

GO:0097027 : ubiquitin-protein transferase activator activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0097027>)

GO - Biological Process

GO:0048477 : oogenesis (<https://www.ebi.ac.uk/QuickGO/term/GO:0048477>)

GO:0045143 : homologous chromosome segregation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045143>)

GO:0031145 : anaphase-promoting complex-dependent catabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0031145>)

GO:0007349 : cellularization (<https://www.ebi.ac.uk/QuickGO/term/GO:0007349>)

GO:0007343 : egg activation (<https://www.ebi.ac.uk/QuickGO/term/GO:0007343>)

GO:0007144 : female meiosis I (<https://www.ebi.ac.uk/QuickGO/term/GO:0007144>)

GO:0007147 : female meiosis II (<https://www.ebi.ac.uk/QuickGO/term/GO:0007147>)

GO:0007143 : female meiotic nuclear division
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007143>)

GO:0007279 : pole cell formation (<https://www.ebi.ac.uk/QuickGO/term/GO:0007279>)

GO:1905786 : positive regulation of anaphase-promoting complex-dependent catabolic process (<https://www.ebi.ac.uk/QuickGO/term/GO:1905786>)

GO:1904668 : positive regulation of ubiquitin protein ligase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:1904668>)

GO - Cellular Component

GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)

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

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Experimental Evidence

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

Main Reference

The evolution and diversification of oakleaf butterflies. (2022) (<https://pubmed.ncbi.nlm.nih.gov/35926506>)

Authors

Wang S; Teng D; Li X; Yang P; Da W; Zhang Y; Zhang Y; Liu G; Zhang X; Wan W; Dong Z; Wang D; Huang S; Jiang Z; Wang Q; Lohman DJ; Wu Y; Zhang L; Jia F; Westerman E; Zhang L; Wang W; Zhang W

Abstract

Oakleaf butterflies in the genus *Kallima* have a polymorphic wing phenotype, enabling these insects to masquerade as dead leaves. This iconic example of protective resemblance provides an interesting evolutionary paradigm that can be employed to study biodiversity. We integrated multi-omic data analyses and functional validation to infer the evolutionary history of *Kallima* species and investigate the genetic basis of their variable leaf wing patterns. We find that *Kallima* butterflies diversified in the eastern Himalayas and dispersed to East and Southeast Asia. Moreover, we find that leaf wing polymorphism is controlled by the wing patterning gene cortex, which has been maintained in *Kallima* by long-term balancing selection. Our results provide macroevolutionary and microevolutionary insights into a model species originating from a mountain ecosystem.

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Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

3 (<https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=~cortex~/and+Taxon+ID=~311037~/or+Gene+Gephebase=~cortex~/and+Taxon+ID=~311037~#gephebase-summary-title>)

EXTERNAL LINKS

COMMENTS

@Parallelism - There are at least 5 distinct cortex haplotypes associated with 5 wing morphs. These diverse haplotypes are also found in closely related species of *Kallima* butterflies, suggesting that the balanced polymorphism has been maintained over millions of years. @Inversion

