

Supplementary Material

Mild to Virulent: Coat Protein Mutations Restore Mosaic Symptom Induction in a Korean PepMV Isolate

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Table S1: Primers used for PepMV analysis in this study

Purpose	Primer	Sequence (5'-3')	Target size
Detection	PepMV-det-F	CCCCAGTTTGAAATGGAAAGATC	720 bp
	PepMV-det-R	CTAGGAGTCAGACCTGGCAT	
Infectious clone construction	PepMV-F1-F	<u>CATTTCATTGGAGAGGGAAAACAAAACAT</u> AACACTTAATATC	3225 bp
	PepMV-F1-R	<u>AGTGTCTCATCTTTCGCCTG</u>	
	PepMV-F2-F	<u>CAGGCGAAAGATGAGACACT</u>	3193 bp
	PepMV-F2-R	<u>ATGCCATGCCGACCCTTTTTATTTAGTAG</u> ATTGAGATACTAAGGG	
Quantitative	qRT-F	ACCCCTGTCAGTGCACTTAC	190 bp
	qRT-R	ATGTGTTTCAGAGGGGTCCAC	

Table S2: Full-length genome accession numbers of PepMV isolates used for phylogenetic analysis.
The table includes strain designations (EU, CH2, LP, PES, and US1), and GenBank® accession numbers.
ToMMV (KP202857) as outgroup.

Strains	GenBank Accession number
EU (European)	JN133846
	AJ438767
	MN395046
	KJ018164
	AF484251
	OR733205
	FJ457098
	JQ314459
	JQ314461
LP (Peruvian)	AJ606361
	MF422616
	MF422614
	MF422612
PES (new Peruvian)	HG313805
	HG313806
	HG313807
US1 (United States 1)	LC656470
	AY509926
	FJ940225
	JQ314462
	KF734961
CH2 (Chilean 2)	LC656469
	DQ000985
	OR733204
	JX417070
	HQ650559
	JN835466
	MK133092

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Table S2: Primer sets used to construct site-mutagenesis of PepMV CP

Mutated residue	Primer	Sequence (5'-3')
5 (S to P)	CP-5-F	GGAAAACCAAccgGCAGCATCAAAC
	CP-5-R	ATAGTTGAGTTAAATTGTTGAATTTAAC
6 (A to T)	CP-6-F	AAACCAATCTaccGCATCAAACACATC
	CP-6-R	TCCATAGTTGAGTTAAATTGTTTG
10 (T to P)	CP-10-F	AGCATCAAACcgcTCAGACGCAC
	CP-10-R	GCAGATTGGTTTTCCATAG
13 (A to V)	CP-13-F	CACATCAGACgtgCCACCAACTG
	CP-13-R	TTTGATGCTGCAGATTG
94 (S to F)	CP-94-F	AAGCTCAAAAtttGCACAACTTATG
	CP-94-R	TGCACGTCAGCATAAG
98 (M to I)	CP-98-F	TGCACAACTTattGGTGCCACAC
	CP-98-R	GATTTTGAGCTTTGCACGTC
155 (E to K)	CP-155-F	AGGCTATCAGaaaGATACCAAATTTG
	CP-155-R	AATTTTGCCCAGTTGG
236 (E to K)	CP-236-F	TGCACCCCCTaaaCTTTAAACAC
	CP-236-R	TCAATTGCGTACATGGTG

Table S3: Predicted binding affinities between viral CP and host proteins. Three host proteins—HSP70, SIOSCA4, and SISTu38—have previously been demonstrated to interact with the CP of PepMV.

Host proteins	Viral CP	Z-score	Haddock Score	Binding energy
HSP70	WT	-1.0	-76.1 +/- 18.3	-7.9
	CP ^{E155K}	-1.0	-117.4 +/- 3.5	-7.8
	CP ^{E236K}	-0.8	-95.9 +/- 7.0	-8.3
	CP ^{E155K/A6T}	-1.3	-68.4 +/- 7.1	-7.5
SIOCA4	WT	-1.3	-88.1 +/- 3.7	-7.9
	CP ^{E155K}	-1.1	-111.9 +/- 12.2	-6.1
	CP ^{E236K}	-2.0	-115.6 +/- 27.4	-9.3
	CP ^{E155K/A6T}	-1.1	-98.0 +/- 4.8	-9.2
SISTU38	WT	-1.5	-112.6 +/- 7.4	-9.4
	CP ^{E155K}	-2.4	-120.8 +/- 11.6	-8.4
	CP ^{E236K}	-1.7	-89.9 +/- 16.3	-7.7
	CP ^{E155K/A6T}	-1.5	-96.4 +/- 11.2	-7.6

Figure S1: Detection of PepMV from asymptomatic samples from the field. (a) Asymptomatic plant samples collected from the field. (b) RT-PCR analysis confirming the presence of PepMV in the collected samples.

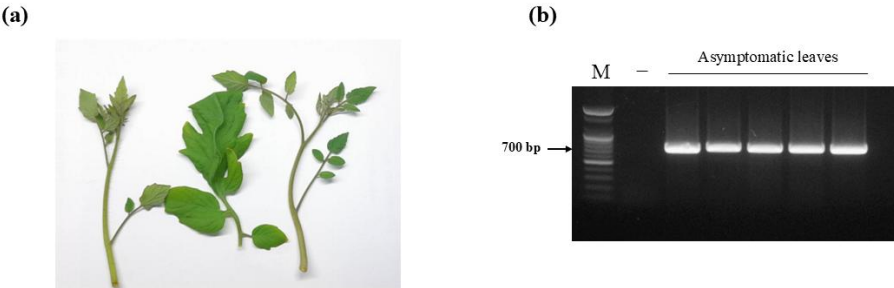


Figure S2: Phenotype of wild-type and mutant clones in *N.benthamiana* at 10 dpi.

Mock



WT



CP^{E155K}



CP^{E236K}

