

TRIM5alpha (https://www.gephebase.org/search-criteria?/and+GeneGephebase=^TRIM5alpha^#gephebase-summary-title)	Gephebase Gene	GP00001135	GepheID
Published	Entry Status	Courtier	Main curator

Trait Category		Trait	
Physiology (#https://www.gephebase.org/search-criteria?/and+Trait+Category=~Physiology)			
Pathogen resistance (retroviruses) (#https://www.gephebase.org/search-criteria?/and+Trait=~Pathogen+resistance+(retroviruses))			
Old World Monkeys	Trait State in Taxon A		
Old World Monkeys	Trait State in Taxon B		
Data not curated	Ancestral State		
Intraspecific (#https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Intraspecific)	Taxonomic Status		
Taxon A	Latin Name	Taxon B	Latin Name
Cercopithecidae (#https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Cercopithecidae)		Cercopithecidae (#https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Cercopithecidae)	
Old World monkeys	Common Name	Old World monkeys	Common Name
Old World monkeys; monkey; monkeys	Synonyms	Old World monkeys; monkey; monkeys	Synonyms
family	Rank	family	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	Lineage	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	Lineage
Cercopithecoidea () - (Rank: superfamily) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=314294)	Parent	Cercopithecoidea () - (Rank: superfamily) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=314294)	Parent
9527 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9527)	NCBI Taxonomy ID	9527 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9527)	NCBI Taxonomy ID
No	is Taxon A an Intraspecies?	No	is Taxon B an Intraspecies?

TRIM5	Generic Gene Name	Q9C035 (http://www.uniprot.org/uniprot/Q9C035)	UniProtKB Homo sapiens
RNF88; TRIM5alpha	Synonyms	AEO45780 (https://www.ncbi.nlm.nih.gov/nuccore/AEO45780)	GenebankID or UniProtKB
9606.ENSPO0000369373 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSPO0000369373)	String		
	Sequence Similarities		
Belongs to the TRIM/RBCC family.			
	GO - Molecular Function		
GO:0042802 : identical protein binding (https://www.ebi.ac.uk/QuickGO/term/GO:0042802)			
GO:0042803 : protein homodimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0042803)			
GO:0008270 : zinc ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0008270)			
GO:0019901 : protein kinase binding (https://www.ebi.ac.uk/QuickGO/term/GO:0019901)			
GO:0030674 : protein binding, bridging			

(<https://www.ebi.ac.uk/QuickGO/term/GO:0030674>)
GO:0008329 : signaling pattern recognition receptor activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0008329>)
GO:0004842 : ubiquitin-protein transferase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0004842>)

GO - Biological Process

GO:0045087 : innate immune response
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045087>)
GO:0043410 : positive regulation of MAPK cascade
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043410>)
GO:0051092 : positive regulation of NF-kappaB transcription factor activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0051092>)
GO:0051607 : defense response to virus
(<https://www.ebi.ac.uk/QuickGO/term/GO:0051607>)
GO:0043123 : positive regulation of I-kappaB kinase/NF-kappaB signaling
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043123>)
GO:0032880 : regulation of protein localization
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032880>)
GO:0060333 : interferon-gamma-mediated signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060333>)
GO:0016032 : viral process (<https://www.ebi.ac.uk/QuickGO/term/GO:0016032>)
GO:0051091 : positive regulation of DNA-binding transcription factor activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0051091>)
GO:0002218 : activation of innate immune response
(<https://www.ebi.ac.uk/QuickGO/term/GO:0002218>)
GO:0006914 : autophagy (<https://www.ebi.ac.uk/QuickGO/term/GO:0006914>)
GO:0046597 : negative regulation of viral entry into host cell
(<https://www.ebi.ac.uk/QuickGO/term/GO:0046597>)
GO:1902187 : negative regulation of viral release from host cell
(<https://www.ebi.ac.uk/QuickGO/term/GO:1902187>)
GO:0070534 : protein K63-linked ubiquitination
(<https://www.ebi.ac.uk/QuickGO/term/GO:0070534>)
GO:0070206 : protein trimerization (<https://www.ebi.ac.uk/QuickGO/term/GO:0070206>)
GO:0031664 : regulation of lipopolysaccharide-mediated signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0031664>)

GO - Cellular Component

GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)
GO:0005829 : cytosol (<https://www.ebi.ac.uk/QuickGO/term/GO:0005829>)
GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)
GO:0000932 : P-body (<https://www.ebi.ac.uk/QuickGO/term/GO:0000932>)

	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
several a.a. substitutions with retrovirus-specific activities; under balancing selection in several species	
	Experimental Evidence
Candidate Gene (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Candidate Gene~#gephebase-summary-title)	

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

	Main Reference
Balancing selection and the evolution of functional polymorphism in Old World monkey TRIM5alpha. (2006) (https://pubmed.ncbi.nlm.nih.gov/17142324)	
	Authors
Newman RM; Hall L; Connoles M; Chen GL; Sato S; Yuste E; Diehl W; Hunter E; Kaur A; Miller GM; Johnson WE	
	Abstract
Retroviral restriction factor TRIM5alpha exhibits a high degree of sequence variation among primate species. It has been proposed that this diversity is the cumulative result of ancient, lineage-specific episodes of positive selection. Here, we describe the contribution of within-species variation to the evolution of TRIM5alpha. Sampling within two geographically distinct Old World monkey species revealed extensive polymorphism, including individual polymorphisms that predate speciation (shared polymorphism). In some instances, alleles were more closely related to orthologues of other species than to one another. Both silent and nonsynonymous changes clustered in two domains. Functional assays revealed consequences of polymorphism, including differential restriction of a small panel of retroviruses by very similar alleles. Together, these features indicate that the primate TRIM5alpha locus has evolved under balancing selection. Except for the MHC there are few, if any, examples of long-term balancing selection in primates. Our results suggest a complex evolutionary scenario, in which fixation of lineage-specific adaptations is superimposed on a subset of critical polymorphisms that predate speciation events and have been maintained by balancing selection for millions of years.	
	Additional References

2 (Mitochondrial antiviral signaling (MAVS), TRIM5alpha-CypA chimeric gene) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=^9527^/and+Trait=Pathogen resistance/and+groupHaplotypes=true#gephebase-summary-title>)

No matches found.

EXTERNAL LINKS

COMMENTS

@BalancingSelection