

Table S1. Plant virga/nege-like virus sequences identified in insect transcriptome shotgun assembly (TSA) database.

Order (databases)				BLASTp result (top Hit)		Sequence name/No.*
Insect species	Sequence ID	Length (nt)	Virus name	e-value	Identity	
Hymenoptera (219)						
<i>Argochrysis armilla</i>	GAXO01029871	10285	Hubei virga-like virus 1	6e-119	37%	AarTSA
<i>Chyphotes</i> sp.	GBLV01021906	11870	Xinzhou nematode virus 1	6e-106	36%	
<i>Chrysis viridula</i>	GATY01002160	10509	Hubei virga-like virus 15	1e-116	36%	CcoTSA
<i>Coelioxys conoidea</i>	GBPZ01003853	9191	Hubei virga-like virus 1	0.0	43%	
<i>Megastigmus spermatrophus</i>	GCPB01032182	12061	Hubei virga-like virus 10	2e-61	32%	
<i>Monosapyga clavicornis</i>	GBWQ01015369	10601	Hubei virga-like virus 17	1e-61	31%	
<i>Sapygina decemguttata</i>	GBPQ01019499	10856	Hubei virga-like virus 21	3e-66	33%	
<i>Solenopsis invicta</i>	LJ378506	10917	Aphis glycines virus 3	5e-52	27%	
<i>Stelis punctulatissima</i>	GBWV01005603	10019	Xingshan nematode virus 1	5e-67	37%	
<i>Trichopria drosophilae</i>	GBUQ01014804	9802	Hubei virga-like virus 21	2e-52	30%	
<i>Vespula germanica</i>	GBNG01008539	9388	Hubei virga-like virus 10	6e-68	30%	
<i>Centris flavifrons</i>			Hubei virga-like virus 1	9e-116	36%	
Diptera (75)						
<i>Bactrocera kraussi</i>	GFNT01032544	10280	Aedes camptorhynchus negev-like virus	e-156	51%	CcaTSA1
<i>Ceratitis capitata</i>	GAMC01017950	9925	Parietaria mottle virus 1	3e-05	30%	
	GAMC01001565	10007	Aedes camptorhynchus negev-like virus	8e-161	46%	
	GAMC01007262	10264	Aedes camptorhynchus negev-like virus	2e-134	44%	CcaTSA3
<i>Musca domestica</i>	GARN01041480	10482	Boutonnet virus	1e-89	34%	CfiTSA
<i>Trichocera saltator</i>	GAXZ02037479	12077	Bofa virus	4e-44	29%	
Hemiptera (66)						
<i>Bemisia tabaci</i>	GARQ01016044	10028	Hubei virga-like virus 2	4e-93	36%	BtaTSA1
	GARQ01015849	9478	Hubei virga-like virus 10	4e-66	27%	BtaTSA2
<i>Okanagana villosa</i>	GAWQ01024725	11997	Hubei virga-like virus 9	2e-66	29%	
Lepidoptera (103)						
<i>Yponomeuta evonymellus</i>	GASG01021114	13110	Hubei virga-like virus 15	5e-52	28%	
Thysanoptera						
<i>Gynaikothrips ficorum</i>	GAXG02092511	11979	Wuhan house centipede virus 1	2e-63	28%	
Megaloptera (12)						
<i>Corydalus cornutus</i>	GATG02018062	9192	Hubei virga-like virus 17	2e-55	34%	
Collembola (9)						
<i>Anurida maritima</i>	GAUE01011802	9420	Wuhan insect virus 8	2e-61	31%	
<i>Sminthurus viridis</i>	GATZ02022882	10627	Hubei virga-like virus 4	9e-30	25%	

* for Fig. 4.

Table S2. GenBank/Refseq accession numbers of replicase or its domain sequences presented in Fig. 1.

Family	Genus	Type member or other members	Sequence ID	
<i>Virgaviridae</i>	<i>Furovirus</i>	soil-borne wheat mosaic virus	NP_049335	
	<i>Goravirus</i>	Gentian ovary ring-spot virus	YP_009047251 +YP_009047252	
	<i>Hordeivirus</i>	barley stripe mosaic virus	NP_604474 +NP_604481	
	<i>Tobamovirus</i>	tobacco mosaic virus	NP_597746	
	<i>Tobravirus</i>	tobacco rattle virus	NP_620669	
	<i>Pecluvirus</i>	peanut clump virus	NP_620047	
	<i>Pomovirus</i>	potato mop-top virus	NP_620444	
	<i>Bromoviridae</i>	<i>Alfamovirus</i>	alfalfa mosaic virus	NP_041192 +YP_053235
<i>Anulavirus</i>		Pelargonium zonate spot virus	NP_619770 +NP_619771	
<i>Bromovirus</i>		brome mosaic virus	NP_041196 +NP_041197	
<i>Cucumovirus</i>		cucumber mosaic virus	NP_049323 +NP_049324	
<i>Iilarvirus</i>		tobacco streak virus	NP_620772 +NP_620768	
<i>Oleavirus</i>		olive latent virus 2	NP_620042 +NP_620043	
Unassigned		raspberry bushy dwarf virus	NP_620465	
<i>Closteroviridae</i>		<i>Ampelovirus</i>	grapevine leafroll-associated virus 3	NP_813795
	<i>Closterovirus</i>	beet yellows virus	NP_041870	
	<i>Crinivirus</i>	lettuce infectious yellows virus	NP_619692	
	<i>Velarivirus</i>	grapevine leafroll-associated virus 7	YP_004935918 + YP_004935919	
Unassigned	<i>Cilevirus</i>	citrus leprosis virus C2	AGE82887	
		citrus leprosis virus C	YP_654538	
Unassigned	<i>Higrevirus</i>	hibiscus green spot virus	AER13445	
Unassigned	<i>Sandewavirus</i>	Santana virus	AFI24675	
		Wallerfield virus	AHH60914	
		Goutanap virus	YP_009094126	
		Dezidoukou virus	AFI24669	
		Tanay virus	YP_009028558	
		Bustos virus	BAU71147	
Unassigned		<i>Nelorpivirus</i>	Negev virus	AFI24672
			Ngewotan virus	AFY98072
	Hubei negev-like virus 2		KX883760	
	Loreto virus		AFI24687	
	Brejeira virus		AIS40884	
	Piura virus		AFI24678	
	Okushiri virus		BAS69360	

Table S3. *Virga/negevirus* replicase-related EVE candidates found in insect genomes.

Order		Length		BLASTp result*		Sequence	
Insect species	Sequence ID	(bp)	Location (aa)	e-value	Identity	name**	
<u>Hymenoptera</u>							
<i>Bombus terrestris</i>	AELG01008530	1788	1766–2133	6e-76	44%	BteVRLS1	
	AELG01005018	57556	1803–2661	0.0	44%	BteVRLS2	
	AELG01005119	21028	382–617, 841–1009, 2175–2690	9e-42	56%	BteVRLS3	
	AELG01005028	20169	2575–2685	2e-17	51%	BteVRLS4	
	AELG01003007	9933	1680–1982	4e-41	35%	BteVRLS5	
	AELG01010115	726	1662–1843	5e-11	28%	BteVRLS5	
	AELG01001606	43014	1540–2180	2e-79	39%	BteVRLS6	
	AELG01009381	512	1913–1997	6e-18	42%	BteVRLS7	
<i>Bombus impatiens</i>	AELG01000464	21553	2210–2354	4e-19	50%	BteVRLS8	
	AEQM02003314	19910	10–660, 857-1034	2e-100	34%	BimVRLS9	
	AEQM02001787	15967	195–412, 1095–1199	1e-29	33%	BimVRLS10	
<i>Cyphomyrmex costatus</i>	LKEX01021423	33880	2644–2737	3e-21	52%	BimVRLS11	
			76-304	5e-113	53%		
<i>Leptopilina clavipes</i>	JUFY01028443	6522	1679-2216	8e-57	50%		
			2435-2576	2e-12	38%		
<i>Lasioglossum albipes</i>	JUFY01033531	7291	2388-2459	2e-10	49%		
			514-609	6e-10	35%		
<i>Megachile rotundata</i>	ANOB01020858	6141	19–699	2e-153	44%		
			1673	160–699	3e-90	43%	
			447	8–120	4e-12	36%	
<i>Pogonomyrmex barbatus</i>	AFJA01010010	5780	110-548	4e-105	46%		
<i>Trachymyrmex cornetzi</i>	ADIH01023611	8301	1667–2478	0.0	61%	TcoVRLS	
			LKEY01019190	156204	15–214	1e-30	49%
<i>T. septentrionalis</i>	LKEY01019191	8943	19–621	7e-166	45%		
<u>Diptera</u>							
<i>Aedes albopictus</i> Rimini	LMAV013327758	3652	2239–2658	2e-77	39%	AalVRLS1	
			2039	2321–2661	2e-70	42%	AalVRLS2
<i>Ae. aegypti</i> Liverpool	NIGP01000002	474425716	1771-2134	2e-37	32%	AaeVRLS1	
			AAGE02029253	59826	1851-2712	5e-70	28%
<i>Anopheles maculatus</i>	LULA01014657	4850	20–480	6e-76	34%		

<i>An. farauti</i>	AXCN02000601	3101	1823-2370	6e-40	29%	AfaVRLS
<i>Drosophila obscura</i>	BDQP01000203	209607	2248-2745	2e-89	41%	DobVRLS
<i>D. rhopaloa</i>	AFPP02003627	1401	2402-2685	1e-66	46%	DrhVRLS
<i>Holcocephala fusca</i>	JXPE010316833	8459	1703-2695	2e-115	42%	HfuVRLS
<i>Neodiprion lecontei</i>	LGIB01001536	23605	13-538	3e-26	27%	
<i>Tipula oleracea</i>	JXPP01070948	7834	396-696	2e-30	32%	
	JXPP01008859	8959	1781-2113	2e-44	35%	
	JXPP01023376	5378	1810-2121	1e-40	37%	
	JXPP01056049	3242	1774-2091	2e-37	35%	
	JXPP01084603	2183	1919-2137	8e-35	40%	
	JXPP01186719	1425	2348-2746	2e-99	47%	
<u>Lepidoptera</u>						
<i>Calycopis cecrops</i>	LUGF01026754	3069	2122-2746	4e-128	41%	CceVRLS
	LUGF01037195	15308	1747-2746	5e-116	32%	
<i>Heliconius hierax</i>	FAQL01006392	1511	1748-2159	7e-64	33%	HhiVRLS
<i>H. xanthocles</i>	FAUE01001035	8156	1721-2142	2e-63	34	
<i>H. timareta</i>	FATD01005043	1622	1748-2159	1e-61	33%	HtiVRLS
<i>H. elevatus:</i>	FAQV01001312	6120	1685-2148	2e-58	32%	HelVRLS
<i>H. cydno cydnides</i>	FAPV01008835	3546	1685-2148	3e-58	31%	HccVRLS
<i>Neruda aoede</i>	FAPZ01000682	8422	1686-2148	3e-58	32%	NaoVRLS
<i>Plodia interpunctella</i>	FXST01009210	12389	1722-2148	8e-57	34%	PinVRLS
<i>Plutella xylostella</i>	AHIO01018779	4482	1685-2153	1e-64	35%	PxyVRLS
<i>Spodoptera frugiperda</i>	FJUZ01002630	60763	1738-2173	3e-64	35%	SfrVRLS
	NJHR010000741	755413	1748-2158	1e-61	36%	
<u>Thysanoptera</u>						
<i>Frankliniella occidentalis</i>	JMDY0102288	10427	16-397	1e-29	27%	FocVRLS1
			2258-2644	3e-66	40%	
	MDY01054944	9727	16-503	1e-28	26%	FocVRLS2
<u>Hemiptera</u>						
<i>Nilaparvata lugens</i>	AOSB01043086	1366	1701-2158	1e-73	36%	NluVRLS1
	AOSB01029478	18157	1756-2172	4e-69	38%	NluVRLS2

–* BLASTp against *Hymenoptera* or other insect WGS sequence databases with HVLV1 replicase.

** for Fig. 4, 5 and S5.