

Genome sequence of a distinct watermelon mosaic virus identified from ginseng (*Panax ginseng*) transcriptome

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Summary. – Watermelon mosaic virus (WMV) is a member of the genus *Potyvirus*, which is the largest genus of plant viruses. WMV is a significant pathogen of crop plants, including *Cucurbitaceae* species. A WMV strain, designated as WMV-Pg, was identified in transcriptome data collected from ginseng (*Panax ginseng*) root. WMV-Pg showed 84% nucleotide sequence identity and 91% amino acid sequence identity with its closest related virus, WMV-Fr. A phylogenetic analysis of WMV-Pg with other WMVs and soybean mosaic viruses (SMVs) indicated that WMV-Pg is a distinct subtype of the WMV/SMV group of the genus *Potyvirus* in the family *Potyviridae*.

Keywords: watermelon mosaic virus; *Potyvirus*; genome; ginseng; *Panax ginseng*

Introduction

Potyvirus, the largest genus of plant viruses, causes considerable crop loss worldwide (Revers and Garcia, 2015). *Potyvirus* virion is a non-enveloped virus, with filamentous and flexuous capsid, and contains a linear positive-sense single-stranded (ss) RNA genome. The genome encodes an open reading frame (ORF) encoding a polyprotein that is cleaved into 10 mature proteins: P1-pro, HC-pro, P3, 6K1, CI, 6K2, VPg, NIa-pro, NIb-RdRp, and CP. The three virus-encoded proteases, P1 protease (P1-pro), helper component protease (HC-pro), and nuclear inclusion a protease (NIa-pro), are involved in this processing. P1-pro and HC-pro cleave a site at their own C-terminus, whereas NIa-pro is responsible for the proteolytic, co-translational processing of the remaining seven sites in *cis* and in *trans* manner (Adams *et al.*, 2005). In addition, a smaller polyprotein is also produced via a polymerase slippage mechanism within the P3 region,

which is cleaved to P1-pro, HC-pro, and P3N-PIPO. These mature proteins are required for replication, translation, packaging, movement, and transmission of the virus.

Watermelon mosaic virus (WMV) is a member of the genus *Potyvirus* with a relatively broad host range, and it is a significant pathogen of the *Cucurbitaceae* family plants (squashes, pumpkins, zucchinis, watermelons, cucumbers, and melons) in temperate and Mediterranean regions (Ali *et al.*, 2006). WMV was also identified in Korean ginseng (*Panax ginseng*), which was designated as WMV-Insam (Jung *et al.*, 2013). WMV belongs to the bean common mosaic virus (BCMV) subgroup. The sequence identity of CP and the 3'-untranslated region (UTR) suggests that WMV and soybean mosaic virus (SMV) are two strains of the same species, although the biological and serological features of WMV and SMV differ (Frenkel *et al.*, 1989). There is evidence suggesting that WMV originated via interspecific recombination event between SMV-like and BCMV-like viruses within the P1 region (Desbiez and Lecoq, 2004). Moreover, multiple intraspecific recombinants among WMV strains have been identified; therefore, classification of these viruses solely based on a portion of the genome is difficult (Desbiez and Lecoq, 2008).

In this study, transcriptome data collected from ginseng in China were analyzed to identify RNA viruses that infect ginseng and a genomic sequence of a distinct WMV strain

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Abbreviations: BCMV = bean common mosaic virus; CLLV = calla lily latent virus; EAPV = East Asian passiflora virus; SMV = soybean mosaic virus; WMV = watermelon mosaic virus; WVMV = wisteria vein mosaic virus

was identified. Sequence and phylogenetic analyses were performed to determine the relationship of this strain among various strains in the BCMV subgroup.

Materials and Methods

Sequence analysis. Ginseng RNA-seq data (18 separate runs) were downloaded from the Sequence Read Archive (SRA) of the National Center for Biotechnology Information (NCBI; accession number PRJNA264354) (Wu *et al.*, 2015). Complete genome sequences of double-stranded (ds) RNA and ssRNA viruses were downloaded from the NCBI nucleotide database. BLASTN searches were performed to identify RNA virus-associated reads in the ginseng transcriptome data using the known RNA viral genome sequences as queries (Altschul *et al.*, 1997). SPAdes (version 3.7.1) was used to assemble collected virus reads into a contig (Bankevich *et al.*, 2012). Then, a BLASTN search was repeated using the contig as query to collect leftover virus reads and to extend the contig. The UPARSE agglomerative clustering method implemented in USEARCH was used to cluster viral sequences, with an identity threshold of 0.9 (Edgar, 2013). Multiple sequence alignment was performed with MUSCLE, and a phylogenetic tree was inferred using the neighbor-joining method in MEGA7 (Kumar *et al.*, 2016)

Results and Discussion

To identify novel RNA viruses that infect ginseng, 99.6 gigabases of RNA-seq data (18 separate runs) that were

obtained from ginseng roots, stems, and leaves collected in China were analyzed (Wu *et al.*, 2015). A contig of 10,046 bp was assembled from a RNA-seq run derived from ginseng root (SRA accession number: SRR1653717). A sequence similarity search against all known viral sequences showed that the contig was a full-length genome of a novel member of the genus *Potyvirus*. The closest virus was a WMV-Fr strain with 84% overall nucleotide sequence identity and 91% amino acid sequence identity. Because it was a distinct WMV identified from ginseng (*Panax ginseng*), the putative virus was designated as WMV-Pg.

The WMV-Pg genome (NCBI Acc. No. KX926428) has an ORF encoding a polyprotein of 3,218 amino acids with nine putative cleavage sites, which are predicted to produce 10 mature proteins (Fig. 1 and Supplementary Table S1). The cleavage sites producing P1-pro and HC-pro were concordant with the consensus sequences I-X-H-Y/S and Y-X-V-G/G, respectively, where X is any amino acid and “/” is the cleavage site. The other seven sites cleaved by NIa-pro have conserved motifs of V-X-X-[QE]/[SAG], which are in agreement with previously reported cleavage sites in other *Potyvirus* species (Adams *et al.*, 2005). An alternative ORF PIPO generated by polymerase slippage which would produce the 11th mature protein, P3N-PIPO, was identified.

The overall sequence identities between WMV-Pg and representative *Potyvirus* species of the BCMV subgroup are shown in Table 1 (amino acid) and Supplementary Table S2 (nucleotide). The nucleotide and amino acid sequence identities were 71–84% and 71–91%, respectively, and the

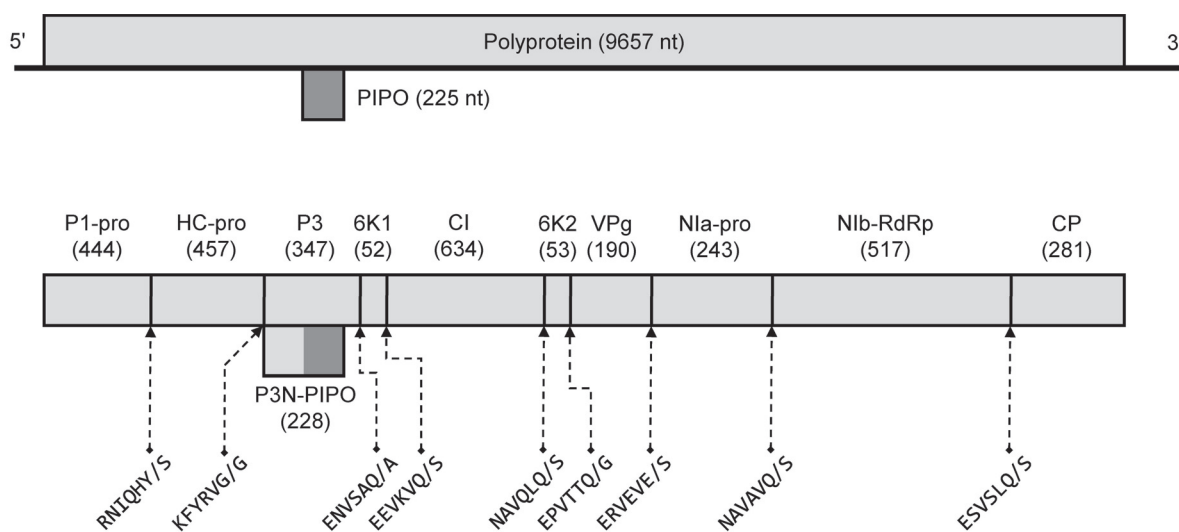


Fig. 1

Genomic structure of WMV-Pg

Open reading frames (top) and mature proteins (bottom) are depicted with their nt and aa sizes shown in parentheses. Predicted proteolytic cleavage sites are presented below.

Table 1. Amino acid sequence identities (%) between WMV-Pg and related *Potyvirus* species

Virus	Acc. No.	Overall	Overall, excluding P1-pro	P1-pro	HC-pro	P3	6K1	CI	6K2	VPg	N1a-pro	N1b-RdRp	CP
WMV-Fr	NC_006262	91	93	77	91	89	100	96	96	91	96	92	90
SMV	NC_002634	86	90	56*	90	80	92	92	94	89	95	92	84
WVMV	NC_007216	81	85	46*	85	72	88	91	83	88	89	86	76
CLLV	NC_021196	82	88	25*	88	81	86	92	93	89	92	91	80
EAPV	NC_007728	72	77	42*	78	58	77	82	74	76	83	82	74
FVY	NC_010954	73	76	38*	79	55	77	82	77	73	79	82	75
BCMV	NC_003397	71	73	52*	73	50	81	78	62	79	79	79	74
BCMNV	NC_004047	72	75	38*	76	48	85	81	71	78	77	83	73

*Partial alignment.

most closely related viruses were WMV-Fr, SMV, wisteria vein mosaic virus (WVMV), calla lily latent virus (CLLV), East Asian passiflora virus (EAPV), fritillary virus Y (FVY), BCMV, and bean common mosaic necrosis virus (BCMNV). The 5'-UTR of WMV-Pg showed sequence similarity to WMV-Fr and BCMV (see Supplementary Table S2), which supported the previous observation that WMV originated from an ancestral recombination event between a BCMV-like virus and a SMV-like virus that occurred within the P1 region (Desbiez and Lecoq, 2004).

For the phylogenetic analysis of WMV-Pg and related *Potyvirus* species, the whole genome sequences of WMV, SMV, CLLV, WVMV, and EAPV strains were identified

using a BLASTN search of the NCBI database. Collected sequences were clustered using the UPARSE agglomerative clustering method implemented in USEARCH, with an identity threshold of 0.9 (Edgar, 2013). When there were multiple sequences in a cluster, one representative sequence was selected (Supplementary Table S3). A multiple alignment of representative sequences was constructed and a phylogenetic tree was inferred using the neighbor-joining method (Fig. 2). In this tree, WMV-Pg did not form a cluster with any other strains, indicating that WMV-Pg is a distinct subtype. All previously reported WMVs, except WMV-KF274031, were clustered into one group represented by WMV-Fr, which is the virus most closely

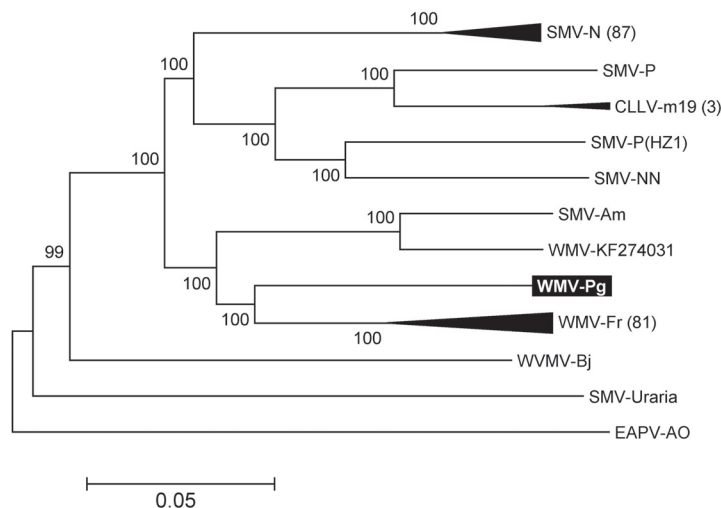


Fig. 2

Phylogenetic tree of WMV-Pg and related representative *Potyvirus* isolates

The isolates were clustered based on sequence similarity. The SMV-N, CLLV-m19, and WMV-Fr clusters contain 87, 3, and 81 sequences, respectively. Numbers at the nodes are the bootstrap values (percentages) of 1,000 replicates. The EAPV-AO strain was used as an outgroup. See Supplementary Table S3 for the list of sequences analyzed.

related to WMV-Pg. The WMV-Fr cluster contained 81 strains and isolates collected from various plant species in wide geographic regions. The strains were isolated from various *Cucurbitaceae* species, *Dendrobium anosmum* (orchid), and *Minthostachys verticillata* (peperina) in Europe (France and Italy), America (USA, Argentina, Venezuela, and Chile) and Asia (Turkey, Iran, Pakistan, India, China, and South Korea). Interestingly, there were at least 23 WMV isolates collected from *Panax ginseng* in South Korea (see Supplementary Table S3). However, these isolates were clustered with WMV-Fr but not with WMV-Pg. Therefore, we conclude that WMV-Pg is a distinct strain that may infect ginseng.

The phylogenetic relationships among WMV/SMV-related viruses suggest that a taxonomic reorganization of these viruses should be considered. For example, SMV-Am formed a clade with WMV-KF274031, which, in turn, was in a sister clade of the WMV-Pg/WMV-Fr clade; the CLLV-m19 cluster was in a clade embedded within the SMVs; and SMV-Uraria was more distant from the WMV/SMV group than WVMV-Bj. Therefore, a systematic regrouping of these viruses is required.

In conclusion, the genome sequence of WMV-Pg was identified in an analysis of *Panax ginseng* root RNA-seq data. We have showed that, WMV-Pg is a novel distinct subtype of the WMV/SMV group of the genus *Potyvirus* of the family *Potyviridae*.

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Supplementary information is available in the online version of the paper.

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Supplementary information

Genome sequence of a distinct watermelon mosaic virus identified from ginseng (*Panax ginseng*) transcriptome

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Supplementary Table S1. Genomic features of WMV-Pg

Feature	Mature protein	Genome position	Protein position
5'-UTR		1-116	
polyprotein		117-9773	1-3218
	P1-pro	117-1448	1-444
	HC-pro	1449-2819	445-901
	P3	2820-3860	902-1248
	6K1	3861-4016	1249-1300
	CI	4017-5918	1301-1934
	6K2	5919-6077	1935-1987
	VPg	6078-6647	1988-2177
	NIa-pro	6648-7376	2178-2420
	NIb-RdRp	7377-8927	2421-2937
	CP	8928-9770	2938-3218
PIPO		3278-3502*	1-65*
3'-UTR		9774-10046	

*Only the PIPO ORF is shown. The mature protein P3N-PIPO is 227 amino acids long.

Supplementary Table S2. Nucleotide sequence identities (%) between WMV-Pg and related *Potyvirus* species

Virus	Acc. No.	Overall	Overall excluding 5'-UTR & P1-pro												
				5'-UTR	P1-pro	HC-pro	P3	6K1	CI	6K2	VPg	NIa-pro	NIb-RdRp	CP	3'-UTR
WMV-Fr	NC_006262	84	85	81*	79	84	86	86	85	83	85	86	84	86	88
SMV	NC_002634	80	81	-	75*	81	80	84	82	87	81	82	81	85	77
WVMV	NC_007216	77	77	-	70*	76	75	84	79	82	79	78	77	81	76
CLLV	NC_021196	81	81	-	-	80	80	82	81	82	82	82	81	85	78
EAPV	NC_007728	73	73	-	-	71	71	78	74	79	74	74	75	76	-
FVY	NC_010954	73	73	-	-	72	69	-	72	78	75	73	75	74	71
BCMNV	NC_003397	71	71	71*	74*	73	67	75	72	79	77	73	73	75	69
BCMNV	NC_004047	73	73	-	-	72	67	76	72	83	74	74	74	74	78

*Partial alignment.

Supplementary Table S3. List of the Potyvirus species used for the phylogenetic analysis

A. List of the representative viruses

Label	Acc. No.	Species	Strain	Isolate	Host	Country
SMV-N	NC_002634	SMV	N	-	-	-
SMV-P	AJ507388	SMV	P	-	Pinellia ternata	China:Zhejiang
CLLV-m19	NC_021196	CLLV	m19	-	Calla lily	Taiwan
SMV-P(HZ1)	AJ628750	SMV	P	HZ1	Pinellia ternata	China:Zhejiang: Hangzhou
SMV-NN	KF982784	SMV	-	NN	Pinellia pedatisecta	China
SMV-Am	KC845322	SMV	-	Am	Atractylodes macrocephala	China
WMV-KF274031	KF274031	WMV	-	-	Ailanthus altissima	China
WMV-Fr	NC_006262	WMV	WMV-Fr	-	-	-
WVMV-Bj	NC_007216	WVMV	-	Beijing	Wisteria	China
SMV-Uraria	LC037232	SMV	Uraria	-	Uraria crinita	Taiwan:Pingtung
EAPV-AO	NC_007728	EAPV	AO	AO	-	Japan:Kagoshima, Amami-O-shima

B. List of the 87 viruses of the "SMV-N" cluster

No.	Acc. No.	Species	Strain	Isolate	Host	Country
1	AB100442	SMV	-	Aa	-	-
2	AB100443	SMV	-	Aa15-M2	-	-
3	AF241739	SMV	G7	-	-	-
4	AJ310200	SMV	Huanghuai strain 5	SAAS	soybean	China:Shandong
5	AJ312439	SMV	severe	Hangzhou	soybean	China:Zhejiang
6	AJ619757	SMV	-	CN18	-	South Korea:Daejeon
7	AY216010	SMV	G7	-	-	-
8	AY216987	SMV	G7d	-	-	-
9	AY294044	SMV	G5	-	Glycine max	South Korea
10	AY294045	SMV	G7H	-	Glycine max	South Korea
11	NC_002634	SMV	N	-	-	-
12	EU871724	SMV	-	L	Glycine max	Canada
13	EU871725	SMV	-	L-RB	Glycine max	Canada
14	FJ376388	SMV	G5H	-	Glycine max	South Korea
15	FJ548849	SMV	-	WS200	wild soybean	South Korea
16	FJ640954	SMV	-	WS32	wild soybean	South Korea
17	FJ640955	SMV	-	WS37	wild soybean	South Korea
18	FJ640956	SMV	-	WS84	wild soybean	South Korea
19	FJ640957	SMV	-	WS101	wild soybean	South Korea
20	FJ640958	SMV	-	WS105	wild soybean	South Korea
21	FJ640959	SMV	-	WS109	wild soybean	South Korea
22	FJ640960	SMV	-	WS110	wild soybean	South Korea
23	FJ640961	SMV	-	WS116	wild soybean	South Korea
24	FJ640962	SMV	-	WS117	wild soybean	South Korea
25	FJ640963	SMV	-	WS128	wild soybean	South Korea
26	FJ640964	SMV	-	WS132	wild soybean	South Korea
27	FJ640965	SMV	-	WS135	wild soybean	South Korea
28	FJ640966	SMV	-	WS144	wild soybean	South Korea
29	FJ640967	SMV	-	WS145	wild soybean	South Korea
30	FJ640968	SMV	-	WS149	wild soybean	South Korea
31	FJ640969	SMV	-	WS151	wild soybean	South Korea
32	FJ640970	SMV	-	WS155	wild soybean	South Korea
33	FJ640971	SMV	-	WS156	wild soybean	South Korea
34	FJ640972	SMV	-	WS160	wild soybean	South Korea

B. List of the 87 viruses of the "SMV-N" cluster (continued)

No.	Acc. No.	Species	Strain	Isolate	Host	Country
35	FJ640973	SMV	-	WS162	wild soybean	South Korea
36	FJ640974	SMV	-	WS202	wild soybean	South Korea
37	FJ640975	SMV	-	WS205	wild soybean	South Korea
38	FJ640976	SMV	-	WS209	wild soybean	South Korea
39	FJ640977	SMV	G1	-	Glycine max	South Korea
40	FJ640978	SMV	G3	-	Glycine max	South Korea
41	FJ640979	SMV	G4	-	Glycine max	South Korea
42	FJ640980	SMV	G6	-	Glycine max	South Korea
43	FJ640981	SMV	G6H	-	Glycine max	South Korea
44	FJ640982	SMV	G7A	-	Glycine max	South Korea
45	FJ807700	SMV	G7H	-	Glycine max	South Korea
46	FJ807701	SMV	G5H	-	Glycine max	South Korea
47	GU015011	SMV	-	413	Glycine max (soybean)	USA: Illinois
48	HM590054	SMV	-	Sc6	soybean	China
49	HM590055	SMV	-	Apr-69	soybean	China
50	HQ166265	SMV	-	NP-C-L	Glycine max cv. Williams 82	Canada
51	HQ166266	SMV	-	NP-L	Glycine max cv. Williams 82	Canada
52	HQ396725	SMV	4547/CHN/2004	-	soybean	China
53	HQ845735	SMV	TNP	-	soybean; genotype V94-5152 (Rsv4)	USA
54	HQ845736	SMV	KY	-	soybean; genotype V94-5152 (Rsv4)	USA
55	JF833013	SMV	-	SC3	Glycine max	China
56	JF833014	SMV	-	Feb-02	Glycine max	China
57	JF833015	SMV	-	Jan-67	Glycine max	China
58	JN416770	SMV	-	Rsv4-RB3	Glycine max	Canada
59	KC845321	SMV	-	SX	soybean	China
60	KF135488	SMV	-	Ar13	soybean	Iran
61	KF135489	SMV	-	Ar33	soybean	Iran
62	KF135490	SMV	-	Lo3	soybean	Iran
63	KF135491	SMV	-	Go11	soybean	Iran
64	KF297335	SMV	-	Ar33	soybean	Iran
65	KM979229	SMV	-	India	soybean	India
66	KP710861	SMV	-	BYX006	Glycine max	China: Nanchang city
67	KP710862	SMV	-	HGT005	Glycine max	China: Nanchang city
68	KP710863	SMV	-	HGT008	Glycine max	China: Nanchang city
69	KP710864	SMV	-	HGT009	Glycine max	China: Nanchang city
70	KP710865	SMV	-	LJZ002	Glycine max	China: Nanchang city
71	KP710866	SMV	-	LJZ010	Glycine max	China: Nanchang city
72	KP710867	SMV	-	SC6-N	Glycine max	China
73	KP710868	SMV	-	SC7-N	Glycine max	China
74	KP710869	SMV	-	NE-N1	Glycine max	China: Northeast area
75	KP710870	SMV	-	SX-Z	Glycine max	China: Yangling city
76	KP710871	SMV	-	XFQ001	Glycine max	China: Harbin city
77	KP710872	SMV	-	XFQ005	Glycine max	China: Harbin city
78	KP710873	SMV	-	XFQ008	Glycine max	China: Harbin city
79	KP710874	SMV	-	XFQ010	Glycine max	China: Harbin city
80	KP710875	SMV	-	XFQ012	Glycine max	China: Harbin city
81	KP710876	SMV	-	XFQ014	Glycine max	China: Harbin city
82	KP710877	SMV	-	XFQ018	Glycine max	China: Harbin city

B. List of the 87 viruses of the “SMV-N” cluster (continued)

No.	Acc. No.	Species	Strain	Isolate	Host	Country
83	KP710878	SMV	–	XFQ020	Glycine max	China: Harbin city
84	KR024718	SMV	–	JAAS-6	soybean	China: Nanjing
85	KR065437	SMV	–	HB-RS	Glycine max	China: Hebei
86	KT285170	SMV	–	Jan-78	Glycine max	China
87	S42280	SMV	G2	–	–	–

C. List of the 3 viruses of the “CLLV-m19” cluster

No.	Acc. No.	Species	Strain	Isolate	Host	Country
1	NC_021196	CLLV	m19	-	Calla lily	Taiwan
2	EF105298	CLLV	BM19	-	Calla lily	Taiwan
3	EF105299	CLLV	E49	-	Calla lily	Taiwan

D. List of the 81 viruses of the “WMV-Fr” cluster

No.	Acc. No.	Species	Strain	Isolate	Host	Country
1	AB218280	WMV	WMV-Pk	–	–	Pakistan
2	AB369278	WMV	Watermelon	–	–	South Korea
3	NC_006262	WMV	WMV-Fr	–	–	–
4	DQ399708	WMV	WMV-CHN	–	watermelon	China
5	EU660578	WMV	–	FMF00-LL2	–	France
6	EU660579	WMV	–	TURK91	–	Turkey
7	EU660580	WMV	–	CHI87-620	–	Chile
8	EU660581	WMV	–	FMF00-LL1	–	France
9	EU660582	WMV	–	CHI02-481	–	Chile
10	EU660583	WMV	–	FMF03-141	–	France
11	EU660584	WMV	–	IR02-54	–	Iran
12	EU660585	WMV	–	C05-270	–	France
13	EU660586	WMV	–	FBR04-37	–	France
14	EU660587	WMV	–	C06-188	–	France
15	EU660588	WMV	–	C06-666	–	France
16	EU660589	WMV	–	C05-337	–	France
17	EU660590	WMV	–	ITA00-G	–	Italy
18	FJ823122	WMV	–	Lecce	Citrullus lanatus	Italy: Lecce
19	HQ384216	WMV	Dendrobium	–	Dendrobium anos- mum (orchid)	USA
20	JF273458	WMV	–	C05-463	zucchini	France: Garons, Gard
21	JF273459	WMV	–	C05-464	zucchini	France: Garons, Gard
22	JF273460	WMV	–	C05-465	zucchini	France: Garons, Gard
23	JF273461	WMV	–	C07-349	melon	France: Saint Chaptes, Gard
24	JF273462	WMV	–	C06-526	melon	France: Bourdic, Gard
25	JF273463	WMV	–	C06-257	melon	France: Saint Chaptes, Gard
26	JF273464	WMV	–	C07-014	melon	France: Aubignan, Vaucluse
27	JF273465	WMV	–	A08-160	zucchini	France: Aubignan, Vaucluse
28	JF273466	WMV	–	A08-170	zucchini	France: Aubignan, Vaucluse

D. List of the 81 viruses of the “WMV-Fr” cluster (continued)

No.	Acc. No.	Species	Strain	Isolate	Host	Country
29	JF273467	WMV	-	Cg09-640	zucchini	France: Montfavet, Vaucluse
30	JF273468	WMV	-	C07-284	zucchini	France: La Tour d'Aigues, Vaucluse
31	JF273469	WMV	-	C04-106	melon	France: Maillane, Bouches-du-Rhone
32	JX079685	WMV	WMV-ShanXi	-	watermelon	China
33	KC292915	WMV	-	VE10-099	Cucumis anguria L.	Venezuela
34	KM597070	WMV	-	RKG	watermelon	India
35	KM597071	WMV	-	RKG2	watermelon	India
36	KP100058	WMV	-	SangJu6-1	Panax ginseng	South Korea
37	KP164988	WMV	-	WMV 1 SDE FF	-	Argentina
38	KT992068	WMV	-	Bonghwa7-2_2014	Panax ginseng C.A. Meyer	South Korea
39	KT992069	WMV	-	Buan2_2014	Citrullus vulgaris	South Korea
40	KT992070	WMV	-	Buan4-1_2013	Panax ginseng C.A. Meyer	South Korea
41	KT992071	WMV	-	Cheongsong5_2013	Panax ginseng C.A. Meyer	South Korea
42	KT992072	WMV	-	Cungju10-1_2014	Panax ginseng C.A. Meyer	South Korea
43	KT992073	WMV	-	Eumseong1-5_2014	Panax ginseng C.A. Meyer	South Korea
44	KT992074	WMV	-	Eumseong2-10_2014	Panax ginseng C.A. Meyer	South Korea
45	KT992075	WMV	-	Hongseong1_2013	Panax ginseng C.A. Meyer	South Korea
46	KT992076	WMV	-	Naju2-1_2013	Panax ginseng C.A. Meyer	South Korea
47	KT992077	WMV	-	Naju2-2_2013	Panax ginseng C.A. Meyer	South Korea
48	KT992078	WMV	-	Sangju2_2014	Panax ginseng C.A. Meyer	South Korea
49	KT992079	WMV	-	Sangju3_2013	Panax ginseng C.A. Meyer	South Korea
50	KT992080	WMV	-	Uiseong3-5(sq)_2013	Cucurbita pepo	South Korea
51	KT992081	WMV	-	Yeongam2_2013	Panax ginseng C.A. Meyer	South Korea
52	KT992082	WMV	-	Yeongam4-2_2014	Panax ginseng C.A. Meyer	South Korea
53	KT992083	WMV	-	Yeongju1-2_2013	Panax ginseng C.A. Meyer	South Korea
54	KT992084	WMV	-	Yeongju2-1_2014	Panax ginseng C.A. Meyer	South Korea
55	KT992085	WMV	-	Yeongju2-3_2013	Panax ginseng C.A. Meyer	South Korea
56	KT992086	WMV	-	Yeongju6-1_2013	Panax ginseng C.A. Meyer	South Korea
57	KT992087	WMV	-	Yeongju7-1_2014	Panax ginseng C.A. Meyer	South Korea
58	KT992088	WMV	-	Yeongju7-2_2013	Panax ginseng C.A. Meyer	South Korea
59	KT992089	WMV	-	Yeongju7-2(cm)_2013	Malva verticillata	South Korea
60	KT992090	WMV	-	Yeongju7-3_2013	Panax ginseng C.A. Meyer	South Korea

D. List of the 81 viruses of the "WMV-Fr" cluster (continued)

No.	Acc. No.	Species	Strain	Isolate	Host	Country
61	KT992091	WMV	-	Yeongju7-5(sq)_2013	Cucurbita pepo	South Korea
62	KT992092	WMV	-	Yeongju9_2014	Panax ginseng C.A. Meyer	South Korea
63	KT992093	WMV	-	Yeongyang8-1_2013	Panax ginseng C.A. Meyer	South Korea
64	KU240094	WMV	-	Buan2-1_2012	-	South Korea
65	KU240095	WMV	-	Gimcheon1_2012	-	South Korea
66	KU240096	WMV	-	Gochang2_2012	-	South Korea
67	KU240097	WMV	-	Gumi4_2012	-	South Korea
68	KU240098	WMV	-	Jeongeup1-1_2012	-	South Korea
69	KU240099	WMV	-	Jeongeup_3-1_2012	-	South Korea
70	KU240100	WMV	-	Naju3-1_2012	-	South Korea
71	KU240101	WMV	-	Pungjeonglee1_2012	-	South Korea
72	KU240102	WMV	-	Pungjeonglee3_2012	-	South Korea
73	KU240103	WMV	-	Sangju2_2012	-	South Korea
74	KU240104	WMV	-	Sangju6-1_2012	-	South Korea
75	KU240105	WMV	-	Sangju6_2012	-	South Korea
76	KU240106	WMV	-	Sangju7-1_2012	-	South Korea
77	KU240107	WMV	-	Yeongam2-1_2012	-	South Korea
78	KU240108	WMV	-	Yeongju5_2012	-	South Korea
79	KU240109	WMV	-	Yeongju9_2012	-	South Korea
80	KU240110	WMV	-	Yeongyang3_2012	-	South Korea
81	KU246036	WMV	-	TX29	watermelon	USA