

# GEPHE SUMMARY

	Gephebase Gene	GephelD
apicoplast ribosomal protein S10 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^apicoplast ribosomal protein S10^#gephebase-summary-title)	GP00001531	Main curator
	Entry Status	Prigent
Published		

## PHENOTYPIC CHANGE

	Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)	
Xenobiotic resistance (artemisinin) (https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic resistance (artemisinin)^#gephebase-summary-title)	Trait
Artemisinin-sensitive Plasmodium with mean parasite clearance half-life of 2.6 hours	Trait State in Taxon A
Artemisinin-resistant Plasmodium with parasite clearance half-life estimated prolongation of 0.58 h	Trait State in Taxon B
	Ancestral State
Taxon A	Taxonomic Status
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#gephebase-summary-title)	

Taxon A	Latin Name	Taxon B	Latin Name
Plasmodium falciparum (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Plasmodium falciparum^#gephebase-summary-title)		Plasmodium falciparum (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Plasmodium falciparum^#gephebase-summary-title)	
malaria parasite P. falciparum	Common Name	malaria parasite P. falciparum	Common Name
Plasmodium (Laverania) falciparum; malaria parasite P. falciparum	Synonyms	Plasmodium (Laverania) falciparum; malaria parasite P. falciparum	Synonyms
species	Rank	species	Rank
	Lineage		Lineage
cellular organisms; Eukaryota; Alveolata; Apicomplexa; Aconoidasida; Haemosporida; Plasmodiidae; Plasmodium; Plasmodium (Laverania)		cellular organisms; Eukaryota; Alveolata; Apicomplexa; Aconoidasida; Haemosporida; Plasmodiidae; Plasmodium; Plasmodium (Laverania)	
Plasmodium (Laverania) () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 418107 )	Parent	Plasmodium (Laverania) () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 418107 )	Parent
5833 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 5833 )	NCBI Taxonomy ID	5833 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 5833 )	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

## GENOTYPIC CHANGE

PF3D7_1460900.1	Generic Gene Name	UniProtKB Plasmodium falciparum (isolate 3D7)
	Synonyms	Q8IKM3 (http://www.uniprot.org/uniprot/Q8IKM3)
PF3D7_1460900.1	String	GenebankID or UniProtKB
-	Sequence Similarities	0
-	GO - Molecular Function	
GO:0003735 : structural constituent of ribosome (https://www.ebi.ac.uk/QuickGO/term/GO:0003735)	GO - Biological Process	
GO:0006412 : translation (https://www.ebi.ac.uk/QuickGO/term/GO:0006412)	GO - Cellular Component	
GO:0005739 : mitochondrion (https://www.ebi.ac.uk/QuickGO/term/GO:0005739)		
GO:0005840 : ribosome (https://www.ebi.ac.uk/QuickGO/term/GO:0005840)		
No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title)		Presumptive Null
		Molecular Type

Coding ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular%20Type=%Coding))

Aberration Type

SNP ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration%20Type=%SNP))

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

p.Val127Met

Experimental Evidence

Association Mapping ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental%20Evidence=%Association%20Mapping))

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

Main Reference

Genetic architecture of artemisinin-resistant *Plasmodium falciparum*. (2015) (<https://pubmed.ncbi.nlm.nih.gov/25599401>)

Authors

Miotto O; Amato R; Ashley EA; Maclnnis B; Almagro-Garcia J; Amaratunga C; Lim P; Mead D; Oyola SO; Dhorda M; Imwong M; Woodrow C; Manske M; Stalker J; Drury E; Campino S; Amenga-Etego L; Thanh TN; Tran HT; Ringwald P; Bethell D; Nosten F; Phy AP; Pukrittayakamee S; Chotivanich K; Chuor CM; Nguon C; Suon S; Sreng S; Newton PN; Mayxay M; Khanthavong M; Hongvanthong B; Htut Y; Han KT; Kyaw MP; Faiz MA; Fanello CI; Onyamboko M; Mokuolu OA; Jacob CG; Takala-Harrison S; Plowe CV; Day NP; Dondorp AM; Spencer CC; McVean G; Fairhurst RM; White NJ; Kwiatkowski DP

Abstract

We report a large multicenter genome-wide association study of *Plasmodium falciparum* resistance to artemisinin, the frontline antimalarial drug. Across 15 locations in Southeast Asia, we identified at least 20 mutations in kelch13 (PF3D7\_1343700) affecting the encoded propeller and BTB/POZ domains, which were associated with a slow parasite clearance rate after treatment with artemisinin derivatives. Nonsynonymous polymorphisms in fd (ferredoxin), arps10 (apicoplast ribosomal protein S10), mdr2 (multidrug resistance protein 2) and crt (chloroquine resistance transporter) also showed strong associations with artemisinin resistance. Analysis of the fine structure of the parasite population showed that the fd, arps10, mdr2 and crt polymorphisms are markers of a genetic background on which kelch13 mutations are particularly likely to arise and that they correlate with the contemporary geographical boundaries and population frequencies of artemisinin resistance. These findings indicate that the risk of new resistance-causing mutations emerging is determined by specific predisposing genetic factors in the underlying parasite population.

Additional References

## RELATED GEPHE

Related Genes

6 (chloroquine resistance transporter, ferredoxin, kelch 13, kelch 13 (K13), multidrug resistance protein 2, protein phosphatase) ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+TaxonID=%583%27+and+Trait=Xenobiotic+resistance+and+groupHaplotypes=true))

Related Haplotypes

No matches found.

## EXTERNAL LINKS

## COMMENTS