

GEPHE SUMMARY

opsin - rhodopsin1 (RH1) (https://www.gephebase.org/search-criteria?/and+Gene)		Gephebase Gene	GP00002535	GepheID
Gephebase="opsin - rhodopsin1 (RH1)"#gephebase-summary-title)				Main curator
Published		Entry Status	Courtier	

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+Trait)		Trait Category		
Category="Physiology"#gephebase-summary-title)				
Color vision (green-shift) (<a color"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="Color)		Trait		
vision (green-shift)"#gephebase-summary-title)				
Stomoxys calcitrans - old Rh1 gene cluster paralogs with blue-shifted wavelength specificity		Trait State in Taxon A		
Stomoxys calcitrans - three younger S. calcitrans Rh1 paralogs with green sensitivity		Trait State in Taxon B		
Data not curated		Ancestral State		
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic)		Taxonomic Status		
Status="Intraspecific"#gephebase-summary-title)				

Taxon A		Taxon B	
Latin Name	Latin Name	Latin Name	Latin Name
Stomoxys calcitrans	Stomoxys calcitrans	Stomoxys calcitrans	Stomoxys calcitrans
(https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="Stomoxys)			
stable fly	stable fly	stable fly	stable fly
Stomoxys calcitrans; stable fly; biting house fly			
species	species	species	species
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Eremoneura; Cyclorrhapha; Schizophora; Calypratae; Muscoidea; Muscidae; Muscinae; Stomoxyini; Stomoxys	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Eremoneura; Cyclorrhapha; Schizophora; Calypratae; Muscoidea; Muscidae; Muscinae; Stomoxyini; Stomoxys	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Eremoneura; Cyclorrhapha; Schizophora; Calypratae; Muscoidea; Muscidae; Muscinae; Stomoxyini; Stomoxys	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Eremoneura; Cyclorrhapha; Schizophora; Calypratae; Muscoidea; Muscidae; Muscinae; Stomoxyini; Stomoxys
Stomoxys () - (Rank: genus)			
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=35569)			
35570	35570	35570	35570
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=35570)			
is Taxon A an Intraspecies?	is Taxon A an Intraspecies?	is Taxon B an Intraspecies?	is Taxon B an Intraspecies?
No	No	No	No

GENOTYPIC CHANGE

RHO	Generic Gene Name	P08100 (http://www.uniprot.org/uniprot/P08100)	UniProtKB Homo sapiens
RP4; OPN2; CSNBAD1	Synonyms	()	GenebankID or UniProtKB
9606.ENSP00000296271	String		
(http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSP00000296271)			
Belongs to the G-protein coupled receptor 1 family. Opsin subfamily.	Sequence Similarities		
	GO - Molecular Function		
GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)			
GO:0004930 : G protein-coupled receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004930)			
GO:0008020 : G protein-coupled photoreceptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008020)			
GO:0005502 : 11-cis retinal binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005502)			

GO - Biological Process

- GO:0007186 : G protein-coupled receptor signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007186>)
- GO:0001523 : retinoid metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0001523>)
- GO:0006468 : protein phosphorylation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006468>)
- GO:0018298 : protein-chromophore linkage
(<https://www.ebi.ac.uk/QuickGO/term/GO:0018298>)
- GO:0007601 : visual perception (<https://www.ebi.ac.uk/QuickGO/term/GO:0007601>)
- GO:0071482 : cellular response to light stimulus
(<https://www.ebi.ac.uk/QuickGO/term/GO:0071482>)
- GO:0007602 : phototransduction (<https://www.ebi.ac.uk/QuickGO/term/GO:0007602>)
- GO:0016038 : absorption of visible light
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016038>)
- GO:0045494 : photoreceptor cell maintenance
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045494>)
- GO:0007603 : phototransduction, visible light
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007603>)
- GO:0022400 : regulation of rhodopsin mediated signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0022400>)
- GO:0060041 : retina development in camera-type eye
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060041>)
- GO:0016056 : rhodopsin mediated signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016056>)

GO - Cellular Component

- GO:0016021 : integral component of membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)
- GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)
- GO:0000139 : Golgi membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0000139>)
- GO:0005887 : integral component of plasma membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005887>)
- GO:0005794 : Golgi apparatus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005794>)
- GO:0005911 : cell-cell junction (<https://www.ebi.ac.uk/QuickGO/term/GO:0005911>)
- GO:0001750 : photoreceptor outer segment
(<https://www.ebi.ac.uk/QuickGO/term/GO:0001750>)
- GO:0097381 : photoreceptor disc membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0097381>)
- GO:0060170 : ciliary membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0060170>)
- GO:0030660 : Golgi-associated vesicle membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030660>)
- GO:0001917 : photoreceptor inner segment
(<https://www.ebi.ac.uk/QuickGO/term/GO:0001917>)
- GO:0060342 : photoreceptor inner segment membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060342>)
- GO:0042622 : photoreceptor outer segment membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042622>)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

Met>Leucine residue present at tuning site 17 which is extremely rare across insect LW opsins. In a survey of over 100 insect LW opsins it was detected only in the two corresponding Rh1 orthologs from *M. domestica* in addition to one in the distantly related species of thrips (Thysanoptera). The site is residue 17 based on the numbering system developed for butterflies which corresponds to residue 57 in *Drosophila* Rh1.

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Met	Leu	17

Main Reference

The genome of the stable fly, *Stomoxys calcitrans*, reveals potential mechanisms underlying reproduction, host interactions, and novel targets for pest control. (2021)
(<https://pubmed.ncbi.nlm.nih.gov/33750380>)

Authors

Olafson PU; Aksoy S; Attardo GM; Buckmeier G; Chen X; Coates CJ; Davis M; Dykema J; Emrich SJ; Friedrich M; Holmes CJ; Ioannidis P; Jansen EN; Jennings EC; Lawson D; Martinson EO; Maslen GL; Meisel RP; Murphy TD; Nayduch D; Nelson DR; Oyen KJ; Raszcik TJ; Ribeiro JMC; Robertson HM; Rosendale AJ; Sackton TB; Saelao P; Swiger SL; Sze SH; Tarone AM; Taylor DB; Warren WC; Waterhouse RM; Weirauch MT; Werren JH; Wilson RK; Zdobnov EM; Benoit JB

Abstract

The stable fly, *Stomoxys calcitrans*, is a major blood-feeding pest of livestock that has near worldwide distribution, causing an annual cost of over \$2 billion for control and product loss in the

USA alone. Control of these flies has been limited to increased sanitary management practices and insecticide application for suppressing larval stages. Few genetic and molecular resources are available to help in developing novel methods for controlling stable flies.

This study examines stable fly biology by utilizing a combination of high-quality genome sequencing and RNA-Seq analyses targeting multiple developmental stages and tissues. In conjunction, 1600 genes were manually curated to characterize genetic features related to stable fly reproduction, vector host interactions, host-microbe dynamics, and putative targets for control. Most notable was characterization of genes associated with reproduction and identification of expanded gene families with functional associations to vision, chemosensation, immunity, and metabolic detoxification pathways.

The combined sequencing, assembly, and curation of the male stable fly genome followed by RNA-Seq and downstream analyses provide insights necessary to understand the biology of this important pest. These resources and new data will provide the groundwork for expanding the tools available to control stable fly infestations. The close relationship of *Stomoxys* to other blood-feeding (horn flies and *Glossina*) and non-blood-feeding flies (house flies, medflies, *Drosophila*) will facilitate understanding of the evolutionary processes associated with development of blood feeding among the Cyclorrhapha.

[Additional References](#)

RELATED GEPHE

No matches found.

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EXTERNAL LINKS

COMMENTS