GEPHE SUMMARY

Gephebase Gene

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

Entry Status

Published

GepheID

GP00001964

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 orena - lower enzyme activity

Trait State in Taxon B

Drosophila erecta - higher enzyme activity

Ancestral State

Unknown

Taxonomic Status

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

Taxon A

Latin Name

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

7233 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7233)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

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

7220 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7220)

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)

UniProtKB Drosophila melanogaster

P00334 (http://www.uniprot.org/uniprot/P00334)

GenebankID or UniProtKB

()

GO:0004022 : alcohol dehydrogenase (NAD) activity
(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

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

In vitro assay by replacement of the entire coding region. Four possible amino acid changes. Exact causal amino acid change(s) not identified.

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

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.

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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

5′ flanking 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 #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

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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Authors

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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

3′ UTR region. Exact mutation(s) not identified. Effect on Ads activity in the opposite direction compared to the other Adh regions.

Experimental Evidence

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

Main Reference

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Authors

Loehlin DW; Ames JR; Vaccaro K; Carroll SB

Abstract

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Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@SeveralMutationsWithEffect - There is a consensus phenotype of moderate ADH activity in the broader taxonomic group (Mercot et al. 1994). With the transformed alleles David Loehlin also observed ”moderate” activity in mel-slow; D. erecta and D. yakuba. This suggests that D. santomea and D. orena have derived low phenotypes but the phylogenetic signal is weak. - Entry validated by David Loehlin