

GEPHE SUMMARY

	Gephebase Gene	GepheID
adenosine deaminase (AgADA) (https://www.gephebase.org/search-criteria?/and+GeneGephebase=^adenosine deaminase (AgADA)^#gephebase-summary-title)	GP00001463	
	Entry Status	Prigent
Published		Main curator

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=^Physiology^#gephebase-summary-title)		Trait	
Pathogen resistance (parasite) (https://www.gephebase.org/search-criteria?/and+Trait=^Pathogen resistance (parasite)^#gephebase-summary-title)		Trait State in Taxon A	
Anopheles gambiae susceptible to Plasmodium falciparum infection		Trait State in Taxon B	
Anopheles gambiae resistant to Plasmodium falciparum infection		Ancestral State	
Taxon A		Taxonomic Status	
Intraspecific (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=^Intraspecific^#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
Anopheles gambiae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Anopheles gambiae^#gephebase-summary-title)		Anopheles gambiae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Anopheles gambiae^#gephebase-summary-title)	
	Common Name		Common Name
African malaria mosquito		African malaria mosquito	
	Synonyms		Synonyms
Anopheles gambiae S; African malaria mosquito; Anopheles gambiae Giles, 1902; Anopheles gambia		Anopheles gambiae S; African malaria mosquito; Anopheles gambiae Giles, 1902; Anopheles gambia	
	Rank		Rank
species		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Diptera; Nematocera; Culicomorpha; Culicoidea; Culicidae; Anophelinae; Anopheles; Cellia; Pyretophorus; gambiae species complex		cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Diptera; Nematocera; Culicomorpha; Culicoidea; Culicidae; Anophelinae; Anopheles; Cellia; Pyretophorus; gambiae species complex	
	Parent		Parent
gambiae species complex () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=44542)		gambiae species complex () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=44542)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
7165 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7165)		7165 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7165)	
	is Taxon A an Infrappecies?		is Taxon B an Infrappecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Homo sapiens
ADA		P00813 (http://www.uniprot.org/uniprot/P00813)
	Synonyms	GenebankID or UniProtKB
ADA1		XM_565288 (https://www.ncbi.nlm.nih.gov/nuccore/XM_565288)
	String	
9606.ENSPP00000361965 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSPP00000361965)		
	Sequence Similarities	
Belongs to the metallo-dependent hydrolases superfamily. Adenosine and AMP deaminases family.		
	GO - Molecular Function	
GO:0008270 : zinc ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0008270)		
GO:0004000 : adenosine deaminase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004000)		
GO:0001883 : purine nucleoside binding		

(<https://www.ebi.ac.uk/QuickGO/term/GO:0001883>)

GO - Biological Process

GO:0007155 : cell adhesion (<https://www.ebi.ac.uk/QuickGO/term/GO:0007155>)
GO:0043101 : purine-containing compound salvage
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043101>)
GO:0050728 : negative regulation of inflammatory response
(<https://www.ebi.ac.uk/QuickGO/term/GO:0050728>)
GO:0010460 : positive regulation of heart rate
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010460>)
GO:0042542 : response to hydrogen peroxide
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042542>)
GO:0001666 : response to hypoxia (<https://www.ebi.ac.uk/QuickGO/term/GO:0001666>)
GO:0007568 : aging (<https://www.ebi.ac.uk/QuickGO/term/GO:0007568>)
GO:0001829 : trophectodermal cell differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0001829>)
GO:0001889 : liver development (<https://www.ebi.ac.uk/QuickGO/term/GO:0001889>)
GO:0048286 : lung alveolus development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048286>)
GO:0030890 : positive regulation of B cell proliferation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030890>)
GO:0042110 : T cell activation (<https://www.ebi.ac.uk/QuickGO/term/GO:0042110>)
GO:0050862 : positive regulation of T cell receptor signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0050862>)
GO:0006154 : adenosine catabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006154>)
GO:0046061 : dATP catabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0046061>)
GO:0006157 : deoxyadenosine catabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006157>)
GO:0048566 : embryonic digestive tract development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048566>)
GO:0002314 : germinal center B cell differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0002314>)
GO:0001821 : histamine secretion (<https://www.ebi.ac.uk/QuickGO/term/GO:0001821>)
GO:0043103 : hypoxanthine salvage (<https://www.ebi.ac.uk/QuickGO/term/GO:0043103>)
GO:0046103 : inosine biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0046103>)
GO:0060169 : negative regulation of adenosine receptor signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060169>)
GO:0042323 : negative regulation of circadian sleep/wake cycle, non-REM sleep
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042323>)
GO:0002686 : negative regulation of leukocyte migration
(<https://www.ebi.ac.uk/QuickGO/term/GO:0002686>)
GO:0002906 : negative regulation of mature B cell apoptotic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0002906>)
GO:0070256 : negative regulation of mucus secretion
(<https://www.ebi.ac.uk/QuickGO/term/GO:0070256>)
GO:0060407 : negative regulation of penile erection
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060407>)
GO:0070244 : negative regulation of thymocyte apoptotic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0070244>)
GO:0048541 : Peyer's patch development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048541>)
GO:0001890 : placenta development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0001890>)
GO:0046638 : positive regulation of alpha-beta T cell differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0046638>)
GO:0050850 : positive regulation of calcium-mediated signaling
(<https://www.ebi.ac.uk/QuickGO/term/GO:0050850>)
GO:0002636 : positive regulation of germinal center formation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0002636>)
GO:0045987 : positive regulation of smooth muscle contraction
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045987>)
GO:0033089 : positive regulation of T cell differentiation in thymus
(<https://www.ebi.ac.uk/QuickGO/term/GO:0033089>)
GO:0032261 : purine nucleotide salvage
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032261>)
GO:0009168 : purine ribonucleoside monophosphate biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009168>)
GO:0033632 : regulation of cell-cell adhesion mediated by integrin
(<https://www.ebi.ac.uk/QuickGO/term/GO:0033632>)
GO:0043278 : response to morphine (<https://www.ebi.ac.uk/QuickGO/term/GO:0043278>)
GO:0033197 : response to vitamin E (<https://www.ebi.ac.uk/QuickGO/term/GO:0033197>)
GO:0046111 : xanthine biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0046111>)

GO - Cellular Component

GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)
GO:0005829 : cytosol (<https://www.ebi.ac.uk/QuickGO/term/GO:0005829>)

GO:0016020 : membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0016020>)
GO:0030054 : cell junction (<https://www.ebi.ac.uk/QuickGO/term/GO:0030054>)
GO:0005615 : extracellular space (<https://www.ebi.ac.uk/QuickGO/term/GO:0005615>)
GO:0043025 : neuronal cell body (<https://www.ebi.ac.uk/QuickGO/term/GO:0043025>)
GO:0009986 : cell surface (<https://www.ebi.ac.uk/QuickGO/term/GO:0009986>)
GO:0005764 : lysosome (<https://www.ebi.ac.uk/QuickGO/term/GO:0005764>)
GO:0009897 : external side of plasma membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009897>)
GO:0060205 : cytoplasmic vesicle lumen
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060205>)
GO:0032839 : dendrite cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0032839>)

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

c.C427T p.R143C

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

Genome-block expression-assisted association studies discover malaria resistance genes in *Anopheles gambiae*. (2013) (<https://pubmed.ncbi.nlm.nih.gov/24297936>)

Authors

Li J; Wang X; Zhang G; Githure JI; Yan G; James AA

Abstract

The malaria parasite-resistance island (PRI) of the African mosquito vector, *Anopheles gambiae*, was mapped to five genomic regions containing 80 genes, using coexpression patterns of genomic blocks. High-throughput sequencing identified 347 nonsynonymous single-nucleotide polymorphisms within these genes in mosquitoes from malaria-endemic areas in Kenya. Direct association studies between nonsynonymous single-nucleotide polymorphisms and *Plasmodium falciparum* infection identified three naturally occurring genetic variations in each of three genes (*An. gambiae* adenosine deaminase, fibrinogen-related protein 30, and fibrinogen-related protein 1) that were associated significantly with parasite infection. A role for these genes in the resistance phenotype was confirmed by RNA interference knockdown assays. Silencing fibrinogen-related protein 30 increased parasite infection significantly, whereas ablation of fibrinogen-related protein 1 transcripts resulted in mosquitoes nearly free of parasites. The discovered genes and single-nucleotide polymorphisms are anticipated to be useful in the development of tools for malaria control in endemic areas in Africa.

Additional References

RELATED GEPHE

Related Genes

4 (APL1 cluster, fibrinogen-related protein 1 (FREP1), fibrinogen-related protein 30 (FBN30), thioester-containing protein 1) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=~7165^/and+Trait=Pathogen resistance/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

the role of the gene is confirmed by RNA interference knockdown assays. Silencing of the gene slightly reduced parasite infection by *P. berghei*

