GEPHE SUMMARY

Gephebase Gene
slowpoke (slo) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^slowpoke (slo)^#gephebase-summary-title)

Entry Status
Published

GepheID
GP00001066

Main curator
Martin

PHENOTYPIC CHANGE

Trait Category
Behavior (https://www.gephebase.org/search-criteria?/and+Trait Category=^Behavior^#gephebase-summary-title)

Trait
Courtship song (sine song frequency) (https://www.gephebase.org/search-criteria?/and+Trait=^Courtship song (sine song frequency)^#gephebase-summary-title)

Trait State in Taxon A
Drosophila mauritiana; and other Drosophila simulans strains

Trait State in Taxon B
Drosophila simulans - strain sim5 (7.8Hz lower sine song frequency than D. mauritiana)

Ancestral State
Taxon A

Taxonomic Status
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#gephebase-summary-title)

Taxon A

Latin Name
Drosophila simulans (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Drosophila simulans^#gephebase-summary-title)

Common Name
-

Synonyms
-

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Diptera; Brachycera; Muscomorpha; Eremoneura; Cyclorrhapha; Schizophora; Acalyptratae; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup

Parent
melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32351)

NCBI Taxonomy ID
7240 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7240)

is Taxon A an Infraspecies?
No

Taxon B

Latin Name
Drosophila simulans (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Drosophila simulans^#gephebase-summary-title)

Common Name
-

Synonyms
-

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Diptera; Brachycera; Muscomorpha; Eremoneura; Cyclorrhapha; Schizophora; Acalyptratae; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup

Parent
melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32351)

NCBI Taxonomy ID
7240 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7240)

is Taxon B an Infraspecies?
Yes

Taxon B Description
Drosophila simulans - strain sim5 (7.8Hz lower sine song frequency than D. mauritiana)

GENOTYPIC CHANGE

Generic Gene Name
slo

Synonyms
BcDNA:GH10751; CG10693; Dmel\CG10693; dslo; dSlo; Dslo; dSlo1; fSlo; Slo; Slo1

String
-

Sequence Similarities
Belongs to the potassium channel family. Calcium-activated (TC 1.A.1.3) subfamily. Slo sub-subfamily.

GO - Molecular Function
GO:0015271 : outward rectifier potassium channel activity (https://www.ebi.ac.uk/QuickGO/term/GO:0015271)
GO:0015269 : calcium-activated potassium channel activity (https://www.ebi.ac.uk/QuickGO/term/GO:0015269)

UniProtKB Drosophila melanogaster
Q03720 (http://www.uniprot.org/uniprot/Q03720)

GenebankID or UniProtKB
NP_001260212 (https://www.ncbi.nlm.nih.gov/nuccore/NP_001260212)

GO:0060072 : large conductance calcium-activated potassium channel activity (https://www.ebi.ac.uk/QuickGO/term/GO:0060072)

GO - Biological Process

GO:0006813 : potassium ion transport (https://www.ebi.ac.uk/QuickGO/term/GO:0006813)
GO:0042493 : response to drug (https://www.ebi.ac.uk/QuickGO/term/GO:0042493)
GO:0042391 : regulation of membrane potential (https://www.ebi.ac.uk/QuickGO/term/GO:0042391)
GO:0007623 : circadian rhythm (https://www.ebi.ac.uk/QuickGO/term/GO:0007623)
GO:0045433 : male courtship behavior, veined wing generated song production (https://www.ebi.ac.uk/QuickGO/term/GO:0045433)
GO:0034765 : regulation of ion transmembrane transport (https://www.ebi.ac.uk/QuickGO/term/GO:0034765)
GO:0048512 : circadian behavior (https://www.ebi.ac.uk/QuickGO/term/GO:0048512)
GO:1900074 : negative regulation of neuromuscular synaptic transmission (https://www.ebi.ac.uk/QuickGO/term/GO:1900074)
GO:0008582 : regulation of synaptic growth at neuromuscular junction (https://www.ebi.ac.uk/QuickGO/term/GO:0008582)

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:0016020 : membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016020)
GO:0043025 : neuronal cell body (https://www.ebi.ac.uk/QuickGO/term/GO:0043025)
GO:0043005 : neuron projection (https://www.ebi.ac.uk/QuickGO/term/GO:0043005)
GO:0045211 : postsynaptic membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0045211)
GO:0008076 : voltage-gated potassium channel complex (https://www.ebi.ac.uk/QuickGO/term/GO:0008076)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

Insertion Size

1-10 kb

Molecular Details of the Mutation

6.7kb "Shelder" retroelement insertion in slowpoke intron; with effect on splicing

Experimental Evidence

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

Main Reference

Natural courtship song variation caused by an intronic retroelement in an ion channel gene. (2016) (https://pubmed.ncbi.nlm.nih.gov/27509856)

Authors

Ding Y; Berrocal A; Morita T; Longden KD; Stern DL

Abstract

Animal species display enormous variation for innate behaviours, but little is known about how this diversity arose. Here, using an unbiased genetic approach, we map a courtship song difference between wild isolates of Drosophila simulans and Drosophila mauritiana to a 966 base pair region within the slowpoke (slo) locus, which encodes a calcium-activated potassium channel. Using the reciprocal hemizygosity test, we confirm that slo is the causal locus and resolve the causal mutation to the evolutionarily recent insertion of a retroelement in a slo intron within D. simulans. Targeted deletion of this retroelement reverts the song phenotype and alters slo splicing. Like many ion channel genes, slo is expressed widely in the nervous system and influences a variety of behaviours; slo-null males sing little song with severely disrupted features. By contrast, the natural variant of slo alters a specific component of courtship song, illustrating that regulatory evolution of a highly pleiotropic ion channel gene can cause modular changes in behaviour.

Additional References

RELATED GEPHE

Related Genes

1 (Period (per)) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^7240^/and+Trait=Courtship song/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@Splicing The sim5 strain insertion is rare and derived within D. simulans - http://flybase.org/reports/FBal0343839