

Table S1 The detailed information of collected samples

Population	Sample size	Latitude	Longitude	Altitude
1	8	23°9'15''	113°21'13''	40.2m
2	14	23°40'49''	114°15'39''	72.8
3	18	23°9'14''	113°22'0''	50.5m

Table S2 Primers used in the experiment

Product name	Primer sequences (5'-3')	Length (bp)	Use of primers
S1	F: CGCGAGTTATTTCTCCCCGT R: GTCTTCTATTCACCTGCAGAGC	1621	Full length cloning
S2	F: GTCAGGAGAAGGATGACCAGAA R: ACCATTTGCCGCTAGACACG	2331	
S3	F: GTGAGACGGTAAGAACATTGC R: CACCGGTCTTCTCTGGGAT	2191	
S4	F: GTGAGACGGTAAGAACATTGC R: CACCGGTCTTCTCTGGGAT	856	
S5	F: ATGACGGATATTGCACCGGACAGCATTGAAAACATCCGCA R: TCCCGATCCTTCTTCTTCTCTCT	3365	Alternative splice
S6	GGATGGAATATTGAACACAGCGAGGCAGATGTGCCT AACGCTGCAAGAGTTCATAAGAC	3183	
S7	F: TGGTGATGAAAACCTCTACAGCTGGGTATTGCTGTGCTACG R: CGGATTTACAGTCTCACAGTTG	3846	
5'-UTR	F: CCAGATTTCGACAGAGAACTTAG R: GATAGGTCAGGAGGGATGTTCTTGTACGCAATATTCTCGA	961	
3'-UTR	F: CATCTGTGGTATAGGCAAGGAC R: CGGATTTACAGTCTCACAGTTG	482	
ASI	F: CCAGGTAGAAAATGATTCACTGAC R: AGTGCCGATTACCGAAACCT	292	
ASII	F: CCAGGTAGAAAATGATTCACTGAC R: TGTGACTAACTCCTGGAGTGC	399	
ASIII	F: CCTGACCTATCCCAATGTGTG R: CATATCACTGTTCTGATGGCG	168	
ASIV	F: CTGGACACAGAACACTTCTC R: TACGGTCCACCAACACGCTTC	161	
ASV	F: CGAGCAGAGAAGAATTATGCC R: AATACTTGAGCTGGTTCACATCCT	415	
M4752	F: CGATATATCCGGTCTAGGCAG R: CGTTATTGATCGACGTGGATCG	245	Sanger sequencing
G4909	F: CGTTCTTGTACAGTCTATGGTATTTTC R: TAACGTCAGTGTACAGCTGC	217	

Note: F, forward primer; R, reverse primer.

Table S3 Characterization of the Ryanodine receptor gene from *Diaphorina citri*

Sequence ID	Number of Amino Acid	Molecular Weight	Theoretical pI	Instability Index	Aliphatic Index	Grand Average of Hydropathicity
DcRyR	5130	580830.34	5.41	46.18	84.36	-0.335

Table S4 The accession numbers of the sequences used in this study

Name	Accession no.	Species
SifRyR	XP_025425821.1	<i>Sipha_flava</i>
MsRyR	XP_025202171.1	<i>Melanaphis sacchari</i>
HhRyR	XP_024217614.1	<i>Halyomorpha halys</i>
ClRyR	XP_024086009.1	<i>Cimex lectularius</i>
ApRyR	XP_016661950.1	<i>Acyrtosiphon pisum</i>
DnRyR	XP_015367530.1	<i>Diuraphis noxia</i>
BrmRyR	XP_001900491.1	<i>Brugia malayi</i>
AaRyR	XP_001657320.2	<i>Aedes aegypti</i>
MmRyR1	NP_033135.2	<i>Mus musculus</i>
MmRyR2	NP_076357.2	<i>Mus musculus</i>
MmRyR3	NP_808320.2	<i>Mus musculus</i>
DrRyR1b	NP_001096041.1	<i>Danio rerio</i>
OcRyR1	NP_001095188.1	<i>Oryctolagus cuniculus</i>
OcRyR2	NP_001076226.1	<i>Oryctolagus cuniculus</i>
OcRyR3	NP_001076231.1	<i>Oryctolagus cuniculus</i>
HsRyR1	NP_000531.2	<i>Homo sapiens</i>
HsRyR2	NP_001026.2	<i>Homo sapiens</i>
HsRyR3	NP_001027.3	<i>Homo sapiens</i>
LhRyR	JAQ15715.1	<i>Lygus hesperus</i>
BmRyR	XP_012544769	<i>Bombyx mori</i>
SrRyR1	CEF62113.1	<i>Strongyloides ratti</i>
TtRyR	CDW52896.1	<i>Trichuris trichiura</i>
DmRyR	BAA41470.1	<i>Drosophila melanogaster</i>
CeRyR	BAA08309.1	<i>Caenorhabditis elegans</i>
LcRyRbeta	BAA04647.2	<i>Lithobates catesbeianus</i>
LcRyRalpha	BAA04646.1	<i>Lithobates catesbeianus</i>
AcRyR	AKM95171.1	<i>Aphis citricidus</i>
DicRyR	AKM95170.1	<i>Dialeurodes citri</i>
MpRyR	AJA41114.1	<i>Myzus persicae</i>
TcRyR	AIU40166.1	<i>Tribolium castaneum</i>
GmRyR	AIP90097.1	<i>Grapholitha molesta</i>
LsRyR	AIA23858.1	<i>Laodelphax striatellus</i>
NIrRyR	AIA23857.1	<i>Nilaparvata lugens</i>
CsRyR	AIA23856.1	<i>Chilo suppressalis</i>
HaRyR	AIA23855.1	<i>Helicoverpa armigera</i>
BdRyR	AHY02115.1	<i>Bactrocera dorsalis</i>
LdRyR	AHW99830.1	<i>Leptinotarsa decemlineata</i>
SfRyR	AHW99829.1	<i>Sogatella furcifera</i>
CasRyR	AHN16453.1	<i>Carposina sasakii</i>
PrRyR	AGI62938.1	<i>Pieris rapae</i>
OfRyR	AGH68757.1	<i>Ostrinia furnacalis</i>

BtRyR	AFK84957.1	<i>Bemisia tabaci</i>
CmRyR	AFI80904.1	<i>Cnaphalocrocis medinalis</i>
SeRyR	AFC36359.1	<i>Spodoptera exigua</i>
PxRyR	AET09964.1	<i>Plutella xylostella</i>
AmRyR	XP_006569098.1	<i>Apis mellifera</i>
BotRyR	XP_048270099.1	<i>Bombus terrestris</i>
SiRyR	XP_039305071.1	<i>Solenopsis invicta</i>
PdRyR	XP_015173032.1	<i>Polistes dominula</i>
FaRyR	XP_011300758.1	<i>Fopius arisanus</i>
AeRyR	XP_011054963.1	<i>Acromyrmex echinator</i>
TpRyR	XP_023317849.1	<i>Trichogramma pretiosum</i>
HyhRyR	QEE14187.1	<i>Hypothenemus hampei</i>
PpRyR	XP_031356017.1	<i>Photinus pyralis</i>
SoRyR	XP_030749978.1	<i>Sitophilus oryzae</i>
AgRyR	XP_018566920.1	<i>Anoplophora glabripennis</i>

Table S5 Sequence identity (I) and similarity (S) between *Diaphorina citri* and other species ryanodine receptor

I S	DcRyR	BtRyR	NlRyR	AeRyR	DmRyR	CeRyR	TcRyR	BmRyR	PxRyR	DrRyR1b	OcRyR1	OcRyR2	OcRyR3	MmRyR1	MmRyR2	MmRyR3	HsRyR1	HsRyR2	HsRyR3
DcRyR		83.59	83.26	77.38	76.57	44.97	80.97	79.63	78.34	42.86	43.25	45.62	43.81	43.45	45.51	43.65	43.14	45.60	43.94
BtRyR	93.69		83.35	76.95	75.76	45.03	80.60	78.96	77.76	42.63	43.20	45.71	43.74	43.37	45.59	43.78	43.08	45.73	43.94
NlRyR	92.73	93.41		78.15	76.62	44.61	80.99	79.38	78.40	42.80	43.01	45.30	43.57	43.10	45.23	43.47	42.75	45.32	43.70
AeRyR	90.03	89.74	89.85		80.86	44.31	78.27	78.11	76.87	42.77	43.12	45.38	43.74	43.36	45.35	43.63	43.03	45.40	43.91
DmRyR	89.74	89.04	89.03	92.32		44.33	77.54	77.66	76.40	41.70	42.50	44.43	42.94	42.64	44.40	42.80	42.38	44.39	43.03
CeRyR	73.47	73.25	72.86	72.87	72.48		45.69	45.16	44.56	36.83	37.66	39.64	37.88	37.71	39.59	37.89	37.53	39.75	38.23
TcRyR	92.28	91.86	91.51	90.61	90.21	74.11		81.56	79.96	42.74	43.096	45.33	44.06	43.30	45.17	43.82	42.87	45.33	44.05
BmRyR	91.19	90.81	90.09	90.01	89.71	73.81	91.64		89.96	43.04	43.554	45.55	43.99	43.71	45.46	43.79	43.43	45.57	44.10
PxRyR	90.08	89.93	89.45	89.19	88.83	72.93	90.51	95.35		42.19	42.906	44.99	43.29	42.98	44.90	42.94	42.82	45.01	43.28
DrRyR1b	70.83	71.02	70.92	71.00	70.54	66.60	70.95	71.23	70.3		75.443	64.51	64.32	75.19	64.29	64.13	74.98	64.51	64.77
OcRyR1	70.67	70.79	70.63	70.95	70.42	66.52	71.15	70.98	70	88.69		64.40	64.18	95.86	64.22	63.90	96.29	64.46	64.39
OcRyR2	72.40	72.75	72.04	72.23	71.88	68.71	72.69	72.76	72.19	85.76	85.06		67.12	64.37	97.062	66.95	64.15	98.67	67.41
OcRyR3	70.94	70.90	70.47	70.54	70.29	67.45	71.37	71.11	70.51	84.49	84.34	86.81		64.19	66.91	94.74	63.93	67.08	96.35
MmRyR1	70.70	70.81	70.49	70.84	70.46	66.52	70.95	70.86	69.91	88.87	98.47	85.37	84.42		64.18	63.96	95.38	64.43	64.42
MmRyR2	72.55	72.72	72.06	72.28	71.85	68.73	72.77	72.63	72.06	85.60	84.98	99.20	86.73	85.19		66.90	64.01	97.20	67.31
MmRyR3	70.52	70.67	70.33	70.43	70.07	67.29	71.22	70.96	70.09	84.55	84.13	86.68	97.97	84.14	86.58		63.75	66.97	95.56
HsRyR1	70.89	70.80	70.62	71.09	70.53	66.55	71.06	71.13	70.03	88.94	98.53	85.13	84.16	98.42	84.99	83.98		64.19	64.18
HsRyR2	72.51	72.85	72.14	72.39	71.94	68.73	72.86	72.89	72.36	85.76	85.16	99.72	86.87	85.41	99.32	86.74	85.21		67.35
HsRyR3	70.93	70.99	70.45	70.71	70.31	67.69	71.48	71.26	70.40	84.77	84.59	86.99	98.71	84.56	86.97	98.53	84.36	87.07	

The percentage of similarity (lower left triangle) and identity (upper right triangle) are illustrated. Abbreviations and GenBank entries for the RyR isoforms are described in Table S4.