

GEPHE SUMMARY

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

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category= [^] Physiology [^] #gephebase-summary-title)			
	Trait		
Xenobiotic resistance (artemisinin) (<a href="https://www.gephebase.org/search-criteria?/and+Trait=<sup>^</sup>Xenobiotic resistance (artemisinin)<sup>^</sup>#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Trait=[^]Xenobiotic resistance (artemisinin)[^]#gephebase-summary-title)			
	Trait State in Taxon A		
Artemisinin-sensitive Plasmodium with mean parasite clearance half-life of 2.6 hours			
	Trait State in Taxon B		
Artemisinin-resistant Plasmodium with parasite clearance half-life estimated prolongation of 0.58 h			
	Ancestral State		
Taxon A			
	Taxonomic Status		
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status= [^] Intraspecific [^] #gephebase-summary-title)			
Taxon A		Taxon B	
	Latin Name		Latin Name
Plasmodium falciparum (<a href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=<sup>^</sup>Plasmodium falciparum<sup>^</sup>#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=[^]Plasmodium falciparum[^]#gephebase-summary-title)		Plasmodium falciparum (<a href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=<sup>^</sup>Plasmodium falciparum<sup>^</sup>#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=[^]Plasmodium falciparum[^]#gephebase-summary-title)	
	Common Name		Common Name
malaria parasite P. falciparum		malaria parasite P. falciparum	
	Synonyms		Synonyms
Plasmodium (Laverania) falciparum; malaria parasite P. falciparum		Plasmodium (Laverania) falciparum; malaria parasite P. falciparum	
	Rank		Rank
species		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Alveolata; Apicomplexa; Aconoidasida; Haemosporida; Plasmodiidae; Plasmodium; Plasmodium (Laverania)		cellular organisms; Eukaryota; Alveolata; Apicomplexa; Aconoidasida; Haemosporida; Plasmodiidae; Plasmodium; Plasmodium (Laverania)	
	Parent		Parent
Plasmodium (Laverania) () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=418107)		Plasmodium (Laverania) () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=418107)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
5833 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=5833)		5833 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=5833)	
	is Taxon A an Infrappecies?		is Taxon B an Infrappecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Plasmodium falciparum (isolate 3D7)
PF3D7_1460900.1		Q81KM3 (http://www.uniprot.org/uniprot/Q81KM3)	
	Synonyms		GenebankID or UniProtKB
PF3D7_1460900.1		()	
-	String		
-			
	Sequence Similarities		
-			
	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)			
			Presumptive Null
No (<a href="https://www.gephebase.org/search-criteria?/and+Presumptive Null=<sup>^</sup>No<sup>^</sup>#gephebase-summary-title">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.Val127Met

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

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

Authors

Miotto O; Amato R; Ashley EA; MacInnis 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; Phyo AP; Pukrittayakamee S; Chotivanich K; Chhor 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) (<https://www.gephebase.org/search-criteria?/or+Taxon+ID=^5833^/and+Trait=Xenobiotic+resistance/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS