GEPHE SUMMARY

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

Entry Status
Published

GepheID
GP00002360

Main curator
Courtier

PHENOTYPIC CHANGE

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

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

Trait State in Taxon A
reduced scales

Trait State in Taxon B
reduced scales

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
EDAR

Synonyms
DL; ED3; ED5; ED1R; EDA3; HRM1; EDA1R; ECTD10A; ECTD10B; EDA-A1R

String
9606.ENSP00000258443 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 9606.ENSP00000258443)

Sequence Similarities
-

GO - Molecular Function
GO:0004888 : transmembrane signaling receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004888)
GO:0038023 : signaling receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0038023)

UniProtKB Homo sapiens
Q9UNE0 (http://www.uniprot.org/uniprot/Q9UNE0)

GenebankID or UniProtKB
()

GO - Biological Process

GO:0030154 : cell differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0030154)
GO:0043473 : pigmentation (https://www.ebi.ac.uk/QuickGO/term/GO:0043473)
GO:0010628 : positive regulation of gene expression (https://www.ebi.ac.uk/QuickGO/term/GO:0010628)
GO:0001942 : hair follicle development (https://www.ebi.ac.uk/QuickGO/term/GO:0001942)
GO:0042475 : odontogenesis of dentin-containing tooth (https://www.ebi.ac.uk/QuickGO/term/GO:0042475)
GO:0043123 : positive regulation of I-kappaB kinase/NF-kappaB signaling (https://www.ebi.ac.uk/QuickGO/term/GO:0043123)
GO:1901224 : positive regulation of NIK/NF-kappaB signaling (https://www.ebi.ac.uk/QuickGO/term/GO:1901224)
GO:0060662 : salivary gland cavitation (https://www.ebi.ac.uk/QuickGO/term/GO:0060662)
GO:0006915 : apoptotic process (https://www.ebi.ac.uk/QuickGO/term/GO:0006915)
GO:0008544 : epidermis development (https://www.ebi.ac.uk/QuickGO/term/GO:0008544)
GO:0046330 : positive regulation of JNK cascade (https://www.ebi.ac.uk/QuickGO/term/GO:0046330)
GO:0033209 : tumor necrosis factor-mediated signaling pathway (https://www.ebi.ac.uk/QuickGO/term/GO:0033209)

GO - Cellular Component

GO:0016021 : integral component of membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016021)
GO:0005886 : plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005886)
GO:0045177 : apical part of cell (https://www.ebi.ac.uk/QuickGO/term/GO:0045177)

Presumptive Null

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

Molecular Type

Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Coding^#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

Deletion of a large part of the EDAR2 coding region.

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

No matches found.

Related Haplotypes

1 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^EDAR^/and+Taxon ID=^75366^/or+Gene Gephebase=^EDAR^/and+Taxon ID=^1608454^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS

Deleterious mutations in the EDAR1 gene also.