

GEPHE SUMMARY

	Gephebase Gene		GepheID
foxo (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^foxo^#gephebase-summary-title)		GP00002661	
	Entry Status	Courtier	Main curator
Published			

PHENOTYPIC CHANGE

Trait #1	Trait Category
Morphology (https://www.gephebase.org/search-criteria?/and+Trait+Category=^Morphology^#gephebase-summary-title)	
	Trait
Body size (wing) (https://www.gephebase.org/search-criteria?/and+Trait=^Body size (wing)^#gephebase-summary-title)	
	Trait State in Taxon A
smaller - low latitude allele	
	Trait State in Taxon B
larger - high latitude allele	

Trait #2	Trait Category
Morphology, Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=^Morphology^/and+Trait+Category=^Physiology^#gephebase-summary-title)	
	Trait
Starvation resistance (https://www.gephebase.org/search-criteria?/and+Trait=^Starvation resistance^#gephebase-summary-title)	
	Trait State in Taxon A
higher starvation resistance - low latitude allele	
	Trait State in Taxon B
lower starvation resistance - high latitude allele	

	Ancestral State		
Unknown			
	Taxonomic Status		
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Intraspecific^#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
Drosophila melanogaster (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Drosophila melanogaster^#gephebase-summary-title)		Drosophila melanogaster (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Drosophila melanogaster^#gephebase-summary-title)	
	Common Name		Common Name
fruit fly		fruit fly	
	Synonyms		Synonyms
Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster		Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster	
	Rank		Rank
species		species	
	Lineage		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		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		Parent
melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32351)		melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32351)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7227)		7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7227)	
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
No		No	

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Drosophila melanogaster
foxo	Q95V55 (http://www.uniprot.org/uniprot/Q95V55)	
	Synonyms	GenebankID or UniProtKB
3143; Afx; Akh; anon-WO0118547.374; cg3143; CG3143; dfoxo; dfoxO; dFoxo; dFoxO; dFOXO; Dfoxo; DfoxO; DFOXO; Dmel\CG3143; DmQ95V5; fd88A; FKHR; foxO; fOXO; Foxo; FoxO; FOXO; Foxo1; FOXO1; Q95V55	()	
	String	
7227.FBpp0293589 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7227.FBpp0293589)		
	Sequence Similarities	
-		
	GO - Molecular Function	
GO:0001228 : DNA-binding transcription activator activity, RNA polymerase II-specific (https://www.ebi.ac.uk/QuickGO/term/GO:0001228)		
GO:0003700 : DNA-binding transcription factor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003700)		
GO:0000977 : RNA polymerase II regulatory region sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0000977)		
GO:0000981 : DNA-binding transcription factor activity, RNA polymerase II-specific (https://www.ebi.ac.uk/QuickGO/term/GO:0000981)		
GO:0000978 : RNA polymerase II proximal promoter sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0000978)		
	GO - Biological Process	
GO:0009617 : response to bacterium (https://www.ebi.ac.uk/QuickGO/term/GO:0009617)		
GO:0045944 : positive regulation of transcription by RNA polymerase II (https://www.ebi.ac.uk/QuickGO/term/GO:0045944)		
GO:0006357 : regulation of transcription by RNA polymerase II (https://www.ebi.ac.uk/QuickGO/term/GO:0006357)		
GO:0006355 : regulation of transcription, DNA-templated (https://www.ebi.ac.uk/QuickGO/term/GO:0006355)		
GO:0000122 : negative regulation of transcription by RNA polymerase II (https://www.ebi.ac.uk/QuickGO/term/GO:0000122)		
GO:0008285 : negative regulation of cell proliferation (https://www.ebi.ac.uk/QuickGO/term/GO:0008285)		
GO:0030308 : negative regulation of cell growth (https://www.ebi.ac.uk/QuickGO/term/GO:0030308)		
GO:0007623 : circadian rhythm (https://www.ebi.ac.uk/QuickGO/term/GO:0007623)		
GO:0035206 : regulation of hemocyte proliferation (https://www.ebi.ac.uk/QuickGO/term/GO:0035206)		
GO:0045475 : locomotor rhythm (https://www.ebi.ac.uk/QuickGO/term/GO:0045475)		
GO:0008340 : determination of adult lifespan (https://www.ebi.ac.uk/QuickGO/term/GO:0008340)		
GO:0008286 : insulin receptor signaling pathway (https://www.ebi.ac.uk/QuickGO/term/GO:0008286)		
GO:0040015 : negative regulation of multicellular organism growth (https://www.ebi.ac.uk/QuickGO/term/GO:0040015)		
GO:0034198 : cellular response to amino acid starvation (https://www.ebi.ac.uk/QuickGO/term/GO:0034198)		
GO:0034599 : cellular response to oxidative stress (https://www.ebi.ac.uk/QuickGO/term/GO:0034599)		
GO:0042594 : response to starvation (https://www.ebi.ac.uk/QuickGO/term/GO:0042594)		
GO:0040008 : regulation of growth (https://www.ebi.ac.uk/QuickGO/term/GO:0040008)		
GO:0006979 : response to oxidative stress (https://www.ebi.ac.uk/QuickGO/term/GO:0006979)		
GO:0061057 : peptidoglycan recognition protein signaling pathway (https://www.ebi.ac.uk/QuickGO/term/GO:0061057)		
GO:0009267 : cellular response to starvation (https://www.ebi.ac.uk/QuickGO/term/GO:0009267)		
GO:0036099 : female germ-line stem cell population maintenance (https://www.ebi.ac.uk/QuickGO/term/GO:0036099)		
GO:0042593 : glucose homeostasis (https://www.ebi.ac.uk/QuickGO/term/GO:0042593)		
GO:0046620 : regulation of organ growth (https://www.ebi.ac.uk/QuickGO/term/GO:0046620)		
GO:0046627 : negative regulation of insulin receptor signaling pathway (https://www.ebi.ac.uk/QuickGO/term/GO:0046627)		
GO:0001745 : compound eye morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0001745)		
GO:0048813 : dendrite morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0048813)		
GO:0019216 : regulation of lipid metabolic process (https://www.ebi.ac.uk/QuickGO/term/GO:0019216)		
GO:0007049 : cell cycle (https://www.ebi.ac.uk/QuickGO/term/GO:0007049)		
GO:0010508 : positive regulation of autophagy (https://www.ebi.ac.uk/QuickGO/term/GO:0010508)		
GO:0010506 : regulation of autophagy		

(<https://www.ebi.ac.uk/QuickGO/term/GO:0010506>)
GO:0045824 : negative regulation of innate immune response
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045824>)
GO:2000253 : positive regulation of feeding behavior
(<https://www.ebi.ac.uk/QuickGO/term/GO:2000253>)
GO:0048542 : lymph gland development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048542>)
GO:0070345 : negative regulation of fat cell proliferation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0070345>)
GO:0045792 : negative regulation of cell size
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045792>)
GO:0010888 : negative regulation of lipid storage
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010888>)
GO:0061045 : negative regulation of wound healing
(<https://www.ebi.ac.uk/QuickGO/term/GO:0061045>)
GO:0061965 : positive regulation of entry into reproductive diapause
(<https://www.ebi.ac.uk/QuickGO/term/GO:0061965>)
GO:2000130 : positive regulation of octopamine signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:2000130>)
GO:0010898 : positive regulation of triglyceride catabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010898>)
GO:0016241 : regulation of macroautophagy
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016241>)

GO - Cellular Component

GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)
GO:0005829 : cytosol (<https://www.ebi.ac.uk/QuickGO/term/GO:0005829>)
GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)

No (<a #gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Presumptive Null=" no"="">https://www.gephebase.org/search-criteria?/and+Presumptive Null="No" #gephebase-summary-title)	Presumptive Null
Unknown (<a #gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Molecular Type=" unknown"="">https://www.gephebase.org/search-criteria?/and+Molecular Type="Unknown" #gephebase-summary-title)	Molecular Type
Unknown (<a #gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Aberration Type=" unknown"="">https://www.gephebase.org/search-criteria?/and+Aberration Type="Unknown" #gephebase-summary-title)	Aberration Type
-	Molecular Details of the Mutation
Candidate Gene (<a #gephebase-summary-title"="" candidate="" gene"="" href="https://www.gephebase.org/search-criteria?/and+Experimental Evidence=">https://www.gephebase.org/search-criteria?/and+Experimental Evidence="Candidate Gene" #gephebase-summary-title)	Experimental Evidence
Allelic polymorphism at foxo contributes to local adaptation in Drosophila melanogaster. (2021) (https://pubmed.ncbi.nlm.nih.gov/33914989)	Main Reference
Betancourt NJ; Rajpurohit S; Durmaz E; Fabian DK; Kapun M; Flatt T; Schmidt P	Authors
The insulin/insulin-like growth factor signalling pathway has been hypothesized as a major determinant of life-history profiles that vary adaptively in natural populations. In Drosophila melanogaster, multiple components of this pathway vary predictably with latitude; this includes foxo, a conserved gene that regulates insulin signalling and has pleiotropic effects on a variety of fitness-associated traits. We hypothesized that allelic variation at foxo contributes to genetic variance for size-related traits that vary adaptively with latitude. We first examined patterns of variation among natural populations along a latitudinal transect in the eastern United States and show that thorax length, wing area, wing loading, and starvation tolerance exhibit significant latitudinal clines for both males and females but that development time does not vary predictably with latitude. We then generated recombinant outbred populations and show that naturally occurring allelic variation at foxo, which exhibits stronger clinality than expected, is associated with the same traits that vary with latitude in the natural populations. Our results suggest that allelic variation at foxo contributes to adaptive patterns of life-history variation in natural populations of this genetic model.	Abstract
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A clinal polymorphism in the insulin signaling transcription factor foxo contributes to life-history adaptation in Drosophila. (2019) (https://pubmed.ncbi.nlm.nih.gov/31111462)	Additional References

RELATED GEPHE

2 (fiz, lnR) (<a 7227"="" and+grouphaplotypes='true#gephebase-summary-title"' and+trait="Starvation" href="https://www.gephebase.org/search-criteria?/or+Taxon ID=" id="7227" or+taxon="" resistance="" size="">https://www.gephebase.org/search-criteria?/or+Taxon ID="7227"/and+Trait=Body size/or+Taxon ID="7227"/and+Trait=Starvation resistance/and+groupHaplotypes=true#gephebase-summary-title)	Related Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS

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