

GEPHE SUMMARY

	Gephebase Gene		GepheID
Multidrug resistance protein 1 (pvmdr1) (<a +multidrug+resistance+protein+1+(pvmdr1)+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+Multidrug+resistance+protein+1+(pvmdr1)+"#gephebase-summary-title)		GP00001482	
	Entry Status	Prigent	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (<a +physiology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">https://www.gephebase.org/search-criteria?/and+Trait+Category="+Physiology+"#gephebase-summary-title)		Trait	
Xenobiotic resistance (mefloquine) (<a +xenobiotic+resistance+(mefloquine)+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">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 (<a +intraspecific+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status="+Intraspecific+"#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
Plasmodium vivax (<a +plasmodium+vivax+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Plasmodium+vivax+"#gephebase-summary-title)		Plasmodium vivax (<a +plasmodium+vivax+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Plasmodium+vivax+"#gephebase-summary-title)	
	Common Name		Common Name
malaria parasite P. vivax		malaria parasite P. vivax	
	Synonyms		Synonyms
Haemamoeba vivax; malaria parasite P. vivax		Haemamoeba vivax; malaria parasite P. vivax	
	Rank		Rank
species		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Alveolata; Apicomplexa; Aconoidasida; Haemosporida; Plasmodiidae; Plasmodium; Plasmodium (Plasmodium)		cellular organisms; Eukaryota; Alveolata; Apicomplexa; Aconoidasida; Haemosporida; Plasmodiidae; Plasmodium; Plasmodium (Plasmodium)	
	Parent		Parent
Plasmodium (Plasmodium) () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=418103)		Plasmodium (Plasmodium) () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=418103)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
5855 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=5855)		5855 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=5855)	
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Plasmodium vivax
-		B7STB0 (http://www.uniprot.org/uniprot/B7STB0)	
	Synonyms		GenebankID or UniProtKB
-		KX299009.1 (https://www.ncbi.nlm.nih.gov/nuccore/KX299009.1)	
	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 (<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)			

Gene Amplification (https://www.gephebase.org/search-criteria?/and+Molecular+Type=~Gene+Amplification~#gephebase-summary-title)	Molecular Type
Insertion (https://www.gephebase.org/search-criteria?/and+Aberration+Type=~Insertion~#gephebase-summary-title)	Aberration Type
10-100 kb	Insertion Size
37 kb duplication on chromosome 10 that includes pvmdr1	Molecular Details of the Mutation
Association Mapping (https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=~Association+Mapping~#gephebase-summary-title)	Experimental Evidence
Genomic analysis of local variation and recent evolution in <i>Plasmodium vivax</i> . (2016) (https://pubmed.ncbi.nlm.nih.gov/27348299)	Main Reference
Pearson RD; Amato R; Auburn S; Miotto O; Almagro-Garcia J; Amaratunga 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; Randrianarivelosia M; Gao Q; Hubbart 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	Authors
The widespread distribution and relapsing nature of <i>Plasmodium vivax</i> 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 <i>P. vivax</i> .	Abstract
	Additional References

RELATED GEPHE

5 (ABC transporter pvmp1, Dihydrofolate reductase (pvdhfr), Dihydropteroate synthase (pvdhps), PVX_084940, PVX_101445) (https://www.gephebase.org/search-criteria?/or+TaxonID=~5855~/and+Trait=Xenobiotic+resistance/and+groupHaplotypes=true#gephebase-summary-title)	Related Genes
No matches found.	Related Haplotypes

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* .