1008	55.81-100	44-100
	East Asian Passiflora virus	<i>Potyviridae</i>	38	202-2405	50-100	50-100
	Broad bean wilt virus 2	<i>Secoviridae</i>	3	408-1039	91.85-98.27	52-99
PX-3	Patchouli chlorosis-associated cytorhabdovirus	<i>Rhabdoviridae</i>	2	1703-7261	71.55-84.95	67-81
	Telosma mosaic virus	<i>Potyviridae</i>	26	200-869	58.76-100	60-100
	East Asian Passiflora virus	<i>Potyviridae</i>	42	200-3568	62.61-100	56-100
	Broad bean wilt virus 2	<i>Secoviridae</i>	3	346-663	84.62-98.29	48-99