

GEPHE SUMMARY

	Gephebase Gene		GepheID
DNA replication factor CDT1 (<a +dna+replication+factor+cdt1~#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?and+Gene=Gephebase=">https://www.gephebase.org/search-criteria?and+Gene=Gephebase="+DNA+replication+factor+CDT1~#gephebase-summary-title)		GP00001507	
	Entry Status	Prigent	Main curator
Published			

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=*Physiology*#gephebase-summary-title)		Trait Category
Resistance to UV irradiation (https://www.gephebase.org/search-criteria?/and+Trait=*Resistance to UV irradiation*#gephebase-summary-title)		Trait
Snub-nosed monkey of lowland regions (R. avunculus)		Trait State in Taxon A
Snub-nosed monkey of high-altitude habitats (R. strykeri & R. bieti)		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 Rhinopithecus avunculus (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=*Rhinopithecus avunculus*#gephebase-summary-title) Tonkin snub-nosed monkey Pygathrix avunculus; Tonkin snub-nosed monkey; Dollman’s snub-nosed monkey; Rhinopithecus avunculus (Dollman, 1912) species cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Euarchontoglires; Primates; Haplorrhini; Simiiformes; Catarrhini; Cercopithecoidea; Cercopithecidae; Colobinae; Rhinopithecus Rhinopithecus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 542827) 66062 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 66062) No Taxon B #1 Rhinopithecus strykeri (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=*Rhinopithecus strykeri*#gephebase-summary-title) Burmese snub-nosed monkey Burmese snub-nosed monkey; Myanmar snub-nosed monkey; Rhinopithecus strykeri Geissmann et al., 2010 species cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Euarchontoglires; Primates; Haplorrhini; Simiiformes; Catarrhini; Cercopithecoidea; Cercopithecidae; Colobinae; Rhinopithecus Rhinopithecus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 542827) 1194336 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 1194336) No Latin Name Common Name Synonyms Rank Lineage Parent NCBI Taxonomy ID is Taxon A an Intraspecies? Latin Name Common Name Synonyms Rank Lineage Parent NCBI Taxonomy ID is Taxon B an Intraspecies?		

Taxon B #2	
Rhinopithecus bieti	Latin Name
(<a bieti"="" href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms~" rhinopithecus="">#gephebase-summary-title)	
black snub-nosed monkey	Common Name
Pygathrix bieti; black snub-nosed monkey	Synonyms
species	Rank
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Euarchontoglires; Primates; Haplorrhini; Simiiformes; Catarrhini; Cercopithecoidea; Cercopithecidae; Colobinae; Rhinopithecus	Lineage
Rhinopithecus () - (Rank: genus)	Parent
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=542827)	

NCBI Taxonomy ID

61621

(<https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=61621>)

is Taxon B an Intraspecies?

No

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Homo sapiens
CDT1		Q9H211 (http://www.uniprot.org/uniprot/Q9H211)
	Synonyms	GenebankID or UniProtKB
DUP; RIS2		XM_017859270.1 (https://www.ncbi.nlm.nih.gov/nucore/XM_017859270.1)
	String	
9606.ENSPP00000301019 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSPP00000301019)		
	Sequence Similarities	
Belongs to the Cdt1 family.		
	GO - Molecular Function	
GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)		
GO:0003682 : chromatin binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003682)		
GO:0070182 : DNA polymerase binding (https://www.ebi.ac.uk/QuickGO/term/GO:0070182)		
	GO - Biological Process	
GO:0051301 : cell division (https://www.ebi.ac.uk/QuickGO/term/GO:0051301)		
GO:0000082 : G1/S transition of mitotic cell cycle (https://www.ebi.ac.uk/QuickGO/term/GO:0000082)		
GO:0000278 : mitotic cell cycle (https://www.ebi.ac.uk/QuickGO/term/GO:0000278)		
GO:0000076 : DNA replication checkpoint (https://www.ebi.ac.uk/QuickGO/term/GO:0000076)		
GO:0007059 : chromosome segregation (https://www.ebi.ac.uk/QuickGO/term/GO:0007059)		
GO:0006260 : DNA replication (https://www.ebi.ac.uk/QuickGO/term/GO:0006260)		
GO:0000083 : regulation of transcription involved in G1/S transition of mitotic cell cycle (https://www.ebi.ac.uk/QuickGO/term/GO:0000083)		
GO:0051315 : attachment of mitotic spindle microtubules to kinetochore (https://www.ebi.ac.uk/QuickGO/term/GO:0051315)		
GO:1902426 : deactivation of mitotic spindle assembly checkpoint (https://www.ebi.ac.uk/QuickGO/term/GO:1902426)		
GO:0071163 : DNA replication preinitiation complex assembly (https://www.ebi.ac.uk/QuickGO/term/GO:0071163)		
GO:0051383 : kinetochore organization (https://www.ebi.ac.uk/QuickGO/term/GO:0051383)		
GO:0000281 : mitotic cytokinesis (https://www.ebi.ac.uk/QuickGO/term/GO:0000281)		
GO:1905341 : negative regulation of protein localization to kinetochore (https://www.ebi.ac.uk/QuickGO/term/GO:1905341)		
GO:0035563 : positive regulation of chromatin binding (https://www.ebi.ac.uk/QuickGO/term/GO:0035563)		
GO:0045740 : positive regulation of DNA replication (https://www.ebi.ac.uk/QuickGO/term/GO:0045740)		
GO:2000105 : positive regulation of DNA-dependent DNA replication (https://www.ebi.ac.uk/QuickGO/term/GO:2000105)		
GO:2001178 : positive regulation of mediator complex assembly (https://www.ebi.ac.uk/QuickGO/term/GO:2001178)		
GO:0031334 : positive regulation of protein complex assembly (https://www.ebi.ac.uk/QuickGO/term/GO:0031334)		
GO:1905342 : positive regulation of protein localization to kinetochore (https://www.ebi.ac.uk/QuickGO/term/GO:1905342)		
GO:0033044 : regulation of chromosome organization (https://www.ebi.ac.uk/QuickGO/term/GO:0033044)		
GO:1902595 : regulation of DNA replication origin binding (https://www.ebi.ac.uk/QuickGO/term/GO:1902595)		
GO:0030174 : regulation of DNA-dependent DNA replication initiation (https://www.ebi.ac.uk/QuickGO/term/GO:0030174)		
GO:0033262 : regulation of nuclear cell cycle DNA replication (https://www.ebi.ac.uk/QuickGO/term/GO:0033262)		
GO:0072708 : response to sorbitol (https://www.ebi.ac.uk/QuickGO/term/GO:0072708)		
	GO - Cellular Component	
GO:0005829 : cytosol (https://www.ebi.ac.uk/QuickGO/term/GO:0005829)		
GO:0005654 : nucleoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005654)		
GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)		
GO:0016604 : nuclear body (https://www.ebi.ac.uk/QuickGO/term/GO:0016604)		
GO:0000777 : condensed chromosome kinetochore (https://www.ebi.ac.uk/QuickGO/term/GO:0000777)		
GO:0000776 : kinetochore (https://www.ebi.ac.uk/QuickGO/term/GO:0000776)		
		Presumptive Null

No (<https://www.gephebase.org/search-criteria?/and+Presumptive+Null=~No~#gephebase-summary-title>)

Molecular Type

Coding (<https://www.gephebase.org/search-criteria?/and+Molecular+Type=~Coding~#gephebase-summary-title>)

Aberration Type

SNP (<https://www.gephebase.org/search-criteria?/and+Aberration+Type=~SNP~#gephebase-summary-title>)

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

p.Ala537Val

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

Main Reference

Genomic analysis of snub-nosed monkeys (*Rhinopithecus*) identifies genes and processes related to high-altitude adaptation. (2016) (<https://pubmed.ncbi.nlm.nih.gov/27399969>)

Authors

Yu L; Wang GD; Ruan J; Chen YB; Yang CP; Cao X; Wu H; Liu YH; Du ZL; Wang XP; Yang J; Cheng SC; Zhong L; Wang L; Wang X; Hu JY; Fang L; Bai B; Wang KL; Yuan N; Wu SF; Li BG; Zhang JG; Yang YQ; Zhang CL; Long YC; Li HS; Yang JY; Irwin DM; Ryder OA; Li Y; Wu CI; Zhang YP

Abstract

The snub-nosed monkey genus *Rhinopithecus* includes five closely related species distributed across altitudinal gradients from 800 to 4,500 m. *Rhinopithecus bieti*, *Rhinopithecus roxellana*, and *Rhinopithecus strykeri* inhabit high-altitude habitats, whereas *Rhinopithecus brelichi* and *Rhinopithecus avunculus* inhabit lowland regions. We report the de novo whole-genome sequence of *R. bieti* and genomic sequences for the four other species. Eight shared substitutions were found in six genes related to lung function, DNA repair, and angiogenesis in the high-altitude snub-nosed monkeys. Functional assays showed that the high-altitude variant of CDT1 (Ala537Val) renders cells more resistant to UV irradiation, and the high-altitude variants of RNASE4 (Asn89Lys and Thr128Ile) confer enhanced ability to induce endothelial tube formation in vitro. Genomic scans in the *R. bieti* and *R. roxellana* populations identified signatures of selection between and within populations at genes involved in functions relevant to high-altitude adaptation. These results provide valuable insights into the adaptation to high altitude in the snub-nosed monkeys.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

Common substitution observed in high-altitude snub-nosed monkeys. identified as evolving under positive selection along the lineage containing *R. bieti* and *R. strykeri* and the lineage leading to *R. roxellana*. Experimental validation: UV irradiation assays showed that CDT1 Ala537Val was more stable than the reference CDT1 protein after irradiation with 100 J/m² UV light. CDT1 is a licensing factor for DNA replication that is tightly controlled to maintain genome integrity and the encoded protein is rapidly degraded by the SCF Skp2 complex upon UV-induced DNA damage