

GEPHE SUMMARY

	Gephebase Gene		GepheID
Mitochondrial antiviral signaling (MAVS) (<a +mitochondrial+antiviral+signaling+(mavs)+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+Mitochondrial+antiviral+signaling+(MAVS)+"#gephebase-summary-title)		GP00001456	
	Entry Status	Prigent	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (<a +physiology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">https://www.gephebase.org/search-criteria?/and+Trait+Category="+Physiology+"#gephebase-summary-title)		Trait	
Pathogen resistance (hepaciviruses) (<a +pathogen+resistance+(hepaciviruses)+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="+Pathogen+resistance+(hepaciviruses)+"#gephebase-summary-title)		Trait State in Taxon A	
Patas monkey and others		Trait State in Taxon B	
Allen’s swamp monkey		Ancestral State	
Taxon A		Taxonomic Status	
Interspecific (<a +interspecific+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status="+Interspecific+"#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
Erythrocebus patas (<a +erythrocebus+patas+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Erythrocebus+patas+"#gephebase-summary-title)		Allenopithecus nigroviridis (<a +allenopithecus+nigroviridis+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Allenopithecus+nigroviridis+"#gephebase-summary-title)	
	Common Name		Common Name
red guenon		Allen’s swamp monkey	
	Synonyms		Synonyms
Cercopithecus patas; red guenon; hussar; patas monkey		Allen’s swamp monkey	
	Rank		Rank
species		species	
	Lineage		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; Cercopithecidae; Cercopithecinae; Erythrocebus		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; Cercopithecinae; Allenopithecus	
	Parent		Parent
Erythrocebus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9537)		Allenopithecus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=54134)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
9538 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9538)		54135 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=54135)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Homo sapiens
MAVS		Q7Z434 (http://www.uniprot.org/uniprot/Q7Z434)	
	Synonyms		GenebankID or UniProtKB
IPS1; VISA; IPS-1; CARDIF; KIAA1271		KC415015 (https://www.ncbi.nlm.nih.gov/nucore/KC415015)	
	String		
9606.ENSP00000401980 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSP00000401980)			
	Sequence Similarities		
-			
	GO - Molecular Function		
GO:0019901 : protein kinase binding (https://www.ebi.ac.uk/QuickGO/term/GO:0019901)			
GO:0050700 : CARD domain binding (https://www.ebi.ac.uk/QuickGO/term/GO:0050700)			
GO:0035591 : signaling adaptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0035591)			

GO - Biological Process

GO:0045087 : innate immune response
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045087>)
GO:0007165 : signal transduction (<https://www.ebi.ac.uk/QuickGO/term/GO:0007165>)
GO:0045944 : positive regulation of transcription by RNA polymerase II
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045944>)
GO:0042742 : defense response to bacterium
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042742>)
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:0001934 : positive regulation of protein phosphorylation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0001934>)
GO:0016032 : viral process (<https://www.ebi.ac.uk/QuickGO/term/GO:0016032>)
GO:0002230 : positive regulation of defense response to virus by host
(<https://www.ebi.ac.uk/QuickGO/term/GO:0002230>)
GO:0033160 : positive regulation of protein import into nucleus, translocation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0033160>)
GO:0051091 : positive regulation of DNA-binding transcription factor activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0051091>)
GO:0002735 : positive regulation of myeloid dendritic cell cytokine production
(<https://www.ebi.ac.uk/QuickGO/term/GO:0002735>)
GO:0032760 : positive regulation of tumor necrosis factor production
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032760>)
GO:0002218 : activation of innate immune response
(<https://www.ebi.ac.uk/QuickGO/term/GO:0002218>)
GO:0071360 : cellular response to exogenous dsRNA
(<https://www.ebi.ac.uk/QuickGO/term/GO:0071360>)
GO:0032480 : negative regulation of type I interferon production
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032480>)
GO:0045071 : negative regulation of viral genome replication
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045071>)
GO:0071651 : positive regulation of chemokine (C-C motif) ligand 5 production
(<https://www.ebi.ac.uk/QuickGO/term/GO:0071651>)
GO:0032727 : positive regulation of interferon-alpha production
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032727>)
GO:1902741 : positive regulation of interferon-alpha secretion
(<https://www.ebi.ac.uk/QuickGO/term/GO:1902741>)
GO:0032728 : positive regulation of interferon-beta production
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032728>)
GO:0035549 : positive regulation of interferon-beta secretion
(<https://www.ebi.ac.uk/QuickGO/term/GO:0035549>)
GO:2000778 : positive regulation of interleukin-6 secretion
(<https://www.ebi.ac.uk/QuickGO/term/GO:2000778>)
GO:0032757 : positive regulation of interleukin-8 production
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032757>)
GO:0071660 : positive regulation of IP-10 production
(<https://www.ebi.ac.uk/QuickGO/term/GO:0071660>)
GO:0060760 : positive regulation of response to cytokine stimulus
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060760>)
GO:1904469 : positive regulation of tumor necrosis factor secretion
(<https://www.ebi.ac.uk/QuickGO/term/GO:1904469>)
GO:0060340 : positive regulation of type I interferon-mediated signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060340>)
GO:1900063 : regulation of peroxisome organization
(<https://www.ebi.ac.uk/QuickGO/term/GO:1900063>)

GO - Cellular Component

GO:0016021 : integral component of membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)
GO:0031966 : mitochondrial membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0031966>)
GO:0005739 : mitochondrion (<https://www.ebi.ac.uk/QuickGO/term/GO:0005739>)
GO:0005741 : mitochondrial outer membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005741>)
GO:0005778 : peroxisomal membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005778>)

Presumptive Null

No ([https://www.gephebase.org/search-criteria?/and+Presumptive Null="+No`"#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive+Null=))

Molecular Type

Coding ([https://www.gephebase.org/search-criteria?/and+Molecular Type="+Coding`"#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular+Type=))

Aberration Type

SNP ([https://www.gephebase.org/search-criteria?/and+Aberration Type="+SNP`"#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration+Type=))

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

Val506Met less susceptible to cleavage

Experimental Evidence

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

Convergent evolution of escape from hepaciviral antagonism in primates. (2012) (<https://pubmed.ncbi.nlm.nih.gov/22427742>)

Main Reference

Patel MR; Loo YM; Horner SM; Gale M; Malik HS

Authors

Abstract

The ability to mount an interferon response on sensing viral infection is a critical component of mammalian innate immunity. Several viruses directly antagonize viral sensing pathways to block activation of the host immune response. Here, we show that recurrent viral antagonism has shaped the evolution of the host protein MAVS--a crucial component of the viral-sensing pathway in primates. From sequencing and phylogenetic analyses of MAVS from 21 simian primates, we found that MAVS has evolved under strong positive selection. We focused on how this positive selection has shaped MAVS' susceptibility to Hepatitis C virus (HCV). We functionally tested MAVS proteins from diverse primate species for their ability to resist antagonism by HCV, which uses its protease NS3/4A to cleave human MAVS. We found that MAVS from multiple primates are resistant to inhibition by the HCV protease. This resistance maps to single changes within the protease cleavage site in MAVS, which protect MAVS from getting cleaved by the HCV protease. Remarkably, most of these changes have been independently acquired at a single residue 506 that evolved under positive selection. We show that "escape" mutations lower affinity of the NS3 protease for MAVS and allow it to better restrict HCV replication. We further show that NS3 proteases from all other primate hepaciviruses, including the highly divergent GBV-A and GBV-C viruses, are functionally similar to HCV. We conclude that convergent evolution at residue 506 in multiple primates has resulted in escape from antagonism by hepaciviruses. Our study provides a model whereby insights into the ancient history of viral infections in primates can be gained using extant host and virus genes. Our analyses also provide a means by which primates might clear infections by extant hepaciviruses like HCV.

Additional References

RELATED GEPHE

	Related Genes
No matches found.	
	Related Haplotypes
No matches found.	

EXTERNAL LINKS

COMMENTS

in this species mutation provides significant protection against protease of GBV-B virus compared to HCV