

GEPHE SUMMARY

	Gephebase Gene	GepheID
Svb/ovo (<a +svb="" href="https://www.gephebase.org/search-criteria?/and+GeneGephebase=" ovo^#gephebase-summary-title"="">https://www.gephebase.org/search-criteria?/and+GeneGephebase="+Svb/ovo^#gephebase-summary-title)	GP00001085	
	Entry Status	Courtier
Published		

PHENOTYPIC CHANGE

Morphology (#gephebase-summary-title)		Trait Category
Trichome pattern (larva) (https://www.gephebase.org/search-criteria?/and+Trait=~Trichome pattern (larva)^#gephebase-summary-title)		Trait
Drosophila simulans; D. mauritiana : more trichomes		Trait State in Taxon A
Drosophila sechellia : fewer trichomes		Trait State in Taxon B
Taxon A		Ancestral State
Interspecific (#gephebase-summary-title)		Taxonomic Status
Taxon A #1		Taxon B
Drosophila simulans (#gephebase-summary-title)		Drosophila sechellia (#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
7240 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7240)		7238 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7238)
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		No

Taxon A #2	
<i>Drosophila mauritiana</i>	Latin Name
(<a +drosophila+mauritiana`#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Drosophila+mauritiana`#gephebase-summary-title)	
-	Common Name
-	Synonyms
species	Rank
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; Acalyptrae; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup	Lineage
	Parent

melanogaster subgroup () - (Rank: species subgroup)
(<https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351>)
NCBI Taxonomy ID
7226
(<https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7226>)
is Taxon A an Intraspecies?
No

GENOTYPIC CHANGE

ovo

Generic Gene Name

UniProtKB Drosophila melanogaster

P51521 (<http://www.uniprot.org/uniprot/P51521>)

Synonyms

GenebankID or UniProtKB

CG15467; CG6824; Dmel\CG6824; Fs(1)K1103; fs(1)K1237; Fs(1)K1237; Fs(1)K155; fs(1)M1; fs(1)M38; Ovo; OVO; Ovo-D; ovo/shavenbaby; ovo/svb; ovoD; Shv; svb; Sv; Sv/Ovo

ABO38688 (<https://www.ncbi.nlm.nih.gov/nuccore/ABO38688>)

String

7227.FBpp0291128
(http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7227.FBpp0291128)

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:0043565 : sequence-specific DNA binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043565>)
GO:0046872 : metal ion binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0046872>)
GO:0003677 : DNA binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0003677>)
GO:0001078 : proximal promoter DNA-binding transcription repressor activity, RNA polymerase II-specific (<https://www.ebi.ac.uk/QuickGO/term/GO:0001078>)

GO - Biological Process

GO:0045944 : positive regulation of transcription by RNA polymerase II
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045944>)
GO:0006355 : regulation of transcription, DNA-templated
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006355>)
GO:0008343 : adult feeding behavior
(<https://www.ebi.ac.uk/QuickGO/term/GO:0008343>)
GO:0000122 : negative regulation of transcription by RNA polymerase II
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000122>)
GO:0045892 : negative regulation of transcription, DNA-templated
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045892>)
GO:0045893 : positive regulation of transcription, DNA-templated
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045893>)
GO:0007010 : cytoskeleton organization
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007010>)
GO:0008360 : regulation of cell shape
(<https://www.ebi.ac.uk/QuickGO/term/GO:0008360>)
GO:0048477 : oogenesis (<https://www.ebi.ac.uk/QuickGO/term/GO:0048477>)
GO:0048067 : cuticle pigmentation (<https://www.ebi.ac.uk/QuickGO/term/GO:0048067>)
GO:0009913 : epidermal cell differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009913>)
GO:0035017 : cuticle pattern formation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0035017>)
GO:0019099 : female germ-line sex determination
(<https://www.ebi.ac.uk/QuickGO/term/GO:0019099>)
GO:0018992 : germ-line sex determination
(<https://www.ebi.ac.uk/QuickGO/term/GO:0018992>)
GO:0016348 : imaginal disc-derived leg joint morphogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016348>)
GO:0035316 : non-sensory hair organization
(<https://www.ebi.ac.uk/QuickGO/term/GO:0035316>)
GO:0070896 : positive regulation of transposon integration
(<https://www.ebi.ac.uk/QuickGO/term/GO:0070896>)

GO - Cellular Component

GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)
GO:0005654 : nucleoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005654>)
GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)

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
Enhancer A	
	Experimental Evidence
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=~Linkage+Mapping~#gephebase-summary-title)	
	Main Reference
Morphological evolution through multiple cis-regulatory mutations at a single gene. (2007) (https://pubmed.ncbi.nlm.nih.gov/17632547)	
	Authors
McGregor AP; Orgogozo V; Delon I; Zanet J; Srinivasan DG; Payre F; Stern DL	
	Abstract
<p>One central, and yet unsolved, question in evolutionary biology is the relationship between the genetic variants segregating within species and the causes of morphological differences between species. The classic neo-darwinian view postulates that species differences result from the accumulation of small-effect changes at multiple loci. However, many examples support the possible role of larger abrupt changes in the expression of developmental genes in morphological evolution. Although this evidence might be considered a challenge to a neo-darwinian micromutationist view of evolution, there are currently few examples of the actual genes causing morphological differences between species. Here we examine the genetic basis of a trichome pattern difference between <i>Drosophila</i> species, previously shown to result from the evolution of a single gene, shavenbaby (svb), probably through cis-regulatory changes. We first identified three distinct svb enhancers from <i>D. melanogaster</i> driving reporter gene expression in partly overlapping patterns that together recapitulate endogenous svb expression. All three homologous enhancers from <i>D. sechellia</i> drive expression in modified patterns, in a direction consistent with the evolved svb expression pattern. To test the influence of these enhancers on the actual phenotypic difference, we conducted interspecific genetic mapping at a resolution sufficient to recover multiple intragenic recombinants. This functional analysis revealed that independent genetic regions upstream of svb that overlap the three identified enhancers are collectively required to generate the <i>D. sechellia</i> trichome pattern. Our results demonstrate that the accumulation of multiple small-effect changes at a single locus underlies the evolution of a morphological difference between species. These data support the view that alleles of large effect that distinguish species may sometimes reflect the accumulation of multiple mutations of small effect at select genes.</p>	
	Additional References

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
Enhancer 7	
	Experimental Evidence
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=~Linkage+Mapping~#gephebase-summary-title)	
	Main Reference
Morphological evolution through multiple cis-regulatory mutations at a single gene. (2007) (https://pubmed.ncbi.nlm.nih.gov/17632547)	
	Authors
McGregor AP; Orgogozo V; Delon I; Zanet J; Srinivasan DG; Payre F; Stern DL	
	Abstract
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	Additional References

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
Enhancer Z	
	Experimental Evidence
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=~Linkage+Mapping~#gephebase-summary-title)	
	Main Reference
Phenotypic robustness conferred by apparently redundant transcriptional enhancers. (2010) (https://pubmed.ncbi.nlm.nih.gov/20512118)	
	Authors
Frankel N; Davis GK; Vargas D; Wang S; Payre F; Stern DL	
	Abstract
<p>Genes include cis-regulatory regions that contain transcriptional enhancers. Recent reports have shown that developmental genes often possess multiple discrete enhancer modules that drive transcription in similar spatio-temporal patterns: primary enhancers located near the basal promoter and secondary, or ‘shadow’, enhancers located at more remote positions. It has been proposed that the seemingly redundant activity of primary and secondary enhancers contributes to phenotypic robustness. We tested this hypothesis by generating a deficiency that removes two newly discovered enhancers of shavenbaby (svb, a transcript of the ovo locus), a gene encoding a transcription factor that directs development of <i>Drosophila</i> larval</p>	

trichomes. At optimal temperatures for embryonic development, this deficiency causes minor defects in trichome patterning. In embryos that develop at both low and high extreme temperatures, however, absence of these secondary enhancers leads to extensive loss of trichomes. These temperature-dependent defects can be rescued by a transgene carrying a secondary enhancer driving transcription of the svb cDNA. Finally, removal of one copy of wingless, a gene required for normal trichome patterning, causes a similar loss of trichomes only in flies lacking the secondary enhancers. These results support the hypothesis that secondary enhancers contribute to phenotypic robustness in the face of environmental and genetic variability.

Additional References

Mutation #4

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

Enhancer DG2

Experimental Evidence

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

Main Reference

Phenotypic robustness conferred by apparently redundant transcriptional enhancers. (2010) (<https://pubmed.ncbi.nlm.nih.gov/20512118>)

Authors

Frankel N; Davis GK; Vargas D; Wang S; Payre F; Stern DL

Abstract

Genes include cis-regulatory regions that contain transcriptional enhancers. Recent reports have shown that developmental genes often possess multiple discrete enhancer modules that drive transcription in similar spatio-temporal patterns: primary enhancers located near the basal promoter and secondary, or ‘shadow’, enhancers located at more remote positions. It has been proposed that the seemingly redundant activity of primary and secondary enhancers contributes to phenotypic robustness. We tested this hypothesis by generating a deficiency that removes two newly discovered enhancers of shavenbaby (svb, a transcript of the ovo locus), a gene encoding a transcription factor that directs development of Drosophila larval trichomes. At optimal temperatures for embryonic development, this deficiency causes minor defects in trichome patterning. In embryos that develop at both low and high extreme temperatures, however, absence of these secondary enhancers leads to extensive loss of trichomes. These temperature-dependent defects can be rescued by a transgene carrying a secondary enhancer driving transcription of the svb cDNA. Finally, removal of one copy of wingless, a gene required for normal trichome patterning, causes a similar loss of trichomes only in flies lacking the secondary enhancers. These results support the hypothesis that secondary enhancers contribute to phenotypic robustness in the face of environmental and genetic variability.

Additional References

Mutation #5

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

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

Molecular Details of the Mutation

Enhancer E6; first epistatic mutation (5 in total)

Experimental Evidence

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

Main Reference

Morphological evolution caused by many subtle-effect substitutions in regulatory DNA. (2011) (<https://pubmed.ncbi.nlm.nih.gov/21720363>)

Authors

Frankel N; Erezyilmaz DF; McGregor AP; Wang S; Payre F; Stern DL

Abstract

Morphology evolves often through changes in developmental genes, but the causal mutations, and their effects, remain largely unknown. The evolution of naked cuticle on larvae of Drosophila sechellia resulted from changes in five transcriptional enhancers of shavenbaby (svb), a transcript of the ovo locus that encodes a transcription factor that governs morphogenesis of microtrichiae, hereafter called ‘trichomes’. Here we show that the function of one of these enhancers evolved through multiple single-nucleotide substitutions that altered both the timing and level of svb expression. The consequences of these nucleotide substitutions on larval morphology were quantified with a novel functional assay. We found that each substitution had a relatively small phenotypic effect, and that many nucleotide changes account for this large morphological difference. In addition, we observed that the substitutions had non-additive effects. These data provide unprecedented resolution of the phenotypic effects of substitutions and show how individual nucleotide changes in a transcriptional enhancer have caused morphological evolution.

Additional References

Evolved Repression Overcomes Enhancer Robustness. (2016) (<https://pubmed.ncbi.nlm.nih.gov/27840106>)

Mutation #6

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

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

Molecular Details of the Mutation

Enhancer E6; 2nd epistatic mutation (5 in total)

Experimental Evidence

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

Main Reference

Morphological evolution caused by many subtle-effect substitutions in regulatory DNA. (2011) (https://pubmed.ncbi.nlm.nih.gov/21720363)	Authors
Frankel N; Erezylmaz DF; McGregor AP; Wang S; Payre F; Stern DL	
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	Additional References
Evolved Repression Overcomes Enhancer Robustness. (2016) (https://pubmed.ncbi.nlm.nih.gov/27840106)	

Mutation #7	
No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No~#gephebase-summary-title)	Presumptive Null
	Molecular Type
Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular Type=~Cis-regulatory~#gephebase-summary-title)	Aberration Type
SNP (https://www.gephebase.org/search-criteria?/and+Aberration Type=~SNP~#gephebase-summary-title)	Molecular Details of the Mutation
Enhancer E6; 3rd epistatic mutation (5 in total)	Experimental Evidence
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Linkage Mapping~#gephebase-summary-title)	Main Reference
Morphological evolution caused by many subtle-effect substitutions in regulatory DNA. (2011) (https://pubmed.ncbi.nlm.nih.gov/21720363)	
	Authors
Frankel N; Erezylmaz DF; McGregor AP; Wang S; Payre F; Stern DL	
	Abstract
Morphology evolves often through changes in developmental genes, but the causal mutations, and their effects, remain largely unknown. The evolution of naked cuticle on larvae of <i>Drosophila sechellia</i> resulted from changes in five transcriptional enhancers of shavenbaby (svb), a transcript of the ovo locus that encodes a transcription factor that governs morphogenesis of microtrichiae, hereafter called ‘trichomes’. Here we show that the function of one of these enhancers evolved through multiple single-nucleotide substitutions that altered both the timing and level of svb expression. The consequences of these nucleotide substitutions on larval morphology were quantified with a novel functional assay. We found that each substitution had a relatively small phenotypic effect, and that many nucleotide changes account for this large morphological difference. In addition, we observed that the substitutions had non-additive effects. These data provide unprecedented resolution of the phenotypic effects of substitutions and show how individual nucleotide changes in a transcriptional enhancer have caused morphological evolution.	
	Additional References
Evolved Repression Overcomes Enhancer Robustness. (2016) (https://pubmed.ncbi.nlm.nih.gov/27840106)	

Mutation #8	
No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No~#gephebase-summary-title)	Presumptive Null
	Molecular Type
Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular Type=~Cis-regulatory~#gephebase-summary-title)	Aberration Type
SNP (https://www.gephebase.org/search-criteria?/and+Aberration Type=~SNP~#gephebase-summary-title)	Molecular Details of the Mutation
Enhancer E6; 4th epistatic mutation (5 in total)	Experimental Evidence
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Linkage Mapping~#gephebase-summary-title)	Main Reference
Morphological evolution caused by many subtle-effect substitutions in regulatory DNA. (2011) (https://pubmed.ncbi.nlm.nih.gov/21720363)	
	Authors
Frankel N; Erezylmaz DF; McGregor AP; Wang S; Payre F; Stern DL	
	Abstract
Morphology evolves often through changes in developmental genes, but the causal mutations, and their effects, remain largely unknown. The evolution of naked cuticle on larvae of <i>Drosophila sechellia</i> resulted from changes in five transcriptional enhancers of shavenbaby (svb), a transcript of the ovo locus that encodes a transcription factor that governs morphogenesis of microtrichiae, hereafter called ‘trichomes’. Here we show that the function of one of these enhancers evolved through multiple single-nucleotide substitutions that altered both the timing and level of svb expression. The consequences of these nucleotide substitutions on larval morphology were quantified with a novel functional assay. We found that each substitution had a relatively small phenotypic effect, and that many nucleotide changes account for this large morphological difference. In addition, we observed that the substitutions had non-additive effects. These data provide unprecedented resolution of the phenotypic effects of substitutions and show how individual nucleotide changes in a transcriptional enhancer have caused morphological evolution.	
	Additional References
Evolved Repression Overcomes Enhancer Robustness. (2016) (https://pubmed.ncbi.nlm.nih.gov/27840106)	

Mutation #9	
No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No~#gephebase-summary-title)	Presumptive Null
	Molecular Type
Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular Type=~Cis-regulatory~#gephebase-summary-title)	Aberration Type

Deletion (https://www.gephebase.org/search-criteria?/and+Aberration+Type=^Deletion^#gephebase-summary-title)	Deletion Size
1-9 bp	
Enhancer E6; 5th epistatic mutation = 1-bp deletion (5 in total)	Molecular Details of the Mutation
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=^Linkage+Mapping^#gephebase-summary-title)	Experimental Evidence
Morphological evolution caused by many subtle-effect substitutions in regulatory DNA. (2011) (https://pubmed.ncbi.nlm.nih.gov/21720363)	Main Reference
Frankel N; Erezylmaz DF; McGregor AP; Wang S; Payre F; Stern DL	Authors
Morphology evolves often through changes in developmental genes, but the causal mutations, and their effects, remain largely unknown. The evolution of naked cuticle on larvae of <i>Drosophila sechellia</i> resulted from changes in five transcriptional enhancers of shavenbaby (svb), a transcript of the ovo locus that encodes a transcription factor that governs morphogenesis of microtrichiae, hereafter called ‘trichomes’. Here we show that the function of one of these enhancers evolved through multiple single-nucleotide substitutions that altered both the timing and level of svb expression. The consequences of these nucleotide substitutions on larval morphology were quantified with a novel functional assay. We found that each substitution had a relatively small phenotypic effect, and that many nucleotide changes account for this large morphological difference. In addition, we observed that the substitutions had non-additive effects. These data provide unprecedented resolution of the phenotypic effects of substitutions and show how individual nucleotide changes in a transcriptional enhancer have caused morphological evolution.	Abstract
Evolved Repression Overcomes Enhancer Robustness. (2016) (https://pubmed.ncbi.nlm.nih.gov/27840106)	Additional References

RELATED GEPHE

1 (Ultrabithorax (Ubx)) (https://www.gephebase.org/search-criteria?/or+Taxon+ID=^7240^/and+Trait=Trichome+pattern/or+Taxon+ID=^7226^/and+Trait=Trichome+pattern/or+Taxon+ID=^7238^/and+Trait=Trichome+pattern/and+groupHaplotypes=true#gephebase-summary-title)	Related Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS

@SeveralMutationsWithEffect - Entry validated by Ella Preger-Ben-Noon