GEPHE SUMMARY

Gephebase Gene
Svb/ovo (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Svb/ovo^#gephebase-summary-title)
Entry Status
Published

GepheID
GP00001086
Main curator
Martin

PHENOTYPIC CHANGE

Trait Category
Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Morphology^#gephebase-summary-title)
Trait
Trichome pattern (larva) (https://www.gephebase.org/search-criteria?/and+Trait=^Trichome pattern (larva)^#gephebase-summary-title)
Trait State in Taxon A
Other Drosophila spp. (virilis group)
Trait State in Taxon B
Drosophila ezoana
Ancestral State
Data not curated
Taxonomic Status
Interspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Interspecific^#gephebase-summary-title)

Taxon A

Latin Name
virilis group (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^virilis group^#gephebase-summary-title)
Common Name
-
Synonyms
-
Rank
species group
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; Drosophila
Parent
Drosophila () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32281)
NCBI Taxonomy ID
32335 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32335)
is Taxon A an Infraspecies?
No

Taxon B

Latin Name
Drosophila ezoana (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Drosophila ezoana^#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; Drosophila; virilis group
Parent
virilis group () - (Rank: species group) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32335)
NCBI Taxonomy ID
47313 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 47313)
is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
ovo
Synonyms
CG15467; CG6824; Dmel\CG6824; Fs(1)K1103; fs(1)K1237; Fs(1)K1237; Fs(1)K155; fs(1)M1; fs(1)M38; Ovo; OVO; Ovo-D; ovo/shavenbaby; ovo/svb; ovoD; Shv; svb; Svb; Svb/Ovo
String
7227.FBpp0291128 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0291128)
Sequence Similarities
-
GO - Molecular Function
GO:0001228 : DNA-binding transcription activator activity, RNA polymerase II-specific (https://www.ebi.ac.uk/QuickGO/term/GO:0001228)
GO:0043565 : sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043565)
GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)

UniProtKB Drosophila melanogaster
P51521 (http://www.uniprot.org/uniprot/P51521)
GenebankID or UniProtKB
()

GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)
GO:0001078 : proximal promoter DNA-binding transcription repressor activity, RNA polymerase II-specific (https://www.ebi.ac.uk/QuickGO/term/GO:0001078)

GO - Biological Process

GO:0045944 : positive regulation of transcription by RNA polymerase II (https://www.ebi.ac.uk/QuickGO/term/GO:0045944)
GO:0006355 : regulation of transcription, DNA-templated (https://www.ebi.ac.uk/QuickGO/term/GO:0006355)
GO:0008343 : adult feeding behavior (https://www.ebi.ac.uk/QuickGO/term/GO:0008343)
GO:0000122 : negative regulation of transcription by RNA polymerase II (https://www.ebi.ac.uk/QuickGO/term/GO:0000122)
GO:0045892 : negative regulation of transcription, DNA-templated (https://www.ebi.ac.uk/QuickGO/term/GO:0045892)
GO:0045893 : positive regulation of transcription, DNA-templated (https://www.ebi.ac.uk/QuickGO/term/GO:0045893)
GO:0007010 : cytoskeleton organization (https://www.ebi.ac.uk/QuickGO/term/GO:0007010)
GO:0008360 : regulation of cell shape (https://www.ebi.ac.uk/QuickGO/term/GO:0008360)
GO:0048477 : oogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0048477)
GO:0048067 : cuticle pigmentation (https://www.ebi.ac.uk/QuickGO/term/GO:0048067)
GO:0009913 : epidermal cell differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0009913)
GO:0035017 : cuticle pattern formation (https://www.ebi.ac.uk/QuickGO/term/GO:0035017)
GO:0019099 : female germ-line sex determination (https://www.ebi.ac.uk/QuickGO/term/GO:0019099)
GO:0018992 : germ-line sex determination (https://www.ebi.ac.uk/QuickGO/term/GO:0018992)
GO:0016348 : imaginal disc-derived leg joint morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0016348)
GO:0035316 : non-sensory hair organization (https://www.ebi.ac.uk/QuickGO/term/GO:0035316)
GO:0070896 : positive regulation of transposon integration (https://www.ebi.ac.uk/QuickGO/term/GO:0070896)

GO - Cellular Component

GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)
GO:0005654 : nucleoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005654)
GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)

Presumptive Null

Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Unknown^#gephebase-summary-title)

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

unknown

Experimental Evidence

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

Main Reference

Conserved regulatory architecture underlies parallel genetic changes and convergent phenotypic evolution. (2012) (https://pubmed.ncbi.nlm.nih.gov/23197832)

Authors

Frankel N; Wang S; Stern DL

Abstract

Similar morphological, physiological, and behavioral features have evolved independently in different species, a pattern known as convergence. It is known that morphological convergence can occur through changes in orthologous genes. In some cases of convergence, cis-regulatory changes generate parallel modifications in the expression patterns of orthologous genes. Our understanding of how changes in cis-regulatory regions contribute to convergence is hampered, usually, by a limited understanding of the global cis-regulatory structure of the evolving genes. Here we examine the genetic causes of a case of precise phenotypic convergence between Drosophila sechellia and Drosophila ezoana, species that diverged ~40 Mya. Previous studies revealed that changes in multiple transcriptional enhancers of shavenbaby (svb, a transcript of the ovo locus) caused phenotypic evolution in the D. sechellia lineage. It has also been shown that the convergent phenotype of D. ezoana was likely caused by cis-regulatory evolution of svb. Here we show that the large-scale cis-regulatory architecture of svb is conserved between these Drosophila species. Furthermore, we show that the D. ezoana orthologs of the evolved D. sechellia enhancers have also evolved expression patterns that correlate precisely with the changes in the phenotype. Our results suggest that phenotypic convergence resulted from multiple noncoding changes that occurred in parallel in the D. sechellia and D. ezoana lineages.

Additional References

Regulatory evolution of shavenbaby/ovo underlies multiple cases of morphological parallelism. (2003) (https://pubmed.ncbi.nlm.nih.gov/12931187)

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS