

GEPHE SUMMARY

PVX_101445 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=^PVX_101445^#gephebase-summary-title)	Gephebase Gene	GP00001483	GepheID
Published	Entry Status	Prigent	Main curator

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=^Physiology^#gephebase-summary-title)		Trait Category
Xenobiotic resistance (chloroquine) (https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic resistance (chloroquine)^#gephebase-summary-title)		Trait
Malaria parasite - sensitive	Trait State in Taxon A	
Malaria parasite - resistant	Trait State in Taxon B	
Taxon A	Ancestral State	
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Intraspecific^#gephebase-summary-title)	Taxonomic Status	
Taxon A	Taxon B	
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

PVX_101445	Generic Gene Name	UniProtKB Plasmodium vivax (strain Salvador I)
	Synonyms	A5K913 (http://www.uniprot.org/uniprot/A5K913)
PVX_101445	String	GenebankID or UniProtKB
	Sequence Similarities	XM_001613986.1 (https://www.ncbi.nlm.nih.gov/nucore/XM_001613986.1)
-	GO - Molecular Function	
-	GO - Biological Process	
-	GO - Cellular Component	
GO:0016021 : integral component of membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016021)		
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)		Presumptive Null
Gene Amplification (<a +gene+amplification`#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?and+Molecular+Type=">https://www.gephebase.org/search-criteria?and+Molecular Type=`Gene Amplification`#gephebase-summary-title)		Molecular Type
		Aberration Type

Insertion (https://www.gephebase.org/search-criteria?/and+Aberration+Type=~Insertion~#gephebase-summary-title)	Insertion Size
1-10 kb	
3 kb duplication on chromosome 14 that includes PVX_101445	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; 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	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), Multidrug resistance protein 1 (pvmdr1), PVX_084940) (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

seen only in Papua Indonesia. With strong evidence of recent selection in Papua Indonesia. The signal of selection encompasses 22 genes on chromosome 14 such that we cannot be certain of the specific gene under selection. PVX_101445 appears to be the strongest candidate