GEPHE SUMMARY

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

Entry Status
Published

GepheID
GP00002431

Main curator
Courtier

PHENOTYPIC CHANGE

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

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

Trait State in Taxon A
Danaus chrysippus - chrysippus morph - orange background with black forewing tip - formerly bbcc

Trait State in Taxon B
Danaus chrysippus - dorippus morph - orange without black tip - formerly bbCC

Ancestral State
Data not curated

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

Taxon A

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

Common Name
African queen

Synonyms
Anosia chrysippus; African queen; common tiger; lesser wanderer; plain tiger; Danaus chrysippus (Linnaeus, 1758); Danaus chryssipus

Rank
species

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; Danainae; Danaini; Danaina; Danaus; Anosia

Parent
Anosia () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 151543)

NCBI Taxonomy ID
151541 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 151541)

is Taxon A an Infraspecies?
Yes

Taxon A Description
Danaus chrysippus - chrysippus morph

Taxon B

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

Common Name
African queen

Synonyms
Anosia chrysippus; African queen; common tiger; lesser wanderer; plain tiger; Danaus chrysippus (Linnaeus, 1758); Danaus chryssipus

Rank
species

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; Danainae; Danaini; Danaina; Danaus; Anosia

Parent
Anosia () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 151543)

NCBI Taxonomy ID
151541 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 151541)

is Taxon B an Infraspecies?
Yes

Taxon B Description
Danaus chrysippus - dorippus morph

GENOTYPIC CHANGE

Generic Gene Name
cnn

Synonyms
cen; CG 4832; CG18370; CG4832; Cnn; CNN; Cnn1; Dmel\CG4832; mat(2)syn-C; mat(2)synHK21; mfs; obv; Arr

String
7227.FBpp0301625 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0301625)

Sequence Similarities
-

GO - Molecular Function
GO:0060090 : molecular adaptor activity

UniProtKB Drosophila melanogaster
P54623 (http://www.uniprot.org/uniprot/P54623)

GenebankID or UniProtKB
()

(https://www.ebi.ac.uk/QuickGO/term/GO:0060090)

GO - Biological Process

GO:0007417 : central nervous system development (https://www.ebi.ac.uk/QuickGO/term/GO:0007417)
GO:0007422 : peripheral nervous system development (https://www.ebi.ac.uk/QuickGO/term/GO:0007422)
GO:0008356 : asymmetric cell division (https://www.ebi.ac.uk/QuickGO/term/GO:0008356)
GO:0051321 : meiotic cell cycle (https://www.ebi.ac.uk/QuickGO/term/GO:0051321)
GO:0055059 : asymmetric neuroblast division (https://www.ebi.ac.uk/QuickGO/term/GO:0055059)
GO:0007494 : midgut development (https://www.ebi.ac.uk/QuickGO/term/GO:0007494)
GO:0007279 : pole cell formation (https://www.ebi.ac.uk/QuickGO/term/GO:0007279)
GO:0007099 : centriole replication (https://www.ebi.ac.uk/QuickGO/term/GO:0007099)
GO:0007098 : centrosome cycle (https://www.ebi.ac.uk/QuickGO/term/GO:0007098)
GO:0040016 : embryonic cleavage (https://www.ebi.ac.uk/QuickGO/term/GO:0040016)
GO:0007052 : mitotic spindle organization (https://www.ebi.ac.uk/QuickGO/term/GO:0007052)
GO:0008594 : photoreceptor cell morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0008594)
GO:0090063 : positive regulation of microtubule nucleation (https://www.ebi.ac.uk/QuickGO/term/GO:0090063)
GO:0030997 : regulation of centriole-centriole cohesion (https://www.ebi.ac.uk/QuickGO/term/GO:0030997)
GO:1903358 : regulation of Golgi organization (https://www.ebi.ac.uk/QuickGO/term/GO:1903358)

GO - Cellular Component

GO:0005794 : Golgi apparatus (https://www.ebi.ac.uk/QuickGO/term/GO:0005794)
GO:0005814 : centriole (https://www.ebi.ac.uk/QuickGO/term/GO:0005814)
GO:0031514 : motile cilium (https://www.ebi.ac.uk/QuickGO/term/GO:0031514)
GO:0005813 : centrosome (https://www.ebi.ac.uk/QuickGO/term/GO:0005813)
GO:0036064 : ciliary basal body (https://www.ebi.ac.uk/QuickGO/term/GO:0036064)
GO:0000242 : pericentriolar material (https://www.ebi.ac.uk/QuickGO/term/GO:0000242)
GO:0000922 : spindle pole (https://www.ebi.ac.uk/QuickGO/term/GO:0000922)

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

The strongest associations with forewing tip (C locus) occur at the gene arrow and a phylogenetic network for a 100-kb region around this gene similarly clusters individuals by phenotype. In Drosophila Arrow is essential for Wnt signalling in wing development

Experimental Evidence

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

Main Reference

Whole-chromosome hitchhiking driven by a male-killing endosymbiont. (2020) (https://pubmed.ncbi.nlm.nih.gov/32108180)

Authors

Martin SH; Singh KS; Gordon IJ; Omufwoko KS; Collins S; Warren IA; Munby H; BrattstrÃ¶m O; Traut W; Martins DJ; Smith DAS; Jiggins CD; Bass C; Ffrench-Constant RH

Abstract

Neo-sex chromosomes are found in many taxa, but the forces driving their emergence and spread are poorly understood. The female-specific neo-W chromosome of the African monarch (or queen) butterfly Danaus chrysippus presents an intriguing case study because it is restricted to a single ′contact zone′ population, involves a putative colour patterning supergene, and co-occurs with infection by the male-killing endosymbiont Spiroplasma. We investigated the origin and evolution of this system using whole genome sequencing. We first identify the ′BC supergene′, a broad region of suppressed recombination across nearly half a chromosome, which links two colour patterning loci. Association analysis suggests that the genes yellow and arrow in this region control the forewing colour pattern differences between D. chrysippus subspecies. We then show that the same chromosome has recently formed a neo-W that has spread through the contact zone within approximately 2,200 years. We also assembled the genome of the male-killing Spiroplasma, and find that it shows perfect genealogical congruence with the neo-W, suggesting that the neo-W has hitchhiked to high frequency as the male-killer has spread through the population. The complete absence of female crossing-over in the Lepidoptera causes whole-chromosome hitchhiking of a single neo-W haplotype, carrying a single allele of the BC supergene and dragging multiple non-synonymous mutations to high frequency. This has created a population of infected females that all carry the same recessive colour patterning allele, making the phenotypes of each successive generation highly dependent on uninfected male immigrants. Our findings show how hitchhiking can occur between the physically unlinked genomes of host and endosymbiont, with dramatic consequences.

Additional References

RELATED GEPHE

Related Genes

1 (yellow) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^151541^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

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