

GEPHE SUMMARY

Gephebase Gene		GepheID
InR (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=~InR^#gephebase-summary-title)	GP00000500	
Entry Status		Main curator
Published		

PHENOTYPIC CHANGE

Trait Category	
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=~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 sechellia	
Trait State in Taxon B	
Drosophila simulans	
Ancestral State	
Data not curated	
Taxonomic Status	
Interspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=~Interspecific^#gephebase-summary-title)	
Taxon A	Taxon B
Latin Name	Latin Name
Drosophila sechellia (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Drosophila sechellia^#gephebase-summary-title)	Drosophila simulans (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Drosophila simulans^#gephebase-summary-title)
Common Name	Common Name
-	-
Synonyms	Synonyms
Drosophila sechellia Tsacas and Bachli, 1981	-
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
7238 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7238)	7240 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7240)
is Taxon A an Intraspecies?	is Taxon B an Intraspecies?
No	No

GENOTYPIC CHANGE

Generic Gene Name		UniProtKB Drosophila melanogaster
InR	P09208 (http://www.uniprot.org/uniprot/P09208)	
Synonyms		GenebankID or UniProtKB
18402; CG18402; DIHR; DILR; dinr; dInr; dlnR; dlnR; dlnR; Dlnr; DlnR; dlnsR; dlnSR; 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; I(3)05545; I(3)93Dj; I(3)er10; InR; sprout; Inr-a		CAY93033 (https://www.ncbi.nlm.nih.gov/nuccore/CAY93033)
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>)
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

Unknown (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=~Unknown~#gephebase-summary-title>)

Molecular Type

Unknown (<https://www.gephebase.org/search-criteria?/and+Molecular Type=~Unknown~#gephebase-summary-title>)

Aberration Type

Unknown (<https://www.gephebase.org/search-criteria?/and+Aberration Type=~Unknown~#gephebase-summary-title>)

Molecular Details of the Mutation

unknown; loss of function reduces ovariole number

Experimental Evidence

Linkage Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Linkage Mapping~#gephebase-summary-title>)

Main Reference

Convergent evolution of a reproductive trait through distinct developmental mechanisms in Drosophila. (2012) (<https://pubmed.ncbi.nlm.nih.gov/23022298>)

Authors

Green DA; Extavour CG

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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Additional References

High-resolution quantitative trait locus mapping reveals sign epistasis controlling ovariole number between two *Drosophila* species. (2006) (<https://pubmed.ncbi.nlm.nih.gov/16489225>)

RELATED GEPHE

No matches found.

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS