

GEPHE SUMMARY

PVX_084940 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=%PVX_084940%#gephebase-summary-title)	Gephebase Gene	GP00001487	GephelD
	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%#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)			
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) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 418103)	Parent	Plasmodium (Plasmodium) () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 418103)	Parent
5855 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 5855)	NCBI Taxonomy ID	5855 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 5855)	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

PVX_084940	Generic Gene Name	UniProtKB Plasmodium vivax (strain Salvador I) A5KoTo (http://www.uniprot.org/uniprot/A5KoTo)
PVX_084940	Synonyms	GenebankID or UniProtKB XM_001616604.1 (https://www.ncbi.nlm.nih.gov/nuccore/XM_001616604.1)
-	String	
-	Sequence Similarities	
GO:0008308 : voltage-gated anion channel activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008308)	GO - Molecular Function	
-	GO - Biological Process	
GO:0005741 : mitochondrial outer membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005741)	GO - Cellular Component	
Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive+Null=%Unknown%#gephebase-summary-title)		Presumptive Null Molecular Type

Unknown ([https://www.gephebase.org/search-criteria?/and+Molecular Type=%5EUnknown%23gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular%20Type=%5EUnknown%23gephebase-summary-title))

Aberration Type

Unknown ([https://www.gephebase.org/search-criteria?/and+Aberration Type=%5EUnknown%23gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration%20Type=%5EUnknown%23gephebase-summary-title))

Molecular Details of the Mutation

unknown

Experimental Evidence

Association Mapping ([https://www.gephebase.org/search-criteria?/and+Experimental Evidence=%5EAssociation Mapping%23gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental%20Evidence=%5EAssociation%20Mapping%23gephebase-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; Randrianarvelosoa M; Gao Q; Hubbard C; Hart L; Jeffery B; Drury E; Mead D; Kekre M; Campino S; Manske M; Cornelius VJ; Maclnnis 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), Multidrug resistance protein 1 (pvmdr1), PVX_101445) ([https://www.gephebase.org/search-criteria?/or+Taxon ID=%5E5855%23gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon%20ID=%5E5855%23gephebase-summary-title))

Related Haplotypes

No matches found.

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