

GEPHE SUMMARY

	Gephebase Gene	GephelD
Multidrug resistance protein 1 (pvmdr1) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Multidrug resistance protein 1 (pvmdr1)^#gephebase-summary-title)	GP00001482	Main curator
	Prigent	
	Entry Status	
Published		

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)	Trait		
Xenobiotic resistance (mefloquine) (https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic resistance (mefloquine)^#gephebase-summary-title)	Trait State in Taxon A		
Malaria parasite - sensitive	Trait State in Taxon B		
Malaria parasite - resistant	Ancestral State		
Taxon A	Taxonomic Status		
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#gephebase-summary-title)			
Taxon A		Taxon B	
Plasmodium vivax	Latin Name	Plasmodium vivax	Latin Name
(https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Plasmodium vivax^#gephebase-summary-title)		(https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Plasmodium vivax^#gephebase-summary-title)	
malaria parasite P. vivax	Common Name	malaria parasite P. vivax	Common Name
Haemamoeba vivax; malaria parasite P. vivax	Synonyms	Haemamoeba vivax; malaria parasite P. vivax	Synonyms
species	Rank	species	Rank
cellular organisms; Eukaryota; Alveolata; Apicomplexa; Aconoidasida; Haemosporida; Plasmodiidae; Plasmodium; Plasmodium (Plasmodium)	Lineage	cellular organisms; Eukaryota; Alveolata; Apicomplexa; Aconoidasida; Haemosporida; Plasmodiidae; Plasmodium; Plasmodium (Plasmodium)	Lineage
Plasmodium (Plasmodium) () - (Rank: subgenus)	Parent	Plasmodium (Plasmodium) () - (Rank: subgenus)	Parent
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 418103)	NCBI Taxonomy ID	(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 418103)	NCBI Taxonomy ID
5855		5855	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 5855)	is Taxon A an Infraspecies?	(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 5855)	is Taxon B an Infraspecies?
No		No	

GENOTYPIC CHANGE

-	Generic Gene Name	UniProtKB Plasmodium vivax
-	Synonyms	GenebankID or UniProtKB
-	String	
-	Sequence Similarities	
-	GO - Molecular Function	
GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)		
GO:0042626 : ATPase activity, coupled to transmembrane movement of substances (https://www.ebi.ac.uk/QuickGO/term/GO:0042626)		
-	GO - Biological Process	
-	GO - Cellular Component	
GO:0016021 : integral component of membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016021)		Presumptive Null
No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title)		

Molecular Type

Gene Amplification ([https://www.gephebase.org/search-criteria?/and+Molecular Type=%27Gene Amplification%27#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular%20Type=%27Gene%20Amplification%27#gephebase-summary-title))

Aberration Type

Insertion ([https://www.gephebase.org/search-criteria?/and+Aberration Type=%27Insertion%27#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration%20Type=%27Insertion%27#gephebase-summary-title))

Insertion Size

10-100 kb

Molecular Details of the Mutation

37 kb duplication on chromosome 10 that includes pvmdr1

Experimental Evidence

Association Mapping ([https://www.gephebase.org/search-criteria?/and+Experimental Evidence=%27Association Mapping%27#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental%20Evidence=%27Association%20Mapping%27#gephebase-summary-title))

Main Reference

Genomic analysis of local variation and recent evolution in *Plasmodium vivax*. (2016) (<https://pubmed.ncbi.nlm.nih.gov/27348299>)

Authors

Pearson RD; Amato R; Auburn S; Miotto O; Almagro-Garcia J; Amaralunga C; Suon S; Mao S; Noviyanti R; Trimarsanto H; Marfurt J; Anstey NM; William T; Boni MF; Dolecek C; Hien TT; White NJ; Michon P; Siba P; Tavul L; Harrison G; Barry A; Mueller I; Ferreira MU; Karunaweera N; Randrianarivojosua M; Gao Q; Hubbard C; Hart L; Jeffery B; Drury E; Mead D; Kekre M; Campino S; Manske M; Cornelius VJ; MacInnis B; Rockett KA; Miles A; Rayner JC; Fairhurst RM; Nosten F; Price RN; Kwiatkowski DP

Abstract

The widespread distribution and relapsing nature of *Plasmodium vivax* infection present major challenges for the elimination of malaria. To characterize the genetic diversity of this parasite in individual infections and across the population, we performed deep genome sequencing of >200 clinical samples collected across the Asia-Pacific region and analyzed data on >300,000 SNPs and nine regions of the genome with large copy number variations. Individual infections showed complex patterns of genetic structure, with variation not only in the number of dominant clones but also in their level of relatedness and inbreeding. At the population level, we observed strong signals of recent evolutionary selection both in known drug resistance genes and at new loci, and these varied markedly between geographical locations. These findings demonstrate a dynamic landscape of local evolutionary adaptation in the parasite population and provide a foundation for genomic surveillance to guide effective strategies for control and elimination of *P. vivax*.

Additional References

RELATED GEPHE

Related Genes

5 (ABC transporter pvmrp1, Dihydrofolate reductase (pvdhfr), Dihydropteroate synthase (pvdhps), PVX_084940, PVX_101445) (<https://www.gephebase.org/search-criteria?/or+TaxonID=%275855%27/and+Trait=Xenobiotic+resistance/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

present in 19% of Western Thailand samples. Duplication of pvmdr1 has previously been associated with resistance to mefloquine and is homologous to the pfmdr1 amplification responsible for mefloquine resistance in *P. falciparum*.