

GEPHE SUMMARY

	Gephebase Gene		GepheID
PVX_084940 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=^PVX_084940^#gephebase-summary-title)		GP00001487	
	Entry Status	Prigent	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=^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+TaxonomicStatus=^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_084940		A5K0T0 (http://www.uniprot.org/uniprot/A5K0T0)	
	Synonyms		GenebankID or UniProtKB
PVX_084940		XM_001616604.1 (https://www.ncbi.nlm.nih.gov/nucore/XM_001616604.1)	
	String		
-			
	Sequence Similarities		
-			
	GO - Molecular Function		
GO:0008308 : voltage-gated anion channel activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008308)			
	GO - Biological Process		
-			
	GO - Cellular Component		
GO:0005741 : mitochondrial outer membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005741)			
			Presumptive Null
Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Unknown^#gephebase-summary-title)			
			Molecular Type

Unknown (https://www.gephebase.org/search-criteria?/and+Molecular+Type=~Unknown^#gephebase-summary-title)	Aberration Type
Unknown (https://www.gephebase.org/search-criteria?/and+Aberration+Type=~Unknown^#gephebase-summary-title)	Molecular Details of the Mutation
unknown	Experimental Evidence
Association Mapping (https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=~Association+Mapping^#gephebase-summary-title)	Main Reference
Genomic analysis of local variation and recent evolution in <i>Plasmodium vivax</i> . (2016) (https://pubmed.ncbi.nlm.nih.gov/27348299)	Authors
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; Randrianarivelojosia 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	
Abstract	
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> .	
Additional References	

RELATED GEPHE

5 (ABC transporter pvmp1, Dihydrofolate reductase (pvdhfr), Dihydropteroate synthase (pvdhps), Multidrug resistance protein 1 (pvmdr1), 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. The signal includes PVX_084940 which encodes a putative voltage-dependent anion-selective channel containing a porin domain proposed to be implicated in antibiotic resistance