GEPHE SUMMARY

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

GepheID
GP00001987

Entry Status
Published

Main curator
Courtier

PHENOTYPIC CHANGE

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

Trait
Color vision (eye; photoreceptor composition) (https://www.gephebase.org/search-criteria?/and+Trait=^Color vision (eye; photoreceptor composition)^#gephebase-summary-title)

Trait State in Taxon A
Drosophila melanogaster

Trait State in Taxon B
Drosophila melanogaster -

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

Common Name
fruit fly

Synonyms
Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster

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
7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7227)

is Taxon A an Infraspecies?
No

Taxon B

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

Common Name
fruit fly

Synonyms
Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster

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
7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7227)

is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
ss

Synonyms
SS; AhR; AHR; CG6993; Dmel\CG6993; Ss; ssa; Dmel_CG6993

String
7227.FBpp0297168 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0297168)

Sequence Similarities
-

GO - Molecular Function
GO:0046982 : protein heterodimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0046982)
GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)

UniProtKB Drosophila melanogaster
E1JIM6 (http://www.uniprot.org/uniprot/E1JIM6)

GenebankID or UniProtKB
()

GO - Biological Process

GO:0045944 : positive regulation of transcription by RNA polymerase II (https://www.ebi.ac.uk/QuickGO/term/GO:0045944)
GO:0000122 : negative regulation of transcription by RNA polymerase II (https://www.ebi.ac.uk/QuickGO/term/GO:0000122)
GO:0048814 : regulation of dendrite morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0048814)
GO:0006805 : xenobiotic metabolic process (https://www.ebi.ac.uk/QuickGO/term/GO:0006805)
GO:0048800 : antennal morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0048800)
GO:0036011 : imaginal disc-derived leg segmentation (https://www.ebi.ac.uk/QuickGO/term/GO:0036011)
GO:0007469 : antennal development (https://www.ebi.ac.uk/QuickGO/term/GO:0007469)
GO:0010092 : specification of animal organ identity (https://www.ebi.ac.uk/QuickGO/term/GO:0010092)
GO:0008049 : male courtship behavior (https://www.ebi.ac.uk/QuickGO/term/GO:0008049)
GO:0007613 : memory (https://www.ebi.ac.uk/QuickGO/term/GO:0007613)
GO:0009410 : response to xenobiotic stimulus (https://www.ebi.ac.uk/QuickGO/term/GO:0009410)
GO:0045466 : R7 cell differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0045466)
GO:0045676 : regulation of R7 cell differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0045676)
GO:0007468 : regulation of rhodopsin gene expression (https://www.ebi.ac.uk/QuickGO/term/GO:0007468)

GO - Cellular Component

GO:0005829 : cytosol (https://www.ebi.ac.uk/QuickGO/term/GO:0005829)
GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)

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

1-9 bp

Molecular Details of the Mutation

Single base insertion in the ss regulatory region upstream of the ss transcription start site. The insertion affects the stochastic on/off expression of the ss protein seen in the R7 photoreceptors: the presence of the insertion results in a significant decrease in the ratio of ss expressing to non-expressing R7 cells.

Experimental Evidence

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

Main Reference

Natural variation in stochastic photoreceptor specification and color preference in Drosophila. (2017) (https://pubmed.ncbi.nlm.nih.gov/29251595)

Authors

Anderson C; Reiss I; Zhou C; Cho A; Siddiqi H; Mormann B; Avelis CM; Deford P; Bergland A; Roberts E; Taylor J; Vasiliauskas D; Johnston RJ

Abstract

Each individual perceives the world in a unique way, but little is known about the genetic basis of variation in sensory perception. In the fly eye, the random mosaic of color-detecting R7 photoreceptor subtypes is determined by stochastic on/off expression of the transcription factor Spineless (Ss). In a genome-wide association study, we identified a naturally occurring insertion in a regulatory DNA element in ss that lowers the ratio of Ss to Ss cells. This change in photoreceptor fates shifts the innate color preference of flies from green to blue. The genetic variant increases the binding affinity for Klumpfuss (Klu), a zinc finger transcriptional repressor that regulates ss expression. Klu is expressed at intermediate levels to determine the normal ratio of Ss to Ss cells. Thus, binding site affinity and transcription factor levels are finely tuned to regulate stochastic expression, setting the ratio of alternative fates and ultimately determining color preference.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

http://flybase.org/reports/FBal0337841