GEPHE SUMMARY

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

GepheID
GP00001707

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

Trait State in Taxon A
Black-nSpots - hA allele (recessive)

Trait State in Taxon B
Black-4Spots - hSp allele (dominant)

Ancestral State
Unknown

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

Taxon A

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

Common Name
-

Synonyms
Coccinella axyridis; Harmonia axyridis (Pallas, 1773)

Rank
species

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

Parent
Harmonia () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 115356)

NCBI Taxonomy ID
115357 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 115357)

is Taxon A an Infraspecies?
No

Taxon B

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

Common Name
-

Synonyms
Coccinella axyridis; Harmonia axyridis (Pallas, 1773)

Rank
species

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

Parent
Harmonia () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 115356)

NCBI Taxonomy ID
115357 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 115357)

is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
pnr

Synonyms
CG3978; CG3978-PA; dGATAa; dGATAa/pannier; Dmel\CG3978; GATA; GATA4; GATAa; GATAa/Pannier; l(3)89B3; Pnr; PNR; prn; GATA-A

String
7227.FBpp0082675 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0082675)

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)

UniProtKB Drosophila melanogaster
P52168 (http://www.uniprot.org/uniprot/P52168)

GenebankID or UniProtKB
A0A348BEZ5 (https://www.ncbi.nlm.nih.gov/nuccore/A0A348BEZ5)

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)

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

exact mutation(s) unknown

Experimental Evidence

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

Main Reference

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

Authors

Ando T; Niimi T

Abstract

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.Â 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

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 56-76Â 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)

EXTERNAL LINKS

COMMENTS

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