

Supplementary Information for:

## **Evolutionary shifts in pheromone receptors contribute to speciation in four *Helicoverpa* species**

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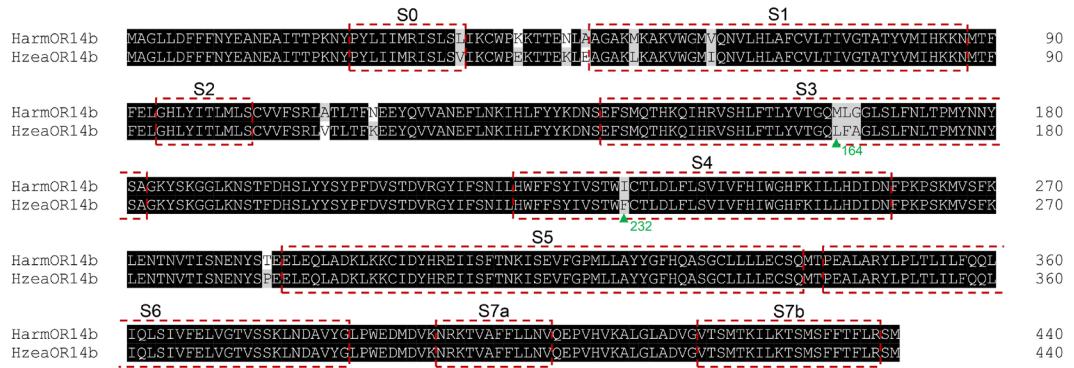
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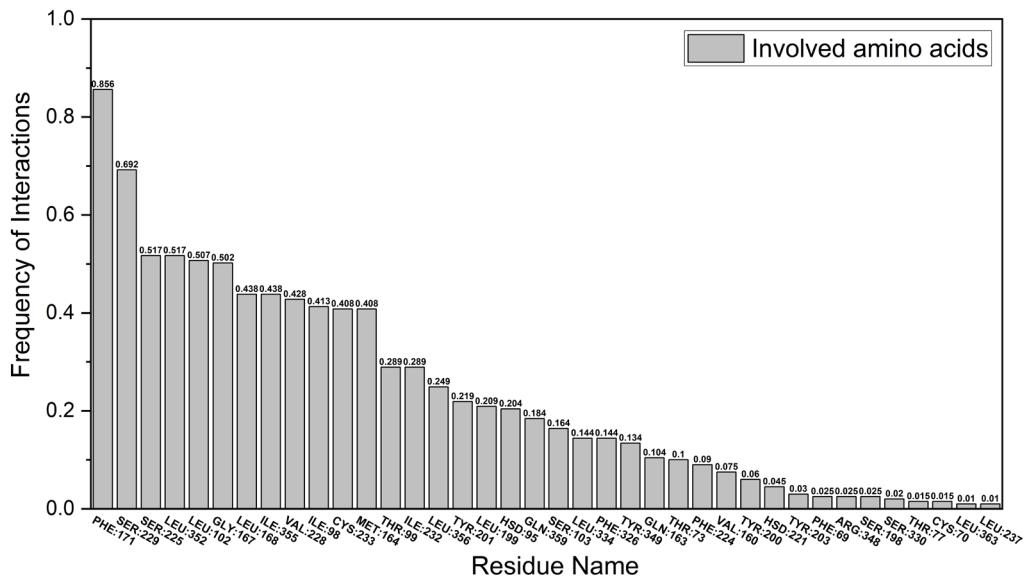
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**Fig. S1** Multiple sequence alignment of HarmOR14b and HzeaOR14b. Residues 164, 232 are two possible specific sites that contribute to the binding process and marked in green.



**Fig. S2** Substrate interaction frequency of HarmOR14b with Z9-14:Ald obtained from the 1 $\mu$ s MD simulation of the Z9-14:Ald bound HarmOR14b.

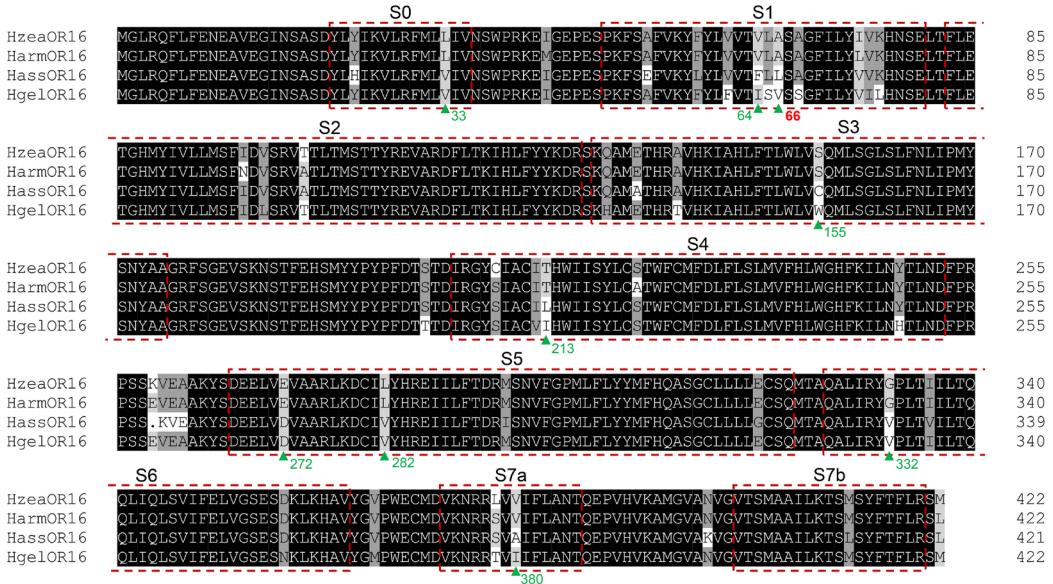


Table S1 Primers used in this study. The Kozak sequence (GCCACC) and the candidate mutated sites are marked in green and red, respectively.

Primer	Forward (5' to 3')	Reverse (5' to 3')
<b>Primers for gene clone</b>		
HgelOrco	ATGATGACCAAAAGTGAAGGC	TTACTTGAGTTGTACCAACACC
HgelOR6	ATGAGCTTAAAAAATTCTTTTC	TCACATACTGCGTAAAAAGGTG
HgelOR11	ATGTATGCCGGAAATGCTG	TTAAAACGTGCGCAGAAAG
HgelOR13	ATGAAAATTCTATCAGATGGTC	TCACTGTTCTTCTGCAAC
HgelOR14b	ATGGCAGGGTTGCTTGATT	TCACATACTGCGTAGGAAGGTG
HgelOR16	ATGGGTCTCGACAATTCTAT	TTACATACTCCTAGAAACGTGAAG
HzeaOrco	ATGATGACCAAGGTGAAGG	TTACTTGAGTTGTACCAACACC
HzeaOR6	ATGAGCTTCAGAAAATTCTTTTC	TCACATACTGCGTAGAAAGGTG
HzeaOR11	ATGTATGCCGGCAATGCTG	TTAGAACGTGCGTAGAAAGGC
HzeaOR13	ATGAAAATTCTATCAGACGGTC	TCACTGTTCTTCTGCAACT
HzeaOR14	ATGAGAGGCATACGTGACTTTAT	TCACTTACTGCGAAGAAAGGT
HzeaOR14b	ATGGCAGGATTGCTTGATT	TCACATACTCCGTAAGAAGGTG
HzeaOR15	ATGACTGGTTTGACATTATC	TTACATGCTGCGTAGAAAAGC
HzeaOR16	ATGGGACTTCGTCAATTCT	TTACATACTCCTAGAAACGTGA
<b>Primers for pT7Ts vector construction</b>		
HgelOrco	TCAGGGCCC <u>GCCACC</u> ATGATGACCAAAAGTGAAGGC	TCAC <u>TCGAGTT</u> ACTTGAGTTGTACCAACAC
HgelOR6	TCA <u>ACTAGT</u> <u>GCCACC</u> ATGAGCTTAAAAAATTTC	TCAC <u>TCGAGT</u> CACATACTGCGTAAAAAGG
HgelOR11	TCAGATATC <u>GCCACC</u> ATGTATGCCGGAAATGCTG	TCAG <u>CATGCT</u> AAAACGTGCGCAGAAAGG
HgelOR13	TCA <u>ACTAGT</u> <u>GCCACC</u> ATGAAAATTCTATCAGATGG	TCAG <u>CGGCCGCT</u> CACTGTTCTTCTGCAA
HgelOR14b	TCA <u>AGATCT</u> <u>GCCACC</u> ATGGCAGGGTTGCTTGATT	TCAG <u>GCATGCT</u> CACATACTGCGTAGGAAG
HgelOR16	TCA <u>ACTAGT</u> <u>GCCACC</u> ATGGGTCTTCGACAATTTC	TCAC <u>TCGAGT</u> TACATACTCCTTAGAAACGTG
HzeaOrco	TCAGGGCCC <u>GCCACC</u> ATGATGACCAAGGTGAAGG	TCAC <u>TCGAGT</u> ACTTGAGTTGTACCAACAC
HzeaOR6	TCA <u>ACTAGT</u> <u>GCCACC</u> ATGAGCTTCAGAAAATTCT	TCAC <u>TCGAGT</u> CACATACTGCGTAGAAAG
HzeaOR11	TCAGATATC <u>GCCACC</u> ATGTATGCCGGCAATGCTG	TCAG <u>CATGCT</u> AGAACGTGCGTAGAAAG
HzeaOR13	TCA <u>ACTAGT</u> <u>GCCACC</u> ATGAAAATTCTATCAGACGG	TCAC <u>TCGAGT</u> CACTGTTCTTCTGCAAC
HzeaOR14	TCA <u>AGATCT</u> <u>GCCACC</u> ATGAGAGGCATACGTGAC	TCAC <u>TCGAGT</u> CACTTACTGCGAAGAAAG
HzeaOR14b	TCA <u>AGATCT</u> <u>GCCACC</u> ATGGCAGGATTGCTTGAT	TCAG <u>GCATGCT</u> CACATACTCCGTAAGAAGG

Primer	Forward (5' to 3')	Reverse (5' to 3')
HzeaOR15	TCA <u>AGATCT</u> <b>GCCACC</b> ATGACTGGTTTGTGACAT	TC <u>ACTCGAG</u> TTACATGCTGCGTAGAAAAG
HzeaOR16	TCA <u>ACTAGT</u> <b>GCCACC</b> ATGGGACTTCGTCAATTTC	TC <u>ACTCGAG</u> TTACATACTCCTAGAAACG
<b>Mutation (HarmOR14b to HzeaOR14b)</b>		
HarmOR14b-M164L	CTGGTCAA <b>CTG</b> CTTGGTGGTC	AGTGTAA <u>GTGGTAA</u> ATAGCGGGC
HarmOR14b-I232F	TGTCAACCTGG <b>TTC</b> TGTACTCTCG	AACATCCGCTTGCGCTGGT
<b>Mutation (HzeaOR14b to HarmOR14b)</b>		
HzeaOR14b-L164M	TACTGGTCAA <b>ATG</b> TTGCTGGTC	TGGAAACCATA <u>GTAA</u> AGCCAACAG
HzeaOR14b-F232I	GTATCAACCTGG <b>ATC</b> TGTACGCTCG	TTAATGTGAGTGGCAAATAACGGGC
<b>Mutation (HarmOR16 to HgelOR16)</b>		
HarmOR16-L33V	TACTGCGATTCATGCTA <b>GTT</b> ATCG	GTTAGCGTAGCA <u>ACTCTGG</u> ACAC
HarmOR16-V64I	GA <u>CTATT</u> GGCCTCTGCTG	AAACTTCTCCTGAAAATCTGCC
HarmOR16-A66V	GA <u>CTGTTTG</u> GTTCTGCTG	AAACTTCTCCTGAAAATCTGCC
HarmOR16-L74V	TGGATTCA <u>TTTATAT</u> GTCGTTAAC	GTGGACAGCACGGTGAGTCTC
HarmOR16-S155W	CATTATGGCTTGTAT <u>G</u> GGCAGATG	AGTAATAGACAGCCGCTTGC
HarmOR16-T213I	CTATTGCGTGTATT <u>A</u> TA CATTGG	ATCTGCGAACATTGAGAAG
HarmOR16-E272D	GTT <u>GAT</u> GTGGCTGCAAGGC	GTC <u>ACTCTCGCTCCC</u> ACC
HarmOR16-L282V	GGATTGTATT <u>GTT</u> TATCATCGTGAG	CCAACCAATTGAAAATAACTG
HarmOR16-G332V	GCTCTTATACGTTAT <u>G</u> TACCACTAAC	CTGGTTCTGAGTATTAGCGAGG
HarmOR16-V380I	AACAGAAGGTGGTG <u>ATC</u> ATC	AAACGTGAAGTAGGACATAGAGGTC
<b>Mutation (HarmOR16 to HassOR16)</b>		
HarmOR16-A66L	GA <u>CTGTTTG</u> <b>CTC</b> TCTGCTG	AAACTTCTCCTGAAAATCTGCC
<b>Mutation (HgelOR16 to HarmOR16)</b>		
HgelOR16-V66A	T <u>GACTATT</u> CG <b>GCC</b> TCTTCTGG	AACTTCTCCTGAAAACCTGCC
<b>Mutation (HassOR16 to HarmOR16)</b>		
HassOR16-L66A	GA <u>CTTTTG</u> <b>GCCT</b> CAGCTGG	AACTTCTCCTGAAAACCTGCC

Table S2 Information for MD stimulations in this study.

<b>MD simulations</b>			
<b>OR Complex</b>	<b>Substrate</b>	<b>Repeat No.</b>	<b>Simulation time</b>
(OR14b) <sub>2</sub> : (Orco) <sub>2</sub>	Z9-14:Ald	2	1 μs
(OR14b) <sub>2</sub> : (Orco) <sub>2</sub>	Z9-16:Ald	2	1 μs
(OR16 <sub>Wild Type</sub> ) <sub>2</sub> : (Orco) <sub>2</sub>	Z11-16:OH	2	500 ns
(OR16 <sub>A66L</sub> ) <sub>2</sub> : (Orco) <sub>2</sub>	Z11-16:OH	2	500 ns