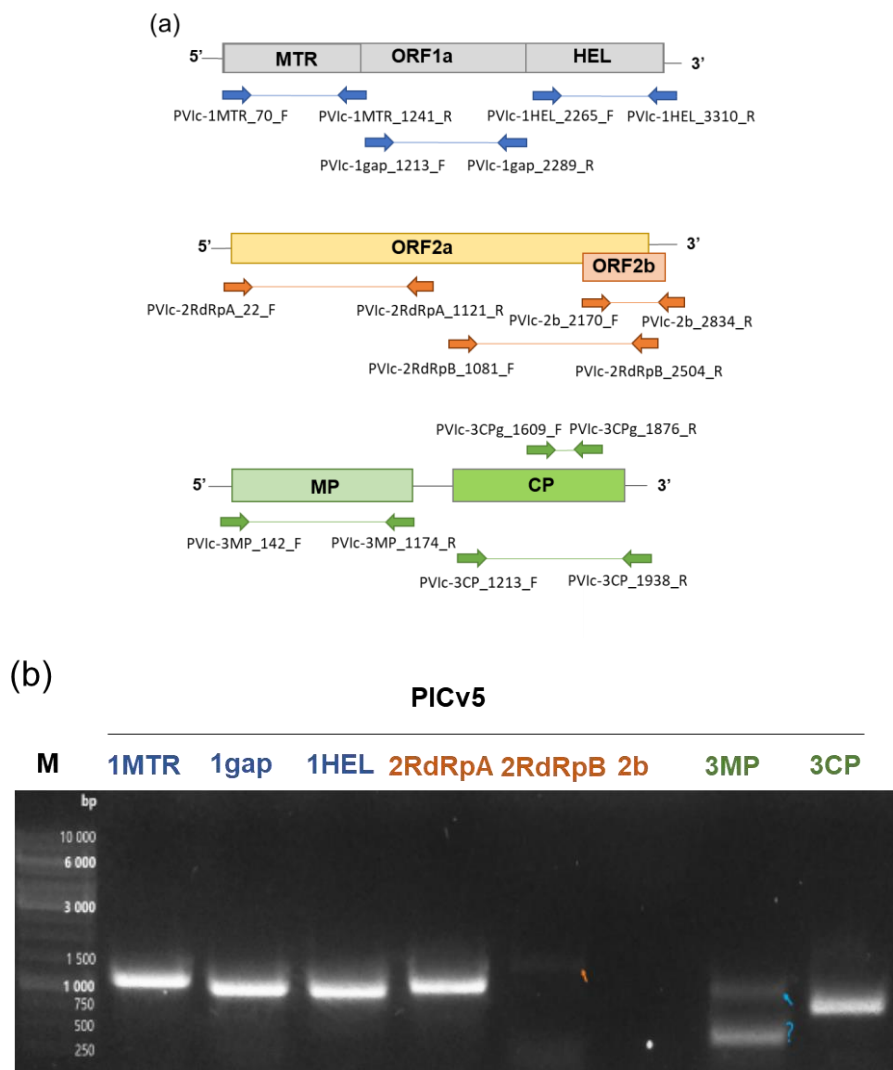


Supplementary Figures to

## *Clematis vitalba* is a natural host of a novel ilarvirus, Prunus virus I

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**Figure S1.** Validation of RNA sequencing. (a) Primers were designed based on the ilarvirus specific contig sequences able to amplify almost all three RNAs of the entire genome. (b) result of the RT-PCR. M corresponds to GeneRuler 1kb DNA Ladder (Thermo Fisher Scientific, Waltham, MA, USA). Arrows indicate the positive products.

Tobacco streak virus gene for movement protein, complete cds, isolate: dahlia  
Sequence ID: [LC030107.1](#) Length: 873 Number of Matches: 11  
Range 1: 1 to 753 [GenBank](#) Next Match Previous Match

Alignment statistics for match #1

	Score	Expect	Identities	Positives	Gaps	Frame
	502 bits(1091)	7e-143	203/251(81%)	234/251(93%)	0/251(0%)	+3/+1
Query	210	MALTPSYRALTFSADESSLEKSVSDALSGCVELNMGLRRCFAFPATNTEAFLCELTKE				389
		MAL P+ +ALTFSADDE+SLEK++++ALSG VE+NMGLRRCFAFP NT AFLCELTKE				
Sbjct	1	MALVPTMKALTFSAEDETSLEKAITALSVEINMGLRRCFAFPVNTGAFCELTKE				180
Query	390	TKTILGKFADKVRGRVFDHAVIHMMYIPVILSTTHAVAEKIRNMTGDELYGGTKVNL				569
		TK+ +GKF+DKVRGRVFDHAVIH+MYIPVIL+TTHA+AELK++N+ATGDELYGGTKVNL				
Sbjct	181	TKSFIGKFSDKVRGRVFDHAVIHLMYIPVILNTTHAIAELKLNLATGDELYGGTKVNL				360
Query	570	NEAFILMTWPRSLFADAVHAHKGGLYLGGTVNCATSVKGCNIGMWYPMWSEKVSNNKQLY				749
		++AFILMTWPRSLFA+AVH+H+GLYLGGTV+CA+SVP IGMWYPMWSEKVSNNKQLY				
Sbjct	361	SKAFILMTWPRSLFAEAVHSHRGLYLGGTVSCASSVPANAKIGMWYPMWSEKVSNNKQLY				540
Query	750	QNTTNIVNTKALETFTTRTMISSDREMRSLRSRASIDIAAKTAEKPVLCSSHVNLLDQHT				929
		QNT NI NT+ALETFTTRTMISSDREMRSLRSRASIDIAAKT EKPV+CS V+LLDQHT				
Sbjct	541	QNTVNIHNTAELETFTTRTMISSDREMRSLRSRASIDIAAKTLEKPVICSERVSLDQHT				720
Query	930	SGVDFTVKQVQ 962				
		GVDFTV +++				
Sbjct	721	QGVDFTVAEIE 753				

Tobacco streak virus movement protein gene, complete cds  
Sequence ID: [MK307506.1](#) Length: 873 Number of Matches: 12  
Range 1: 1 to 750 [GenBank](#) Next Match Previous Match

Alignment statistics for match #1

	Score	Expect	Identities	Positives	Gaps	Frame
	492 bits(1068)	1e-139	198/250(79%)	231/250(92%)	0/250(0%)	+3/+1
Query	210	MALTPSYRALTFSADESSLEKSVSDALSGCVELNMGLRRCFAFPATNTEAFLCELTKE				389
		MAL P+ +ALTFSADDE+SLEK++++ALSG VELNMGLRRCFAFP NT AFLCELTKE				
Sbjct	1	MALVPTMKALTFSADDETSLEKAITALSVELNMGLRRCFAFPVNTGAFCELTKE				180
Query	390	TKTILGKFADKVRGRVFDHAVIHMMYIPVILSTTHAVAEKIRNMTGDELYGGTKVNL				569
		TK+ +GKF+DKVRGR FVDHAVIH++Y+PVIL TT+A++ELK++N+ATGDELYGGTKV+L				
Sbjct	181	TKSFIGKFSDKVRGRVFDHAVIHLMLPVILKTTYAISELKLKNLATGDELYGGTKVDL				360
Query	570	NEAFILMTWPRSLFADAVHAHKGGLYLGGTVNCATSVKGCNIGMWYPMWSEKVSNNKQLY				749
		++AFILMTWPRSLFA+AVHAH+GLYLGGTV+CA+SVP IGMWYPMWSEKVSNNKQLY				
Sbjct	361	SKAFILMTWPRSLFAEAVHSHRGLYLGGTVSCASSVPSNAKIGMWYPMWSEKVSNNKQLY				540
Query	750	QNTTNIVNTKALETFTTRTMISSDREMRSLRSRASIDIAAKTAEKPVLCSSHVNLLDQHT				929
		QNT NI +T+ALETFTTRTMISSDREMRSLRSRASIDIAA+T EKPV+CS V+LLDQHT				
Sbjct	541	QNTVNIHSTAELETFTTRTMISSDREMRSLRSRASIDIAARTPEKPVICSERVSLDQHT				720
Query	930	SGVDFTVKQV 959				
		GVDFTV ++				
Sbjct	721	QGVDFTVSEI 750				

**Figure S2. Alignment of the amino-acid sequences of the PV-0309 PrVI isolate to closely related TSV isolates**  
TBLASTX search of the RNA sequence of PRVI DSMZ PV-0309 strain (OL584350) showed high identity in the amino-acid sequence of the movement protein encoded by TSV dahlia strain (LC030107) or by a TSV strain infecting summer squash in Georgia, U.S.A.