GEPHE SUMMARY

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

GepheID
GP00001085

Entry Status
Published

Main curator
Courtier

PHENOTYPIC CHANGE

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

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

Trait State in Taxon A
Drosophila simulans; D. mauritiana : more trichomes

Trait State in Taxon B
Drosophila sechellia : fewer trichomes

Ancestral State
Taxon A

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

Taxon A #1

Latin Name
Drosophila simulans (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Drosophila simulans^#gephebase-summary-title)

Common Name
-

Synonyms
-

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
7240 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7240)

is Taxon A an Infraspecies?
No

Taxon A #2

Latin Name
Drosophila mauritiana (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Drosophila mauritiana^#gephebase-summary-title)

Common Name
-

Synonyms
-

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

Taxon B

Latin Name
Drosophila sechellia (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Drosophila sechellia^#gephebase-summary-title)

Common Name
-

Synonyms
Drosophila sechellia Tsacas and Bachli, 1981

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
7238 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7238)

is Taxon B an Infraspecies?
No

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 Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

ovo

Synonyms

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; Svb; Svb/Ovo

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)

UniProtKB Drosophila melanogaster

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

GenebankID or UniProtKB

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

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

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 Drosophila 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 D. melanogaster driving reporter gene expression in partly overlapping patterns that together recapitulate endogenous svb expression. All three homologous enhancers from D. sechellia 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 D. sechellia 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.

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

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 Drosophila 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 D. melanogaster driving reporter gene expression in partly overlapping patterns that together recapitulate endogenous svb expression. All three homologous enhancers from D. sechellia 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 D. sechellia 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.

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

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 #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; 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 #7

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

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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 #8

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; 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

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Additional References

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

Mutation #9

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

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

Deletion Size

1-9 bp

Molecular Details of the Mutation

Enhancer E6; 5th epistatic mutation = 1-bp deletion (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)

RELATED GEPHE

Related Genes

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 Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

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