

GEPHE SUMMARY

	Gephebase Gene		GepheID
bab2 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~bab2~#gephebase-summary-title)		GP00000132	
	Entry Status	Martin	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Physiology~#gephebase-summary-title)			
	Trait		
Fertility (ovariole number) (https://www.gephebase.org/search-criteria?/and+Trait=~Fertility(ovariole number)~#gephebase-summary-title)			
	Trait State in Taxon A		
Drosophila melanogaster			
	Trait State in Taxon B		
Drosophila melanogaster			
	Ancestral State		
Data not curated			
	Taxonomic Status		
Intraspecific (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~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 Infraspecies?		is Taxon B an Infraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Drosophila melanogaster
bab2		Q9W0K4 (http://www.uniprot.org/uniprot/Q9W0K4)	
	Synonyms		GenebankID or UniProtKB
bab; BAB; bab-II; Bab2; BAB2; BTB-II; BtbII; CG13911; CG9102; Dmel\CG9102		AJ252173 (https://www.ncbi.nlm.nih.gov/nuccore/AJ252173)	
	String		
7227.FBpp0072535 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier= 7227.FBpp0072535)			
	Sequence Similarities		
-			
	GO - Molecular Function		
GO:0003700 : DNA-binding transcription factor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003700)			
GO:0003680 : AT DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003680)			
	GO - Biological Process		

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:0006351 : transcription, DNA-templated
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006351>)
GO:0007455 : eye-antennal disc morphogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007455>)
GO:0007478 : leg disc morphogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007478>)
GO:0061040 : female gonad morphogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0061040>)
GO:2000736 : regulation of stem cell differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:2000736>)

GO - Cellular Component

GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)
GO:0005700 : polytene chromosome
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005700>)

Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive Null=~Unknown~#gephebase-summary-title)	Presumptive Null
Unknown (https://www.gephebase.org/search-criteria?/and+Molecular Type=~Unknown~#gephebase-summary-title)	Molecular Type
Unknown (https://www.gephebase.org/search-criteria?/and+Aberration Type=~Unknown~#gephebase-summary-title)	Aberration Type
unknown ; loss of function reduces ovariole number	Molecular Details of the Mutation
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Linkage Mapping~#gephebase-summary-title)	Experimental Evidence
Convergent evolution of a reproductive trait through distinct developmental mechanisms in Drosophila. (2012) (https://pubmed.ncbi.nlm.nih.gov/23022298)	Main Reference
Green DA; Extavour CG	Authors
	Abstract

Convergent morphologies often arise due to similar selective pressures in independent lineages. It is poorly understood whether the same or different developmental genetic mechanisms underlie such convergence. Here we show that independent evolution of a reproductive trait, ovariole number, has resulted from changes in distinct developmental mechanisms, each of which may have a different underlying genetic basis in Drosophila. Ovariole number in Drosophila is species-specific, highly variable, and largely under genetic control. Convergent changes in Drosophila ovariole number have evolved independently within and between species. We previously showed that the number of a specific ovarian cell type, terminal filament (TF) cells, determines ovariole number. Here we examine TF cell development in different Drosophila lineages that independently evolved a significantly lower ovariole number than the D. melanogaster Oregon R strain. We show that in these Drosophila lineages, reduction in ovariole number occurs primarily through variations in one of two different developmental mechanisms: (1) reduced number of somatic gonad precursors (SGP cells) specified during embryogenesis; or (2) alterations of somatic gonad cell morphogenesis and differentiation in larval life. Mutations in the D. melanogaster Insulin Receptor (InR) alter SGP cell number but not ovarian morphogenesis, while targeted loss of function of bric-Å -brac 2 (bab2) affects morphogenesis without changing SGP cell number. Thus, evolution can produce similar ovariole numbers through distinct developmental mechanisms, likely controlled by different genetic mechanisms.

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Quantitative trait loci affecting phenotypic plasticity and the allometric relationship of ovariole number and thorax length in Drosophila melanogaster. (2008) (https://pubmed.ncbi.nlm.nih.gov/18716336)	Additional References
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RELATED GEPHE

6 (Drip, PPAR-gamma, Sdic gene cluster, InR, PHGPx, RnrS) (https://www.gephebase.org/search-criteria?/or+Taxon ID=~7227~/and+Trait=Fertility/and+groupHaplotypes=true#gephebase-summary-title)	Related Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS

