

GEPHE SUMMARY

	Gephebase Gene	GepheID
FAR (pheromone gland FAR) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase="FAR (pheromone gland FAR)"#gephebase-summary-title)	GP00000304	
	Entry Status	Main curator
Published	Martin	

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category="Physiology"#gephebase-summary-title)		Trait	
Pheromone production (isomeric/chirality divergence) (<a (isomeric="" chirality="" divergence)"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=" pheromone="" production="">https://www.gephebase.org/search-criteria?/and+Trait="Pheromone production (isomeric/chirality divergence)"#gephebase-summary-title)			
	Trait State in Taxon A		
Ostrinia nubilalis Z		Trait State in Taxon B	
Ostrinia nubilalis E; other Ostrinia spp. In 2013 update			
	Ancestral State		
Data not curated		Taxonomic Status	
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status="Intraspecific"#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
Ostrinia nubilalis (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Ostrinia nubilalis"#gephebase-summary-title)		Ostrinia nubilalis (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Ostrinia nubilalis"#gephebase-summary-title)	
	Common Name		Common Name
European corn borer		European corn borer	
	Synonyms		Synonyms
Pyralis nubilalis; Pyrausta nubilalis; European corn borer; Ostrinia nubilalis (Hubner, 1796)		Pyralis nubilalis; Pyrausta nubilalis; European corn borer; Ostrinia nubilalis (Hubner, 1796)	
	Rank		Rank
species		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Amphiesmenoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Ditrysia; Obtectomera; Pyraloidea; Crambidae; Pyraustinae; Ostrinia		cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Amphiesmenoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Ditrysia; Obtectomera; Pyraloidea; Crambidae; Pyraustinae; Ostrinia	
	Parent		Parent
Ostrinia () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=29056)		Ostrinia () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=29056)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
29057 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=29057)		29057 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=29057)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
Yes		Yes	
	Taxon A Description		Taxon B Description
Ostrinia nubilalis Z		Ostrinia nubilalis E; other Ostrinia spp. In 2013 update	

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Ostrinia nubilalis
pgFAR		D3U9W3 (http://www.uniprot.org/uniprot/D3U9W3)
	Synonyms	GenebankID or UniProtKB
-		GU808264 (https://www.ncbi.nlm.nih.gov/nuccore/GU808264)
	String	
-		
	Sequence Similarities	
Belongs to the fatty acyl-CoA reductase family.		
	GO - Molecular Function	
GO:0102965 : alcohol-forming fatty acyl-CoA reductase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0102965)		
GO:0080019 : fatty-acyl-CoA reductase (alcohol-forming) activity (https://www.ebi.ac.uk/QuickGO/term/GO:0080019)		
	GO - Biological Process	

GO:0006629 : lipid metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006629>)

GO - Cellular Component

GO:0016021 : integral component of membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)

No (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title>)

Coding (<https://www.gephebase.org/search-criteria?/and+Molecular Type=^Coding^#gephebase-summary-title>)

Unknown (<https://www.gephebase.org/search-criteria?/and+Aberration Type=^Unknown^#gephebase-summary-title>)

Candidate a.a. substitutions with effect validated in vitro

Linkage Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title>)

Allelic variation in a fatty-acyl reductase gene causes divergence in moth sex pheromones. (2010) (<https://pubmed.ncbi.nlm.nih.gov/20592730>)

Lassance JM; Groot AT; LiÅ©nard MA; Antony B; Borgwardt C; Andersson F; HedenstrÅ¶m E; Heckel DG; LÅ¶fstedt C

Pheromone-based behaviours are crucial in animals from insects to mammals, and reproductive isolation is often based on pheromone differences. However, the genetic mechanisms by which pheromone signals change during the evolution of new species are largely unknown. In the sexual communication system of moths (Insecta: Lepidoptera), females emit a species-specific pheromone blend that attracts males over long distances. The European corn borer, *Ostrinia nubilalis*, consists of two sex pheromone races, Z and E, that use different ratios of the cis and trans isomers of acetate pheromone components. This subtle difference leads to strong reproductive isolation in the field between the two races, which could represent a first step in speciation. Female sex pheromone production and male behavioural response are under the control of different major genes, but the identity of these genes is unknown. Here we show that allelic variation in a fatty-acyl reductase gene essential for pheromone biosynthesis accounts for the phenotypic variation in female pheromone production, leading to race-specific signals. Both the cis and trans isomers of the pheromone precursors are produced by both races, but the precursors are differentially reduced to yield opposite ratios in the final pheromone blend as a result of the substrate specificity of the enzymes encoded by the Z and E alleles. This is the first functional characterization of a gene contributing to intraspecific behavioural reproductive isolation in moths, highlighting the importance of evolutionary diversification in a lepidopteran-specific family of reductases. Accumulation of substitutions in the coding region of a single biosynthetic enzyme can produce pheromone differences resulting in reproductive isolation, with speciation as a potential end result.

Functional consequences of sequence variation in the pheromone biosynthetic gene pgFAR for *Ostrinia* moths. (2013) (<https://pubmed.ncbi.nlm.nih.gov/23407169>)
bric Å brac controls sex pheromone choice by male European corn borer moths. (2021) (<https://pubmed.ncbi.nlm.nih.gov/33990556>)

RELATED GEPHE

No matches found.

No matches found.

EXTERNAL LINKS

COMMENTS

@SexualTrait

Presumptive Null

Molecular Type

Aberration Type

Molecular Details of the Mutation

Experimental Evidence

Main Reference

Authors

Abstract

Additional References

Related Genes

Related Haplotypes