Table S1. Number of reads mapped to the genome of the putative viruses in the China sample.

Putative Virus	**Number of Reads**[a]	**% of Reads**
Total RNA	11,216,334	100
DcRV-Seg.1	1,831,120	16.33
DcRV-Seg.2	1,393,426	12.42
DcRV-Seg.3	1,602,937	14.29
DcRV-Seg.4	1,539,470	13.73
DcRV-Seg.7	488,079	4.35
DcRV-Seg.8	483,744	4.31
DcRV-Seg.10	366,619	3.27
DcPLV	87,537	0.78
DcDNV	8,843	0.08
DcBV-Seg. L	23,843	0.5
DcBV-Seg. M	2,646	0.02
DcBV-Seg. S	750	<0.01
DcACV- RNA1	814	0.01
DcACV- RNA2	2,601	0.02
Small RNA	8,319,921	100
DcRV-Seg.1	177,671	2.14
DcRV-Seg.2	131,100	1.58
DcRV-Seg.3	159,437	1.92
DcRV-Seg.4	145,184	1.75
DcRV-Seg.7	87,778	1.06
DcRV-Seg.8	100,271	1.21
DcRV-Seg.10	93,111	1.12
DcPLV	122,044	1.47
DcDNV	161	<0.01
DcBV-Seg. L	2,260	0.02
DcBV-Seg. M	2,145	0.02
DcBV-Seg. S	676	0.01

DcPLV, *Diaphorina citri Picorna-like virus*; DcRV, *Diaphorina citri reovirus*; DcDNV, *Diaphorina citri densovirus*; DcACV, *Chronic bee paralysis virus;* DcBV, *Diaphorina citri bunyavirus;* Seg., Segment; L, Large; M, Medium; S, Small. [a] number of reads after subtracting *D. citri* reads.

Table S2. Significant BLASTx hits to the viral database using contigs created from small RNA/RNA-seq libraries as query sequences.

Virus Category	**Virus Family**	**Virus Genus**	**Virus Species**	**Assembled contigs from representative *D. citri* Populations**
Insect virus	*Reoviridae*	*Fijivirus*	*Nilaparvata lugens reovirus*	CH, TW, FL, HW
Insect virus	*Iflaviridae*	*Iflavirus*	*Deformed wing virus*	BR, CH, TW
Insect virus	*Parvoviridae*	Various	Densovirus SC1065, *Mythimna loreyi densovirus*, Uncharacterized protein in *D. citri*	CH, TW
Insect virus	Unclassified	Unclassified	*Chronic bee paralysis virus*	CH
Insect virus	*Bunyaviridae*	Unclassified	*Wuhan mosquito virus, Wuchang cockraoch virus 1, Kigluaik phantom virus*	CH, TW
Bacteriophage	*Unclassified phages*	Unclassified	*WO prophage*	BR, CH, TW, FL, HW

CH) China; TW) Taiwan; FL) Florida, BR) Brazil; HW) Hawaii.

Table S3. Accession numbers of reference isolates and out-groups used to construct the phylogenetic trees.

Name	Abbreviation	Accession Number	Name	Abbreviation	Accession Number
Antheraea pernyi iflavirus	ApIFV	YP_009002581	*Drosophila C virus*	DCV	NP_044945
Deformed wing virus	DWV	AAP49283	*Cricket paralysis virus*	CrPV	AAF80998
Minute virus of mice	MVM	P07300	Rice strip virus	RSV	20428590
Sacbrood virus	SBV	NP_049374	*Acute bee paralysis virus*	ABPV	NP_066241
Brevicoryne brassicae picorna-like virus	BbPLV	YP_001285409	*Aphid lethal paralysis virus*	ALPV	NP_733845
Bunyamwera virus	BUNV	9630657	*Encephalomyocarditis virus*	EMCV	NP_056777
Varroa destructor virus-1	VdV-1	YP_145791	*Hepatitis A virus*	HAV	AAA45472
Slow bee paralysis virus	SBPV	YP_003622540	*Nilaparvata lugens reovirus*	NLRV	BAA08542
Nilaparvata lugens honeydew virus1	NlHDV1	BAN19725	*Fiji disease virus*	FDV	YP_249762
Kakugo virus	KV	YP_015696	*Acinopterus angulatus reovirus*	AcARV	AFA28393
Formica exsecta virus 2	FeV2	YP_008888537	*Raspberry latent virus*	RpLV	YP_003934917
Heliconius erato ifavirus	HeIFV	YP_009026409	*Aedes pseudoscutellaris reovirus*	ApRV	YP_443935
Lymantria dispar iflavirus 1	LdIFV	YP_009047245	*Heliothis armigera cypovirus 5*	HaCPV5	YP_001883323
Graminella nigrifrons virus 1	GnV-1	YP_009129265	*Rice black streaked dwarf virus*	RBSDV	NP_620452
Laodelphax striatella honeydew virus 1	LsHDV1	YP_009010941	*Mal de Rio Cuarto virus*	MRCV	YP_956848
Southern rice black-streaked dwarf virus	SRBSDV	YP_004021936	*Casphalia extranea densovirus*	CeDNV	NP_694838
Spissistilus festinus reovirus	SpFRV	YP_005255246	*Halyomorpha halys virus*	HhV	YP_008719809
Homalodisca vitripennis reovirus	HoVRV	YP_002790884	*Human rotavirus A*	HuRV	ACV73799
Denrdrolimus punctatus densovirus	DpDNV	YP_164339	*Rice dwarf Virus*	RDV	NP_620544
Aedes aegypti densovirus	AeDNV	P27454	*Diatraea saccharalis* densovirus	DsDNV	O71153
Pseudoplusia includes densovirus	PiDNV	YP_007003823	*sea star-associated*densovirus	SSaDV	AIQ82699
Acheta domesticus densovirus	AdDNV	YP_227600	*Mythimna loreyi densovirus*	MlDNV	NP_958099
Blattela germanica densovirus	BgDNV	NP_874381	*Galleria mellonella densovirus*	GmDNV	NP_899650
Planococcus citri densovirus	PcDNV	NP_694843	*Junonia coenia* densovirus	JcDNV	NP_694824
Periplaneta fuliginosa densovirus	PfDNV	NP_051020	*Heterosigma akashiwo RNA virus*	HaRNAv	AY337486
Myzus persicae densovirus	MpDNV	NP_874376	Densovirus SC116	sc116	AFH02761
Culex pipiens densovirus	CpDNV	YP_002887625	*adeno-associated virus-2*	AAV2	YP_680422
Encephalomyocarditis virus	EMCV	M67473	*Hepatitis A virus*	HAV	M14707
Feline calicivirus	FCV	M86379	*Rabbit hemorrhagic disease virus*	RHDV	M67473

Name	Abbreviation	Accession Number	Name	Abbreviation	Accession Number
Parsnip yellow fleck virus	PYFV	D14066	*Rice tungro spherical virus*	RTSV	M95497
Anopheles gambiae densovirus	AgDNV	YP_002265406	*Human poliovirus 1*	PV	AAV91151
Cherax quadricarinatus densovirus	CqDNV	YP_009134732			

Table S4. Viral sequences identified in global *D. citri* populations.

D. citri population	Putative virus					Identification method	*D. citri* population	Putative virus					Identification method
	DcRV	DcPLV	DcDNV	DcACV	DcBV			DcRV	DcPLV	DcDNV	DcACV	DcBV	
China 1	+	+	+	-	-	1, 3	Florida 4	-	-	-	+	-	3
China 2	+	+	+	+	+	2, 3	Florida 5	-	-	-	-	-	3
China 3	+	+	+	+	+	3	Florida 6	-	-	-	-	-	3
China 4	+	+	+	-	+	3	Florida 7	-	-	-	+	-	3
China 5	+	+	+	-	+	3	California 1	-	-	-	-	-	3
Taiwan 1	+	+	+	-	+	1, 3	California 2	-	-	-	+	-	3
Taiwan 2	+	-	+	-	-	3	California 3	-	-	-	+	-	3
Taiwan 3	-	-	+	-	-	3	California 4	-	-	-	+	-	3
Taiwan 4	+	+	+	-	-	3	Texas 1	-	-	-	-	-	3
Brazil 1	-	+	-	-	-	1, 3	Texas 2	+	-	-	+	-	3
Brazil 2	-	+	-	-	-	2, 3	Texas 3	-	-	-	-	-	3
Brazil 3	-	+	-	-	-	3	Texas 4	-	-	-	+	-	3
Brazil 4	-	+	-	-	-	3	Hawaii 1	+	-	-	-	-	2, 3
Brazil 5	-	+	-	-	-	3	Hawaii 2	+	-	-	-	-	3
Florida 1	+	-	-	-	-	1, 3	Hawaii 3	-	-	-	-	-	3
Florida 2	-	-	-	+	-	2, 3	Hawaii 4	+	-	-	-	-	3
Florida 3	-	-	-	+	-	3	Pakistan	-	-	+	-	-	3

DcPLV, *Diaphorina citri Picorna-like virus*; DcRV, *Diaphorina citri reovirus*; DcDNV, *Diaphorina citri densovirus*; DcACV, *Chronic bee paralysis virus;* DcBV, *Diaphorina citri bunyavirus.* 1) small RNA deep sequencing; 2) Total RNA sequencing (RNA-seq); 3) RT-PCR