

GEPHE SUMMARY

<p>WntA (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=~WntA^#gephebase-summary-title)</p> <p>Published</p>	<p>Gephebase Gene</p> <p>Entry Status</p>	<p>GP00001213</p> <p>Martin</p>	<p>GepheID</p> <p>Main curator</p>
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PHENOTYPIC CHANGE

<p>Morphology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Morphology^#gephebase-summary-title)</p>		<p>Trait Category</p>		
<p>Coloration (wing, Mullerian mimicry) (https://www.gephebase.org/search-criteria?/and+Trait=~Coloration+(wing,+Mullerian+mimicry)^#gephebase-summary-title)</p>		<p>Trait</p>		
<p>Heliconius himera - central color patch</p>		<p>Trait State in Taxon A</p>		
<p>Heliconius erato notabilis - "split" color patch</p>		<p>Trait State in Taxon B</p>		
<p>Data not curated</p>		<p>Ancestral State</p>		
<p>Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Intraspecific^#gephebase-summary-title)</p>		<p>Taxonomic Status</p>		
<p>Taxon A</p>	<p>Latin Name</p>	<p>Taxon B</p>	<p>Latin Name</p>	
<p>Heliconius himera (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Heliconius+himera^#gephebase-summary-title)</p>	<p>Heliconius erato (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Heliconius+erato^#gephebase-summary-title)</p>	<p>Heliconius erato (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Heliconius+erato^#gephebase-summary-title)</p>	<p>Heliconius erato (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Heliconius+erato^#gephebase-summary-title)</p>	
<p>-</p>	<p>Common Name</p>	<p>crimson-patched longwing</p>	<p>Common Name</p>	
<p>-</p>	<p>Synonyms</p>	<p>crimson-patched longwing</p>	<p>Synonyms</p>	
<p>species</p>	<p>Rank</p>	<p>crimson-patched longwing; Heliconius erato (Linnaeus, 1764)</p>	<p>Rank</p>	
<p>cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Amphimesnoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Ditrysia; Obtectomera; Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius</p>	<p>Lineage</p>	<p>cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Amphimesnoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Ditrysia; Obtectomera; Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius</p>	<p>Lineage</p>	
<p>Heliconius () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=33416)</p>	<p>Parent</p>	<p>Heliconius () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=33416)</p>	<p>Parent</p>	
<p>33442 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=33442)</p>	<p>NCBI Taxonomy ID</p>	<p>33431 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=33431)</p>	<p>NCBI Taxonomy ID</p>	
<p>No</p>	<p>is Taxon A an Intraspecies?</p>	<p>Yes</p>	<p>is Taxon B an Intraspecies?</p>	
			<p>Taxon B Description</p>	
			<p>Heliconius erato notabilis - "split" color patch</p>	

GENOTYPIC CHANGE

<p>WntA</p>	<p>Generic Gene Name</p>	<p>A0A077DF90 (http://www.uniprot.org/uniprot/A0A077DF90)</p>	<p>UniProtKB Vanessa cardui</p>
<p>-</p>	<p>Synonyms</p>	<p>JN944589 (https://www.ncbi.nlm.nih.gov/nucleotide/JN944589)</p>	<p>GenebankID or UniProtKB</p>
<p>-</p>	<p>String</p>		
<p>Belongs to the Wnt family.</p>	<p>Sequence Similarities</p>		
<p>GO:0005102 : signaling receptor binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005102)</p>	<p>GO - Molecular Function</p>		
<p>GO:0007275 : multicellular organism development (https://www.ebi.ac.uk/QuickGO/term/GO:0007275)</p>	<p>GO - Biological Process</p>		
<p>GO:0016055 : Wnt signaling pathway</p>			

(<https://www.ebi.ac.uk/QuickGO/term/GO:0016055>)

GO - Cellular Component

GO:0005576 : extracellular region (<https://www.ebi.ac.uk/QuickGO/term/GO:0005576>)

Presumptive Null

No ([https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No~#gephebase-summary-title](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](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](https://www.gephebase.org/search-criteria?/and+Aberration+Type=~Unknown~#gephebase-summary-title))

Molecular Details of the Mutation

Not identified

Experimental Evidence

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

Main Reference

Diversification of complex butterfly wing patterns by repeated regulatory evolution of a Wnt ligand. (2012) (<https://pubmed.ncbi.nlm.nih.gov/22802635>)

Authors

Martin A; Papa R; Nadeau NJ; Hill RI; Counterman BA; Halder G; Jiggins CD; Kronforst MR; Long AD; McMillan WO; Reed RD

Abstract

Although animals display a rich variety of shapes and patterns, the genetic changes that explain how complex forms arise are still unclear. Here we take advantage of the extensive diversity of *Heliconius* butterflies to identify a gene that causes adaptive variation of black wing patterns within and between species. Linkage mapping in two species groups, gene-expression analysis in seven species, and pharmacological treatments all indicate that cis-regulatory evolution of the WntA ligand underpins discrete changes in color pattern features across the *Heliconius* genus. These results illustrate how the direct modulation of morphogen sources can generate a wide array of unique morphologies, thus providing a link between natural genetic variation, pattern formation, and adaptation.

Additional References

RELATED GEPHE

Related Genes

1 (Optix) ([https://www.gephebase.org/search-criteria?/or+Taxon ID=~33442~/and+Trait=Coloration/or+Taxon ID=~33431~/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon+ID=~33442~/and+Trait=Coloration/or+Taxon+ID=~33431~/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title))

Related Haplotypes

2 ([https://www.gephebase.org/search-criteria?/or+Gene Gephebase=~WntA~/and+Taxon ID=~33442~/or+Gene Gephebase=~WntA~/and+Taxon ID=~33431~#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=~WntA~/and+Taxon+ID=~33442~/or+Gene+Gephebase=~WntA~/and+Taxon+ID=~33431~#gephebase-summary-title))

EXTERNAL LINKS

COMMENTS

See follow-up paper : Van Belleghem et al. for high-resolution Association Mapping of the *H. erato notabilis* allele