

Sexual isolation of male moths explained by a single pheromone response QTL containing four receptor genes

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Long distance sexual communication in moths has fascinated biologists because of the complex, precise female pheromone signals and the extreme sensitivity of males to specific pheromone molecules. Progress has been made in identifying some genes involved in female pheromone production and in male response. However, we have lacked information on the genetic changes involved in evolutionary diversification of these mate-finding mechanisms that is critical to understanding speciation in moths and other taxa. We used a combined quantitative trait locus (QTL) and candidate gene approach to determine the genetic architecture of sexual isolation in males of two congeneric moths, *Heliothis subflexa* and *Heliothis virescens*. We report behavioral and neurophysiological evidence that differential male responses to three female-produced chemicals (Z9-14:Ald, Z9-16:Ald, Z11-16:OAc) that maintain sexual isolation of these species are all controlled by a single QTL containing at least four odorant receptor genes. It is not surprising that pheromone receptor differences could control *H. subflexa* and *H. virescens* responses to Z9-16:Ald and Z9-14:Ald, respectively. However, central rather than peripheral level control over the positive and negative responses of *H. subflexa* and *H. virescens* to Z11-16:OAc had been expected. Tight linkage of these receptor genes indicates that mutations altering male response to complex blends could be maintained in linkage disequilibrium and could affect the speciation process. Other candidate genes such as those coding for pheromone binding proteins did not map to this QTL, but there was some genetic evidence of a QTL for response to Z11-16:OH associated with a sensory neuron membrane protein gene.

mating | speciation | AFLP | odorant receptor | *Heliothis*

Evolutionary diversification of sexual communication traits remains paradoxical (1, 2) because signal production and signal reception are under independent genetic control, and a mutation causing an alteration in one component of the system is predicted to reduce efficiency of communication and to cause a loss of fitness. The resulting stabilizing selection is expected to promote evolutionary stasis, not diversification (3–5). Systems in which changes in signals and responses are governed by the same genetic alterations (i.e., pleiotropy) should be less evolutionarily constrained in many cases (6), and studies of mating communication have revealed a few systems that appear to have this property (7–9). However, no pleiotropy has been found between signal production and response in moths (e.g., 5, 10). Because female and male moths with divergent signals and responses appear to be selected against (11, 12), we have no simple explanation for the great diversity of moths (~180,000 species) and moth pheromones (5, 13, 14).

Beyond capturing the attention of evolutionary biologists, the diversity of long distance, pheromone-based sexual communication traits in moths has become a focus of some molecular biologists, biochemists, neurophysiologists, and communications specialists because of the surprisingly high specificity of signals and responses within a species and the clear differentiation in signaling systems among species (15, 16). In the past 20 years, a

great deal has been learned about the biosynthetic pathways that result in precise ratios of specific compounds in pheromone blends (17), and major breakthroughs have recently been made in our understanding of the mechanisms that enable a male to detect incredibly low concentrations of pheromone molecules (18, 19). We now know that peripheral reception of pheromones involves a number of proteins in male antennae, including pheromone binding proteins (PBP), general odorant binding proteins (GOBP), chemosensory proteins (CSP), two classes of odorant receptors (OR), pheromone degrading enzymes (PDE), and sensory neuron membrane proteins (SNMP) (19–21). Genetic changes in the structure/expression of any or all of these proteins could have been involved in evolutionary diversification of moth sexual communication systems, but it is also possible that the crucial changes were in the male moth central nervous system (5, 22).

One pioneering study tested two races of the pyralid moth *Ostrinia nubilalis* (European corn borer) for a relationship between genetic traits for antennal neuron spike patterns and male pheromone response but found none (23). A related study on *Ctenopseustis* moths (brownheaded leafrollers) did find a correlation (24) but did not examine the genes that could be involved. More recently, correlations have been found between neuron targeting and pheromone responses (25, 26), but their genetic basis is unknown. As pointed out by Smadja and Butlin (5), a critical next step in understanding how mate communication systems diversified is the determination of what kinds of changes in which genes resulted in divergent signals and responses of closely related species and races.

Here we focus on understanding the genetic architecture and genes involved in the sexual communication differences between two closely related, nonsister species of heliothine moths with a divergence time of approximately 2 million years based on CO-I divergence (27). *Heliothis virescens* (hereafter referred to as *Hv*) is a generalist, feeding on plants in over 14 families, whereas *Heliothis subflexa* (*Hs*) specializes on plants within the genus *Physalis* (28, 29). These two species are not attracted to each other in field locations where they cooccur because of differential response to pheromone blends (28), but they can be mated and backcrossed in

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the laboratory (28). Our previous quantitative trait locus (QTL) studies with backcross (BC) families demonstrated that genes on at least nine of the 31 *Heliothis* chromosomes contribute to the differences between the species in the volatile compounds produced by the pheromone gland and indicate that there can be epistatic interactions among the QTL (29, 30). In the current experiments, we used a combined QTL/candidate gene approach to determine what classes of genes code for the differences between males of the two species in their response to pheromone blends.

Hv males must perceive Z11-16:Ald and Z9-14:Ald to maintain flight toward a pheromone source in a wind tunnel (31). The presence of Z11-16:Ald is also critical for *Hs*, but these males do not respond to Z9-14:Ald at normal concentrations in pheromone blends. Instead, they require Z9-16:Ald and Z11-16:OH (32). The response of *Hs* is significantly enhanced by Z11-16:OAc, a compound that inhibits response of male *Hv* (28). The chemicals in the female sex pheromones of the two species and their ratios match to the male responses.

A series of papers by Krieger et al. (33, 34) identified a set of ORs in *Hv* with much higher expression in male antennae compared to those of females. Subsequent studies elucidated some of their pheromone ligands and their localization to specific sensilla (35–37). Other studies of *Hv* identified PBPs (38), GOBPs (39), SNMPs (40), and CSPs (41). Genetic alleles associated with any of these molecules could control differences between *Hv* and *Hs* male response. If coding or *cis*-regulatory sequence differences between the two species in one or more of these genes have an impact on male response specificity, then in segregating BCs between the two species, QTL including these genes would cosegregate with the pheromone response phenotype of BC males.

Heliothis species are especially well suited for QTL analysis because they have 30 autosomes of similar size with no recombination in females. Therefore, when female hybrids are used in a BC, there are 30 unambiguous linkage groups that could contain QTL (29). Mapping of a QTL within a chromosome is subsequently accomplished by BCs using hybrid males that have normal recombination. Furthermore, repeated BCs to one of the parental species can be used to introgress a single chromosome from the second species into the genome of the first. QTL analysis relies on efficient and accurate assessment of the phenotype of interest. Response of individual *Hv* and *Hs* males to synthetic pheromone blends can fortunately be measured in a wind tunnel based on whether they take flight and how far they fly along a 1-m path toward the pheromone source.

Results

BC-Male Response. We conducted four BCs, each starting with a cross of one *Hv* female to an *Hs* male. Hybrid females resulting from these crosses were individually mated to *Hs* and *Hv* males to establish two *Hs* BC families (*Hs*-BC) and two *Hv*-BC families, respectively. The genetically segregating *Hs*-BC and *Hv*-BC male offspring were tested for behavioral response to pheromone blends containing one of the species-specific compounds, Z9-14:Ald or Z9-16:Ald. We measured response qualitatively by whether an individual male flew at least halfway to the source. More quantitatively, we ranked degree of each male's response on a scale of 0–7 described in *Materials and Methods*. We first tested response of *Hs*-BC males to a blend containing Z11-16:Ald, Z9-14:Ald, and Z11-16:OH in a 1.0:0.1:0.1 ratio, which was previously found to attract F₁ males but not *Hs* males in a wind tunnel (32, 42). Because *Hv* was the nonrecurrent parent in these crosses, each BC offspring could have one or no copies of each complete *Hv* autosome. Our expectation was that males that inherited one copy of an *Hv* chromosome with pheromone-response gene(s) would be more likely to respond positively to the blend with Z9-14:Ald than those that did not inherit this chromosome. Of 90 *Hs*-BC males presented with this blend in a wind tunnel, 36 flew at least halfway

toward the pheromone source, suggesting that these males had inherited an *Hv* chromosome with gene(s) for response to Z9-14:Ald. In a smaller experiment, *Hv*-BC males were tested for flight toward a blend with Z11-16:Ald, Z9-16:Ald, and Z11-16:OH, in a 1.0:0.5:0.1 ratio, which is attractive to F₁ males but not to *Hv* males (31, 42). Fifteen of 28 males flew at least halfway to the pheromone source, suggesting that they had inherited *Hs* gene(s) for response to the Z9-16:Ald.

Genetic Maps and QTL Analysis. To determine which *Hv* chromosomes each *Hs*-BC male inherited and which *Hs* chromosomes each *Hv*-BC inherited, we used previously developed Amplified Fragment Length Polymorphism (AFLP) methods (29) to build genetic maps of the segregating BC families (BC to *Hv*, 230 AFLP markers, range 3–18 per chromosome; BC to *Hs*, 211 AFLP markers, range 3–19 per chromosome) (see *SI Text*, Table S1 for specific primers used).

Once the genotyping was completed, we used G-tests with Yates corrections (43) to check for associations between male response and the presence/absence of specific chromosomes from the nonrecurrent parent (44). In the *Hs*-BC, only one of the *Hv* chromosomes [chromosome 27 (*Hv*-C27)] showed a statistically significant association with male flight toward the blend. Of the males with one copy of *Hv*-C27, 34 of 40 had flown at least halfway toward the Z9-14:Ald-containing blend, but only 2 of 50 males without *Hv*-C27 had flown at least halfway toward the blend ($\chi^2 = 58.88$, $P < 0.000000001$; with Bonferroni correction $P < 0.000000003$). In the *Hv*-BC, 14 of 18 moths with a copy of *Hs*-C27 had flown at least halfway to the blend with Z9-16:Ald, although only 1 of 10 without *Hs*-C27 had flown at least halfway to this blend ($\chi^2 = 9.98$, $P = 0.0016$; Bonferroni correction = 0.048). No other *Hs* or *Hv* chromosomes were associated with male response ($P = 0.05$ without Bonferroni correction). To better visualize the differences between responses of males with and without C27 from the nonrecurrent parental species Fig. 1 presents the degree of response by males of each genotype. Clearly, C27 contained one or more critical DNA sequences that differentiate male responses of the two species with respect to the preference of either Z9-14:Ald or Z9-16:Ald.

Maps of Candidate Genes. We mapped genes coding for 11 ORs, 2 PBPs, 1 SNMP, 2 CSPs, and 1 GOBP to individual autosomes or to the sex chromosome (*Materials and Methods*). We included some ORs that are expressed in both males and females because recent evidence indicates that females perceive certain components present in their own pheromonal mixtures (45, 46). We first mapped these genes in an *Hv*-BC family, testing for non-independent segregation of the *Hs* allele of each candidate gene and the *Hs* form of one of the autosomes. Genes were mapped to the sex chromosome based on presence of the *Hs* allele of the candidate gene in BC males but not in females (females are the heterogametic sex). For confirmation, we then mapped the genes in an *Hs*-BC family. Table 1 presents the chromosomal locations of all 17 candidate genes. Five chromosomes had only a single OR gene, although chromosome 19 and chromosome 27 had two and four OR genes, respectively. Genes for all of the PBPs, CSPs, and GOBP1 were found on the same chromosome (C19).

HR13, which is the OR for Z11-16:Ald (36), the most abundant pheromone component of *Hv* and *Hs*, was the only receptor that mapped to the sex chromosome. Genes coding for HR14, HR15, and HR16, which have been associated with response to other critical *Hv* pheromone compounds (35, 47), all mapped to C27, which was the one chromosome that cosegregated with male response to the Z9-14:Ald and Z9-16:Ald in our QTL analysis above. *HR6* was the only other candidate gene that mapped to C27. This OR could also be involved in pheromone response but its lack of tissue-specific expression makes it a less likely candidate (35, 47). These results suggest that changes in coding and/or regulatory regions of one or more of these OR genes are

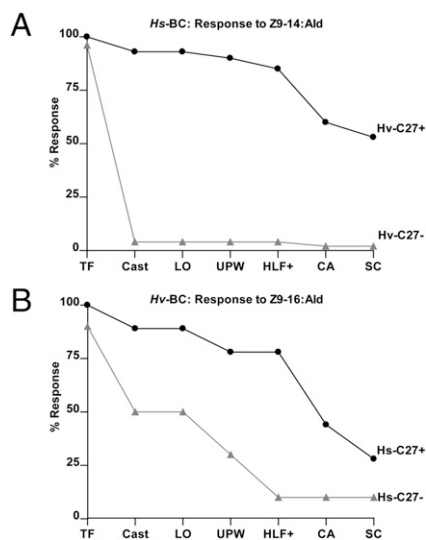


Fig. 1. Response of backcross (BC) males to pheromone blends with species-specific aldehydes. The graphs show the percentage of male moths of each C27 genotype with successively stronger responses to the test pheromone blends. TF = took flight, Cast = cast back and forth in search of pheromone plume, LO = locked-on to the plume, UPW = flew upwind less than halfway to the source of pheromone, HLF+ = flew at least halfway to the source, CA = close approach to the source (<5 cm), SC = source contact by male. (A) Males tested were progeny from a first BC to *Hs* and the blend tested contained the *Hv* compound, Z9-14:Ald. The two genotypes are homozygotes for *Hs-C27* (no copies of *Hv-C27*; solid gray triangle) and heterozygotes for C27 (one copy from *Hv*; solid black circles) (B) Males tested were progeny from a first BC to *Hv* and the blend tested contained the *Hs* compound, Z9-16:Ald. The two genotypes are homozygotes for *Hv-C27* (no copies of *Hs-C27*; solid gray triangle) and heterozygotes for C27 (one copy from *Hv*; solid black circles). See main text for details.

responsible for altered male response to the two aldehydes, Z9-14:Ald and Z9-16:Ald.

Introgressing and Mapping Chromosome 27. To further examine the role of genes within C27 in male response, *Hs-C27* was introgressed into the *Hv* genomic background by repeatedly backcrossing females with *Hs-C27* to *Hv* males (for general methods see refs. 28, 48). This resulted in a BC line that was identical to *Hv* except that about 1/2 of the individuals inherited one copy of *Hs-C27* (checked with AFLPs and *HR14* sequences). Males from the fifth BC generation were tested in a wind tunnel for their response to blends containing Z9-16:Ald. Seven of 15 males with one copy of *Hs-C27* flew at least halfway toward the blend with Z9-16:Ald, whereas only 5 of 30 males without *Hs-C27* flew at least halfway toward the Z9-16:Ald blend (χ^2 with Yates correction = 4.14; $P = 0.042$). The mean degree of response for the

Table 1. Candidate genes mapped to *Heliothis* chromosomes

Candidate Gene	Chromosome	Candidate Gene	Chromosome
HR2	1	HR16	27
HR5	4	HR18	7
HR6	27	CSP1	19
HR7	8	CSP2	19
HR11	3	GOBP1	19
HR12	8	PBP1	19
HR13	Z	PBP2	19
HR14	27	SNMP1	24
HR15	27		

males with *Hs-C27* was 4.40 on our scale from 0 to 7 (*Materials and Methods*), whereas for those without *Hs-C27* it was only 1.97.

After the fifth BC, males that were heterozygous (one copy of *Hs-C27* and one of *Hv-C27*) were crossed to *Hv* females to allow recombination within C27. No recombination among the four OR genes was found among the 62 offspring analyzed, but we were able to use this male BC to map the general location (within approximately 6 cM) of the OR genes within C27 by use of 14 recombining AFLP markers and the *HR14* codominant marker (Fig. S1). In a final attempt to separate the OR genes through recombination, we analyzed a total of 574 BC offspring (six male *Hv-BC* families) for *Hv* and *Hs* alleles of *HR14*, *HR15*, and *HR16*, but we did not find a single recombinant. This suggests that the HR genes are a tightly linked cluster of duplicated genes.

Further Backcrossing to Isolate a Smaller QTL Region for Response to Z9-16:Ald. Backcrossing of males that were positive for the *Hs-HR14* allele, as determined by PCR, was continued for 15 more generations to allow for recombination and eventual loss of segments of *Hs-C27* that were not tightly linked to the OR gene cluster. One half of the male offspring from the 15th BC generation of backcrossing were expected to be identical to *Hv* for all autosomes, sex chromosomes, and mitochondria, with the exception of being heterozygous for *Hs* genes that are physically linked to *Hs-HR14*. The other half of the offspring were expected to be genetically identical to *Hv*. Male offspring ($n = 80$) were flown in a wind tunnel to blends containing Z9-16:Ald. If a male did not respond to this blend (by more than simply taking flight), it was flown to a blend with Z9-14:Ald. Of 58 males with one copy of the *Hs-HR14* allele, 45 responded to the blend with Z9-16:Ald with a mean degree of response equal to 3.89. The 13 males with *Hs-HR14* that did not respond to this blend also did not respond to the blend with Z9-14:Ald. Of 22 males without the *Hs-HR14* allele, none responded to the blend containing Z9-16:Ald and 19 responded to the blend with Z9-14:Ald with a mean degree of response of 5.58. AFLP analysis of nine markers on C27 revealed that four of the males with the *Hs-HR14* allele only had one or two of the AFLP markers from *Hs*. All of these males responded to the Z9-16:Ald blend. Furthermore, no relationship was found between the number of *Hs-C27* AFLP markers (range 1–9) and the degree of response (0–7 scale) to the Z9-16:Ald-containing blend (Spearman rank order correlation = -0.18 ; $P = 0.203$). This indicates that only the four HR genes and genes tightly linked to them could be controlling male response to the Z9-16:Ald.

Response to the Acetate, Z11-16:OAc. The Z11-16:OAc component of the *Hs* blend enhances *Hs* male response but decreases that of *Hv* (28, 49). Grosse-Wilde et al. (35) found, evidence that Z11-16:OAc is a ligand for HR14 based on expression of *HR14* in receptor neurons neighboring those expressing *HR16* (also see ref. 47) as well as binding affinity in a heterologous system. These results suggest that the *Hv* and *Hs* alleles of *HR14* on C27 could impact male response to Z11-16:OAc. Therefore, we flew BC males to pheromone blends with and without this odorant. Previous work had established that F₁ males were partially deterred by Z11-16:OAc (42), so we considered its deterrent effect to be codominant. In one test, single pair crosses were conducted between males and females that were each genetically identical to *Hv* except for being heterozygous for the full *Hs-C27* chromosome (as determined by the codominant *HR14* genetic marker). The offspring of this cross were expected to segregate into three genotypes: homozygotes for *Hs-C27*, heterozygotes, and homozygotes for *Hv-C27*. Male offspring from these crosses ($n = 62$) were first flown to a blend of Z11-16:Ald/Z9-16:Ald/Z11-16:OH/Z11-16:OAc in a 1:0.5:0.1:0.1 ratio. They were then flown to a similar blend that lacked the acetate, which was expected to be more attractive to males that were heterozygous for *Hs-C27*. Males that did not respond to either of these blends were flown to the *Hv* blend of Z11-16:Ald/

Z9-14:Ald in a 1.0:0.05 ratio. We specifically chose this order of exposure because males generally respond more strongly to their first exposure and preliminary tests indicated that this order resulted in more response to blends with the acetate. Nine males did not respond at all, and of the 16 responsive males that were homozygous for *Hv*-C27 chromosome, 15 only responded to the *Hv* blend. Of the males that were heterozygous for *Hs*-C27 ($n = 25$), 80% responded less to the blend with the acetate than to the blend lacking the acetate. In contrast, only 25% of males homozygous for the *Hs*-C27 ($n = 12$) responded less to the acetate-containing blend (χ^2 with Yates correction = 7.80; $P = 0.0052$ —no need for Bonferonni correction).

To confirm this finding, we tested males from a typical BC of a hybrid female to an *Hv* male where there were only two C27 genotypes, those that were homozygous for the *Hv*-C27 chromosome and those that were heterozygous (one copy of C27 from *Hs* and one copy from *Hv*). We tested these males to a blend of Z11-16:Ald/Z9-14:Ald/Z11-16:OH/Z11-16:OAc in a 1:0.1:0.1:0.1 ratio and then to this blend without the acetate. We expected the blend with acetate to be more deterrent to homozygotes for *Hv*-C27. Of males homozygous for *Hv*-C27 ($n = 34$), 44.1% responded less to the blend with the acetate. In contrast only 6.9% of heterozygous males ($n = 29$) responded less to the blend with the acetate (χ^2 with Yates correction = 11.37, $P = 0.0007$). For both heterozygotes and homozygotes, more males responded positively to the blend with acetate than we had expected. The higher relative responsiveness to the acetate blend could be due to the fact that their first exposure was to this blend.

Response to the Alcohol, Z11-16:OH. Results from Grosse-Wilde et al. (35) demonstrate that Z11-16:OH is a ligand for HR16, the gene for which is found on C27. Therefore, we also tested the potential involvement of C27 in the differential response of *Hv* and *Hs* to Z11-16:OH. *Hs* males require this compound to be attracted, although *Hv* males respond to blends without it (32). Because F_1 hybrid males are more responsive to blends without Z11-16:OH than *Hs* males, we treated response to this compound as a codominant trait and tested response of male offspring from a first female BC to *Hs*. About 50% of these males were expected to be heterozygous for C27, and the other 50% were expected to be homozygous for *Hs*-C27. Males were first flown to a blend of Z11-16:Ald/Z9-16:Ald in a 1.0/0.5 ratio, after which they were flown to a similar blend with the addition of Z11-16:OH at a 0.1 ratio. We tested whether males that were heterozygous for *Hs*-C27 were more likely to respond to the blend without the alcohol than males homozygous for the *Hs* form. Of 55 heterozygotes, 67% responded to the blend without the alcohol, and of 48 homozygotes, 77% responded ($\chi^2 = 1.228$, $P = 0.2678$). This indicates that *Hs* homozygote and heterozygote males do not differ. The data from this experiment were also analyzed based on degree of response. Of 54 heterozygotes that could be scored, 72% had a higher score when the alcohol was present, although 57% of 47 homozygous males had a higher score with the alcohol present ($\chi^2 = 2.394$, $P = 0.1218$). This indicated clearly that C27 did not affect the requirement for Z11-16:OH by males.

To follow up on these results, we used AFLPs to map all 30 autosomes from this BC to *Hs*. We tested each autosome for effects on the ratio of males that responded more to the blend that included the alcohol. Only chromosome 24, which includes an SNMP gene, showed a significant P value ($\chi^2 = 6.88$, $P = 0.0087$) but when adjusted using a Bonferonni correction the P value became 0.261. Therefore, no single autosome appears to strongly affect male response to Z11-16:OH. We could not test for a relationship between the species origin of two male Z sex chromosomes and response to the alcohol because all males in this BC are homozygous for the Z chromosome of *Hs*.

Recordings from Single Antennal Neurons. Previous single cell recordings from male antennal sensilla have shown differences in response of male *Hv* and *Hs* neurons to specific pheromone components (50). We hypothesized that if alleles of the HR genes in *Hv* and *Hs* were responsible for the behavioral differences among male genotypes, then we should find distinct electrophysiological responses in moths with *Hs* versus *Hv* receptor alleles. We compared the electrophysiological responses of the following types of males: (i) pure *Hv*, (ii) pure *Hs*, (iii) *Hv* except for being homozygous for *Hs*-C27. We recorded independently from B-type and C-type sensilla that are described in Baker et al. (50). As expected from Baker et al. (50), the neurons in B-type sensilla of pure *Hv* were activated by low concentrations of Z9-14:Ald but not Z9-16:Ald (Fig. 2*A* and *B*). B-type sensilla of *Hs* males were somewhat more sensitive to Z9-16:Ald than to Z9-14:Ald. The males that were identical to *Hv* except for having *Hs*-C27 responded much like the pure *Hs* males. The neurons of C-type sensilla of *Hv* responded strongly to both Z11-16:OH and Z11-16:OAc (Fig. 2*C* and *D*). *Hs* C-type sensilla also responded strongly to Z11-16:OH but only weakly to Z11-16:OAc. The response to Z11-16:OAc by *Hv* males with *Hs*-C27 was generally similar to the pure *Hs* males. Curiously, the *Hs*-C27 males had a stronger response to Z11-16:OH than the pure *Hv* and *Hs* males, which were quite similar to each other (Fig. 2*D*). These electrophysiological results reinforce the behavioral genetic studies in that the C27 genotype affected response to the two aldehydes and the acetate, but did not affect response to the alcohol.

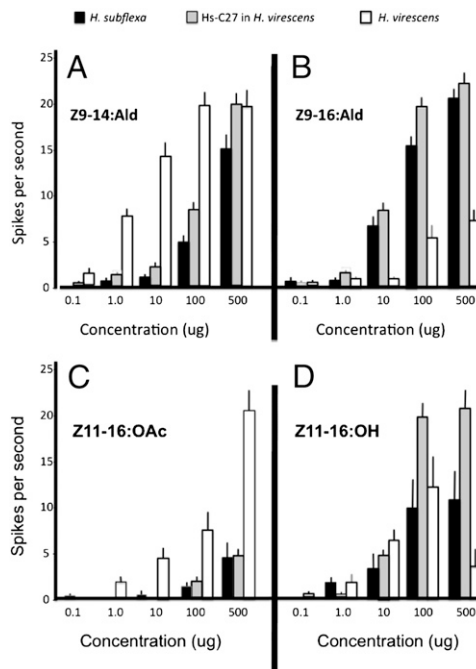


Fig. 2. Single cell recordings from males of (1) pure line *Hs*, (2) *Hv* with *Hs*-C27, (3) pure line *Hv*. A cut-tip recording method was used to measure activity from olfactory receptor neurons housed within B-Type sensilla during stimulation with either Z9-14:Ald or Z9-16:Ald (*A* and *B*) and C-Type sensilla (*C* and *D*) sensilla during stimulation with Z11-16:OAc or Z11-16:OH. For each recording, a dose series (0.1–500 μ g) was used to determine relative responses to each odorant. Responses by introgressed male *Hv* with *Hs*-C27 to Z9-14:Ald, Z9-16:Ald and Z11-16:OAc were more similar to pure line *Hs* than pure line *Hv*. *Hv* with *Hs*-C27 responded more strongly to Z11-16:OH than either pure line. ** Number of olfactory receptor neurons recorded Type Bs: *H. subflexa*, $n = 7$; *H. virescens* with *Hs*-C27, $n = 27$; *H. virescens*, $n = 11$ Type Cs: *H. subflexa*, $n = 4$; *H. virescens* with *Hs*-C27, $n = 11$; *H. virescens*, $n = 3$.

Discussion

DNA sequence differences in a tightly linked portion of C27 cause major differences between *Hs* and *Hv* males in their responses to Z9-16:Ald and Z9-14:Ald, and are also responsible for at least a substantial portion of the difference between the two species in their responses to Z11-16:OAc. It is surprising to find that a change in receptors for Z11-16:OAc could be responsible for the switch between the positive behavioral response of *Hs* and the negative response of *Hv* to this compound. In *Drosophila* where *cis*-vacenyl acetate is attractive to females but repulsive to males, it is a central nervous system difference that controls the switch between positive and negative response (22). Furthermore, previous work showed that acetate responsive receptor neurons of *Hv* converge on a different glomerulus of the male macroglomerular complex compared to those of *Hs* (51). In mammals, a change in the receptor gene expressed in a neuron can affect glomerular targeting, but it is thought that such targeting does not occur in any insects based on work with *Drosophila melanogaster* (19). If this assumption is incorrect, it could be that changes in the acetate receptor amino acid sequence could alter the targeting of the neurons. We have not yet determined if the differential glomerular targeting in *Hv* and *Hs* maps to C27.

From work with *Drosophila* and other insect genomes it is apparent that OR genes are often clustered within small chromosomal regions and appear to have arisen from gene duplication (52). Our finding of four OR genes in a segment of C27 that rarely if ever recombines is in line with this previous information. However, our recombination data cannot differentiate between linkage due to close tandem genes versus species-specific inversions (53). A phylogenetic analysis of *Hv* OR proteins indicates that HR6, HR14, HR15, and HR16 are more closely related to each other than any other known *Hv* OR proteins, arguing for gene duplication (34). HR11 and HR13 are also closely related to this group of four, but their genes map to chromosome 3 and the Z sex chromosome, respectively. HR13 is the receptor for the major component of the *Hv* and *Hs* pheromones and HR11 has recently been shown to have time and cell-specific expression patterns linked with HR13 (37). The receptor for bombykol, the major component of the silkworm (*Bombyx mori*) pheromone, clusters phylogenetically with HR13 (54) and is also located on the sex chromosome (55). Functional and comparative genomic studies of *Hv*, *Hs*, and related moth species will help to determine the evolutionary processes that have shaped the location and sequence divergence of these pheromone-related OR genes.

Our study revealed that the genes for three other classes of proteins associated with peripheral reception of odors (CSP1, CSP2, GOBP1, PBP1, and PBP2) are all found on the same chromosome. We have yet to perform fine-scale mapping of chromosome 19 to determine their locations relative to each other. Although these genes could all be involved in differential perception and response to species-specific pheromones, our QTL analysis found no evidence of their involvement in differences between *Hv* and *Hs* male response. Although an SNMP gene on chromosome 24 may influence response to Z11-16:OH, the data are not strong because the multiple tests involved increase the chance of type I errors. An independent test of this association would be useful.

The tight genetic linkage of receptors that are critical to species isolation could have important evolutionary consequences both in terms of the build-up of linkage disequilibrium between novel alleles of multiple receptor genes early in the process of speciation (56) and for evolution of strong isolation after speciation occurs (57). A number of theoretical analyses suggest that the number of independently assorting sexual isolation genes can affect the likelihood of speciation (e.g., 6, 58, 59). Our current data cannot test whether the tight linkage of OR genes involved in pheromone reception is simply an outcome of genome evolution that has a side-effect on speciation, or if selection acted to

build this linkage through species-specific inversions (60). Our data also bring up the question of whether selection or a general property of the genome led to *HRI3* and *HRI1* being on different chromosomes. Only more detailed comparative studies will shed light on these questions.

Even though our study suggests that a few genes can strongly impact differential male response to important pheromone components, we do not know how many independent changes in base pairs, or indels within these genes affect male behavior. Sequence comparisons among moth species and heterologous expression of mutated receptor genes would help in assessing which differences in the C27 receptor gene region have significant impacts on male behavior.

Materials and Methods

Mapping Candidate Genes. The DNA processing and assignment of specific AFLP markers to specific chromosomes followed procedures described in Sheek et al. (29). The primers used and the number of markers per chromosome are presented in Table S2. We designed PCR primers for 11 ORs, 2 PBPs, 1 SNMP, 2 CSPs, and 1 GOBP based on *Hv* sequences in GenBank (Table S2). Only primers that reliably amplified both *Hv* and *Hs* genomic DNA and produced bands with species-specific migration patterns on agarose gels were used as codominant markers (see Table S2 and S3 for specific genes, restriction enzymes, primers, PCR conditions, and migration values). PCR products were sequenced to check for identity with the candidate gene sequence in GenBank. DNA of *Hv*-BC offspring and the *Hs*-BC offspring was amplified using each of the 17 primer pairs separately, and the products were run on agarose gels [number of BC offspring tested for each candidate gene: mean (SD) = 19.3 (1.5)]. For each of the candidate genes, the correspondence was assessed between the presence of bands representing *Hv* and *Hs* alleles of the candidate gene in the BC and the presence/absence of bands from the *Hv* or *Hs* AFLP markers for the 30 autosomal linkage groups in the same insects (see ref. 61). In all cases, an obvious match between the codominant marker for a candidate gene and a single AFLP-identified chromosome was found (three mismatches in 328 comparisons). Fine scale mapping of C27 was done with JoinMap (62) using default parameter settings.

Chemicals. Test compounds for both flight tunnel assays and neurophysiology were obtained from Bedoukian Research, Inc. (>95% purity by gas chromatography), and stock solutions were diluted in steps from 100 ng to 1 mg in hexane and stored at -20 °C until use. Five compounds were used in the wind tunnel assays: Z11-16:Ald, Z9-14:Ald, Z9-16:Ald, Z11-16:OAc, and Z11-16:OH. The blends were created by admixing the required components directly onto a circular piece of filter paper (1-cm diameter). Stimulus cartridges for single sensillum recording had single compounds loaded on filter paper at dosages between 100 ng and 500 ng.

Wind Tunnel Assays. Wind tunnel assays followed procedures in Vickers (32) in which the filter paper with the pheromone blend being tested is placed 1 m upwind from a platform upon which the test male is initially placed. As in Vickers (32, 42) males were typically 3–5 days old when tested. On the day of testing, males were placed in the wind tunnel for at least 1 h to acclimate to the conditions therein. Responses of individual male moths ranges from simply remaining on the take-off platform without taking flight to taking flight, casting back and forth, locking-on to the pheromone plume, upwind flight in a zigzag pattern and eventual contact with the pheromone source. To quantify the degree to which an individual male responded to a pheromone blend we established a ranking of the successive behavioral responses as follows: 0 = no flight, 1 = took flight without orientation, 2 = casting flight above take-off platform, 3 = lock-on to the pheromone plume, 4 = upwind flight less than halfway to source, 5 = upwind flight at least halfway to the source, 6 = close approach to source (<5 cm), 7 = contact with source. The mean degree of response of a genotype was calculated by multiplying each rank number by the number of males with that response, taking the sum of all of these products and dividing by the total number of males.

Electrophysiological Recordings from Single Sensilla. The general methods used are described in Hillier et al. (63). Briefly, male moths were restrained on a depression slide and a reference electrode introduced to the contralateral eye. Long trichoidsensilla were selected randomly from the proximal ventral surface of the antenna and cut using a glass capillary piezoelectric cutter (64). Once cut, a saline-filled silver-chloride glass electrode was placed over the sensillum tip and activity of sensory neurons within recorded during odor presentation.

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Supporting Information

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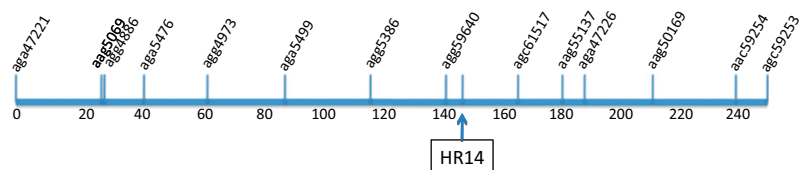


Fig. S1. Location of HR14 within chromosome 27 based on mapping of a backcross in which the male parent was heterozygous for chromosome 27 and the female parent was from the pure *Hv* colony. Based on JoinMap (1) analysis of 46 individuals using default parameters.

1. Van Ooijen JW (2006) *JoinMap 4. Software for the Calculation of Genetic Linkage Maps in Experimental Populations* (Kyazma B. V., Wageningen, Netherlands).

Other Supporting Information Files

[Table S1 \(DOC\)](#)

[Table S2 \(DOCX\)](#)

[Table S3 \(DOCX\)](#)

Table S2. Primers used for candidate genes along with matches to specific chromosomes

Candidate Gene Primers

Gene	Forward Primer (5'-3')	Reverse Primer (5'-3')
HR14 (Krieger Paper)	-S GTTCACACTGTACCTCACTGG	-AS GAACAACATTGGCCCGAATAC
HR13 (Krieger Paper)	-S CGGTCTACTTACTCGGCTTGG	-AS CTGTGCGACTGTCTGAGCATC
HR11 (Krieger Paper)	-S CAGGCATTACGGGTCCAATGG	-AS GGTCAAACATCGACACGCTGC
HR5 (Krieger Paper)	-S CTGTCCTGCTCATGCAACTTC	-AS TGCATCATTGCCTTGATCATC
HR15	4F TGTTGCGCAAATGACCGTGGCTG	3R TGCCTTACATGCACAGGCTC
HR16	3F TCATCAGGCAAGTGGCTGTC	1R TGGCAGTCCATATACCGCGTGC
HR2	5F GAAGCGGCTTACTCCTGCCAGTGG	5R CATGAAGTAGGTTACCACGGCTCC
HR6	1F TCATCAGAACTTGGCCTCGGAA	2R CCATAGCATGCTTAGAACGATCC
HR7	9F CAACTGCAGGTGGTATTCCGCCAA	10R CGAAATACGACCACGCTGAGCTT
CSP1	2F ACCTGGACGAGATCCTCAGCAACC	4R CATTGGTTCCAAGCTACAGGA
CSP2	2F GAAATCTTGGAGTCTCAGCGCCT	4R AAAGCTTTGGTAACTGCGTCTG
PBP1	2F ACAGACACAAGGGCTGCGCCAT	3R GGCTACGTTGAGGGCCTTCATGCA
PBP2	3F TTTGCCAAGAGCCACGGCGCTGAC	4R GATGACCTCCATGCTGGGAGCCCA
GOBP1	4F CGAGGCACGCTAGTGCGTCTCAT	4R AGCAGCACTCGCTTGCATCAGCA
HR12	4F TGGCCTTGGGTGTATCTGCGACAG	4R CTCGATACAGTGTGTTGAGCAATCG
HR18	1F TTACCATATCATCAAGGAGCGTG	5R AGGGCCCATAAACGTTCTGCAGCT

Candidate Gene Primers	Restriction Enzyme	Chr (04 V-dir)	MW Hv DNA Band (bp)	MW Hs DNA Band (bp)	PCR Program
Gene		27	1300	1000	57
HR14 (Krieger Paper)	BamHI	Sex	1400	1000, 400	57
HR13 (Krieger Paper)		26	1100	1000	57
HR11 (Krieger Paper)	EcoRI	3	950, 900	1600	57
HR5 (Krieger Paper)		27	600, 450	500	57
HR15		27	1700, 800	550	57
HR16		9	700	350	614
HR2		27	750	1400, 750	614
HR6		19	1200	1000	57
HR7		7	900	650	57
CSP1	Tsp45I	7	400	287, 85	57
CSP2		7	585	600	57
PBP1		7	430	450	57
PBP2		7	350	300	57
GOBP2					57
HR9		19	350	300	57
HR12	HindIII	10	750, 100	850	57

Table S1. AFLP Markers used for maps and number of markers per chromosome.

04 Hs-BC map - 78 individuals used to make map

Chrom. Numb.	Marker ID	Number of markers	Chrom. Numb.	Marker ID	Number of markers
C01	*aac47111	8	C15	*aac50115	10
C01	*aac50310		C15	*aac50182	
C01	*aac59156		C15	*aac53191	
C01	*aag51253		C15	*aag52303	
C01	*aag59375		C15	*aag59232	
C01	*aca47166		C15	*aca47250	
C01	*aca47426		C15	*aca51141	
C01	*aga4778		C15	*aca59215	
C02	*aac47114	7	C15	*aga47224	
C02	*aag4981		C15	*agc54240	
C02	*aag50213		C16	*aac50146	6
C02	*aag50326		C16	*aac51194	
C02	*aag56244		C16	*aac53241	
C02	*aca4974		C16	*aag5695	
C02	*aca5164		C16	*aca59272	
C03	*aac47141	6	C16	*aga49352	
C03	*aac48343		C17	*aac50170	15
C03	*aac5490		C17	*aac50193	
C03	*aag49200		C17	*aac59325	
C03	*aga4763		C17	*aag49278	
C03	*aga49207		C17	*aag49376	
C04	*aac47163	7	C17	*aag60217	
C04	*aac51290		C17	*aca47174	
C04	*aac53124		C17	*aca59100	
C04	*aac55327		C17	*aca59114	
C04	*aac59302		C17	*aga48264	
C04	*agc4997		C17	*aga48291	
C04	*agc54105		C17	*aga49121	
C05	*aac47269	9	C17	*agc51-72	
C05	*aac49163		C17	*agc59327	
C05	*aac50144		C17	*agc62125	
C05	*aac50153		C18	*aac50177	9
C05	*aca59474		C18	*aac50340	
C05	*aga47207		C18	*aac55238	
C05	*aga47491		C18	*aac5988	

C05	*aga48377		C18	*aag56155	
C05	*agc54142		C18	*aca47100	
C06	*aac47280	8	C18	*aca48240	
C06	*aac5290		C18	*agc51129	
C06	*aag51464		C18	*agc51235	
C06	*aag60403		C19	*aac50210	5
C06	*aca47198		C19	*aag59164	
C06	*aca51288		C19	*aca47342	
C06	*aga49168		C19	*aca48115	
C06	*agc47298		C19	*agc47123	
C07	*aac47289	7	C20	*aac50343	7
C07	*aac54284		C20	*aac54169	
C07	*aac59203		C20	*aca55269	
C07	*aag51243		C20	*agc47337	
C07	*aga47312		C20	*agc4986	
C07	*agc47137		C20	*agc59174	
C07	*agc51302		C20	*agc62206	
C08	*aac47327	10	C21	*aac5091	9
C08	*aac51185		C21	*aac5483	
C08	*aac54291		C21	*aag49356	
C08	*aac55270		C21	*aag49560	
C08	*aag51471		C21	*aag56102	
C08	*aca51118		C21	*aag59298	
C08	*aca51179		C21	*aca48319	
C08	*aca55308		C21	*aga49211	
C08	*aca55349		C21	*agc47141	
C08	*aca5978		C22	*aac51126	7
C09	*aac47363	4	C22	*aac52132	
C09	*aac50140		C22	*aca60223	
C09	*agc51326		C22	*aga47300	
C09	*agc62181		C22	*aga47353	
C10	*aac47684	6	C22	*aga4895	
C10	*aac51382		C22	*agc47174	
C10	*aac53184		C23	*aac51161	7
C10	*aac55110		C23	*aac54313	
C10	*aca51169		C23	*aac59383	
C10	*agc54178		C23	*aag59138	
C11	*aac48169	6	C23	*aca48336	
C11	*aac48260		C23	*aga49126	
C11	*aac52353		C23	*agc49268	
C11	*aag49274		C24	*aac51197	8
C11	*aag52261		C24	*aac59164	
C11	*aag59131		C24	*aag60149	
C12	*aac48462	3	C24	*aca51313	
C12	*aac54121		C24	*aca59150	
C12	*aca47356		C24	*aga48206	

C13	*aac49136	5	C24	*aga49140	
C13	*aac49575		C24	*agc54273	
C13	*aac5269		C25	*aac52227	3
C13	*aac54193		C25	*aca49336	
C13	*aca60171		C25	*agc5485	
C14	*aac49248	19	C26	*aac53109	4
C14	*aac50102		C26	*aag59174	
C14	*aac52186		C26	*aag59-81	
C14	*aac52195		C26	*agc59296	
C14	*aac53207		C27	*aac59237	3
C14	*aac54201		C27	*aga49159	
C14	*aac59206		C27	*agc59237	
C14	*aag50261		C28	*aag51261	5
C14	*aca4889		C28	*aca48127	
C14	*aca49147		C28	*agc59208	
C14	*aca59121		C28	*agc59222	
C14	*aca59291		C28	*agc59512	
C14	*aca60177		C29	*aag59182	3
C14	*aca60246		C29	*aag60388	
C14	*aga47251		C29	*aca48263	
C14	*aga48278		C30	*aca51161	5
C14	*aga49214		C30	*aca59233	
C14	*aga49260		C30	*aga48379	
C14	*agc49247		C30	*agc54113	
			C30	*agc62224	

04 Hv-BC map - 48 individuals used to make map

Chrom. Numb.	Marker ID	Number of markers	Chrom. Numb.	Marker ID	Number of markers
C01	*aac47176	8	C12	*aac48271	10
C01	*aac49270		C12	*aac55115	
C01	*aac49356		C12	*aac57353	
C01	*aac51240		C12	*aag60128	
C01	*aag60170		C12	*aca48298	
C01	*aca59423		C12	*aca55271	
C01	*agc49271		C12	*aga49275	
C01	*agc51415		C12	*agc51292	
C02	*aac47180	5	C12	*agc57354	
C02	*aac55151		C12	*agc59278	
C02	*aag48177		C13	*aac48506	6
C02	*aag49226		C13	*aag51420	
C02	*aga5380		C13	*aca47162	
C03	*aac47194	18	C13	*aca52120	
C03	*aag51-90		C13	*agc55279	
C03	*aag58-69		C13	*agc5788	
C03	*aag59303		C14	*aac49235	7
C03	*aag60115		C14	*aac59149	
C03	*aag60520		C14	*aac62146	
C03	*aca47290		C14	*aag51209	
C03	*aca48186		C14	*aca47224	
C03	*aca48-78		C14	*agc49236	
C03	*aca52288		C14	*agc54102	
C03	*aca52-81		C15	*aac49510	8
C03	*aca56131		C15	*aac58361	
C03	*aca56163		C15	*aag48117	
C03	*aga49167		C15	*aag51282	
C03	*aga50224		C15	*aca49142	
C03	*agc51257		C15	*aca49331	
C03	*agc59281		C15	*aga49288	
C03	*agg56-70		C15	*aga50-77	
C04	*aac47295	9	C16	*aac4988	8
C04	*aac47315		C16	*aac59128	
C04	*aac56191		C16	*aac59129	
C04	*aac58191		C16	*aag49223	
C04	*aag51121		C16	*aag60320	
C04	*aag51417		C16	*aca55155	
C04	*aca53255		C16	*aga52-83	
C04	*aca59222		C16	*aga53276	
C04	*aga51178		C17	*aac51252	4

C05	*aac47310	8	C17	*aag59296	
C05	*aag59201		C17	*aga52276	
C05	*aag59311		C17	*agc5995	
C05	*aca59143		C18	*aac54158	3
C05	*aca60283		C18	*aac62164	
C05	*aga48360		C18	*agc54332	
C05	*agc51207		C19	*aac54211	7
C05	*agc59157		C19	*aac5977	
C06	*aac47319	13	C19	*aca59262	
C06	*aac47436		C19	*aca60187	
C06	*aac57247		C19	*aca60328	
C06	*aac57253		C19	*aga53161	
C06	*aac59116		C19	*agc62361	
C06	*aac59117		C20	*aac55221	10
C06	*aac62239		C20	*aac59238	
C06	*aag51-99		C20	*aac59239	
C06	*aca47130		C20	*aag51110	
C06	*aca56292		C20	*aag54213	
C06	*agc55439		C20	*aag59263	
C06	*agc59213		C20	*aga49426	
C06	*agc5969		C20	*aga4981	
C07	*aac47339	9	C20	*aga50287	
C07	*aac47512		C20	*agc49106	
C07	*aac49205		C21	*aac56-83	4
C07	*aag51179		C21	*aac58-83	
C07	*aca47155		C21	*aca52-78	
C07	*aca53121		C21	*agc55155	
C07	*aga51153		C22	*aac59284	3
C07	*agc49204		C22	*aga48208	
C07	*agc5198		C22	*agc54324	
C08	*aac47380	10	C23	*aac62115	8
C08	*aac48-69		C23	*aag54322	
C08	*aac58336		C23	*aca48163	
C08	*aag48265		C23	*aca55331	
C08	*aag54210		C23	*aga48108	
C08	*aag58350		C23	*aga52-79	
C08	*aca49208		C23	*agc51132	
C08	*aga50157		C23	*agc59482	
C08	*agc49151		C24	*aac62233	5
C08	*agg57250		C24	*aag58163	
C09	*aac47416	9	C24	*aca56278	
C09	*aag47146		C24	*agc59335	
C09	*aag59-98		C24	*agg56164	
C09	*aag60143		C25	*aag48185	4
C09	*aag60175		C25	*aca55143	
C09	*aga51141		C25	*aca59428	

C09	*aga51359		C25	*aga51342	
C09	*aga52158		C26	*aag48333	13
C09	*agc59189		C26	*aag51126	
C10	*aac47539	10	C26	*aag58437	
C10	*aac55149		C26	*aca49146	
C10	*aca55242		C26	*aca60189	
C10	*aca59331		C26	*aga48102	
C10	*aga53114		C26	*aga49290	
C10	*aga53271		C26	*aga51266	
C10	*agc54211		C26	*aga51299	
C10	*agc55148		C26	*agc54229	
C10	*agc59199		C26	*agc55140	
C10	*agc59308		C26	*agc59121	
C11	*aac48130	11	C26	*agc6294	
C11	*aag48-87		C27	*aag49266	3
C11	*aag54180		C27	*agc59253	
C11	*aca56221		C27	*agg5386	
C11	*aca59463		C28	*aag51265	4
C11	*aga48221		C28	*aca47313	
C11	*aga49295		C28	*aca55264	
C11	*aga53301		C28	*aga50172	
C11	*aga53311		C29	*aca47142	5
C11	*agc4966		C29	*aca48197	
C11	*agc54236		C29	*aca60-87	
			C29	*agc55215	
			C29	*agc62170	
			C30	*aca49174	8
			C30	*aca53497	
			C30	*aca53503	
			C30	*aca59164	
			C30	*aga49383	
			C30	*aga51232	
			C30	*agc51244	
			C30	*agc5480	

Table S3. PCR programs for candidate genes

57

- 1 - 94°C for 3 min
- 2 - 94°C for 1 min
- 3 - 57°C for 1 min
- 0.5°C/cycle
- 4 - 72°C for 2 min
- 5 - Goto Step 2 18 times
- 6 - 94°C for 1 min
- 7 - 47°C for 1 min
- 8 - 72°C for 2 min
- 9 - Goto Step 6 18 times
- 10 - 72°C for 7 min
- 11 - 4°C end

614

- 1 - 94°C for 3 min
- 2 - 94°C for 1 min
- 3 - 61.4°C for 1 min
- 0.5°C/cycle
- 4 - 72°C for 2 min
- 5 - Goto Step 2 18 times
- 6 - 94°C for 1 min
- 7 - 51.4°C for 1 min
- 8 - 72°C for 2 min
- 9 - Goto Step 6 18 times
- 10 - 72°C for 7 min
- 11 - 4°C end