

Table 1

Ten putative totivirus-like sequences from the field sample of powdery mildew.

No. contig ^a Name	Sequence name (tentative virus name)	Abbreviation	Size (nt)	Read count	SG ^f	Accession number
1 65-114 ^b	Red clover powdery mildew-associated totivirus 1-a	RPaTV1-a	4781 ^c	2656	I-A	LC075485
2 65-6 ^b	Red clover powdery mildew-associated totivirus 1-b	RPaTV1-b	(4673)	2788	I-A	LC075486
3 75-52	Red clover powdery mildew-associated totivirus 2	RPaTV2	(4178) ^{d, e}	1934	I-B	LC075487
4 75-77	Red clover powdery mildew-associated totivirus 3	RPaTV3	4805 ^c	1897	I-C	LC075488
5 6052	Red clover powdery mildew-associated totivirus 4	RPaTV4	(4455) ^e	2203	I-C	LC075489
6 75-14	Red clover powdery mildew-associated totivirus 5	RPaTV5	5056 ^c	4915	I-D	LC075490
7 75-22	Red clover powdery mildew-associated totivirus 6	RPaTV6	5007 ^c	3719	I-D	LC075491
8 75-7	Red clover powdery mildew-associated totivirus 7	RPaTV7	4942 ^c	2762	I-D	LC075492
9 85-65	Red clover powdery mildew-associated totivirus 8	RPaTV8	(5065) ^e	3950	I-D	LC075493
10 85-21	Red clover powdery mildew-associated totivirus 9	RPaTV9	(5997) ^d	6808	II	LC075494

^a All contigs show sequence heterogeneity (SNPs) probably reflecting infection by quasispecies (see Fig. S2).

^b These sequences are slightly different from each other at the nucleic acid level (13% difference).

^c Complete genome sequence.

^d They lack the 5' terminal sequences.

^e They lack the sequences coding for N- or C-terminal regions of ORF1 and ORF2, respectively (see Figs. 2, S3 and S4).

^f Subgrouping based on the CP-RdRP phylogenetic tree (Fig. 4).

Table 2
Summary of the BLASTp search results for RPaTVs.

Virus/ contig name	Size (aa, kDa)	Best-matched virus	Identity (e-value, QC ^b)
<u>query sequence: ORF1 (CP)</u>			
RPaTV1-a/ 65-114	681, 76	black raspberry virus F	35% ($2e^{-71}$, 97)
RPaTV1-b/ 65-6	681, 76	black raspberry virus F	36% ($1e^{-69}$, 94)
RPaTV2 / 75-52 ^a	>580, >66	Saccharomyces cerevisiae virus L-BC (La)	29% ($5e^{-43}$, 78)
RPaTV3 / 75-77	685, 77	Xanthophyllomyces dendrorhous virus L1b	33% ($7e^{-108}$, 97)
RPaTV4 / 6052	683, 77	Xanthophyllomyces dendrorhous virus L1b	44% (0.0, 99)
RPaTV5 / 75-14	807, 90	Saccharomyces cerevisiae virus L-A-lus	22% (0.007, 44)
RPaTV6 / 75-22	809, 90	Tuber aestivum virus 1	21% (0.001, 44)
RPaTV7 / 75-7	811, 90	Saccharomyces cerevisiae virus L-A-2	22% (0.037, 47)
RPaTV8 / 85-65	820, 91	Tuber aestivum virus 1	26% ($1e^{-04}$, 37)
<u>query sequence: ORF2 (RdRP)</u>			
RPaTV1-a/ 65-114	801, 90	black raspberry virus F	42% (0.0, 99)
RPaTV1-b/ 65-6	835, 90	black raspberry virus F	42% (0.0, 95)
RPaTV2 / 75-52	776, 88	Saccharomyces cerevisiae virus L-BC (La)	39% ($3e^{-113}$, 78)
RPaTV3 / 75-77	799, 90	Xanthophyllomyces dendrorhous virus L1b	44% (0.0, 94)
RPaTV4 / 6052 ^a	>774, >87	Xanthophyllomyces dendrorhous virus L1b	59% (0.0, 97)
RPaTV5 / 75-14	831, 95	Xanthophyllomyces dendrorhous virus L1A	37% ($2e^{-121}$, 76)
RPaTV6 / 75-22	801, 90	Xanthophyllomyces dendrorhous virus L1A	37% ($4e^{-112}$, 74)
RPaTV7 / 75-7	808, 91	Xanthophyllomyces dendrorhous virus L2	34% ($6e^{-106}$, 80)
RPaTV8 / 85-65	$\geq 821, \geq 92$	Xanthophyllomyces dendrorhous virus L2	34% ($4e^{-121}$, 84)
<u>query sequence: ORF (polyprotein)</u>			
RPaTV9 / 85-21	1826, 204	Ustilago maydis virus H1	29% ($2e^{-23}$, 32)

^a They lack the sequences coding for N- or C-terminal regions of ORF1 and ORF2, respectively.

^b QC: query coverage (%).

Table 3
BLASTp against transcriptome shotgun assembly (TSA) database with RPaTVs.

Query sequence Host organism	Accession number	Size (>1000 nt)	Identity (e-value, QC ^c)		TSA No. ^d	
			CP	RdRp		
RPaTV6/75-22 (SG I-D)^a						
<i>Phakopsora pachyrhizi</i> (soybean bean rust)	GACM01000569	4284 nt	32% (2e ⁻⁶⁰ , 56)	37% (9e ⁻¹⁵⁰ , 98)	TSA1	
	GACM01000768 ^b	5179 nt	28% (9e ⁻⁸⁹ , 97)	37% (5e ⁻¹⁴⁸ , 99)	TSA2	
	GACM01002541	2493 nt		40% (9e ⁻¹⁶⁸ , 94)	TSA3	
	GACM01001017 ^b	2296 nt		44% (2e ⁻¹⁴⁷ , 79)	TSA4	
	GACM01003071 ^b	2197 nt		37% (1e ⁻¹⁴² , 79)	TSA5	
	GACM01003023 ^b	1305 nt		47% (7e ⁻¹¹⁷ , 60)		
	GACM01003327 ^b	1827 nt		47% (1e ⁻⁷⁷ , 60)		
	GACM01002865 ^b	1017 nt		43% (5e ⁻⁷² , 39)		
	GACM01000636	2658 nt	38% (1e ⁻¹¹⁴ , 94)		TSA6	
	GACM01000628	3035 nt	32% (1e ⁻⁷⁶ , 83)		TSA7	
	GACM01004032	1307 nt	34% (2e ⁻⁵⁷ , 49)			
	GACM01002992	1383 nt	31% (9e ⁻⁵⁶ , 49)			
	<i>Uromyces appendiculatus</i> (common bean rust)	GACI01004215	4580 nt	30% (2e ⁻³⁸ , 87)	41% (1e ⁻¹⁵⁹ , 85)	TSA1
		GACI01000486 (=GACI01000485)	4647 nt	30% (6e ⁻⁸⁸ , 97)	40% (2e ⁻¹⁴⁸ , 81)	TSA2
GACI01000487		2181 nt	31% (5e ⁻⁹⁴ , 85)		TSA4	
GACI01005442		2137 nt	32% (2e ⁻⁸⁷ , 79)		TSA5	
GACI01004183		1916 nt	32% (1e ⁻⁷⁹ , 78)		TSA6	
GACI01004090		1781 nt	30% (5e ⁻⁶⁴ , 71)			
GACI01006079		1292 nt	29% (1e ⁻³⁶ , 48)			
RPaTV3/75-77 (SG I-C)^a						
<i>Uromyces appendiculatus</i>	GACI01003374	4312 nt	27% (1e ⁻⁴⁸ , 86)	43% (3e ⁻¹⁴¹ , 65)	TSA3	
<i>Helicoverpa assulta</i> (oriental tobacco budworm)	GBTA01063992	2637 nt		32% (5e ⁻¹⁰⁹ , 96)	TSA1	
RPaTV2/75-52 (SG I-B)^a						
<i>Tetradontophora bielensis</i> (springtail)	GAXI01156566	1904 nt	28% (2e ⁻⁴⁰ , 83)			
RPaTV1-a/65-114 (SG I-A)^a						
<i>Boechera gunnisoniana</i> (rockcress)	GBAD01037434	1851 nt		47% (0.0, 73)	TSA1	
	GBAD01037432	2876 nt	28% (3e ⁻⁷⁷ , 97)			
	GBAD01061696	1355 nt	29% (7e ⁻⁴⁹ , 64)			
	GBAD01061697	1154 nt	29% (1e ⁻⁴³ , 53)			
	GBAD01009780	1808 nt	30% (2e ⁻⁴¹ , 62)			
	GBAD01053024	1971 nt	30% (4e ⁻⁴¹ , 49)			
	GBAD01053023	1975 nt	29% (2e ⁻³⁹ , 55)			
	GBAD01053025	1951 nt	31% (8e ⁻³⁹ , 48)			
<i>Camellia taliensis</i> (tea plant)	GCRZ01031143	1986 nt		45% (1e ⁻¹⁶² , 66)		
	GCRZ01056351	1223 nt	33% (2e ⁻²⁶ , 29)			
	<i>Lathyrus sativus</i> (legume)	GBSN01054039	1567 nt		40% (2e ⁻⁷⁵ , 46)	

^a Subgrouping based on the CP-RdRP phylogenetic tree (Fig. 4).

^b Reported sequences in a previous paper (Link et al., 2014).

^c QC: query coverage (%).

^d TSA number: these sequences are used in phylogenetic studies in Figs. 5 or S6.