GEPHE SUMMARY

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

GepheID
GP00001384

Entry Status
Published

Main curator
Courtier

PHENOTYPIC CHANGE

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

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

Trait State in Taxon A
Drosophila melanogaster - no wing spots

Trait State in Taxon B
Drosophila guttifera - wing spots and thoracic stripes

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

Parent
guttifera group () - (Rank: species group) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 66367)

NCBI Taxonomy ID
66368 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 66368)

is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
wg

Synonyms
l; beta-catenin; Br; CG4889; Dint-1; Dm Wg; Dm-1; Dmel\CG4889; DWint-1; dWnt; DWnt-1; fg; Gla; int-1; l(2)02657; l(2)rO727; l(2)SH1281; l(2)SH2 1281; l(2)wg; Sp; spd; Wg; WG; wgl; wnt; Wnt; WNT; Wnt-1; Wnt/Wg; wnt1; Wnt1

String
7227.FBpp0079060 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0079060)

Sequence Similarities
Belongs to the Wnt family.

GO - Molecular Function
GO:0048018 : receptor ligand activity (https://www.ebi.ac.uk/QuickGO/term/GO:0048018)

UniProtKB Drosophila melanogaster
P09615 (http://www.uniprot.org/uniprot/P09615)

GenebankID or UniProtKB
()

GO:0005109 : frizzled binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005109)
GO:0016015 : morphogen activity (https://www.ebi.ac.uk/QuickGO/term/GO:0016015)
GO:0050840 : extracellular matrix binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0050840)
GO:0005539 : glycosaminoglycan binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0005539)
GO:0043395 : heparan sulfate proteoglycan binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0043395)

GO - Biological Process

GO:0061382 : Malpighian tubule tip cell differentiation
(https://www.ebi.ac.uk/QuickGO/term/GO:0061382)
GO:0007616 : long-term memory (https://www.ebi.ac.uk/QuickGO/term/GO:0007616)
GO:0008284 : positive regulation of cell proliferation
(https://www.ebi.ac.uk/QuickGO/term/GO:0008284)
GO:0007398 : ectoderm development
(https://www.ebi.ac.uk/QuickGO/term/GO:0007398)
GO:0007476 : imaginal disc-derived wing morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0007476)
GO:0007498 : mesoderm development
(https://www.ebi.ac.uk/QuickGO/term/GO:0007498)
GO:0030707 : ovarian follicle cell development
(https://www.ebi.ac.uk/QuickGO/term/GO:0030707)
GO:0008587 : imaginal disc-derived wing margin morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0008587)
GO:0048728 : proboscis development
(https://www.ebi.ac.uk/QuickGO/term/GO:0048728)
GO:0035220 : wing disc development
(https://www.ebi.ac.uk/QuickGO/term/GO:0035220)
GO:0008544 : epidermis development
(https://www.ebi.ac.uk/QuickGO/term/GO:0008544)
GO:0035225 : determination of genital disc primordium
(https://www.ebi.ac.uk/QuickGO/term/GO:0035225)
GO:0007391 : dorsal closure (https://www.ebi.ac.uk/QuickGO/term/GO:0007391)
GO:0061331 : epithelial cell proliferation involved in Malpighian tubule morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0061331)
GO:0007444 : imaginal disc development
(https://www.ebi.ac.uk/QuickGO/term/GO:0007444)
GO:0045572 : positive regulation of imaginal disc growth
(https://www.ebi.ac.uk/QuickGO/term/GO:0045572)
GO:0007367 : segment polarity determination
(https://www.ebi.ac.uk/QuickGO/term/GO:0007367)
GO:0035277 : spiracle morphogenesis, open tracheal system
(https://www.ebi.ac.uk/QuickGO/term/GO:0035277)
GO:0010002 : cardioblast differentiation
(https://www.ebi.ac.uk/QuickGO/term/GO:0010002)
GO:2000648 : positive regulation of stem cell proliferation
(https://www.ebi.ac.uk/QuickGO/term/GO:2000648)
GO:0010942 : positive regulation of cell death
(https://www.ebi.ac.uk/QuickGO/term/GO:0010942)
GO:0048754 : branching morphogenesis of an epithelial tube
(https://www.ebi.ac.uk/QuickGO/term/GO:0048754)
GO:0007442 : hindgut morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0007442)
GO:0001745 : compound eye morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0001745)
GO:0044719 : regulation of imaginal disc-derived wing size
(https://www.ebi.ac.uk/QuickGO/term/GO:0044719)
GO:0007448 : anterior/posterior pattern specification, imaginal disc
(https://www.ebi.ac.uk/QuickGO/term/GO:0007448)
GO:0035147 : branch fusion, open tracheal system
(https://www.ebi.ac.uk/QuickGO/term/GO:0035147)
GO:0060070 : canonical Wnt signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0060070)
GO:0061316 : canonical Wnt signaling pathway involved in heart development
(https://www.ebi.ac.uk/QuickGO/term/GO:0061316)
GO:0090254 : cell elongation involved in imaginal disc-derived wing morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0090254)
GO:0035293 : chitin-based larval cuticle pattern formation
(https://www.ebi.ac.uk/QuickGO/term/GO:0035293)
GO:0007450 : dorsal/ventral pattern formation, imaginal disc
(https://www.ebi.ac.uk/QuickGO/term/GO:0007450)
GO:0035153 : epithelial cell type specification, open tracheal system
(https://www.ebi.ac.uk/QuickGO/term/GO:0035153)
GO:0035224 : genital disc anterior/posterior pattern formation
(https://www.ebi.ac.uk/QuickGO/term/GO:0035224)
GO:0035263 : genital disc sexually dimorphic development
(https://www.ebi.ac.uk/QuickGO/term/GO:0035263)
GO:0060914 : heart formation (https://www.ebi.ac.uk/QuickGO/term/GO:0060914)

GO:0007488 : histoblast morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0007488)
GO:0035217 : labial disc development (https://www.ebi.ac.uk/QuickGO/term/GO:0035217)
GO:0035167 : larval lymph gland hemopoiesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0035167)
GO:0007523 : larval visceral muscle development
(https://www.ebi.ac.uk/QuickGO/term/GO:0007523)
GO:0035170 : lymph gland crystal cell differentiation
(https://www.ebi.ac.uk/QuickGO/term/GO:0035170)
GO:0048542 : lymph gland development
(https://www.ebi.ac.uk/QuickGO/term/GO:0048542)
GO:0061332 : Malpighian tubule bud morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0061332)
GO:0048332 : mesoderm morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0048332)
GO:0009996 : negative regulation of cell fate specification
(https://www.ebi.ac.uk/QuickGO/term/GO:0009996)
GO:0032876 : negative regulation of DNA endoreduplication
(https://www.ebi.ac.uk/QuickGO/term/GO:0032876)
GO:0045611 : negative regulation of hemocyte differentiation
(https://www.ebi.ac.uk/QuickGO/term/GO:0045611)
GO:0014019 : neuroblast development
(https://www.ebi.ac.uk/QuickGO/term/GO:0014019)
GO:0061320 : pericardial nephrocyte differentiation
(https://www.ebi.ac.uk/QuickGO/term/GO:0061320)
GO:0046672 : positive regulation of compound eye retinal cell programmed cell death
(https://www.ebi.ac.uk/QuickGO/term/GO:0046672)
GO:0042691 : positive regulation of crystal cell differentiation
(https://www.ebi.ac.uk/QuickGO/term/GO:0042691)
GO:0061328 : posterior Malpighian tubule development
(https://www.ebi.ac.uk/QuickGO/term/GO:0061328)
GO:0048076 : regulation of compound eye pigmentation
(https://www.ebi.ac.uk/QuickGO/term/GO:0048076)
GO:0072091 : regulation of stem cell proliferation
(https://www.ebi.ac.uk/QuickGO/term/GO:0072091)
GO:0060061 : Spemann organizer formation
(https://www.ebi.ac.uk/QuickGO/term/GO:0060061)
GO:0050808 : synapse organization (https://www.ebi.ac.uk/QuickGO/term/GO:0050808)
GO:0051124 : synaptic growth at neuromuscular junction
(https://www.ebi.ac.uk/QuickGO/term/GO:0051124)
GO:0007418 : ventral midline development
(https://www.ebi.ac.uk/QuickGO/term/GO:0007418)
GO:0035311 : wing cell fate specification
(https://www.ebi.ac.uk/QuickGO/term/GO:0035311)

GO - Cellular Component

GO:0005886 : plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005886)
GO:0045121 : membrane raft (https://www.ebi.ac.uk/QuickGO/term/GO:0045121)
GO:0005576 : extracellular region (https://www.ebi.ac.uk/QuickGO/term/GO:0005576)
GO:0030054 : cell junction (https://www.ebi.ac.uk/QuickGO/term/GO:0030054)
GO:0005615 : extracellular space (https://www.ebi.ac.uk/QuickGO/term/GO:0005615)
GO:0005783 : endoplasmic reticulum
(https://www.ebi.ac.uk/QuickGO/term/GO:0005783)
GO:0009986 : cell surface (https://www.ebi.ac.uk/QuickGO/term/GO:0009986)
GO:0005771 : multivesicular body (https://www.ebi.ac.uk/QuickGO/term/GO:0005771)
GO:0043195 : terminal bouton (https://www.ebi.ac.uk/QuickGO/term/GO:0043195)

Mutation #1

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

Complex cis-regulatory evolution by gain of cis-regulatory activity at three sites: 1) Crossvein/Vein-Tip enhancer (3′ of wg) ; and within first intron of distant Wnt10 gene 2) Campaniform Spot enhancer and 3) Thoracic Stripes enhancer

Experimental Evidence

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

Main Reference

Gain of cis-regulatory activities underlies novel domains of wingless gene expression in Drosophila. (2015) (https://pubmed.ncbi.nlm.nih.gov/26034272)

Authors

Koshikawa S; Giorgianni MW; Vaccaro K; Kassner VA; Yoder JH; Werner T; Carroll SB

Abstract

Changes in gene expression during animal development are largely responsible for the evolution of morphological diversity. However, the genetic and molecular mechanisms responsible for the origins of new gene-expression domains have been difficult to elucidate. Here, we sought to identify molecular events underlying the origins of three novel features of wingless (wg) gene expression that are associated with distinct pigmentation patterns in Drosophila guttifera. We compared the activity of cis-regulatory sequences (enhancers) across the wg locus in D. guttifera and Drosophila melanogaster and found strong functional conservation among the enhancers that control similar patterns of wg expression in larval imaginal discs that are essential for appendage development. For pupal tissues, however, we found three novel wg enhancer activities in D. guttifera associated with novel domains of

wg expression, including two enhancers located surprisingly far away in an intron of the distant Wnt10 gene. Detailed analysis of one enhancer (the vein-tip enhancer) revealed that it overlapped with a region controlling wg expression in wing crossveins (crossvein enhancer) in D. guttifera and other species. Our results indicate that one novel domain of wg expression in D. guttifera wings evolved by co-opting pre-existing regulatory sequences governing gene activity in the developing wing. We suggest that the modification of existing enhancers is a common path to the evolution of new gene-expression domains and enhancers.

Additional References

Generation of a novel wing colour pattern by the Wingless morphogen. (2010) (https://pubmed.ncbi.nlm.nih.gov/20376004)

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

Complex cis-regulatory evolution by gain of cis-regulatory activity at three sites: 1) Crossvein/Vein-Tip enhancer (3′ of wg) ; and within first intron of distant Wnt10 gene 2) Campaniform Spot enhancer and 3) Thoracic Stripes enhancer

Experimental Evidence

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

Main Reference

Gain of cis-regulatory activities underlies novel domains of wingless gene expression in Drosophila. (2015) (https://pubmed.ncbi.nlm.nih.gov/26034272)

Authors

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Additional References

Generation of a novel wing colour pattern by the Wingless morphogen. (2010) (https://pubmed.ncbi.nlm.nih.gov/20376004)

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

Complex cis-regulatory evolution by gain of cis-regulatory activity at three sites: 1) Crossvein/Vein-Tip enhancer (3′ of wg) ; and within first intron of distant Wnt10 gene 2) Campaniform Spot enhancer and 3) Thoracic Stripes enhancer

Experimental Evidence

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

Main Reference

Gain of cis-regulatory activities underlies novel domains of wingless gene expression in Drosophila. (2015) (https://pubmed.ncbi.nlm.nih.gov/26034272)

Authors

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Additional References

Generation of a novel wing colour pattern by the Wingless morphogen. (2010) (https://pubmed.ncbi.nlm.nih.gov/20376004)

RELATED GEPHE

Related Genes

5 (bab, bab1, ebony, tan, yellow) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^7227^/and+Trait=Coloration/or+Taxon ID=^66368^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@SeveralMutationsWithEffect Multiple transgenic lines were deployed to demonstrate sufficiency of the derived enhancers to drive gene expression