

## GEPHE SUMMARY

Gephbase Gene  
 chloroquine resistance transporter ([https://www.gepbase.org/search-criteria?/and+Gene+Gephbase=^chloroquine resistance transporter^#gepbase-summary-title](https://www.gepbase.org/search-criteria?/and+Gene+Gephbase=^chloroquine+resistance+transporter^#gepbase-summary-title)) GP00001533  
 Entry Status Prigent  
 Published  
 Main curator

## PHENOTYPIC CHANGE

Trait Category  
 Physiology (<https://www.gepbase.org/search-criteria?/and+Trait+Category=^Physiology^#gepbase-summary-title>)  
 Trait  
 Xenobiotic resistance (artemisinin) ([https://www.gepbase.org/search-criteria?/and+Trait=^Xenobiotic resistance \(artemisinin\)^#gepbase-summary-title](https://www.gepbase.org/search-criteria?/and+Trait=^Xenobiotic+resistance+(artemisinin)^#gepbase-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 0.47 h  
 Ancestral State  
 Taxon A  
 Taxonomic Status  
 Intraspecific (<https://www.gepbase.org/search-criteria?/and+Taxonomic+Status=^Intraspecific^#gepbase-summary-title>)  

Taxon A	Taxon B
Latin Name	Latin Name
Plasmodium falciparum ( <a href="https://www.gepbase.org/search-criteria?/and+Taxon+and+Synonyms=^Plasmodium+falciparum^#gepbase-summary-title">https://www.gepbase.org/search-criteria?/and+Taxon+and+Synonyms=^Plasmodium falciparum^#gepbase-summary-title</a> )	Plasmodium falciparum ( <a href="https://www.gepbase.org/search-criteria?/and+Taxon+and+Synonyms=^Plasmodium+falciparum^#gepbase-summary-title">https://www.gepbase.org/search-criteria?/and+Taxon+and+Synonyms=^Plasmodium falciparum^#gepbase-summary-title</a> )
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) ( <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> )	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> )
NCBI Taxonomy ID	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> )	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> )
is Taxon A an Intraspecies?	is Taxon B an Intraspecies?
No	No

## GENOTYPIC CHANGE

Generic Gene Name  
 CRT Q9N623 (<http://www.uniprot.org/uniprot/Q9N623>) UniProtKB Plasmodium falciparum  
 Synonyms GenebankID or UniProtKB  
 - ()  
 String  
 -  
 Sequence Similarities  
 Belongs to the CRT-like transporter family.  
 GO - Molecular Function  
 GO:0015238 : drug transmembrane transporter activity  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0015238>)  
 GO - Biological Process  
 -  
 GO - Cellular Component  
 GO:0016021 : integral component of membrane  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)  
 GO:0005774 : vacuolar membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005774>)  
 Presumptive Null  
 No ([https://www.gepbase.org/search-criteria?/and+Presumptive Null=^No^#gepbase-summary-title](https://www.gepbase.org/search-criteria?/and+Presumptive+Null=^No^#gepbase-summary-title))

Coding (<https://www.gephebase.org/search-criteria?/and+Molecular+Type=~Coding^#gephebase-summary-title>)

Molecular Type

SNP (<https://www.gephebase.org/search-criteria?/and+Aberration+Type=~SNP^#gephebase-summary-title>)

Aberration Type

Nonsynonymous

SNP Coding Change

p.Ile356Thr

Molecular Details of the Mutation

Association Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=~Association+Mapping^#gephebase-summary-title>)

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; 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 (apicoplast ribosomal protein S10, 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