

GEPHE SUMMARY

Mpv17 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase="Mpv17">#gephebase-summary-title)	Gephebase Gene	GP00002358	GephelD
Published	Entry Status	Courtier	Main curator

PHENOTYPIC CHANGE

Morphology, Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category="Morphology"/and+Trait Category="Physiology">#gephebase-summary-title)	Trait Category
Coloration (albinism; iridophores) (https://www.gephebase.org/search-criteria?/and+Trait=^Coloration (albinism;%20iridophores)^#gephebase-summary-title)	Trait
pigmentation, cavefish	Trait State in Taxon A
loss of pigmentation in the skin, cavefish	Trait State in Taxon B
Taxon A	Ancestral State
Interspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status="Interspecific">#gephebase-summary-title)	Taxonomic Status

Taxon A	Latin Name	Taxon B	Latin Name
Sinocyclocheilus grahami (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=%20Sinocyclocheilus+grahami%23gephebase-summary-title)	Common Name	Sinocyclocheilus anshuiensis (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=%20Sinocyclocheilus+anshuiensis%23gephebase-summary-title)	Common Name
-	Synonyms	-	Synonyms
Barbus grahami; Barbus grahami Regan, 1904; Sinocyclocheilus grahami (Regan, 1904); BMNH:1904.1.26.27		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	
species	Rank	species	Rank
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	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	Lineage
Sinocyclocheilus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=75365)	Parent	Sinocyclocheilus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=75365)	Parent
75366 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=75366)	NCBI Taxonomy ID	1608454 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1608454)	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

mpv17	Generic Gene Name	UniProtKB Danio rerio
roy; zgc:63573	Synonyms	GenebankID or UniProtKB
7955.ENSDARP00000114374 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=7955.ENSDARP00000114374)	String	0
Belongs to the peroxisomal membrane protein PXMP2/4 family.	Sequence Similarities	
-	GO - Molecular Function	
GO:0050935 : iridophore differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0050935)	GO - Biological Process	

GO:0006225 : UDP biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006225>)

GO - Cellular Component

GO:0016021 : integral component of membrane

(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)

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

GO:0005743 : mitochondrial inner membrane

(<https://www.ebi.ac.uk/QuickGO/term/GO:0005743>)

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 which removes 16 amino acids in a conserved region. The Mpv17 mutant in zebrafish displays a strong reduction of iridophores throughout larval and adult stages.

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 (tyrosinase (TYR)) (<https://www.gephebase.org/search-criteria?/or+Taxon+ID=%75366%and+Trait=Coloration/or+Taxon+ID=%1608454%and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS