

GEPHE SUMMARY

	Gephebase Gene	GephelID
WntA (https://www.gephebase.org/search-criteria?/and+Gene Gephebase="WntA">#gephebase-summary-title)	GP00001211	
	Entry Status	Main curator
Published	Martin	

PHENOTYPIC CHANGE

	Trait Category	
Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category="Morphology">#gephebase-summary-title)	Trait	
Coloration (wing, Mullerian mimicry) (https://www.gephebase.org/search-criteria?/and+Trait=^Coloration+(wing,+Mullerian+mimicry)^#gephebase-summary-title)	Trait State in Taxon A	
Heliconius himera - central color patch	Trait State in Taxon B	
Heliconius erato erato - "broken" color patch	Ancestral State	
Data not curated	Taxonomic Status	
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status="Intraspecific">#gephebase-summary-title)		
Taxon A		Taxon B
	Latin Name	Latin Name
Heliconius himera (#gephebase-summary-title)	Heliconius erato (#gephebase-summary-title)	
-	Common Name	Common Name
-	Synonyms	Synonyms
-	Rank	Rank
species	Lineage	Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Amphiesmenoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Ditrysia; Obtectomera; Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius		
Heliconius () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=33416)	Parent	Parent
33442 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=33442)	NCBI Taxonomy ID	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	is Taxon B an Infraspecies?
Belongs to the Wnt family.	Yes	Yes
GO:0005102 : signaling receptor binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005102)		Taxon B Description
GO:0007275 : multicellular organism development (https://www.ebi.ac.uk/QuickGO/term/GO:0007275)		
GO:0016055 : Wnt signaling pathway	Heliconius erato erato - "broken" color patch	

GENOTYPIC CHANGE

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

(<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>)

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

Not identified

Experimental Evidence

Linkage Mapping (<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

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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>)

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>)

EXTERNAL LINKS

COMMENTS

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