GEPHE SUMMARY

Gephebase Gene

Green-sensitive opsin (RH2) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Green-sensitive opsin (RH2)^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00002355

Main curator

Courtier

PHENOTYPIC CHANGE

Trait Category

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

Trait

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

Trait State in Taxon A

color vision

Trait State in Taxon B

loss of vision, no external eyeballs and no lens, degenrated retina

Ancestral State

Taxon A

Taxonomic Status

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

Taxon A

Latin Name

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

Common Name

-

Synonyms

Barbus grahami; Barbus grahami Regan, 1904; Sinocyclocheilus grahami (Regan, 1904); BMNH:1904.1.26.27

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupeocephala; Otomorpha; Ostariophysi; Otophysi; Cypriniphysae; Cypriniformes; Cyprinoidei; Cyprinidae; Cyprininae; Sinocyclocheilus

Parent

Sinocyclocheilus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 75365)

NCBI Taxonomy ID

75366 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 75366)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

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

Common Name

-

Synonyms

Sinocyclocheilus anshuiensis Gan, Wu, Wei & Yang, 2013; KIZ 12060239; KIZ 12070271; KIZ 12070276; KIZ 12070277; KIZ 12070280; KIZ:12060239; KIZ:12070271; KIZ:12070276; KIZ:12070277; KIZ:12070280

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupeocephala; Otomorpha; Ostariophysi; Otophysi; Cypriniphysae; Cypriniformes; Cyprinoidei; Cyprinidae; Cyprininae; Sinocyclocheilus

Parent

Sinocyclocheilus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 75365)

NCBI Taxonomy ID

1608454 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 1608454)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

opn1mw4

Synonyms

RH2-4; rh2.4; zfgr2; grops2; wu:fk64b02; rh24

String

7955.ENSDARP00000000979 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7955.ENSDARP00000000979)

Sequence Similarities

Belongs to the G-protein coupled receptor 1 family. Opsin subfamily.

GO - Molecular Function

GO:0008020 : G protein-coupled photoreceptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008020)
GO:0009881 : photoreceptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0009881)

GO - Biological Process

UniProtKB Danio rerio

Q9W6A6 (http://www.uniprot.org/uniprot/Q9W6A6)

GenebankID or UniProtKB

()

GO:0007186 : G protein-coupled receptor signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0007186)
GO:0018298 : protein-chromophore linkage
(https://www.ebi.ac.uk/QuickGO/term/GO:0018298)
GO:0007601 : visual perception (https://www.ebi.ac.uk/QuickGO/term/GO:0007601)
GO:0071482 : cellular response to light stimulus
(https://www.ebi.ac.uk/QuickGO/term/GO:0071482)
GO:0007602 : phototransduction (https://www.ebi.ac.uk/QuickGO/term/GO:0007602)

GO - Cellular Component

GO:0005887 : integral component of plasma membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0005887)
GO:0001750 : photoreceptor outer segment
(https://www.ebi.ac.uk/QuickGO/term/GO:0001750)

Presumptive Null

Yes (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Yes^#gephebase-summary-title)

Molecular Type

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

Aberration Type

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

Deletion Size

-

Molecular Details of the Mutation

Rh2-4 coding sequence absent from the full genome sequence of S. anshuiensis but present in the genome of Sinocyclocheilus rhinocerous and S. grahami

Experimental Evidence

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

Main Reference

The Sinocyclocheilus cavefish genome provides insights into cave adaptation. (2016) (https://pubmed.ncbi.nlm.nih.gov/26728391)

Authors

Yang J; Chen X; Bai J; Fang D; Qiu Y; Jiang W; Yuan H; Bian C; Lu J; He S; Pan X; Zhang Y; Wang X; You X; Wang Y; Sun Y; Mao D; Liu Y; Fan G; Zhang H; Chen X; Zhang X; Zheng L; Wang J; Cheng L; Chen J; Ruan Z; Li J; Yu H; Peng C; Ma X; Xu J; He Y; Xu Z; Xu P; Wang J; Yang H; Wang J; Whitten T; Xu X; Shi Q

Abstract

An emerging cavefish model, the cyprinid genus Sinocyclocheilus, is endemic to the massive southwestern karst area adjacent to the Qinghai-Tibetan Plateau of China. In order to understand whether orogeny influenced the evolution of these species, and how genomes change under isolation, especially in subterranean habitats, we performed whole-genome sequencing and comparative analyses of three species in this genus, S. grahami, S. rhinocerous and S. anshuiensis. These species are surface-dwelling, semi-cave-dwelling and cave-restricted, respectively.

The assembled genome sizes of S. grahami, S. rhinocerous and S. anshuiensis are 1.75 Gb, 1.73 Gb and 1.68 Gb, respectively. Divergence time and population history analyses of these species reveal that their speciation and population dynamics are correlated with the different stages of uplifting of the Qinghai-Tibetan Plateau. We carried out comparative analyses of these genomes and found that many genetic changes, such as gene loss (e.g. opsin genes), pseudogenes (e.g. crystallin genes), mutations (e.g. melanogenesis-related genes), deletions (e.g. scale-related genes) and down-regulation (e.g. circadian rhythm pathway genes), are possibly associated with the regressive features (such as eye degeneration, albinism, rudimentary scales and lack of circadian rhythms), and that some gene expansion (e.g. taste-related transcription factor gene) may point to the constructive features (such as enhanced taste buds) which evolved in these cave fishes.

As the first report on cavefish genomes among distinct species in Sinocyclocheilus, our work provides not only insights into genetic mechanisms of cave adaptation, but also represents a fundamental resource for a better understanding of cavefish biology.

Additional References

RELATED GEPHE

Related Genes

1 (opsin - rhodopsin (LWS)) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^75366^/and+Trait=Color vision/or+Taxon ID=^1608454^/and+Trait=Color vision/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

2 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^Green-sensitive opsin (RH2)^/and+Taxon ID=^75366^/or+Gene Gephebase=^Green-sensitive opsin (RH2)^/and+Taxon ID=^1608454^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS