GEPHE SUMMARY

Gephebase Gene

protein kinase cAMP-dependent type I regulatory subunit alpha (PRKAR1A) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^protein kinase cAMP-dependent type I regulatory subunit alpha (PRKAR1A)^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00002109

Main curator

Courtier

PHENOTYPIC CHANGE

Trait Category

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

Trait

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

Trait State in Taxon A

lighter black

Trait State in Taxon B

darker black - lizards on Pigash lava flow

Ancestral State

Taxon A

Taxonomic Status

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

Taxon A

Latin Name

Uta stansburiana (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Uta stansburiana^#gephebase-summary-title)

Common Name

-

Synonyms

Uta antiqua; Uta stellata; Uta stansburiana Baird & Girard, 1852; USNM 12666; USNM:12666

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Sauropsida; Sauria; Lepidosauria; Squamata; Bifurcata; Unidentata; Episquamata; Toxicofera; Iguania; Phrynosomatidae; Phrynosomatinae; Uta

Parent

Uta () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 43651)

NCBI Taxonomy ID

43653 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 43653)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

Uta stansburiana (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Uta stansburiana^#gephebase-summary-title)

Common Name

-

Synonyms

Uta antiqua; Uta stellata; Uta stansburiana Baird & Girard, 1852; USNM 12666; USNM:12666

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Sauropsida; Sauria; Lepidosauria; Squamata; Bifurcata; Unidentata; Episquamata; Toxicofera; Iguania; Phrynosomatidae; Phrynosomatinae; Uta

Parent

Uta () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 43651)

NCBI Taxonomy ID

43653 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 43653)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

Prkar1a

Synonyms

Tse1; Tse-1; RIalpha; 1300018C22Rik

String

10090.ENSMUSP00000056500 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 10090.ENSMUSP00000056500)

Sequence Similarities

Belongs to the cAMP-dependent kinase regulatory chain family.

GO - Molecular Function

GO:0034236 : protein kinase A catalytic subunit binding (https://www.ebi.ac.uk/QuickGO/term/GO:0034236)
GO:0031625 : ubiquitin protein ligase binding (https://www.ebi.ac.uk/QuickGO/term/GO:0031625)
GO:0019904 : protein domain specific binding

UniProtKB Mus musculus

Q9DBC7 (http://www.uniprot.org/uniprot/Q9DBC7)

GenebankID or UniProtKB

()

(https://www.ebi.ac.uk/QuickGO/term/GO:0019904)
GO:0047555 : 3',5'-cyclic-GMP phosphodiesterase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0047555)
GO:0030552 : cAMP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0030552)
GO:0004862 : cAMP-dependent protein kinase inhibitor activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0004862)
GO:0008603 : cAMP-dependent protein kinase regulator activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0008603)

GO - Biological Process

GO:0007507 : heart development (https://www.ebi.ac.uk/QuickGO/term/GO:0007507)
GO:0019934 : cGMP-mediated signaling
(https://www.ebi.ac.uk/QuickGO/term/GO:0019934)
GO:0008283 : cell proliferation (https://www.ebi.ac.uk/QuickGO/term/GO:0008283)
GO:0006468 : protein phosphorylation
(https://www.ebi.ac.uk/QuickGO/term/GO:0006468)
GO:0009887 : animal organ morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0009887)
GO:0001707 : mesoderm formation (https://www.ebi.ac.uk/QuickGO/term/GO:0001707)
GO:0045835 : negative regulation of meiotic nuclear division
(https://www.ebi.ac.uk/QuickGO/term/GO:0045835)
GO:0006469 : negative regulation of protein kinase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0006469)
GO:0007143 : female meiotic nuclear division
(https://www.ebi.ac.uk/QuickGO/term/GO:0007143)
GO:0060038 : cardiac muscle cell proliferation
(https://www.ebi.ac.uk/QuickGO/term/GO:0060038)
GO:0046007 : negative regulation of activated T cell proliferation
(https://www.ebi.ac.uk/QuickGO/term/GO:0046007)
GO:2000480 : negative regulation of cAMP-dependent protein kinase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:2000480)
GO:0045859 : regulation of protein kinase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0045859)
GO:0045214 : sarcomere organization
(https://www.ebi.ac.uk/QuickGO/term/GO:0045214)

GO - Cellular Component

GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)
GO:0005829 : cytosol (https://www.ebi.ac.uk/QuickGO/term/GO:0005829)
GO:0098978 : glutamatergic synapse
(https://www.ebi.ac.uk/QuickGO/term/GO:0098978)
GO:0032991 : protein-containing complex
(https://www.ebi.ac.uk/QuickGO/term/GO:0032991)
GO:0045202 : synapse (https://www.ebi.ac.uk/QuickGO/term/GO:0045202)
GO:0031594 : neuromuscular junction
(https://www.ebi.ac.uk/QuickGO/term/GO:0031594)
GO:0044853 : plasma membrane raft
(https://www.ebi.ac.uk/QuickGO/term/GO:0044853)
GO:0031588 : nucleotide-activated protein kinase complex
(https://www.ebi.ac.uk/QuickGO/term/GO:0031588)
GO:0001772 : immunological synapse
(https://www.ebi.ac.uk/QuickGO/term/GO:0001772)
GO:0005930 : axoneme (https://www.ebi.ac.uk/QuickGO/term/GO:0005930)
GO:0005952 : cAMP-dependent protein kinase complex
(https://www.ebi.ac.uk/QuickGO/term/GO:0005952)

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

no coding mutation associated with the phenotype - one differentiated SNP in an intron in the 5' UTR

Experimental Evidence

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

Main Reference

The Genetic Basis of Adaptation following Plastic Changes in Coloration in a Novel Environment. (2018) (https://pubmed.ncbi.nlm.nih.gov/30197088)

Authors

Corl A; Bi K; Luke C; Challa AS; Stern AJ; Sinervo B; Nielsen R

Abstract

Phenotypic plasticity has been hypothesized to precede and facilitate adaptation to novel environments [1-8], but examples of plasticity preceding adaptation in wild populations are rare (but see [9,Â 10]). We studied a population of side-blotched lizards, Uta stansburiana, living on a lava flow that formed 22,500 years ago [11] to understand the origin of their novel melanic phenotype that makes them cryptic on the black lava. We found that lizards living on and off of the lava flow exhibited phenotypic plasticity in coloration but also appeared to have heritable differences in pigmentation. We sequenced the exomes of 104 individuals and identified two known regulators of melanin production, PREP and PRKAR1A, which had markedly increased levels of divergence between lizards living on and off the lava flow. The derived variants in PREP and PRKAR1A were only found in the lava population and were associated with increased pigmentation levels in an experimental cohort of hatchling lizards. Simulations suggest that the derived variants in the PREP and PRKAR1A genes arose recently and were under strong positive selection in the lava population. Overall, our results suggest that ancestral plasticity for coloration facilitated initial survival in the lava environment and was followed by genetic changes that modified the phenotype in the direction of the induced plastic response, possibly through de novo mutations. These observations provide a detailed example supporting the hypothesis that plasticity aids in the initial colonization of a novel habitat, with natural selection subsequently refining the phenotype with genetic adaptations to the new environment. VIDEO ABSTRACT.

Additional References

RELATED GEPHE

Related Genes

1 (prolyl endopeptidase (PREP)) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^43653^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@Plasticity - variation in PRKAR1A has been associated with hyperpigmentation in humans