

GEPHE SUMMARY

Gephebase Gene
Svb/ovo

Entry Status
Published

GepheID
GP00001086

Main curator
Martin

PHENOTYPIC CHANGE

Trait Category
Morphology

Trait
Trichome pattern (larva)

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

Taxon A

Latin Name
virilis group

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; Acalypratae; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Drosophila

Parent
Drosophila () - (Rank: subgenus)

NCBI Taxonomy ID
32335

is Taxon A an Intraspecies?
No

Taxon B

Latin Name
Drosophila ezoana

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; Acalypratae; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Drosophila; virilis group

Parent
virilis group () - (Rank: species group)

NCBI Taxonomy ID
47313

is Taxon B an Intraspecies?
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

Sequence Similarities
-

GO - Molecular Function
GO:0001228 : DNA-binding transcription activator activity, RNA polymerase II-specific
GO:0043565 : sequence-specific DNA binding
GO:0046872 : metal ion binding
GO:0003677 : DNA binding
GO:0001078 : proximal promoter DNA-binding transcription repressor activity, RNA polymerase II-specific

GO - Biological Process
GO:0045944 : positive regulation of transcription by RNA polymerase II

UniProtKB *Drosophila melanogaster*
P51521

GenebankID or UniProtKB

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

GO - Cellular Component

GO:0005737 : cytoplasm
GO:0005654 : nucleoplasm
GO:0005634 : nucleus

Presumptive Null

Unknown

Molecular Type

Cis-regulatory

Aberration Type

Unknown

Molecular Details of the Mutation

unknown

Experimental Evidence

Candidate Gene

Main Reference

Conserved regulatory architecture underlies parallel genetic changes and convergent phenotypic evolution. (2012)

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)

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

COMMENTS