

GEPHE SUMMARY

pannier (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~pannier~#gephebase-summary-title)	Gephebase Gene	GP00001707	GepheID
	Entry Status	Courtier	Main curator
	Published		

PHENOTYPIC CHANGE

Morphology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Morphology~#gephebase-summary-title)	Trait Category		
	Trait		
	Coloration (elytra) (https://www.gephebase.org/search-criteria?/and+Trait=~Coloration(elytra)~#gephebase-summary-title)		
Black-nSpots - hA allele (recessive)	Trait State in Taxon A		
	Trait State in Taxon B		
	Black-4Spots - hSp allele (dominant)		
Unknown	Ancestral State		
	Taxonomic Status		
	Intraspecific (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Intraspecific~#gephebase-summary-title)		

Taxon A		Taxon B	
Harmonia axyridis (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Harmoniaaxyridis~#gephebase-summary-title)	Latin Name	Harmonia axyridis (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Harmoniaaxyridis~#gephebase-summary-title)	Latin Name
	Common Name		Common Name
	-		-
Coccinella axyridis; Harmonia axyridis (Pallas, 1773)	Synonyms	Coccinella axyridis; Harmonia axyridis (Pallas, 1773)	Synonyms
	Rank		Rank
	species		species
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Coleoptera; Polyphaga; Cucujiformia; Cucujoidea; Coccinellidae; Coccinellinae; Coccinellini; Harmonia	Lineage	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Coleoptera; Polyphaga; Cucujiformia; Cucujoidea; Coccinellidae; Coccinellinae; Coccinellini; Harmonia	Lineage
	Parent		Parent
	Harmonia () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=115356)		Harmonia () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=115356)
115357 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=115357)	NCBI Taxonomy ID	115357 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=115357)	NCBI Taxonomy ID
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
	No		No

GENOTYPIC CHANGE

pnr	Generic Gene Name	UniProtKB Drosophila melanogaster
	Synonyms	GenebankID or UniProtKB
	CG3978; CG3978-PA; dGATAa; dGATAa/pannier; Dmel\CG3978; GATA; GATA4; GATAa; GATAa/Pannier; l(3)89B3; Pnr; PNR; prn; GATA-A	A0A348BEZ5 (https://www.ncbi.nlm.nih.gov/nuccore/A0A348BEZ5)
7227.FBpp0082675 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier= 7227.FBpp0082675)	String	
	Sequence Similarities	
	-	
	GO - Molecular Function	
	GO:0003700 : DNA-binding transcription factor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003700)	
	GO:0046982 : protein heterodimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0046982)	
	GO:0043565 : sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043565)	

GO:0008270 : zinc ion binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0008270>)
GO:0000981 : DNA-binding transcription factor activity, RNA polymerase II-specific (<https://www.ebi.ac.uk/QuickGO/term/GO:0000981>)
GO:0001085 : RNA polymerase II transcription factor binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0001085>)
GO:0001103 : RNA polymerase II repressing transcription factor binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0001103>)
GO:0003690 : double-stranded DNA binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0003690>)
GO:0016251 : RNA polymerase II general transcription initiation factor activity (<https://www.ebi.ac.uk/QuickGO/term/GO:0016251>)

GO - Biological Process

GO:0022416 : chaeta development (<https://www.ebi.ac.uk/QuickGO/term/GO:0022416>)
GO:0008407 : chaeta morphogenesis (<https://www.ebi.ac.uk/QuickGO/term/GO:0008407>)
GO:0045944 : positive regulation of transcription by RNA polymerase II (<https://www.ebi.ac.uk/QuickGO/term/GO:0045944>)
GO:0030154 : cell differentiation (<https://www.ebi.ac.uk/QuickGO/term/GO:0030154>)
GO:0007507 : heart development (<https://www.ebi.ac.uk/QuickGO/term/GO:0007507>)
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:0048565 : digestive tract development (<https://www.ebi.ac.uk/QuickGO/term/GO:0048565>)
GO:0007398 : ectoderm development (<https://www.ebi.ac.uk/QuickGO/term/GO:0007398>)
GO:0042440 : pigment metabolic process (<https://www.ebi.ac.uk/QuickGO/term/GO:0042440>)
GO:0007391 : dorsal closure (<https://www.ebi.ac.uk/QuickGO/term/GO:0007391>)
GO:0010002 : cardioblast differentiation (<https://www.ebi.ac.uk/QuickGO/term/GO:0010002>)
GO:0007179 : transforming growth factor beta receptor signaling pathway (<https://www.ebi.ac.uk/QuickGO/term/GO:0007179>)
GO:0007389 : pattern specification process (<https://www.ebi.ac.uk/QuickGO/term/GO:0007389>)
GO:0007350 : blastoderm segmentation (<https://www.ebi.ac.uk/QuickGO/term/GO:0007350>)
GO:0048542 : lymph gland development (<https://www.ebi.ac.uk/QuickGO/term/GO:0048542>)
GO:0061320 : pericardial nephrocyte differentiation (<https://www.ebi.ac.uk/QuickGO/term/GO:0061320>)
GO:0007510 : cardioblast cell fate determination (<https://www.ebi.ac.uk/QuickGO/term/GO:0007510>)
GO:0035051 : cardiocyte differentiation (<https://www.ebi.ac.uk/QuickGO/term/GO:0035051>)
GO:0035050 : embryonic heart tube development (<https://www.ebi.ac.uk/QuickGO/term/GO:0035050>)
GO:0007492 : endoderm development (<https://www.ebi.ac.uk/QuickGO/term/GO:0007492>)
GO:0060047 : heart contraction (<https://www.ebi.ac.uk/QuickGO/term/GO:0060047>)
GO:0002805 : regulation of antimicrobial peptide biosynthetic process (<https://www.ebi.ac.uk/QuickGO/term/GO:0002805>)

GO - Cellular Component

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

No (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title>)

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

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

exact mutation(s) unknown

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

Development and evolution of color patterns in ladybird beetles: A case study in *Harmonia axyridis*. (2019) (<https://pubmed.ncbi.nlm.nih.gov/30644547>)

Ando T; Niimi T

Many organisms show various geometric color patterns on their bodies, and the developmental, evolutionary, genetic, and ecological bases of these patterns have been intensely studied in various organisms. Ladybird beetles display highly diverse patterns of wing (elytral) color and are one of the most attractive model organisms for studying these characteristics. In this study, we reviewed the genetic history of elytral color patterns in the Asian multicolored ladybird beetle *Harmonia axyridis* from the classical genetic studies led by the pupils of Thomas Hunt Morgan and Theodosius Dobzhansky to recent genomic studies that revealed that a single GATA transcription factor gene, pannier, regulates the highly diverse elytral color patterns in this species. We also reviewed and discussed the developmental and evolutionary mechanisms driven by the pannier locus in *H. axyridis*. In the development sections, we focused on the following two topics: (a) how the red (carotenoid) and black (melanin) pigmentation of elytra is regulated by the pannier and pigmentation genes and (b) how the diverse color patterns are formed by

Presumptive Null

Molecular Type

Aberration Type

Molecular Details of the Mutation

Experimental Evidence

Main Reference

Authors

Abstract

integrating regulatory inputs from other genes involved in wing development. In the evolution section, we subsequently focused on the highly diversified DNA sequences within the first intron of pannier that are 56-76 kb long and that were generated through recurrent multiple inversions. Furthermore, we discussed how these recurrent inversions have driven the diversification of color patterns throughout evolution.

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Additional References

The Genomic Basis of Color Pattern Polymorphism in the Harlequin Ladybird. (2018) (<https://pubmed.ncbi.nlm.nih.gov/30146156>)
Development and evolution of color patterns in ladybird beetles: A case study in Harmonia axyridis. (2019) (<https://pubmed.ncbi.nlm.nih.gov/30644547>)

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

2 ([https://www.gephebase.org/search-criteria?/or+Gene+Gephebase="+pannier^"/and+Taxon+ID="+115357^"/or+Gene+Gephebase="+pannier^"/and+Taxon+ID="+115357^"#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=))

EXTERNAL LINKS

COMMENTS

@Inversion - Four alleles of pannier are associated with four distinct color patterns