

kelch 13 (<a +kelch+13^#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene Gephebase="+kelch 13^#gephebase-summary-title)	Gephebase Gene	GP00001514	GepheID
Published	Entry Status	Prigent	Main curator

	Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Physiology^#gephebase-summary-title)	
	Trait
Xenobiotic resistance (artemisinin) (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 mean parasite clearance half-life of 8.38 hours from Thailand (6 samples)	
	Ancestral State
Taxon A	
	Taxonomic Status
Intraspecific (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Intraspecific^#gephebase-summary-title)	

GENOTYPIC CHANGE

PF3D7_1343700	Generic Gene Name	UniProtKB Plasmodium falciparum (isolate 3D7)
	Synonyms	Q8IDQ2 (http://www.uniprot.org/uniprot/Q8IDQ2)
PF3D7_1343700		GenebankID or UniProtKB
	String	KM187892.1 (https://www.ncbi.nlm.nih.gov/nuccore/KM187892.1)
-		
	Sequence Similarities	
-		
	GO - Molecular Function	
-		
	GO - Biological Process	
GO:0042493 : response to drug (https://www.ebi.ac.uk/QuickGO/term/GO:0042493)		
GO:0051260 : protein homooligomerization (https://www.ebi.ac.uk/QuickGO/term/GO:0051260)		
	GO - Cellular Component	
-		
		Presumptive Null
No (<a +no`#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?and+Presumptive+Null=">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

N458Y affecting the encoded propeller and BTB/POZ domains

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; 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, chloroquine resistance transporter, ferredoxin, 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

19 (<https://www.gephebase.org/search-criteria?/or+Gene Gephebase=~kelch 13~/and+Taxon ID=~5833~/or+Gene Gephebase=~kelch 13~/and+Taxon ID=~5833~#gephebase-summary-title>)

EXTERNAL LINKS

COMMENTS