

GEPHE SUMMARY

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

PHENOTYPIC CHANGE

Trait Category			
Morphology, Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Morphology^/and+Trait+Category=~Physiology^#gephebase-summary-title)			
Trait			
Coloration (albinism; iridophores) (https://www.gephebase.org/search-criteria?/and+Trait=~Coloration+albinism;+iridophores^#gephebase-summary-title)			
Trait State in Taxon A			
pigmentation, cavefish			
Trait State in Taxon B			
loss of pigmentation in the skin, cavefish			
Ancestral State			
Taxon A			
Taxonomic Status			
Interspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Interspecific^#gephebase-summary-title)			
Taxon A		Taxon B	
Latin Name		Latin Name	
Sinocyclocheilus grahami (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Sinocyclocheilus+grahami^#gephebase-summary-title)		Sinocyclocheilus anshuiensis (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Sinocyclocheilus+anshuiensis^#gephebase-summary-title)	
Common Name		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	
Rank		Rank	
species		species	
Lineage		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		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		Parent	
Sinocyclocheilus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 75365)		Sinocyclocheilus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 75365)	
NCBI Taxonomy ID		NCBI Taxonomy ID	
75366 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 75366)		1608454 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 1608454)	
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
No		No	

GENOTYPIC CHANGE

Generic Gene Name		UniProtKB Danio rerio
mpv17		Q5TZ51 (http://www.uniprot.org/uniprot/Q5TZ51)
Synonyms		GenebankID or UniProtKB
roy; zgc:63573		0
String		
7955.ENSДАРP00000114374 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7955.ENSДАРP00000114374)		
Sequence Similarities		
Belongs to the peroxisomal membrane protein PXMP2/4 family.		
GO - Molecular Function		
-		
GO - Biological Process		
GO:0050935 : iridophore differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0050935)		

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, <i>S. grahami</i> , <i>S. rhinoceros</i> and <i>S. anshuiensis</i> . These species are surface-dwelling, semi-cave-dwelling and cave-restricted, respectively.	

The assembled genome sizes of *S. grahami*, *S. rhinoceros* 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)	
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS