

## GEPHE SUMMARY

ferredoxin ( <a href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^ferredoxin^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^ferredoxin^#gephebase-summary-title</a> )	Gephebase Gene	GP00001530	GepheID
Published	Entry Status	Prigent	Main curator

## PHENOTYPIC CHANGE

Physiology ( <a href="https://www.gephebase.org/search-criteria?/and+Trait+Category=^Physiology^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Trait+Category=^Physiology^#gephebase-summary-title</a> )	Trait Category		
Xenobiotic resistance (artemisinin) ( <a href="https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic+resistance+(artemisinin)^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic+resistance+(artemisinin)^#gephebase-summary-title</a> )	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 0.53 h	Trait State in Taxon B		
	Ancestral State		
Intraspecific ( <a href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Intraspecific^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Intraspecific^#gephebase-summary-title</a> )	Taxonomic Status		
	Taxon A		Taxon B
Plasmodium falciparum ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Plasmodium+falciparum^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Plasmodium+falciparum^#gephebase-summary-title</a> )	Latin Name	Plasmodium falciparum ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Plasmodium+falciparum^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Plasmodium+falciparum^#gephebase-summary-title</a> )	Latin Name
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
cellular organisms; Eukaryota; Alveolata; Apicomplexa; Aconoidasida; Haemosporida; Plasmodiidae; Plasmodium; Plasmodium (Laverania)	Lineage	cellular organisms; Eukaryota; Alveolata; Apicomplexa; Aconoidasida; Haemosporida; Plasmodiidae; Plasmodium; Plasmodium (Laverania)	Lineage
Plasmodium (Laverania) () - (Rank: subgenus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=418107">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=418107</a> )	Parent	Plasmodium (Laverania) () - (Rank: subgenus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=418107">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=418107</a> )	Parent
5833 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=5833">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=5833</a> )	NCBI Taxonomy ID	5833 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=5833">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=5833</a> )	NCBI Taxonomy ID
No	is Taxon A an Intraspecies?	No	is Taxon B an Intraspecies?

## GENOTYPIC CHANGE

PF3D7_1318100	Generic Gene Name	UniProtKB Plasmodium falciparum (isolate 3D7)
PF3D7_1318100	Synonyms	Q8IED5 ( <a href="http://www.uniprot.org/uniprot/Q8IED5">http://www.uniprot.org/uniprot/Q8IED5</a> )
-	String	GenebankID or UniProtKB
	Sequence Similarities	
Belongs to the 2Fe2S plant-type ferredoxin family.		
GO:0046872 : metal ion binding ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0046872">https://www.ebi.ac.uk/QuickGO/term/GO:0046872</a> )	GO - Molecular Function	
GO:0009055 : electron transfer activity ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0009055">https://www.ebi.ac.uk/QuickGO/term/GO:0009055</a> )		
GO:0051537 : 2 iron, 2 sulfur cluster binding ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0051537">https://www.ebi.ac.uk/QuickGO/term/GO:0051537</a> )		
GO:0055114 : oxidation-reduction process ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0055114">https://www.ebi.ac.uk/QuickGO/term/GO:0055114</a> )	GO - Biological Process	
GO:0020011 : apicoplast ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0020011">https://www.ebi.ac.uk/QuickGO/term/GO:0020011</a> )	GO - Cellular Component	

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

Presumptive Null

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

Molecular Type

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

Aberration Type

Nonsynonymous

SNP Coding Change

p.Asp193Tyr

Molecular Details of the Mutation

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

Experimental Evidence

	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; Chuor CM; Nguon C; Suon S; Sreng S; Newton PN; Mayxay M; Khantavong 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 (apicoplast ribosomal protein S10, chloroquine resistance transporter, 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](https://www.gephebase.org/search-criteria?/or+Taxon+ID=))

Related Haplotypes

No matches found.

## EXTERNAL LINKS

## COMMENTS