

**Table S1.** Primers used for full-length sequencing of the two genomic segments (DNA-A and DNA-B) of PepGMV and PHYVV.

<b>Virus</b>		<b>Primer name</b>	<b>Primer Sequence 5'→3'</b>	<b>Position</b>	<b>T<sub>m</sub> (°C)</b>
PepGMV	DNA-A <sup>1</sup>	PepGMVA2R	CGA TCV CGH AGY TCG TTC TTC	697-717	58.3
		PepGMVA1R	GTT CCA AAT CCC CTA TTT TTC	1,272-1,293	48.5
		PepGMVA1F	CTC CCA RAT AAA AAC GSM ATT C	1,294-1,315	53.0
		PepGMVA3R	GCT CAA TTC GTC ATC CTC CAC	1,473-1,493	54.4
		PepGMVA2F	GCA TTT ACN GCG TTR TRR TAG ACG	2,074-2,097	59.1
PepGMV	DNA-B <sup>2</sup>	PepGMVB2R	CAT CCT TCR ATR TCT ACC ATG AC	964-986	55.3
		PepGMVB1R	TGG ACT TYW CMC ATG TGG ACT A	1,561-1,582	54.8
		PepGMVB1F	CAT CGT TAT GGG WGA AYT GTT T	1,583-1,604	51.1
		PepGMVB3R	GTC ATT CTT TTC RCT VAA RGA YCC	1,746-1,766	57.4
		PepGMVB2F	GAA GTG TTT YGC GAA TAA GAG G	2,121-2,142	53.0
PHYVV	DNA-A <sup>3</sup>	PHYVVA2F	CCG CMA AGA TTA GCC GAA CTG GC	270-292	60.6
		PHYVVA2R	CGC CAT CTA CGT CAC CAT CG	1,505-1,524	55.9
		PHYVVA3F	GAA ATG GAG GAA CCC ANG GTT CC	1,961-1,983	58.8
		PHYVVA1R	TAG AGG AGG ACA GCA GTC TGC	2,125-2,145	56.3
		PHYVVA1F	GCA GAT CTS CCG TCT ATT TGG	2,146-2,166	54.4
PHYVV	DNA-B <sup>4</sup>	PHYVVB2R	CAC ATG NCG WAT RTA RAA MCG TTC C	953-977	59.3
		PHYVVB1R	CTG ACA ACC AAG GAC ATA GC	1,478-1,497	51.8
		PHYVVB1F	CAT CTG TGT GAG TGG TCC CTA TGG	1,498-1,521	59.1
		PHYVVB3R	GCG TCM TTC TTY TCC YTG AAG G	1,822-1,843	58.6
		PHYVVB2F	GCT AYA CCT AAC AAT GWT AAT GG	2,217-2,239	51.7

<sup>1</sup> Position numbered as in sequence of DNA-A from PepGMV-Mo (Acc. No. AY928512).

<sup>2</sup> Position numbered as in sequence of DNA-B from PepGMV-Mo (Acc. No. AY928513).

<sup>3</sup> Position numbered as in sequence of DNA-A from PHYVV (Acc. No. NC\_001359).

<sup>4</sup> Position numbered as in sequence of DNA-B from PHYVV (Acc. No. NC\_001369).

**Table S2.** Summary of geographical origin and year of sampling of the PepGMV and PHYVV sequences used in this work.

<b>Virus</b>	<b>Isolate</b>	<b>Population</b>	<b>Habitat</b>	<b>Year</b>
<b>PepGMV</b>	BER131W2004	Bernal	Wild	2004
	BER42W2007	Bernal	Wild	2007
	BER52W2007	Bernal	Wild	2007
	BER53W2007	Bernal	Wild	2007
	BER71W2007	Bernal	Wild	2007
	BER129W2009	Bernal	Wild	2009
	CER21W2007	Cerritos	Wild	2007
	CER24W2009	Cerritos	Wild	2009
	DZI03W2007	Dzibilchaltun	Wild	2007
	DZI09W2007	Dzibilchaltun	Wild	2007
	HUA05W2007	Huatulco	Wild	2007
	HUA06W2007	Huatulco	Wild	2007
	HUJ110W2009	El Huajote	Wild	2009
	HUJ111W2009	El Huajote	Wild	2009
	PEL64W2007	Puente Elota	Wild	2007
	PEL93W2007	Puente Elota	Wild	2007
	PEL94W2007	Puente Elota	Wild	2007
	PEL95W2007	Puente Elota	Wild	2007
	TUL511W2009	Tlacuapa	Wild	2009
	CER52L2004	Cerritos	Let-standing	2004
	CER53L2004	Cerritos	Let-standing	2004
	ELO14L2007	Elota	Let-standing	2007
	ELO27L2007	Elota	Let-standing	2007
	ELO35L2007	Elota	Let-standing	2007
	PVE95L2004	Puerto Verde	Let-standing	2004
	TUL2025L2001	Tula	Let-standing	2001
	TUL2028L2001	Tula	Let-standing	2001
	TUL72L2004	Tula	Let-standing	2004
	TUL19L2009	Tula	Let-standing	2009
	CER44C2009	Cerritos	Cultivated	2009
	CER45C2009	Cerritos	Cultivated	2009
	CER46C2009	Cerritos	Cultivated	2009
	CER49C2009	Cerritos	Cultivated	2009
	CHO04C2007	Cholul	Cultivated	2007
	CHO12C2007	Cholul	Cultivated	2007
	CHO13C2007	Cholul	Cultivated	2007
	CHO15C2007	Cholul	Cultivated	2007
	HUJ21C2009	El Huajote	Cultivated	2009
	HUJ23C2009	El Huajote	Cultivated	2009
	HUJ25C2009	El Huajote	Cultivated	2009
	HUJ27C2009	El Huajote	Cultivated	2009
	PVE101C2004	Puerto Verde	Cultivated	2004
	PVE12C2007	Puerto Verde	Cultivated	2007
	PVE17C2007	Puerto Verde	Cultivated	2007
	PVE19C2007	Puerto Verde	Cultivated	2007
	PVE219C2007	Puerto Verde	Cultivated	2007
	TLA31C2007	Tlacuapa	Cultivated	2007

<b>PHYVV</b>				
	BER2114W2001	Bernal	Wild	2001
	BER111W2004	Bernal	Wild	2004
	BER41W2007	Bernal	Wild	2007
	BER52W2007	Bernal	Wild	2007
	BER1210W2009	Bernal	Wild	2009
	BER129W2009	Bernal	Wild	2009
	CER21W2007	Cerritos	Wild	2007
	CER26W2009	Cerritos	Wild	2009
	DZI03W2007	Dzibilchaltun	Wild	2007
	HUA06W2007	Huatulco	Wild	2007
	HUJ111W2009	El Huajote	Wild	2009
	MAU25W2009	Los Mautos	Wild	2009
	MAU30W2009	Los Mautos	Wild	2009
	MAU31W2009	Los Mautos	Wild	2009
	MOC27W2009	Moctezuma	Wild	2009
	PEL93W2007	Puente Elota	Wild	2007
	PEL95W2007	Puente Elota	Wild	2007
	TUL510W2009	Tula	Wild	2009
	TUL59W2009	Tula	Wild	2009
	CER58L2004	Cerritos	Let-standing	2004
	ELO35L2004	Elota	Let-standing	2004
	ELO14L2007	Elota	Let-standing	2007
	ELO22L2007	Elota	Let-standing	2007
	ELO25L2007	Elota	Let-standing	2007
	ELO26L2007	Elota	Let-standing	2007
	PVE91L2004	Puerto Verde	Let-standing	2007
	TUL2011L2001	Tula	Let-standing	2001
	TUL85L2004	Tula	Let-standing	2004
	TUL114L2009	Tula	Let-standing	2009
	TUL312L2009	Tula	Let-standing	2009
	CER43C2009	Cerritos	Cultivated	2009
	CER44C2009	Cerritos	Cultivated	2009
	CHO02C2007	Cholul	Cultivated	2007
	CHO13C2007	Cholul	Cultivated	2007
	HUJ23C2009	El Huajote	Cultivated	2009
	HUJ27C2009	El Huajote	Cultivated	2009
	PVE102C2004	Puerto Verde	Cultivated	2004
	PVE104C2004	Puerto Verde	Cultivated	2004
	PVE107C2004	Puerto Verde	Cultivated	2004
	PVE12C2007	Puerto Verde	Cultivated	2007
	PVE17C2007	Puerto Verde	Cultivated	2007
	TLA31C2007	Tlacuapa	Cultivated	2007

**Table S3.** Genetic diversity ( $\pi$ ),  $d_N/d_S$ ,  $d_N$  and  $d_S$  values for each gene in the PepGMV and PHYVV genomes.

	Habitat <sup>1</sup>	PepGMV						PHYVV					
		CP <sup>2</sup>	REn <sup>2</sup>	TrAP <sup>2</sup>	Rep <sup>2</sup>	MP <sup>2</sup>	NSP <sup>2</sup>	CP <sup>2</sup>	REn <sup>2</sup>	TrAP <sup>2</sup>	Rep <sup>2</sup>	MP <sup>2</sup>	NSP <sup>2</sup>
$\pi^3$	Wild	0.023±0.003	0.022±0.003	0.026±0.004	0.027±0.003	0.077±0.007	0.109±0.009	0.057±0.012	0.061±0.009	0.072±0.015	0.047±0.005	0.080±0.007	0.162±0.014
	Let-standing	0.036±0.004	0.045±0.009	0.045±0.007	0.044±0.004	0.087±0.007	0.105±0.010	0.055±0.006	0.061±0.010	0.066±0.011	0.047±0.006	0.072±0.012	0.084±0.008
	Cultivated	0.065±0.005	0.071±0.009	0.063±0.008	0.072±0.006	0.089±0.009	0.120±0.012	0.052±0.005	0.057±0.009	0.066±0.014	0.045±0.004	0.176±0.014	0.174±0.016
	<b>ALL</b>	<b>0.050±0.006</b>	<b>0.047±0.006</b>	<b>0.047±0.006</b>	<b>0.050±0.004</b>	<b>0.083±0.008</b>	<b>0.111±0.009</b>	<b>0.056±0.005</b>	<b>0.059±0.009</b>	<b>0.069±0.009</b>	<b>0.046±0.005</b>	<b>0.079±0.006</b>	<b>0.170±0.014</b>
$d_N/d_S^3$	Wild	0.041±0.007	0.366±0.024	0.456±0.043	0.186±0.014	0.100±0.006	0.167±0.015	0.047±0.018	0.296±0.015	0.392±0.014	0.111±0.028	0.050±0.006	0.160±0.006
	Let-standing	0.026±0.005	0.450±0.025	0.555±0.038	0.168±0.010	0.076±0.010	0.112±0.023	0.030±0.007	0.311±0.018	0.416±0.020	0.103±0.012	0.036±0.002	0.181±0.006
	Cultivated	0.021±0.003	0.374±0.014	0.336±0.031	0.174±0.016	0.076±0.009	0.152±0.010	0.038±0.008	0.329±0.043	0.405±0.023	0.113±0.009	0.048±0.002	0.171±0.006
	<b>ALL</b>	<b>0.025±0.002</b>	<b>0.363±0.008</b>	<b>0.407±0.011</b>	<b>0.173±0.004</b>	<b>0.087±0.002</b>	<b>0.147±0.004</b>	<b>0.040±0.005</b>	<b>0.307±0.007</b>	<b>0.398±0.006</b>	<b>0.108±0.006</b>	<b>0.047±0.002</b>	<b>0.173±0.005</b>
$d_N^3$	Wild	0.003±0.001	0.015±0.001	0.020±0.001	0.018±0.001	0.037±0.002	0.048±0.003	0.010±0.001	0.036±0.001	0.048±0.002	0.016±0.001	0.015±0.001	0.063±0.002
	Let-standing	0.004±0.001	0.052±0.007	0.047±0.005	0.020±0.001	0.020±0.002	0.031±0.003	0.006±0.001	0.036±0.002	0.045±0.003	0.016±0.001	0.010±0.001	0.074±0.003
	Cultivated	0.004±0.001	0.030±0.001	0.028±0.001	0.032±0.001	0.022±0.002	0.039±0.002	0.008±0.001	0.035±0.002	0.045±0.003	0.013±0.001	0.016±0.001	0.070±0.004
	<b>ALL</b>	<b>0.270±0.08</b>	<b>0.030±0.001</b>	<b>0.031±0.001</b>	<b>0.026±0.001</b>	<b>0.028±0.001</b>	<b>0.042±0.001</b>	<b>0.008±0.001</b>	<b>0.036±0.001</b>	<b>0.046±0.001</b>	<b>0.016±0.001</b>	<b>0.014±0.001</b>	<b>0.069±0.001</b>
$d_S^3$	Wild	0.086±0.006	0.041±0.003	0.043±0.003	0.096±0.004	0.336±0.016	0.290±0.015	0.210±0.007	0.121±0.004	0.122±0.005	0.147±0.005	0.301±0.010	0.396±0.015
	Let-standing	0.141±0.010	0.081±0.004	0.084±0.008	0.119±0.007	0.258±0.012	0.272±0.016	0.216±0.018	0.117±0.008	0.108±0.008	0.151±0.014	0.288±0.018	0.407±0.019
	Cultivated	0.168±0.006	0.115±0.011	0.085±0.003	0.185±0.006	0.288±0.011	0.257±0.007	0.201±0.013	0.108±0.006	0.111±0.006	0.143±0.009	0.323±0.018	0.406±0.024
	<b>ALL</b>	<b>0.153±0.002</b>	<b>0.083±0.002</b>	<b>0.075±0.001</b>	<b>0.150±0.002</b>	<b>0.323±0.005</b>	<b>0.286±0.004</b>	<b>0.213±0.004</b>	<b>0.116±0.002</b>	<b>0.115±0.002</b>	<b>0.145±0.003</b>	<b>0.302±0.004</b>	<b>0.402±0.006</b>

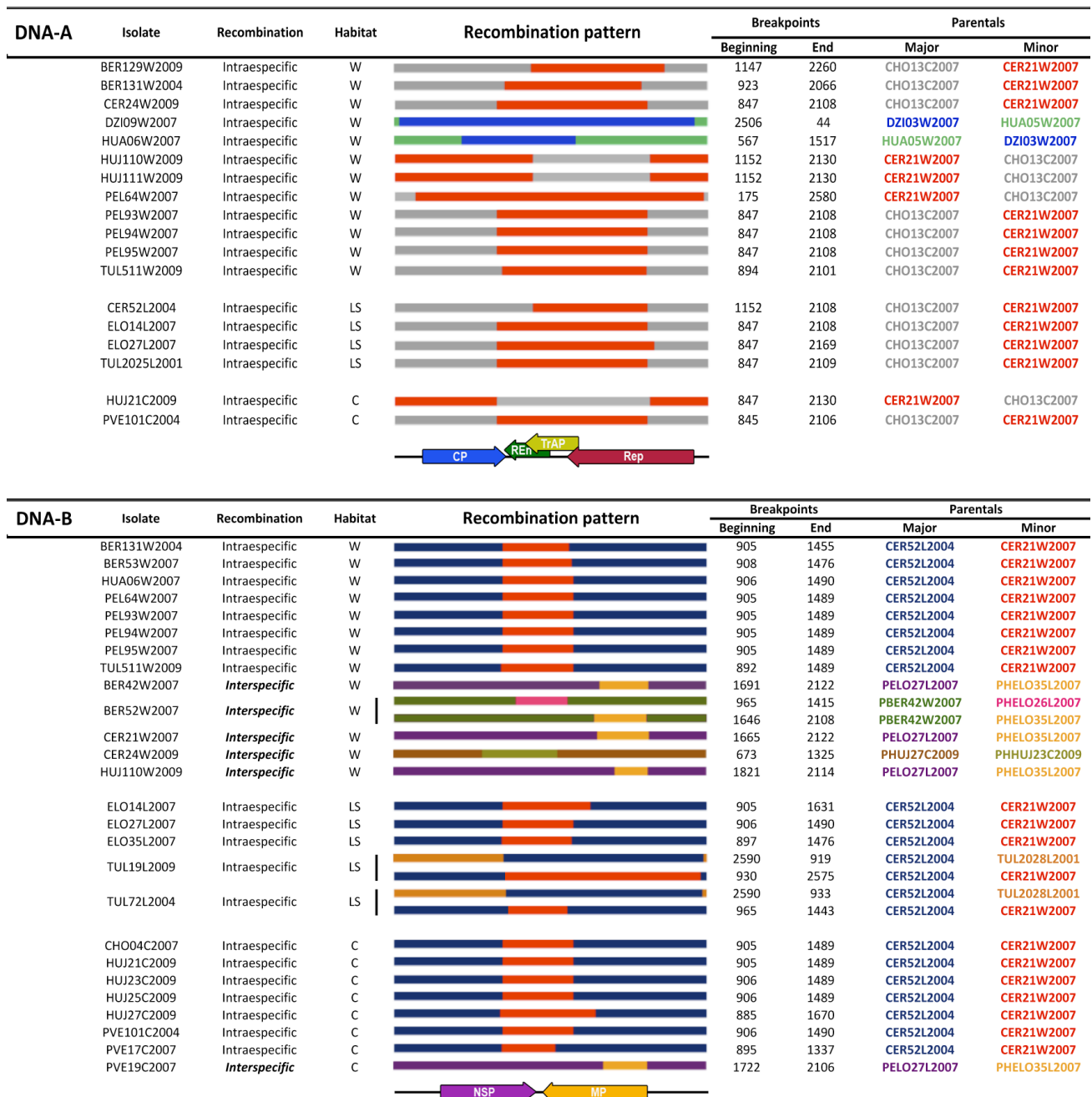
<sup>1</sup> Level of anthropisation (Wild; Let-standing; Cultivated; ALL: Wild + Let-standing + Cultivated).

<sup>2</sup> Genes harbored by the PepGMV and PHYVV genomes. CP: coat protein; REn: replication enhancer protein; Rep: replication-associated protein; TrAP: transcription activation protein; MP: movement protein; NSP: nuclear shuttle protein.

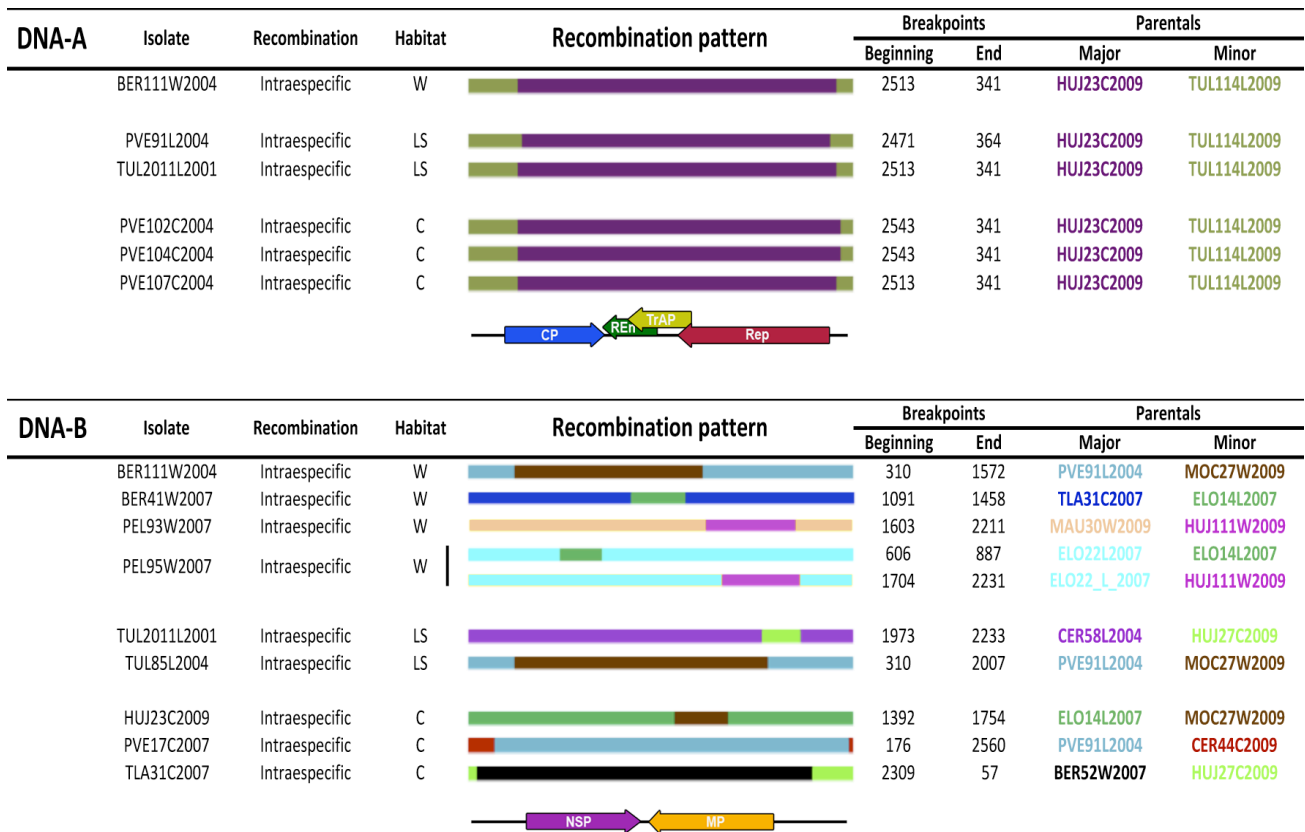
<sup>3</sup> Values are mean ± standard error based on 1000 replicates bootstrap of  $\pi$ , and based on pairwise determination of  $d_N/d_S$ ,  $d_N$  and  $d_S$ .

**Table S4.** Analysis of association between habitat and PepGMV and PHYVV phylogenies. *P*-values for three association indexes are presented: Parsimony Score (PS), Association Index (AI), and Monophyletic Clade Size (MC).

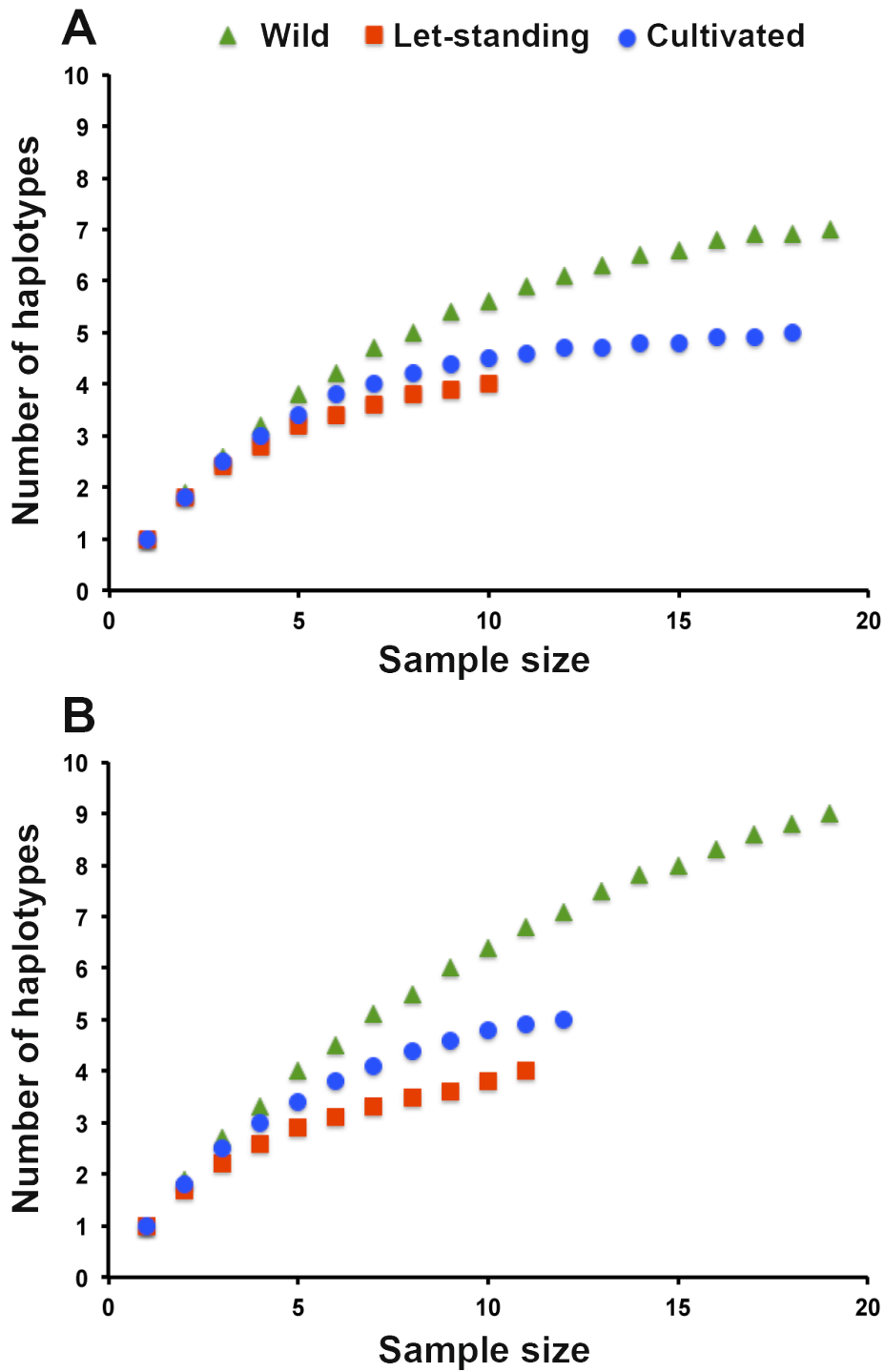
Habitat	PepGMV		PHYVV	
	DNA-A	DNA-B	DNA-A	DNA-B
AI	$1.0 \times 10^{-9}$	$1.0 \times 10^{-9}$	$8.0 \times 10^{-3}$	0.160
PS	$1.9 \times 10^{-4}$	$1.9 \times 10^{-4}$	$6.0 \times 10^{-3}$	0.115
MC (Wild)	$5.0 \times 10^{-4}$	$8.8 \times 10^{-4}$	0.038	0.037
MC (Let-standing)	1.000	0.317	0.424	1.000
MC (Cultivated)	$1.0 \times 10^{-4}$	$6.9 \times 10^{-4}$	0.047	0.487



**Figure S1.** Recombination patterns in the DNA-A and DNA-B of PepGMV isolates. Isolates are presented according to the level of anthropisation of the host population. Recombination patterns are represented by linearizing both genomic DNAs at the nicking site of the invariant nonanucleotide of the origin of replication, and genomic organization of DNA-A and DNA-B is represented accordingly. Colored arrows denote the position and orientation of each gene. CP: Coat protein (blue); REn: Replication Enhancer protein (green); TrAP: Transcriptional Activator Protein (yellow); Rep: Replication protein (red); NSP: Nuclear Shuttle Protein (Purple); MP: Movement Protein (Orange). Data on the type of recombination (intra- or inter-specific), location of recombination breakpoints and parentals is also shown for each recombinant isolate.



**Figure S2.** Recombination patterns in the DNA-A and DNA-B of PHYVV isolates. Isolates are presented according to the level of anthropisation of the host population. Recombination patterns are represented by linearizing both genomic DNAs at the nicking site of the invariant nonanucleotide of the origin of replication, and genomic organization of DNA-A and DNA-B is represented accordingly. Colored arrows denote the position and orientation of each gene. CP: Coat protein (blue); REn: Replication Enhancer protein (green); TrAP: Transcriptional Activator Protein (yellow); Rep: Replication protein (red); NSP: Nuclear Shuttle Protein (Purple); MP: Movement Protein (Orange). Data on the type of recombination (intra- or inter-specific), location of recombination breakpoints and parentals is also shown for each recombinant isolate.



**Figure S3.** Rarefaction curves for PepGMV (A) and PHYVV (B) populations in each of the three levels of habitat anthropisation considered in this study. Curves were obtained using Analytic Rarefaction 1.3 (<http://strata.uga.edu/software/anRareReadme.html>).