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1   ATGCCCTCATGAACGGGTGGTGGATCGCTGCTGGCTGGTGGCTGCTGACGACCGGGCCGCGAGGAGAGGTGGCGGACATCGACGTCGCGAACAGCGGGACCG
1   M P S M N G W W I A F V W L W S L S V T T A A V E E K V C G S I D V R N S G D R
121  CTGTCCGGCTTGCACAACTGCACCACTCCAGGGTTCCTGCGAGTCTGCTGCTGATGCGCACCAACCGCTCCGACTTCGACATCAGCTTCCCGCTTGGCGGAGATCACTGACATG
21  L S A L H N C T I V Q G S V Q I V L L D A T K P S D F D I S F P L L R E I T Q Y
241  CTGTGCTGTACCGGCTGGCGGCTGTACAACCTGGGAAGCTGTCCCGAACCTGATGCTATCCGGGACGACAGTCTCTATTCCCGGACTGGCGCTCATGTCACGCAAC
81  L V V Y R V A G L Y N L G K L F P N L M L I R G T H S P H F P G L A L M H D N
361  CTGACCTCAGGAGATCGGACTGTACAGCTGACCAACATCAGCGGGGTCCTGGTATCTTGGAAAACCTAAATTTGTCAGGGGAACAACATCGATTTGGGGTCAATGGCCAA
121  L D L R E I G L Y S L T N I T R G S V I I S K N P K L C H A T T I D W G Q I A N
481  GGAGTGAGCAACACATACCTGATCAGCAACGAGCACTATAAATGTATGGATGCTCTAATATTGGCTGCGGGAGACCTGTGCTGTCACAGATCCCGTCCAGTCTGAGTAC
161  G V S N D I N V I S N D E P I K C N G C S N I G C P G D L C W S H D P V Q C Q Y
601  GGGAGATGAACGGTTGCCATCCATTGTGCGCTGTGGCTGTGACGAACCGCATCTGCGCAGACATGTTTGGTGCACCGGATCATGTACAAGGGGAATGCATCAAGAATGTCCA
201  G R L N G C H P L C A G G C D E P H S A R H C F A C T A Y M Y K G E C I K E C P
721  TAGCGCTGTATGCTCACATCAGTCTGTTTCCCGCAAGAGTGTCTGCTGCTCCGGTACGAGAGAATGCACCGGAGCTTTTAAACACACACTACATCCCGTTCGAACGC
241  Y G L L Y G H I R S C L T A E E C Y S L P V S R E E S T P D V L N T H Y I P F E R
841  GTTTGTCGGGATGCTCCGATCAGGATCGAGGTGAGGTGGATAAAGAATGTACACTGCTGCACAAGACGAGATCCGACACTGTACGGGAACTGTAATGTTTCAAGATCAGC
281  V C R D E C P Y G F E V T V D K R N C T L C T K T R Y G H C Q R N C N S F K I S
961  GATGACATGTTGGAAGAACTATGAATATGTTTACACACCACTGTACAACAATCAAGTCTCTGGAGATCGAAGTCAAGTACGGCAGGATGAGGATGAGAAGCTGATAGAAGA
321  D D M L R K N Y E Y R L H T N C T T I K S L E I E V K Y G T S E D V E R R L E E
1081  TACATTCGCAAGTAGAAGTATTTGGATCAGTAAAAATCATACGGTGGTATTCGCTGACTCTTGAATTTCTGGGAAGTCTGTAGAAATACCGGTTGAAAATCTGTTAAATA
361  Y I G K V E V I L D Q L K I I R S Y S L N S L N F L R S L Y E I R G E N T V N K
1201  ATGGCTTTGGTATTTCGGCAATAAAAAATTTACAAGACTTTGGACCAACAGTGAACGAGACTGCGCCGTAAGATATTGAACGGCAGCATCTTTTATTCACTCAAGATTA
401  M A L V I R G N K N L Q R L W T N S E N E T R P V K I L N G T V S F H Y N P K L
1321  TGTATGACAAATATAAATTTGGAATTTATCTGCTGCTGCTCTCAGATATAGAAGTGTCTGTATATGAAATGGGATCAGTTCGATGATCTTATAAATTAAGATGA
441  C M S E I Y K F G N L S S L P A F S D I E V S V I S N G D Q F A C T V Y N L Q V
1441  GAAACCGTAAATCGAACCAACTATTGTTGACAAATGCACAACCGTGAAGCAGATCATTGGAAGTTTCTGTGATTTTATGAAGCATTAAGAAAGTAAAGTAA
481  E T V Y K I E P Q S I V L Q M H K P V E A D H L E R F L V Y F I E A S K W N E T I
1561  GAAACACCGTAAATCGAACCAACTATTGTTGAAATGATGATATAGTTCAAAAAGTTTCAACGACTGAAATTTACATGCTATTGAAACCAACACAGACTGAT
521  E T T D C E D S S W K I D D I S S K K V F N D T E I Y H V I T N L E P N T E Y I
1681  TATTATGAAAGACTTACAGGATTTCTCAAGACTAGTATGATGATGATTCGATGTAAGACACTACCATAAAGCCGTCGCTCCTCAATCTCAGTCTCAACCATGCTGCTAGT
561  Y V V K I Y T I S S K T S M S S V F R S K T L P S K P S A P Q Y F T A Q P L S
1801  TCTGAAGTAGACTTACATGAAACCTCTTCCACATCTCTGAAATTAAGTCAATATACATATTAAGGAAATTCATTAACGATGACCAAGCCATTTGGGACAGCTACTGCTG
601  S E V E L T W K P P S H P H G K L V K Y I I K G I H L T D D Q A I L D E R S Y T
1921  AGAACAAAGCAATATGGAACAGGCACTAATAATCCACCACTCAATATTAACCATCCGATGATACATGTAACCAAGCTGAAACAGTGAACCTCAAAAGACTGTTGATGATAAT
641  R N K T I N G N G I T H K S T T S I I K P S D D T C E K Q C E P Q K N T V D N I
2041  TGCAACTTGAACACGGTATAGACATGATTAATTCATTAACAATCAACAGTATACATTTGAATCGTGCAGCAGTAACTTCTTAATATCTTATAATCAAAATTTGGGCA
681  C N T F E H G I D M D L I S L N N H K Y T F E S C S S N I L N I F I N S K L A
2161  ATGCAAAACAAAGCAGCACTATCTTCCAAATATAAATGAAACTGTACAGAAATGGTGGTCAAGTAAATATGAAACAACTCACTATAAAGATGATGATCTATTTTC
721  M Q N N D D T I F P N I I N E N C T E M W S V S N I L N N Y T H K D G S S S Y F
2281  CAGTACCACTAAATGAAATGTTACATCAATTAATCTGTAACCTTAGCCATTACAGTCAATATTTGTTGCCATATGGTTGTAGAGAAGTGGTCAACGAAGATTAACCTAAGT
761  Q I Q L N E N V T S F N L G N L R H Y S Q Y L L S I L L V C R E V Y V K Q E I L S
2401  AATATCAATCTGTAGTCAAGAGACATTAATCTCCGCACTTGGAAAATAGCAGGACAGATATATGATAGGATAGTACAATATGTTGTTGAAATACACACTGTTAAT
801  N I N S C S Q E T L I S F R T L E N K Q A D I D S D S V Q Y V V V N N H T V N
2521  ATATCTGGGAGTCACCACTTATAAATAGTATATACATAGTTCCAGTTGGAATATAAGCGCTCGGATCGCCCAATTTGTTCTGTATGATTAATGAAAGGATGATAAA
841  I S W E S P T L I N S I L H S F Q L E Y K R S D A P N F V S V C I T M K E Y E N
2641  GCTGGCCGATCATGTCTCAAGAACTACAGCCTGGTCTTACCAATACAAAATCAAAGCTGTTCTTTGTATAAAGCTGGCCATTCACACTGGAAGAGTTTAACTTCCATAT
881  A G R S S Y V F K N L Q P G A Y Q Y K I Q A V S L Y K P G P F T T V K E F N L P Y
2761  CCAGACTATTAAACAGTGAACCTTATCTCATAATTTTCAATTTGGCTGTTTAAATTTTAAACAGTATATATATTCGTACACACTTATGCTGAAGATTTTGGAACTGAT
921  P D S F N [ S W N L I L I I F I C G C L L I L L T V Y Y ] R T H F S R K I L E R N
2881  ACCATGTTTAAATAGCCAACTCTGGCTATGTTGTTATATGTTGAGGACAAATTTGAGATACCTCGAGATGATTAATATACAAAAATCTGCGTAGAGGACATTTGGCACA
961  T M F N L A N N P G Y V G I Y V E D E F E I P R D D V I I Q K I L G R G T F G T
3001  GTTCAGCAAGCTGCTATGCTGATCCATACCATGCTGTAATCTGTTAGCAAGACAACTTTTGAATATCATGACAGTCTTAAACGAGCAGCATATAAGAAAGTTG
1001  V H E G L L M P D S I P C A V K S V S K T N F L R Y H A E F L N E A A I M K K F
3121  AGGGAACATACATATAGTGAGATGCTTGGTGGTGAAGCAACCTACCACTACTGTAATGGAACCTATGGCCGCTGGTATTGAAAAGTGTATTTGGTAAAGTCAAGGAT
1041  S E A Y H I V R L L G V V T K T H P P L L V M E L M G R G D L K S V L V K C R D
3241  TCTGATGACCTACCGCACTAACAGATATACTATCATGATGCTGACAAATAGCTGATGATGACATTCAGAAATATAAATAATTTATTCATGCTGATTTGGCAGCCGAAAT
1081  S D D L P P P N R Y T I I R M A A Q I A D G M A F L E Y N K F I H R D L L A A R N
3361  TGTATGCTGCTAATGATGACTGTGAAAATTTGGTATTGTTGATGAGTCGACAAATATAATGTTGATTTATTCGTAAGGAAATAGGGTGAATGCCTATACGGTGGATGGCT
1121  C M V A N D M T V K I G D F G M S R Q I Y N G D Y Y R K G N K G E M P R W M A
3481  CCCGAGACTTATGAAAGTATATTTACTAGTCAATCGGATGTTGGAGTTACGGGTTGTTGCTGGAAATGATGACATAGGAGCACAACCTACTCAGAAAAGATTAACATGAA
1161  P E S L S E G I F T S Q S D V W S Y G V V I W E M M T L G A Q P Y S E K S N N E
3601  GTCATGGCACATGCTGATGATGACTACTACTGCAATATTTGCTGATGTTGGCTGATTTGATGATGATGTTGAAATGGACTGCTTCAACGACCAAGCTTCTTA
1201  V M A H V L D G N L L N L P I F C P D V L A G I V R L C W N W T A S Q R P R F L
3721  AAAATAGTCGAACACTGATGTTATCTGGAGGATGATTCAGATCAGTTTCGTTTATACACAGTGGTTACACAATGAATCACCTGCGATCAATGTTGATGCTGCGCATGACT
1241  K I V E T L D V Y L E D D F R S V S F Y H T R G L H N E S P A D Q S L M S P C T
3841  ACATATGAAGAAGATGATGATAAAGAACTTTCTTTGAAAGTGGTGCACACTGTTGCTGATATAGTGGCTTCCATGTAGACAAAAATAAATGAGTAATGGCATTATTCGCCAATG
1281  T Y E E D V D N E S I S F E G G D T V A V Y S A F H V D K N K M S N G H L S P M
3961  TAA
1321  *

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Figure S2. Nucleotide and deduced amino acid sequences of *AcInR2* from *Aphis (Toxoptera) citricida*. The start codon (ATG), stop codon (TGA) are highlighted in black. The furin-like cysteine-rich (Fu) region is underlined with red wavy lines. Three fibronectin type 3 (FN3) domains are labeled with yellow solid underlines. A single transmembrane (TM) region is highlighted with a box. An “NPXY” motif is shown in green. The highly conserved tyrosine kinase domain (TyrKc) is indicated in blue. A triple tyrosine cluster (YXXXYY) is indicated in red.

Table S1. Primer sequences used for cloning, quantitative real-time PCR and double-stranded RNA (dsRNA) synthesis.

Experiments	Primer Names and Sequence (5' to 3')	Amplification Efficiency	Product Length
Full-length confirmation	<i>InR1</i> -F: ATGTGTGGAGAGTGTGACAA	-	4473
	<i>InR1</i> -R: TCAGCATATAGTGGTATTTAT		
	<i>InR2</i> -F: ATGCCGTCCATGAACGGGTG	-	3963
	<i>InR2</i> -R: TTACATTGGCGATAAATGGCC		
qPCR analysis	Q- <i>InR1</i> -F: ATGGTTCGAGATGCTTGTGGA	98.2%	217
	Q- <i>InR1</i> -R: TGTGGAGGACTTGGAGTTCC		
	Q- <i>InR2</i> -F: TTCCCGAACCTGATGCTGAT	96.3%	204
	Q- <i>InR2</i> -R: GCTCACTCCATTGGCGATTT		
	Q- <i>EF1α</i> -F: GATGCACCTGGTCACAGAGA	96.5%	194
	Q- <i>EF1α</i> -R: CCATCTTGTTCACACCAACG		
dsRNA synthesis	ds <i>AcInR1</i> -F: taatacgaactactatagggTTGTGGGATTGGAGTACTC	-	511
	ds <i>AcInR1</i> -R: taatacgaactactatagggCACTTTGTGCACCATTAGA		
	ds <i>AcInR2</i> -F: taatacgaactactatagggAACCTAAATTGTGTCACG	-	609
	ds <i>AcInR2</i> -R: taatacgaactactatagggGACTTCGATCTCCAGAGAC		
	ds <i>GFP</i> -F: taatacgaactactatagggCAGTTCTTGTGAATTAGATG	-	436
	ds <i>GFP</i> -R: taatacgaactactatagggTTTGGTTTGTCTCCCATGATG		

InR, insulin receptor; dsRNA, double-stranded RNA; *EF1α*, elongation factor 1α; F, forward; R, reverse; Ac, *Aphis (Toxoptera) citricida*. The lower case letters represent the T7 promoter sequences for efficient in vitro transcription in dsRNA synthesis.

Table S2. Sequences and relevant information used for phylogenetic analysis of the insulin receptor genes.

Genes	GenBank No. or Gene ID	Species
<i>BgInR</i>	CDI30232.1	<i>Blattella germanica</i>
<i>ZnInR1</i>	KDR13786.1	<i>Zootermopsis nevadensis</i>
<i>ClInR1</i>	XP_014256336.1	<i>Cimex lectularius</i>
<i>HhInR1</i>	XP_014273515.1	<i>Halyomorpha halys</i>
<i>NlInR1</i>	AIY24638.1	<i>Nilaparvata lugens</i>
<i>AcInR1</i>	KX507134	<i>Aphis (Toxoptera) citricida</i>
<i>DnInR1</i>	XP_015375915.1	<i>Diuraphis noxia</i>
<i>ApInR1</i>	XP_008185917.1	<i>Acyrtosiphon pisum</i>
<i>MpInR1</i>	MYZPE13164_G006_v1.0_000181710	<i>Myzus persicae</i>
<i>PhInR</i>	XP_002430961.1	<i>Pediculus humanus corporis</i>
<i>NvInR</i>	XP_003425750.1	<i>Nasonia vitripennis</i>
<i>AmInR1</i>	NP_001233596.1	<i>Apis mellifera</i>
<i>BiInR1</i>	XP_003490625.1	<i>Bombus impatiens</i>
<i>SiInR1</i>	XP_011158641.1	<i>Solenopsis invicta</i>
<i>CfInR1</i>	XP_011251746.1	<i>Camponotus floridanus</i>
<i>HsaInR1</i>	XP_011144146.1	<i>Harpegnathos saltator</i>
<i>OnInR</i>	AFQ20827.1	<i>Onthophagus nigriventris</i>
<i>TcInR1</i>	XP_008199415.1	<i>Tribolium castaneum</i>
<i>BmInR</i>	XP_012549124.1	<i>Bombyx mori</i>
<i>PxInR</i>	XP_011567916.1	<i>Plutella xylostella</i>
<i>AaInR</i>	AAB17094.1	<i>Aedes aegypti</i>
<i>DmInR</i>	ACY01695.1	<i>Drosophila melanogaster</i>
<i>GmInR</i>	AFQ01096.1	<i>Glossina morsitans morsitans</i>
<i>BdInR</i>	XP_011210333.1	<i>Bactrocera dorsalis</i>
<i>CcInR</i>	XP_004518075.1	<i>Ceratitis capitata</i>
<i>CfInR2</i>	XP_011263722.1	<i>Camponotus floridanus</i>

Table S2. Cont.

Genes	GenBank No. or Gene ID	Species
<i>SlInR2</i>	XP_011175961.1	<i>Solenopsis invicta</i>
<i>HsaInR2</i>	XP_011140707.1	<i>Harpegnathos saltator</i>
<i>AmInR2</i>	XP_394771.4	<i>Apis mellifera</i>
<i>BiInR2</i>	XP_003484422.1	<i>Bombus impatiens</i>
<i>ZnInR2</i>	KDR21367.1	<i>Zootermopsis nevadensis</i>
<i>ClInR2</i>	XP_014242610.1	<i>Cimex lectularius</i>
<i>HhInR2</i>	XP_014273071.1	<i>Halyomorpha halys</i>
<i>NlInR2</i>	AIY24639.1	<i>Nilaparvata lugens</i>
<i>TcInR2</i>	AHF20215.1	<i>Tribolium castaneum</i>
<i>AcInR2</i>	KX507135	<i>Aphis (Toxoptera) citricida</i>
<i>DnInR2</i>	XP_015363980.1	<i>Diuraphis noxia</i>
<i>ApInR2</i>	XP_001942660.2	<i>Acyrthosiphon pisum</i>
<i>MpInR2</i>	MYZPE13164_G006_v1.0_000187240	<i>Myzus persicae</i>
<i>HsInR</i>	NP_001073285.1	<i>Homo sapiens</i>