MTR Ⅰ   MTR Ⅱ   MTR Ⅲ

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PhMV      50 ILSFGIPVSGLGTDPHPHPIHKTIEIHLLFTHW(29)HLLNYRLTSADTCRYPET(74)HHAGSYDQPLDALSWLKIHSIPHP
ChiYMV    50 LISSGIPVSGFGTTPHPHAVHKTIETFLLFNHW(29)ELINYRLTPADTVRYPTT(74)HHAGSYNQPLQALSWLKVNSISHP
OyMV      50 LLAAGIPTSGFGCNPHPHAVHKVIETFLLFNHW(29)ELVNYRLTAADSVRYPST(74)HHAGSYDQPLDAISWLKLNSIHSP
KyMV      50 LLKSGIPINSFGSSPHPHAHKTLETHLLFTHW(29)HLHNYRLTPTDSVRFPST(74)HSAGSYNQPITALSWLKINSILSP
TyMV      50 LNSYGIPTSGLGTSHHPHAAHKTIETFLLCTHW(29)ELKNYRLHPNDSTRYPFT(74)HEAGSYNQPSDAHSWLRINSIRLG
AsAV      50 LLQAGIQTSGLGTTPHPHPVHKVLETNLLFNHW(29)ELLNYRVTPNDSVRYPTT(74)HYAGSYNQPLSAIQWLKISSIHHP
GFKV     163 LNQAGIPATSYGHQSHPHPIHKTIETHLLHEHW(36)HLLNPILTARDADRYTHL(76)NPSSSYTQPLTATQWLTTSSITAG
SsMTV1   189 LGSAGVPTPAYPTMKHAHPGHKRLENYLYQVAW(30)ELVNCDLTHKDLSRYGPK(75)DPAGSYRQPLDAHKLLNPSRVSVV
              :  *:  .   *.*.**:*:*  . . .*  . *   * *  .** **  * . *
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HEL Ⅰ   HEL Ⅱ   HEL Ⅲ   HEL Ⅳ   HEL Ⅴ

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PhMV    1059 ISGFAGCGKTHPIQHLL(49)LVIDECYKCPRYH(10)LLGDPLQGEYHS(20)IDCYCWWTYRLPIKTA(43)HAITISSSQGGTYDEINT
ChiMV    985 IAGFAGCGKTLPVQHLL(48)LVIDEIYKLPRGY(10)ILGDPLQGEYHS(20)IDCYCFWSYRIPTSFA(43)HAITISSSQGTTFQEAHT
TyMV     974 FAGFAGCGKTYPIQQLL(48)LVIDEIYKMPRGY(10)ILGDPLQGEYHS(20)IDMYCWWSYRIPQCIA(43)RSCTISSSQGLTFCDPAI
OyMV     897 IAGFPGCGKSHPIQKLL(48)LVVDEIYKLPRGY(10)MLGDPLQGEYHS(20)IDCYCWWTYRCPKAVA(43)HALTISSSQGMTYSDPVT
KyMV    1000 LAGFAGCGKPKLQSLL(48)LVIDEIYKLPRGY(10)ILGDPLQGEYHS(20)IDHYCWWTYRVPSHIA(47)PATTISASQGVTHHNRVT
AsAV     934 IAGFAGCGKTHPLQHLL(48)LVIDEIYKLPRGY(10)LLGDPLQGEYHS(20)IDHYCWWTYRVPSHIS(47)PSCTISSSQGMTFRKHVT
GFKV    1046 IAGFAGCGKSYPIQQLL(48)LVIDEVYKLPRGY(10)ILGDPLQGSYNP(20)IDFYCLWTRRLPRLVA(43)RAITYAASQGSTYPAPVH
SsMTV1  1118 VLGAPGCGKSAPLQDFL(51)IVIDEISLFPPGY(10)ILGDHCQCRFHS(20)GSQYLLQFHRAPQLLA(43)KAFTFQQAQSRSFPRVQI
              * .****:.*:* :*   :*.**    *  :   :*** *  ::.    .  *    *  * :   :*  :*.
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RdRP Ⅰ   RdRP Ⅱ   RdRP Ⅲ

```
ChiMV   1530 TSVRIFAKAQHKVNDSSIFSNWKACQTLALMHDYIILVLGPVKKYQRIYDQRERPPQIYYHCGHTPTQLSQWCSQHLQS
OyMV    1418 TVVRIFAKSQHKVNDGSIFGSWKACQTLALMHDFVILTLGPVKKYQRIIDHYDRPNFIYTHCGKTPSELSAWSHSFLKG
AsAV    1457 TAVKIFAKSQHKVNDGSIFGPWKACQTLALMHDFVILSLGPVKKYQRLFDQADRPSHLYTHCGKTPQDLSLWCSAHLSH
KyMV    1522 TAVKIFAKSQHKVNDASIFGNWKACQTLALMHDFVILSLGPVKKYQRIFDALDRPPHLYTHCGKSPADLSAWCQTHLTG
TyMV    1492 TTVKIFAKAQHKVNDGSIFGSWKACQTLALMHDYVILVLGPVKKYQRIFDNADRPPNIYSHCGKTPNQLRDWCQEHLTH
PhMV    1582 TSVRIFAKAQHKVNDGSIFSSWKACQTLALMHDYIILTLGPVKKYQRIFDMKDRPPHLYLHCGHTPCQLSAWCTEHFRP
GFKV    1603 TFVRIFSKTQHKVNENSLFTSWKACQTLALMHDYLILVLGPVKKYQRILDSRDRPAHLYIHAGQTPHQLSEWCQNHLTP
SsMTV1  1618 NLVSHFLKSQLKGKMEAFLMPAKPGQTIATCHDLVLILLGAMNRYIRRMEHRDRPKNIFLHCGTSNEDLRDWTIEHWKD
              . *  * * *:*:  :  ::   *. **:*  **::: **.:::* *   :** :: *.*:  :  :*  *   .
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RdRP Ⅳ   RdRP Ⅴ   RdRP Ⅵ

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ChiMV   1609 PV-ATTNDYTAFDQSQHGEAVVFECFK(22)T-QFGPLTCMRLTGEPGTYDDNSDYNLAVIYSQYAIKS-EAIMISGDDSVIDG
OyMV    1497 DA-YICNDYTSFDQSQHGEAVIFESLK(22)T-QFGPLTCMRLTGEPGTYDDNTDYNLAVIFSQYVISD-HPIMVSGDDSVICG
AsAV    1536 KT-KVTNDYTAFDQSQHGESVILEALK(22)T-QFGPLTCMRLTGEPGTYDDNTDYNIAVLYSQYNLQN-TPVMVSGDDSLIDS
KyMV    1599 QI-KLTNDYTAFDQSQHGESVILEALK(22)T-QFGPLTCMRLTGEPGTYDDNSDYNLAVIHSQFDMKD-IPVMVSGDDSLIDR
TyMV    1571 STPKIANDYTAFDQSQHGESVVLEALK(22)T-QFGPLTCMRLTGEPGTYDDNTDYNLAVIYSQYDVGS-CPIMVSGDDSLIDH
PhMV    1659 TI-CTTNDYTAFDQSQHGEAVVWKCLK(22)T-QFGPLTCMRITGEPGTYDDNTDYNLAVIYSQYTMQN-LPLLVSGDDSVIVG
GFKV    1682 SV-HLANDYTAFDQSQHGEAVVLEAWK(22)C-QFGPLTCMRITGEPGTYDDNTDYNLAILYTQYLLHR-TPVLVSGDDSLVDR
SsMTV1  1697 IR-STTNDYTAFDSSQKGESVAFAERH(22)SDIIGEKDLGRDTGEPGTYDDNCRYNLAVIACQYIVPRGLPILIGGDDSALNA
              ****:**.**:**:*        :     : *    * * *********  **:*:: *:  :   :  .::::.****   :
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Figure S1. Multiple alignment of three conserved domains (Mtr, Hel, and RdRp) of Sclerotinia sclerotiorum mycotymovirus 1 (SsMTV1/SZ-150) with corresponding regions in the referenced members of the order *Tymovirales*. The positions of the motifs are indicated by lines above the sequences with numbers from I to VI. Identical residues are shaded and indicated by asterisks; conserved and semi-conserved amino acid residues are indicated by colons and dots, respectively. Numbers in square brackets correspond to the number of amino acid residues separating the motifs. ChiYMV: Chiltepin yellow mosaic virus, OYMV: Ononis yellow mosaic virus, AsAV: Asclepias asymptomatic virus, KyMV: Kennedya yellow mosaic virus, TYMV: Turnip yellow mosaic virus, PhyMV: Physalis mottle virus, GFkV: Grapevine fleck virus.

Table S1 The information of all selected viruses used for phylogenetic analysis

Virus Family	Virus name	Abbreviation	Accession Numbe
Chrysovidae	Colletotrichum gloeosporioides chrysovirus 1	CgCV1	KT581957
	Raphanus sativus chrysovirus 1	RsCV1	JQ045335
	Botryosphaeria dothidea chrysovirus 1	BdCV1	KF688736
	Fusarium graminearum dsRNA mycovirus-2	FgV2	HQ343295
	Magnaporthe oryzae chrysovirus 1-A	MoCV-1A	AB560761
	Macrophomina phaseolina chrysovirus 1	MpCV1	KP900886

	Verticillium dahliae chrysovirus 1	VdCV1	NC_038784
Totiviridae	Saccharomyces cerevisiae virus L-A	ScV-L-A	J04692
	Saccharomyces cerevisiae virus L-BC	ScV-L-BC	U01060
	Magnaporthe oryzae virus 2	MoV2	AB300379
	Gremmeniella abietina RNA virus L1	GaRV-L1	AF337175
	Botryotinia fuckeliana totivirus 1	BfTV1	AM491608
Partitiviridae	Helicobasidium mompa partitivirus V1-1	HmV-V1-1	AB110979
	Rosellinia necatrix virus 1	RnV1	AB113347
	Rhizoctonia solani virus 717	RhsV-717	AF133290
	Rosellinia necatrix partitivirus 2	RnPV2	NC_020234
	Rhizoctonia solani dsRNA virus 2	RsPV2	NC_023684
	Sclerotinia sclerotiorum partitivirus S	SsPV-S	NC_013014
	Sclerotinia sclerotiorum partitivirus 1	SsPV1	JX297511
Reoviridae	Cryphonectria parasitica mycoreovirus 1	CpMYRV1	NC_010743
	Rosellinia necatrix mycoreovirus 3	RnMYRV3	NC_007535
	Sclerotinia sclerotiorum mycoreovirus 3	SsMYRV4	NC_030158
Megabirnaviridae	Pleosporales megabirnavirus 1	PMBV1	KT601119

	Rosellinia necatrix megabirnavirus 1	RnMBV1	NC_013462
	Sclerotinia sclerotiorum megabirnavirus 1	SsMBV1	NC_027221
	Rosellinia necatrix megabirnavirus 2	RnMBV2	NC_029125
Botybirnaviridae	Sclerotinia sclerotiorum botybirnavirus 1	SsBV1	NC_027138
	Sclerotinia sclerotiorum botybirnavirus 2	SsBV2	KT962972
	Bipolaris maydis botybirnavirus 1	BmBRV1	MF034087
	Alternatra botybirnavirus 1	ABRV1	KX784491
	Soybean leaf-associated botybirnavirus 1	SlaBRV1	KT598241
	Botrytis porri botybirnavirus 1	BpBV1	NC_017990
Unclassified	Fusarium graminearum virus DK21	FgV-DK21	AY533037
	Sclerotinia sclerotiorum RNA virus L	SsRV-L	EU779934
	Sclerophthora macrospora virus A	SmV-A	AB083060

Table S2 Primer pairs used in this study.

Primer name	Primer sequence (5′–3′)	Application	Product size (bp)
actin-qF2	GAGCTGTTTTCCCTTCCATTGTC	Used as an internal control	146
actin-qR4	GACGACACCGTGCTCGATTGG		
SsHV1-F	CCAAAACAACCCTGTCGCC	Detection for SsHV1	252
SsHV1-R	CAACAAACCTGTCAGCACCC		
SsBV3-F	GGGTGACGACGGATGGGTA	Detection for SsBV3	462
SsBV3-R	CACAGGCAGCTTCGCTACTCT		
SatH-F	AGAAATTGTTATGGCAAGCT	Detection for SatH	1271
SatH-R	GGGTTGATATATCCGATAAG		
SsMTV1-F	ATTGGTCAAGACTCCGTGAC	Detection for SsMTV1	1020
SsMTV1-R	GGAAGCATGCGCCGCTTGGT		
random dN6	CGATCGATCATGATGCAATGCNNNNNN	To obtain the viral cDNA	
Oligo (dT)18	d(TTTTTTTTTTTTTTTTTT)		
5'Long primer	CTAATACGACTCACTATAGGGCAAGCAGTGGTATCAACGCAGAGT	Termini determination of SsMTV1	
RACE-OLIGO:	GCATTGCATCATGATCGATCGAATTCTTTAGTGAGGGTTAATTGCC-(NH2)		
O5RACE -1	GGCAATTAACCCTCACTAAAG		
O5RACE -2	TCACTAAAGAATTCGATCGATC		
O5RACE -3	CGATCGATCATGATGCAATGC		
SsMTV1_5'1	GAAAGGGTCGTAACGGTATTCG		
SsMTV1_5'2	CTGTGGAGATAGCCATCGTTCA		
C1-F	GACGAAATTTCTCTCTTTCCCCCG	To fill the gap of SsMTV1	
C1-R	TATTATACTgTCTAgTTCCgAC		

C2-F	GTAGAACTCTCTGACACCTCAA		
C2-R	GGGCCGCGATCTGACCATGGCAGT		
SsBV3_L1-1F	GCAAATAAAAGAGCTGCCTT	To determine the genome of SsBV3-L1-dsRNA	
SsBV3_L1-1R	ATCTTCTTCTAATACCACCT		
SsBV3_L1-2F	CACCACAAGCGCAGTGACGA		
SsBV3_L1-2R	ATCTTCTTCTAATACCACCT		
SsBV3_L1-3F	TGAGTCAGAGATGGAGGAGA		
SsBV3_L1-3R	CAGGTAGCGTGATCATGTTG		
SsBV3_L1-4F	TGACAGCAGAAGGATTCAAC		
SsBV3_L1-4R	TCTAACCTGTTCTTGCCCAA		
SsBV3_L1-5F	GCAGAAAGTAGCGCAGGAGA		
SsBV3_L1-5R	AAACTCACCTTTCGCCCACT		
SsBV3_L1-6F	GATCAAAGAAGGGATCTTGA		
SsBV3_L1-6R	CTACCCATCCGTCGTCACCC		
SsBV3_L1-7F	AACCTCACGTACCACCACAT		
SsBV3_L1-7R	GCTATCTATTCACTTCTCCC		
SsBV3_L2-1F	GCAAATAAAAGAGCTGCCTA	To determine the genome of SsBV3-L2-dsRNA	
SsBV3_L2-1R	GGCATCTTGTTTGGTTTGAA		
SsBV3_L2-2F	TGTGCATCGCTATCGCGCGC		
SsBV3_L2-2R	AAGTGAATTGCACAACGGTA		
SsBV3_L2-3F	GTTCAGATACAATAAGACAG		
SsBV3_L2-3R	GCAAATCGGTCTGCACAGTG		
SsBV3_L2-4F	CRAAGGCTCGCCCACACGGG		
SsBV3_L2-4R	GGTGTCTTTGCGGGAAAGAG		
SsBV3_L2-5F	TGGCCGAGTTCGGTGAAAGA		

SsBV3_L2-5R	AGCTTCTCTTCTGTACCCGC		
SsBV3_L2-6F	AAAAGGCACAGGAGAGGGAG		
SsBV3_L2-6R	GCTCTGTAATTACTCCTTCC		