GEPHE SUMMARY

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

GepheID
GP00002663

Main curator

Entry Status
Published

Courtier

PHENOTYPIC CHANGE

Trait #1

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

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

Trait State in Taxon A
-

Trait State in Taxon B
-

Trait #2

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

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

Trait State in Taxon A
-

Trait State in Taxon B
-

Trait #3

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

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

Trait State in Taxon A
-

Trait State in Taxon B
-

Trait #4

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

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

Trait State in Taxon A
-

Trait State in Taxon B
-

Trait #5

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

Trait
Lifespan (https://www.gephebase.org/search-

criteria?/and+Trait=^Lifespan^#gephebase-summary-title)

Trait State in Taxon A

-

Trait State in Taxon B

-

Ancestral State

Unknown

Taxonomic Status

Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#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 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 B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

InR

Synonyms

18402; CG18402; DIHR; DILR; dinr; dInr; dInR; dINR; DInr; DInR; dInsR; dINSR; dir; dIR; DIR; Dir-a; Dir-b; DIRbeta; dIRH; DIRH; Dmel\CG18402; er10; inr; inR; Inr; INR; Inr-alpha; Inr-beta; INS; InsR; insulin/insulin-like growth factor receptor; IR; l(3)05545; l(3)93Dj; l(3)er10; lnR; sprout; Inr-a

String

7227.FBpp0288669 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0288669)

Sequence Similarities

Belongs to the protein kinase superfamily. Tyr protein kinase family. Insulin receptor subfamily.

GO - Molecular Function

GO:0004888 : transmembrane signaling receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004888)
GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)
GO:0042802 : identical protein binding (https://www.ebi.ac.uk/QuickGO/term/GO:0042802)
GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)
GO:0004714 : transmembrane receptor protein tyrosine kinase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004714)
GO:0004713 : protein tyrosine kinase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004713)
GO:0043559 : insulin binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043559)
GO:0043560 : insulin receptor substrate binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043560)
GO:0005009 : insulin-activated receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005009)
GO:0043548 : phosphatidylinositol 3-kinase binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043548)

UniProtKB Drosophila melanogaster

P09208 (http://www.uniprot.org/uniprot/P09208)

GenebankID or UniProtKB

()

GO:0017124 : SH3 domain binding (https://www.ebi.ac.uk/QuickGO/term/GO:0017124)

GO - Biological Process

GO:0055088 : lipid homeostasis (https://www.ebi.ac.uk/QuickGO/term/GO:0055088)
GO:0005975 : carbohydrate metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0005975)
GO:0043066 : negative regulation of apoptotic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0043066)
GO:0007399 : nervous system development
(https://www.ebi.ac.uk/QuickGO/term/GO:0007399)
GO:0030154 : cell differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0030154)
GO:0042632 : cholesterol homeostasis
(https://www.ebi.ac.uk/QuickGO/term/GO:0042632)
GO:0070374 : positive regulation of ERK1 and ERK2 cascade
(https://www.ebi.ac.uk/QuickGO/term/GO:0070374)
GO:0070328 : triglyceride homeostasis
(https://www.ebi.ac.uk/QuickGO/term/GO:0070328)
GO:0008284 : positive regulation of cell proliferation
(https://www.ebi.ac.uk/QuickGO/term/GO:0008284)
GO:0035264 : multicellular organism growth
(https://www.ebi.ac.uk/QuickGO/term/GO:0035264)
GO:0030307 : positive regulation of cell growth
(https://www.ebi.ac.uk/QuickGO/term/GO:0030307)
GO:0006468 : protein phosphorylation
(https://www.ebi.ac.uk/QuickGO/term/GO:0006468)
GO:2000377 : regulation of reactive oxygen species metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:2000377)
GO:0007626 : locomotory behavior (https://www.ebi.ac.uk/QuickGO/term/GO:0007626)
GO:0007623 : circadian rhythm (https://www.ebi.ac.uk/QuickGO/term/GO:0007623)
GO:0030707 : ovarian follicle cell development
(https://www.ebi.ac.uk/QuickGO/term/GO:0030707)
GO:0007166 : cell surface receptor signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0007166)
GO:0008340 : determination of adult lifespan
(https://www.ebi.ac.uk/QuickGO/term/GO:0008340)
GO:0009792 : embryo development ending in birth or egg hatching
(https://www.ebi.ac.uk/QuickGO/term/GO:0009792)
GO:0007390 : germ-band shortening
(https://www.ebi.ac.uk/QuickGO/term/GO:0007390)
GO:0009968 : negative regulation of signal transduction
(https://www.ebi.ac.uk/QuickGO/term/GO:0009968)
GO:0008286 : insulin receptor signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0008286)
GO:0040014 : regulation of multicellular organism growth
(https://www.ebi.ac.uk/QuickGO/term/GO:0040014)
GO:0046777 : protein autophosphorylation
(https://www.ebi.ac.uk/QuickGO/term/GO:0046777)
GO:0007568 : aging (https://www.ebi.ac.uk/QuickGO/term/GO:0007568)
GO:0007411 : axon guidance (https://www.ebi.ac.uk/QuickGO/term/GO:0007411)
GO:0006629 : lipid metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0006629)
GO:0040018 : positive regulation of multicellular organism growth
(https://www.ebi.ac.uk/QuickGO/term/GO:0040018)
GO:0006979 : response to oxidative stress
(https://www.ebi.ac.uk/QuickGO/term/GO:0006979)
GO:0007424 : open tracheal system development
(https://www.ebi.ac.uk/QuickGO/term/GO:0007424)
GO:0009267 : cellular response to starvation
(https://www.ebi.ac.uk/QuickGO/term/GO:0009267)
GO:0048589 : developmental growth
(https://www.ebi.ac.uk/QuickGO/term/GO:0048589)
GO:0001700 : embryonic development via the syncytial blastoderm
(https://www.ebi.ac.uk/QuickGO/term/GO:0001700)
GO:0055116 : entry into reproductive diapause
(https://www.ebi.ac.uk/QuickGO/term/GO:0055116)
GO:0048132 : female germ-line stem cell asymmetric division
(https://www.ebi.ac.uk/QuickGO/term/GO:0048132)
GO:0036099 : female germ-line stem cell population maintenance
(https://www.ebi.ac.uk/QuickGO/term/GO:0036099)
GO:0008585 : female gonad development
(https://www.ebi.ac.uk/QuickGO/term/GO:0008585)
GO:0060180 : female mating behavior
(https://www.ebi.ac.uk/QuickGO/term/GO:0060180)
GO:0042078 : germ-line stem cell division
(https://www.ebi.ac.uk/QuickGO/term/GO:0042078)
GO:0060250 : germ-line stem-cell niche homeostasis
(https://www.ebi.ac.uk/QuickGO/term/GO:0060250)
GO:0042593 : glucose homeostasis (https://www.ebi.ac.uk/QuickGO/term/GO:0042593)
GO:0007446 : imaginal disc growth (https://www.ebi.ac.uk/QuickGO/term/GO:0007446)

GO:0036335 : intestinal stem cell homeostasis
(https://www.ebi.ac.uk/QuickGO/term/GO:0036335)
GO:0048133 : male germ-line stem cell asymmetric division
(https://www.ebi.ac.uk/QuickGO/term/GO:0048133)
GO:0007520 : myoblast fusion (https://www.ebi.ac.uk/QuickGO/term/GO:0007520)
GO:0010507 : negative regulation of autophagy
(https://www.ebi.ac.uk/QuickGO/term/GO:0010507)
GO:0042321 : negative regulation of circadian sleep/wake cycle, sleep
(https://www.ebi.ac.uk/QuickGO/term/GO:0042321)
GO:2000252 : negative regulation of feeding behavior
(https://www.ebi.ac.uk/QuickGO/term/GO:2000252)
GO:0090278 : negative regulation of peptide hormone secretion
(https://www.ebi.ac.uk/QuickGO/term/GO:0090278)
GO:0045793 : positive regulation of cell size
(https://www.ebi.ac.uk/QuickGO/term/GO:0045793)
GO:0070346 : positive regulation of fat cell proliferation
(https://www.ebi.ac.uk/QuickGO/term/GO:0070346)
GO:0010884 : positive regulation of lipid storage
(https://www.ebi.ac.uk/QuickGO/term/GO:0010884)
GO:1904801 : positive regulation of neuron remodeling
(https://www.ebi.ac.uk/QuickGO/term/GO:1904801)
GO:0046622 : positive regulation of organ growth
(https://www.ebi.ac.uk/QuickGO/term/GO:0046622)
GO:0014068 : positive regulation of phosphatidylinositol 3-kinase signaling
(https://www.ebi.ac.uk/QuickGO/term/GO:0014068)
GO:1904263 : positive regulation of TORC1 signaling
(https://www.ebi.ac.uk/QuickGO/term/GO:1904263)
GO:0007285 : primary spermatocyte growth
(https://www.ebi.ac.uk/QuickGO/term/GO:0007285)
GO:0051290 : protein heterotetramerization
(https://www.ebi.ac.uk/QuickGO/term/GO:0051290)
GO:0042127 : regulation of cell proliferation
(https://www.ebi.ac.uk/QuickGO/term/GO:0042127)
GO:0046620 : regulation of organ growth
(https://www.ebi.ac.uk/QuickGO/term/GO:0046620)
GO:0034059 : response to anoxia (https://www.ebi.ac.uk/QuickGO/term/GO:0034059)
GO:0042220 : response to cocaine (https://www.ebi.ac.uk/QuickGO/term/GO:0042220)
GO:0007525 : somatic muscle development
(https://www.ebi.ac.uk/QuickGO/term/GO:0007525)

GO - Cellular Component

GO:0005886 : plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005886)
GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)
GO:0005887 : integral component of plasma membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0005887)
GO:0043235 : receptor complex (https://www.ebi.ac.uk/QuickGO/term/GO:0043235)
GO:0030424 : axon (https://www.ebi.ac.uk/QuickGO/term/GO:0030424)
GO:0005899 : insulin receptor complex
(https://www.ebi.ac.uk/QuickGO/term/GO:0005899)

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

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

Indel Size

1-9 bp

Molecular Details of the Mutation

Deletion of 9 nucleotides in the first exon. The two alleles differ by presence/absence of the three amino acids QHH.

Experimental Evidence

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

Main Reference

A highly pleiotropic amino acid polymorphism in the Drosophila insulin receptor contributes to life-history adaptation. (2014) (https://pubmed.ncbi.nlm.nih.gov/25319083)

Authors

Paaby AB; Bergland AO; Behrman EL; Schmidt PS

Abstract

Finding the specific nucleotides that underlie adaptive variation is a major goal in evolutionary biology, but polygenic traits pose a challenge because the complex genotype-phenotype relationship can obscure the effects of individual alleles. However, natural selection working in large wild populations can shift allele frequencies and indicate functional regions of the genome. Previously, we showed that the two most common alleles of a complex amino acid insertion-deletion polymorphism in the Drosophila insulin receptor show independent, parallel clines in frequency across the North American and Australian continents. Here, we report that the cline is stable over at least a five-year period and that the polymorphism also demonstrates temporal shifts in allele frequency concurrent with seasonal change. We tested the alleles for effects on levels of insulin signaling, fecundity, development time, body size, stress tolerance, and life span. We find that the alleles are associated with predictable differences in these traits, consistent with patterns of Drosophila life-history variation across geography that likely reflect adaptation to the heterogeneous climatic environment. These results implicate insulin signaling as a major mediator of life-history adaptation in Drosophila, and suggest that life-history trade-offs can be explained by extensive pleiotropy at a single locus.

Additional References

Identification of a candidate adaptive polymorphism for Drosophila life history by parallel independent clines on two continents. (2010) (https://pubmed.ncbi.nlm.nih.gov/20074316)

RELATED GEPHE

Related Genes

12 (bab2, Drip, PPAR-gamma, Sdic gene cluster, Catecholamines up, Darkener of apricot (Doa), Dopa-decarboxylase, eve, fiz, foxo, PHGPx, RnrS) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^7227^/and+Trait=Fertility/or+Taxon ID=^7227^/and+Trait=Developmental time/or+Taxon ID=^7227^/and+Trait=Body size/or+Taxon ID=^7227^/and+Trait=Stress response/or+Taxon ID=^7227^/and+Trait=Lifespan/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

Impossible to know the direction of change because there is a lot of variation at this site in the closely related species D. simulans; D. sechellia and D. yakuba. @Cline