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DOI
10.1073/pnas.0910945107

Publication date
2010

Document Version
Final published version

Published in
Proceedings of the National Academy of Sciences of the United States of America

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

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Edited by Gene E. Robinson, University of Illinois at Urbana–Champaign, Urbana, IL, and approved March 22, 2010 (received for review September 30, 2009)

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 (*Z*9-14:Ald, *Z*9-16:Ald, *Z*11-16: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 *Z*9-16:Ald and *Z*9-14:Ald, respectively. However, central rather than peripheral level control over the positive and negative responses of *H. subflexa* and *H. virescens* to *Z*11-16: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 *Z*11-16: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

Author contributions: F.G., M.E., N.K.H., A.T.G., C.S., and N.J.V. designed research; M.E., N.K.H., B.P., C.M.W., J.L.E., and N.J.V. performed research; F.G., M.E., N.K.H., B.P., C.M.W., J.L.E., and N.J.V. analyzed data; and F.G., and N.J.V. wrote the paper.

The authors declare no conflict of interest.

This article is a PNAS Direct Submission.

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This article contains supporting information online at www.pnas.org/lookup/suppl/doi:10.1073/pnas.0910945107/-/DCSupplemental.

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 *Z*11-16:Ald and *Z*9-14:Ald to maintain flight toward a pheromone source in a wind tunnel (31). The presence of *Z*11-16:Ald is also critical for *Hs*, but these males do not respond to *Z*9-14:Ald at normal concentrations in pheromone blends. Instead, they require *Z*9-16:Ald and *Z*11-16:OH (32). The response of *Hs* is significantly enhanced by *Z*11-16: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, *Z*9-14:Ald or *Z*9-16: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 *Z*11-16:Ald, *Z*9-14:Ald, and *Z*11-16:OH in a 1.0:0.1:0.1 ratio, which was previously found to attract F_1 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 *Z*9-14: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 *Z*9-14:Ald. In a smaller experiment, *Hv*-BC males were tested for flight toward a blend with *Z*11-16:Ald, *Z*9-16:Ald, and *Z*11-16:OH, in a 1.0:0.5:0.1 ratio, which is attractive to F_1 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 *Z*9-16: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 *Z*9-14:Ald-containing blend, but only 2 of 50 males without *Hv*-C27 had flown at least halfway toward the blend ($\chi^2 = 58.88$, $P < 0.0000000001$; 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 *Z*9-16: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 *Z*9-14:Ald or *Z*9-16: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 nonindependent 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 *Z*11-16: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 *Z*9-14:Ald and *Z*9-16: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

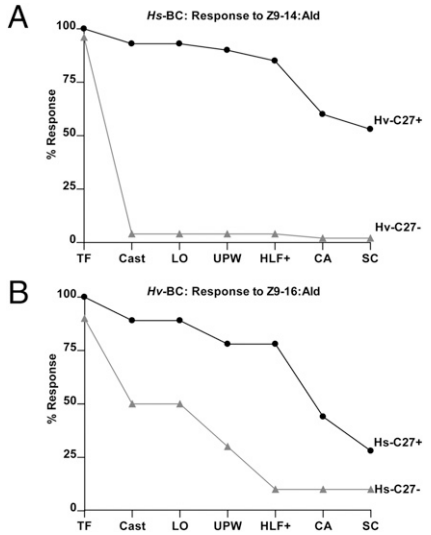

Fig. 1. Response of backcross (BC) males to pheromone blends with species-specific aldehydes. The graphs show the percentage of male moths of each C27 genotype with successively stronger responses to the test pheromone blends. TF = took flight, Cast = cast back and forth in search of pheromone plume, 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, *Z*9-14: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, *Z*9-16: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, *Z*9-14:Ald and *Z*9-16: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 *Z*9-16:Ald. Seven of 15 males with one copy of *Hs*-C27 flew at least halfway toward the blend with *Z*9-16:Ald, whereas only 5 of 30 males without *Hs*-C27 flew at least halfway toward the *Z*9-16:Ald blend (χ^2 with Yates correction = 4.14; $P = 0.042$). The mean degree of response for the 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.

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		

Further Backcrossing to Isolate a Smaller QTL Region for Response to *Z*9-16: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 *Z*9-16:Ald. If a male did not respond to this blend (by more than simply taking flight), it was flown to a blend with *Z*9-14:Ald. Of 58 males with one copy of the *Hs-HR14* allele, 45 responded to the blend with *Z*9-16: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 *Z*9-14:Ald. Of 22 males without the *Hs-HR14* allele, none responded to the blend containing *Z*9-16:Ald blend and 19 responded to the blend with *Z*9-14:Ald blend 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 *Z*9-16: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 *Z*9-16: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 *Z*9-16:Ald.

Response to the Acetate, *Z*11-16:OAc. The *Z*11-16: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 *Z*11-16: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 *Z*11-16:OAc. Therefore, we flew BC males to pheromone blends with and without this odorant. Previous work had established that F_1 males were partially deterred by *Z*11-16: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 *Z*11-16:Ald/*Z*9-16:Ald/*Z*11-16:OH/*Z*11-16: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 *Z*11-16:Ald/

*Z*9-14: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 *Z*11-16:Ald/*Z*9-14:Ald/*Z*11-16:OH/*Z*11-16: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, *Z*11-16:OH. Results from Grosse-Wilde et al. (35) demonstrate that *Z*11-16: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 *Z*11-16: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 *Z*11-16: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 *Z*11-16:Ald/*Z*9-16:Ald in a 1.0/0.5 ratio, after which they were flown to a similar blend with the addition of *Z*11-16: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 (χ^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 (χ^2 = 2.394 P = 0.1218). This indicated clearly that C27 did not affect the requirement for *Z*11-16: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 (χ^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 *Z*11-16: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 *Z*9-14:Ald but not *Z*9-16:Ald (Fig. 2 *A* and *B*). B-type sensilla of *Hs* males were somewhat more sensitive to *Z*9-16:Ald than to *Z*9-14: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 *Z*11-16:OH and *Z*11-16:OAc (Fig. 2 *C* and *D*). *Hs* C-type sensilla also responded strongly to *Z*11-16:OH but only weakly to *Z*11-16:OAc. The response to *Z*11-16: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 *Z*11-16: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.

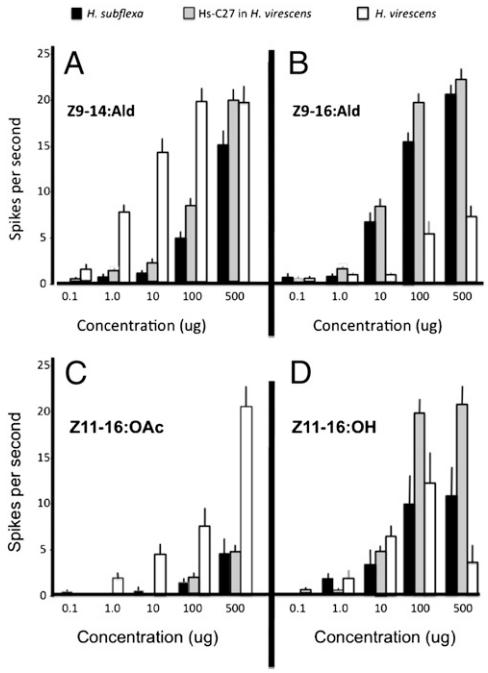

Fig. 2. Single cell recordings from males of (1) pure line Hs, (2) Hv with Hs-C27, (3) pure line Hv. A cut-tip recording method was used to measure activity from olfactory receptor neurons housed within B-Type sensilla during stimulation with either *Z*9-14:Ald or *Z*9-16:Ald (*A* and *B*) and C-Type sensilla (*C* and *D*) sensilla during stimulation with *Z*11-16:OAc or *Z*11-16:OH. For each recording, a dose series (0.1–500 μg) was used to determine relative responses to each odorant. Responses by introgressed male *Hv* with *Hs*-C27 to *Z*9-14:Ald, *Z*9-16:Ald and *Z*11-16:OAc were more similar to pure line *Hs* than pure line *Hv*. *Hv* with *Hs*-C27 responded more strongly to *Z*11-16: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 *Z*9-16:Ald and *Z*9-14:Ald, and are also responsible for at least a substantial portion of the difference between the two species in their responses to *Z*11-16:OAc. It is surprising to find that a change in receptors for *Z*11-16: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*-vaccenyl 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 *Z*11-16: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 *HR13* and *HR11* 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 Sheck 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 autosome 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: *Z*11-16:Ald, *Z*9-14:Ald, *Z*9-16:Ald, *Z*11-16:OAc, and *Z*11-16: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 ug.

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 peizoelectric 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.

ACKNOWLEDGMENTS. We thank K. Lane, K. McDowell, S. Pope, and R. Walsh for help with crosses, rearing of strains, and the running and scoring of gels. M. Servedio offered useful comments on the manuscript. This work was supported by National Science Foundation Grants DEB-0235400 (to F.G. and C.S.) and IOB-0416861 (to N.J.V.) and Department of Agriculture Grant 2007-35607-17824 (to F.G.).

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Supporting Information

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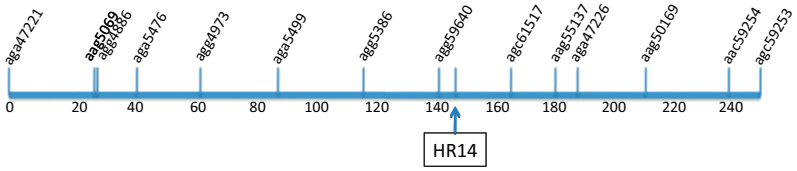

Fig. S1. Location of HR14 within chromosome 27 based on mapping of a backcross in which the male parent was heterozygous for chromosome 27 and the female parent was from the pure *Hv* colony. Based on JoinMap (1) analysis of 46 individuals using default parameters.

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)