

GEPHE SUMMARY

PVX_101445 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^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)	Latin Name	Plasmodium vivax (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Plasmodium+vivax^#gephebase-summary-title)	Latin Name
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 Intraspecies?	No	is Taxon B an Intraspecies?

GENOTYPIC CHANGE

PVX_101445	Generic Gene Name	UniProtKB Plasmodium vivax (strain Salvador I)
PVX_101445	Synonyms	A5K913 (http://www.uniprot.org/uniprot/A5K913)
-	String	GenebankID or UniProtKB XM_001613986.1 (https://www.ncbi.nlm.nih.gov/nuccore/XM_001613986.1)
-	Sequence Similarities	
-	GO - Molecular Function	
-	GO - Biological Process	
-	GO - Cellular Component	
GO:0016021 : integral component of membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016021)		Presumptive Null
No (https://www.gephebase.org/search-criteria?/and+Presumptive+Null=^No^#gephebase-summary-title)		Molecular Type
Gene Amplification (https://www.gephebase.org/search-criteria?/and+Molecular+Type=^Gene+Amplification^#gephebase-summary-title)		Aberration Type

Insertion (<https://www.gephebase.org/search-criteria?/and+Aberration+Type=~Insertion^#gephebase-summary-title>)

Insertion Size

1-10 kb

Molecular Details of the Mutation

3 kb duplication on chromosome 14 that includes PVX_101445

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 *Plasmodium vivax*. (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; Randrianarivelosia M; Gao Q; Hubbard 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 *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 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 Haplotypes

No matches found.

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