GEPHE SUMMARY

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

GepheID
GP00001965

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

Trait State in Taxon A
Drosophila americana - lower enzyme activity

Trait State in Taxon B
Drosophila virilis - higher enzyme activity

Ancestral State
Taxon A

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

Taxon A

Latin Name
Drosophila americana (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Drosophila americana^#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
40366 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 40366)

is Taxon A an Infraspecies?
No

Taxon B

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

Common Name
-

Synonyms
Drosophila virilis Sturtevant, 1916; Drosophila irilis

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
7244 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7244)

is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
Adh

Synonyms
adh; ADH; Adh3; BG:DS01486.8; CG32954; CG3481; dADH; DM-ADH; DmADH; Dmel\CG3481; Dreg-1; Reg-1; T16

String
7227.FBpp0100048 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0100048)

Sequence Similarities
Belongs to the short-chain dehydrogenases/reductases (SDR) family.

GO - Molecular Function
GO:0042803 : protein homodimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0042803)
GO:0008774 : acetaldehyde dehydrogenase (acetylating) activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008774)
GO:0004022 : alcohol dehydrogenase (NAD) activity

UniProtKB Drosophila melanogaster
P00334 (http://www.uniprot.org/uniprot/P00334)

GenebankID or UniProtKB
()

(https://www.ebi.ac.uk/QuickGO/term/GO:0004022)
GO:0016491 : oxidoreductase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0016491)

GO - Biological Process

GO:0006117 : acetaldehyde metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0006117)
GO:0046164 : alcohol catabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0046164)
GO:0006066 : alcohol metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0006066)
GO:0048149 : behavioral response to ethanol
(https://www.ebi.ac.uk/QuickGO/term/GO:0048149)
GO:0006067 : ethanol metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0006067)
GO:0006069 : ethanol oxidation (https://www.ebi.ac.uk/QuickGO/term/GO:0006069)
GO:0055114 : oxidation-reduction process
(https://www.ebi.ac.uk/QuickGO/term/GO:0055114)

GO - Cellular Component

GO:0005829 : cytosol (https://www.ebi.ac.uk/QuickGO/term/GO:0005829)
GO:0032991 : protein-containing complex
(https://www.ebi.ac.uk/QuickGO/term/GO:0032991)

Mutation #1

Presumptive Null

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

Molecular Type

Gene Amplification (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Gene Amplification^#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

Duplication of the Adh gene.

Experimental Evidence

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

Main Reference

A major role for noncoding regulatory mutations in the evolution of enzyme activity. (2019) (https://pubmed.ncbi.nlm.nih.gov/31152141)

Authors

Loehlin DW; Ames JR; Vaccaro K; Carroll SB

Abstract

The quantitative evolution of protein activity is a common phenomenon, yet we know little about any general mechanistic tendencies that underlie it. For example, an increase (or decrease) in enzyme activity may evolve from changes in protein sequence that alter specific activity, or from changes in gene expression that alter the amount of protein produced. The latter in turn could arise via mutations that affect gene transcription, posttranscriptional processes, or copy number. Here, to determine the types of genetic changes underlying the quantitative evolution of protein activity, we dissected the basis of ecologically relevant differences in Alcohol dehydrogenase (Adh) enzyme activity between and within several Drosophila species. By using recombinant Adh transgenes to map the functional divergence of ADH enzyme activity in vivo, we find that amino acid substitutions explain only a minority (0 to 25%) of between- and within-species differences in enzyme activity. Instead, noncoding substitutions that occur across many parts of the gene (enhancer, promoter, and 5′ and 3′ untranslated regions) account for the majority of activity differences. Surprisingly, one substitution in a transcriptional Initiator element has occurred in parallel in two species, indicating that core promoters can be an important natural source of the tuning of gene activity. Furthermore, we show that both regulatory and coding substitutions contribute to fitness (resistance to ethanol toxicity). Although qualitative changes in protein specificity necessarily derive from coding mutations, these results suggest that regulatory mutations may be the primary source of quantitative changes in protein activity, a possibility overlooked in most analyses of protein evolution.

Additional References

Mutation #2

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

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

Molecular Details of the Mutation

segment 1 of the 5′ flanking region (upstream of 5′UTR). The two segments of the 5′ flanking region have significant but opposite effects on activity. Exact mutation(s) not identified.

Experimental Evidence

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

Main Reference

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Additional References

Mutation #3

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

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

Molecular Details of the Mutation

segment 2 of the 5′ flanking region (upstream of 5′UTR). The two segments of the 5′ flanking region have significant but opposite effects on activity. Exact mutation(s) not identified.

Experimental Evidence

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

Main Reference

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Additional References

Mutation #4

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

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

Molecular Details of the Mutation

5′ UTR region. Exact mutation(s) not identified.

Experimental Evidence

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

Main Reference

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Additional References

Mutation #5

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

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

Molecular Details of the Mutation

3′ UTR region. Exact mutation(s) not identified.

Experimental Evidence

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

Main Reference

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Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@SeveralMutationsWithEffect - Entry validated by David Loehlin