

The genetic basis of pheromone evolution in moths

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Supplemental Table 1. Overview of the genetic analyses conducted to determine the heritability and/or mode of inheritance of variation in the female sex pheromone signal and the male preference response.

	Species	Type of analysis	Type of cross	Main findings	# genes involved (sex linked?)	ref
Inheritance of female sex pheromone signal	<i>Ostrinia nubilalis</i> E vs Z	Crossing and selection experiments with pheromone analysis	F1 and backcrosses phenotyped	In heterozygous females much more variation than expected based on a one locus-2 allele model	2 genes: 1 major gene (with two Z alleles) and 1 modifying dominant locus in E	(49)
		Crossing experiments with pheromone analysis	F1, F2 and backcrosses phenotyped	Sex pheromone is controlled by simple Mendelian inheritance involving a single pair of alleles	one gene, two alleles	(27, 38)
		QTL analysis (backcrosses with pheromone analysis) and identifying candidate genes in QTL	Backcrosses phenotyped and genotyped	Not d11desat, but FAR is the gene underlying pheromone differentiation	one autosomal gene: pgFAR (unclear which SNPs are involved, many SNPs between E and Z)	(30, 31)
		Cloning and functional analysis with desaturases (YE _p OLEX for d9, pYES2 for d11, pFastBac1 for d14)	NA	Existence of all desats in both species (d11 in ACB, d14 in ECB) without d11 or d14 products suggest gene duplication and subfunctionalization	one gene (first gene duplication, then subfunctionalization, after which neofunctionalization to d14 happened)	(39)
	<i>O. nubilalis</i> vs <i>O. furnacalis</i>	Crossing experiments with pheromone analysis	F1, F2 and backcrosses phenotyped	F1 produces 14:Ac plus all pheromone components of both parents	one recessive gene, i.e. suppressor of desaturase	(40)
	<i>Ostrinia scapularis</i> E vs <i>O. furnacalis</i>	Crossing experiments with pheromone analysis	F1, F2 and backcrosses phenotyped	Genetic analysis similar to <i>O. nub.</i> but natural variation in EE, ZZ and EZ freqs (in Japan)	one autosomal locus with 2 alleles (plus modifiers for I type)	(45)
	<i>Ostrinia zealis</i> , <i>O. zaguliaevi</i> , and <i>O. sp.</i> near <i>zaguliaevi</i>	Crossing experiments with pheromone analysis	F1 and backcrosses phenotyped	in F ₁ no Z9 produced, thus recessive. In <i>Zea</i> Sca ^Z x <i>Zea</i> : 15/68 females are Sca ^E -like (<i>Zea</i> x Sca ^Z : F ₁ Sca ^L -like)	two genes that are likely linked (one for EZ var and one for the third comp in <i>O. zealis</i>)	(44)
	<i>Ostrinia scapularis</i> vs <i>O. zealis</i>	Crossing experiments with pheromone analyses	F1, F2 and backcrosses	Z9-14:OAc production controlled through an autosomal recessive gene, likely chain-shortening of fatty acid precursor	One major autosomal gene	(43)

<i>Ostrinia zaguliaevi</i>	Selection on female pheromone	Selection for 3 generations for E11-14:OAc, Z11-14:OAc and Z9-14:OAc	Z11 and Z9 showed a heritability of 0.6-0.6. E11 no heritable variation	A few genes, presumably involved in reduction or acetylation	(42)
<i>Planotortrix excessana</i> , <i>P. octo</i>	Crossing experiments with pheromone analysis and qPCR of candidate gene	F1, F2 and backcrosses phenotyped	Crosses were phenotyped, and expression of <i>desat5</i> was measured (also sequenced)	two genes: most likely <i>desat5</i> and a repressor	(2)
<i>Ctenopseustis obliquana</i> (Co) and <i>Planotortrix octo</i> (Po), vs <i>C. herana</i> (Ch) and <i>P. excessana</i> (Pe)	<i>Desat</i> expression & phenotyping in F1 and backcrosses; sequencing, qPCR and functional analyses with d9 and d11 desaturases	F1, F2 and backcrosses phenotyped	Co and Po use Z8-14:Ac as extra sex pheromone component; due to changes in a <i>trans</i> -acting repressor and a <i>cis</i> -regulatory mutation in an activator binding site within the <i>desat5</i> promoter	two genes: a repressor of <i>desat5</i> and a mutation in the <i>desat5</i> promoter	(1)
<i>Ctenopseustis obliquana</i> vs <i>C. herana</i>	Crossing experiments with pheromone analysis	F1, F2 and backcrosses phenotyped	Different crosses yield different pheromone blends, suggesting >1 gene, sex-linked and autosomal	multiple genes, sex-linked and autosomal	(14)
<i>Bombyx mori</i>	Cloning and functional analysis of pheromone gland specific fatty acyl reductase	NA	Identification of the first pg-FAR	NA	(36)
	Cloning and functional analysis of pheromone specific desaturases	NA	Identification of <i>desat1</i> , a bifunctional enzyme that catalyzes both a Z11 desaturation and a d10,12 desaturation	NA	(35)
<i>Helicoverpa armigera</i> and <i>H. assulta</i>	Crossing experiments with pheromone analysis	F1 and backcrosses phenotyped	Ratio of Z9-16:Ald to Z11-16:Ald controlled by one autosomal gene	one autosomal gene, two alleles, with <i>H. armigera</i> dominance	(47)
<i>Heliothis virescens</i> and <i>H. subflexa</i>	QTL analysis on interspecific pheromone variation	Backcrosses phenotyped and genotyped	Complex genetic inheritance, 5-12 QTL found	multiple autosomal genes	(18, 41)
<i>Heliothis virescens</i>	QTL analysis on intraspecific pheromone variation	Backcross phenotyped and genotyped	Major QTL onto which d9-desaturases map, not d11-desaturase	one autosomal gene	(19)
<i>Heliothis subflexa</i>	QTL analysis on intraspecific pheromone variation	Backcross phenotyped and genotyped	Major QTL for acetates overlaps with interspecific QTL	one autosomal gene	(20)
<i>Manduca sexta</i>	Cloning and functional characterization of desaturases KPSE and APTQ	NA	KPSE similar to other KPSE, MsexAPTQThe possesses both Z11 desaturase and 10,12-desaturase activities	NA	(33)
<i>Trichoplusia ni</i>	Crossing experiments with mutant line	F1, F2 and backcrosses	mutant pheromone blend controlled by a single recessive	one gene	(24)

				autosomal gene		
	<i>Spodoptera descoinsi (Sd)</i> and <i>S. latifascia (Sl)</i>	Crossing experiments with pheromone analysis and calling time	F1, F2 and backcrosses	sex pheromone controlled by one autosomal gene, onset time of calling likely polygenic	one major gene, with the Sl allele semi-dominant over the Sd allele	(34)
	<i>Spodoptera frugiperda</i>	QTL analysis on pheromone variation in corn and rice strain	F1 and backcross phenotyped and genotyped	multiple QTL with small effects	multiple autosomal genes	(21)
	<i>Cadra cautella</i>	Selection on female pheromone	Selection (6 generations) for high and low ratios of Z9,E12-14:Ac to Z9-14:Ac	Selection differentials (sd) High line: 3.4-4.2, sd Low lines: 1.9 – 2.6	Response to selection shows additive genetic variance to titers of components, not to ratio	(3, 4)
	<i>Agrotis segetum</i>	Crossing experiments with Scandinavian and Zimbabwean populations	F1, F2 and backcrosses phenotyped	Autosomal inheritance with no dominance for Z5-10/Z7-12 ratio, but more complicated for Z9-14/Z7-12 ratio	Likely one major autosomal gene, with partial dominance for Z5-10:Ac	(29)
	<i>Pectinophora gossypiella</i>	Heritability of intraspecific variation	F1 (heritability analysis, F2 (inbreeding analysis)	Genetic correlation between the two isomers: 0.989 Inbreeding: no effect on ratio, but total amt sign. lower	Not assessed	(7)
		Heritability of variation in pheromone production	Bidirectional selection experiments	Selection for 12 generations to change the ratio of the binary blend showed heritability in one direction only	NA	(9)
Inheritance of male response and preference	<i>Ostrinia nubilalis</i> E vs Z	Crossing experiments with male behavioral response	F1, F2 and backcrosses phenotyped	Male response is heritable, NY (E) males have broader response than P (Z) males	probably one gene	(27)
		Crossing experiments with single sensillum recordings (SSR)	F1, F2, and backcrosses phenotyped	SSRs segregate in Mendelian fashion	one gene, autosomal	(23)
		Crossing experiments with male physiological and behavioral response	F1, F2 and backcrosses phenotyped	SSR response autosomal, behavioral response sex-linked	two genes: one autosomal for the periphery and one sex-linked for the behavior	(10, 38)
		Crossing and behavioral analysis and allozyme tracking of Z chromosome	ExZ strain F1 and F2 crosses	Z chromosome origin(s) determines behavioral response	sex-linked	(16)
		QTL analysis with male behavioral response	F1 and backcrosses phenotyped and genotyped	Behavioral response sex-linked	one gene, sex-linked	(11)
		Crossing experiments with antennal lobe recordings, neuroanatomy and antennal response	F1 and backcrosses phenotyped	Antennal response, antennal lobe neuroanatomy and volume of glomeruli are sex linked	sex-linked	(26)

		Crossing experiments with single sensillum recordings (SSR)	F1 and backcrosses phenotyped	SSR response both autosomal and sex-linked	at least two genes, one autosomal and one E-dominant sex-linked	(37)
		Artificial selection for broader response in ECB Z males to ACB pheromone	NA	Gradual increase in response breadth to selection (and gradual decrease in absence of selection) suggests a quantitative trait	multiple genes	(12)
		Crossing experiments with sensory physiological analysis (SSR)	F1 phenotyped	Hybrids have swapped neuronal identity across all three neurons in the same sensillum	sex-linked	(28)
	<i>Ostrinia nubilalis</i> and <i>O. furnacalis</i>	Pheromone receptor analyses	Comparison of genetics and response profile of candidate pheromone receptor	A single nucleotide shift in one OR underlies swap from <i>E11-14:OAc</i> to <i>E12-14:OAc</i>	One gene, pheromone receptor, OR3	(32)
	<i>Ctenopseustis obliquana</i> , <i>C. herana</i>	Crossing experiments with single sensillum recordings	F1, F2 and backcrosses phenotyped	Phenotype distribution suggests single-sex linked locus with <i>C. herana-type</i> dominance. However, variability in the responses of the hybrids suggests involvement of other genes	one gene, sex-linked, although additional genes seem to be involved too	(22)
		Crossing experiments with male behavioral response	F1, F2 and backcrosses phenotyped	Pattern of male behavioral responses in the crosses also fit a model of inheritance through a single sex-linked locus with <i>C. herana-type</i> dominance	one gene, sex-linked	(14)
	<i>Heliothis virescens</i> and <i>H. subflexa</i>	Crosses and behavioral analysis	F1 crosses phenotyped	Response of F1 hybrids largely <i>H. subflexa</i> dominant	NA	(46)
		Crosses and sensory physiological analysis	F1 crosses phenotyped	Response of F1 hybrids <i>H. subflexa</i> dominant	NA	(6)
		QTL analysis with male physiological and behavioral response	Backcrosses phenotyped and genotyped	One major QTL controlling physiological and behavioral interspecific difference	one gene (cluster), autosomal	(17)
	<i>Helicoverpa armigera</i> and <i>H. assulta</i>	Crosses with behavioral and electrophysiological analyses	F1 and backcrosses phenotyped	<i>H. armigera</i> behavioral and electrophysiological response dominant	NA	(48)
	<i>Trichoplusia ni</i>	Heritability studies on male response to normal/mutant blend	Selection for male response to normal/mutant blend	Heritability of normal males to mutant blend 0.25, heritability of normal and mutant males to normal blend: 0	NA	(13)

		Wind tunnel experiments to assess pheromone response breath and sensitivity	F1 phenotyped	Mutant males have broader response, but are less sensitive than normal males, response profiles of hybrid males similar to wild-type males and reduced sensitivity observed in mutant males	NA	(25)
	<i>Cadra cautella</i>	Genetic linkage of male response in female signal selection lines	NA (tests on selection lines)	Heritability male preference: -0.025, thus no genetic linkage between female pheromone and male response	NA	(5)
	<i>Agrotis segetum</i>	Crossing experiments with Scandinavian and Zimbabwean populations	F1, F2 and backcrosses phenotyped (male behavior in wind tunnel)	Few detectable differences in male response, so that mode of inheritance cannot be determined: males broadly tuned	?	(29)
	<i>Pectinophora gossypiella</i>	Heritability of a) overall responsiveness, b) response specificity	F1 phenotyped	Heritability a: 0.38 Heritability b: 0.117 for the 25% ZE blend, -0.043 for the 65% ZE blend	NA	(8)
	<i>Bombyx mori</i>	Mutant <i>B. mori</i> analyzed on behavioral and antennal lobe response	Mutant versus wildtype analysis	Transcription factor <i>Bmacj6</i> involved in swap in behavior and physiology from bombikol to bombikal	One sex-linked gene, <i>Bmacj6</i>	(15)

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