

GEPHE SUMMARY

	Gephebase Gene		GepheID
ABC transporter pvmrp1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase="ABC transporter pvmrp1"#gephebase-summary-title)	GP00001486		
	Entry Status	Prigent	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category="Physiology"#gephebase-summary-title)			
	Trait		
Xenobiotic resistance (multiresistance to antimalarial drugs) (https://www.gephebase.org/search-criteria?/and+Trait="Xenobiotic resistance (multiresistance to antimalarial drugs)"#gephebase-summary-title)			
	Trait State in Taxon A		
Malaria parasite - sensitive			
	Trait State in Taxon B		
Malaria parasite - resistant			
	Ancestral State		
Unknown			
	Taxonomic Status		
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status="Intraspecific"#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
Plasmodium vivax (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Plasmodium vivax"#gephebase-summary-title)		Plasmodium vivax (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 (strain Salvador I)
PVX_097025		A5KCN4 (http://www.uniprot.org/uniprot/A5KCN4)	
	Synonyms		GenebankID or UniProtKB
PVX_097025		XM_001612630.1 (https://www.ncbi.nlm.nih.gov/nuccore/XM_001612630.1)	
	String		
5855.PVX_097025 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier= 5855.PVX_097025)			
	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)			

Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive Null=~Unknown~#gephebase-summary-title)	Presumptive Null
Unknown (https://www.gephebase.org/search-criteria?/and+Molecular Type=~Unknown~#gephebase-summary-title)	Molecular Type
Unknown (https://www.gephebase.org/search-criteria?/and+Aberration Type=~Unknown~#gephebase-summary-title)	Aberration Type
unknown	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 (Dihydrofolate reductase (pvdhfr), Dihydropteroate synthase (pvdhps), Multidrug resistance protein 1 (pvmdr1), PVX_084940, PVX_101445) (https://www.gephebase.org/search-criteria?/or+Taxon ID=~5855~/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title)	Related Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS

With strong evidence of recent selection in western Thailand and western Cambodia. The signal of selection encompasses 4 genes on chromosome 2 such that we cannot be certain of the specific gene under selection. Pvmp1 is a noteworthy candidate that has been implicated as a drug resistance candidate and whose *P. falciparum* homologues are associated with resistance to multiple anti-malarial drugs