

## GEPHE SUMMARY

|   |                              |                         |
|---|------------------------------|-------------------------|
| protein phosphatase ( <a href="https://www.gephebase.org/search-criteria?/and+Gene">https://www.gephebase.org/search-criteria?/and+Gene</a><br>Gephebase= <sup>^</sup> protein phosphatase <sup>^</sup> #gephebase-summary-title) | Gephebase Gene<br>GP00001534 | GepheID<br>Main curator |
| Published   | Entry Status<br>Prigent      |                         |

## PHENOTYPIC CHANGE

|   |  |  |  |
|---|--|--|--|
| Physiology ( <a href="https://www.gephebase.org/search-criteria?/and+Trait">https://www.gephebase.org/search-criteria?/and+Trait</a><br>Category= <sup>^</sup> Physiology <sup>^</sup> #gephebase-summary-title)  | Trait Category   |  |  |
| Xenobiotic resistance (artemisinin) ( <a href="https://www.gephebase.org/search-criteria?/and+Trait=&lt;sup&gt;^&lt;/sup&gt;Xenobiotic resistance (artemisinin)&lt;sup&gt;^&lt;/sup&gt;#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Trait=<sup>^</sup>Xenobiotic resistance (artemisinin)<sup>^</sup>#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 0.52 h   | Trait State in Taxon B   |  |  |
|   | Ancestral State  |  |  |
| Taxon A   | Taxonomic Status   |  |  |
| Intraspecific ( <a href="https://www.gephebase.org/search-criteria?/and+Taxonomic">https://www.gephebase.org/search-criteria?/and+Taxonomic</a><br>Status= <sup>^</sup> Intraspecific <sup>^</sup> #gephebase-summary-title)  |  |  |  |
|   | Taxon A  | Taxon B  |  |
|   | Latin Name   | Latin Name   |  |
| Plasmodium falciparum<br>( <a href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=&lt;sup&gt;^&lt;/sup&gt;Plasmodium falciparum&lt;sup&gt;^&lt;/sup&gt;#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=<sup>^</sup>Plasmodium falciparum<sup>^</sup>#gephebase-summary-title</a> )              | Plasmodium falciparum<br>( <a href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=&lt;sup&gt;^&lt;/sup&gt;Plasmodium falciparum&lt;sup&gt;^&lt;/sup&gt;#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=<sup>^</sup>Plasmodium falciparum<sup>^</sup>#gephebase-summary-title</a> ) | Plasmodium falciparum<br>( <a href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=&lt;sup&gt;^&lt;/sup&gt;Plasmodium falciparum&lt;sup&gt;^&lt;/sup&gt;#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=<sup>^</sup>Plasmodium falciparum<sup>^</sup>#gephebase-summary-title</a> ) |  |
| malaria parasite P. falciparum  | Common Name  | Common Name  |  |
| Plasmodium (Laverania) falciparum; malaria parasite P. falciparum   | Synonyms   | Synonyms   |  |
| species   | Rank   | Rank   |  |
| cellular organisms; Eukaryota; Alveolata; Apicomplexa; Aconoidasida; Haemosporida; Plasmodiidae; Plasmodium; Plasmodium (Laverania)   | Lineage  | Lineage  |  |
| Plasmodium (Laverania) () - (Rank: subgenus)<br>( <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   | Parent   |  |
| 5833<br>( <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   | NCBI Taxonomy ID   |  |
| is Taxon A an Infrappecies?   |  | is Taxon B an Infrappecies?  |  |
| No  |  | No   |  |

## GENOTYPIC CHANGE

|  |                         |   |
|--|-------------------------|---|
| PF3D7_1012700  | Generic Gene Name       | UniProtKB Plasmodium falciparum (isolate 3D7)<br>Q8LJR8 ( <a href="http://www.uniprot.org/uniprot/Q8LJR8">http://www.uniprot.org/uniprot/Q8LJR8</a> ) |
| PF3D7_1012700  | Synonyms                | GenebankID or UniProtKB<br>()   |
| -  | String                  |   |
| -  | Sequence Similarities   |   |
| GO:0008420 : RNA polymerase II CTD heptapeptide repeat phosphatase activity<br>( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0008420">https://www.ebi.ac.uk/QuickGO/term/GO:0008420</a> )   | GO - Molecular Function |   |
| GO:0070940 : dephosphorylation of RNA polymerase II C-terminal domain<br>( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0070940">https://www.ebi.ac.uk/QuickGO/term/GO:0070940</a> )   | GO - Biological Process |   |
| -  | GO - Cellular Component |   |
| No ( <a href="https://www.gephebase.org/search-criteria?/and+Presumptive Null=&lt;sup&gt;^&lt;/sup&gt;No&lt;sup&gt;^&lt;/sup&gt;#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Presumptive Null=<sup>^</sup>No<sup>^</sup>#gephebase-summary-title</a> ) |                         | Presumptive Null  |
|  |                         | 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.Val1157Leu

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 (apicoplast ribosomal protein S10, chloroquine resistance transporter, ferredoxin, kelch 13, kelch 13 (K13), multidrug resistance protein 2) (<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