

Gephebase Gene		GepheID
Dihydrofolate reductase (pvdhfr) (https://www.gephebase.org/search-criteria?/and+Gene	GP00001484	
Gephebase=~Dihydrofolate reductase (pvdhfr)^#gephebase-summary-title)		Main curator
Published	Entry Status	Prigent

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

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?

DHFR	Generic Gene Name	P00374 (http://www.uniprot.org/uniprot/P00374)	UniProtKB Homo sapiens
DYR; DHFRP1	Synonyms	JN794515.1 (https://www.ncbi.nlm.nih.gov/nucore/JN794515.1)	GenebankID or UniProtKB
9606.ENSPP00000396308 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSPP00000396308)	String		
	Sequence Similarities		
Belongs to the dihydrofolate reductase family.			
	GO - Molecular Function		
GO:0003729 : mRNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003729)			
GO:0008144 : drug binding (https://www.ebi.ac.uk/QuickGO/term/GO:0008144)			
GO:0050661 : NADP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0050661)			
GO:0000900 : translation repressor activity, mRNA regulatory element binding (https://www.ebi.ac.uk/QuickGO/term/GO:0000900)			
GO:0004146 : dihydrofolate reductase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004146)			
GO:0033560 : folate reductase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0033560)			

GO:0005542 : folic acid binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0005542>)
GO:0051870 : methotrexate binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0051870>)
GO:0070402 : NADPH binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0070402>)
GO:1990825 : sequence-specific mRNA binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:1990825>)

GO - Biological Process

GO:0055114 : oxidation-reduction process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0055114>)
GO:0051000 : positive regulation of nitric-oxide synthase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0051000>)
GO:0017148 : negative regulation of translation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0017148>)
GO:0031103 : axon regeneration (<https://www.ebi.ac.uk/QuickGO/term/GO:0031103>)
GO:0046452 : dihydrofolate metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0046452>)
GO:0046655 : folic acid metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0046655>)
GO:0006730 : one-carbon metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006730>)
GO:2000121 : regulation of removal of superoxide radicals
(<https://www.ebi.ac.uk/QuickGO/term/GO:2000121>)
GO:0000083 : regulation of transcription involved in G1/S transition of mitotic cell cycle
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000083>)
GO:0031427 : response to methotrexate
(<https://www.ebi.ac.uk/QuickGO/term/GO:0031427>)
GO:0006729 : tetrahydrobiopterin biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006729>)
GO:0046654 : tetrahydrofolate biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0046654>)
GO:0046653 : tetrahydrofolate metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0046653>)

GO - Cellular Component

GO:0005829 : cytosol (<https://www.ebi.ac.uk/QuickGO/term/GO:0005829>)
GO:0005739 : mitochondrion (<https://www.ebi.ac.uk/QuickGO/term/GO:0005739>)

	Presumptive Null
Unknown (<a +unknown+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Presumptive Null=">https://www.gephebase.org/search-criteria?/and+Presumptive Null="+Unknown+"#gephebase-summary-title)	
	Molecular Type
Unknown (<a +unknown+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Molecular Type=">https://www.gephebase.org/search-criteria?/and+Molecular Type="+Unknown+"#gephebase-summary-title)	
	Aberration Type
Unknown (<a +unknown+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Aberration Type=">https://www.gephebase.org/search-criteria?/and+Aberration Type="+Unknown+"#gephebase-summary-title)	
	Molecular Details of the Mutation
unknown	
	Experimental Evidence
Association Mapping (<a +association="" href="https://www.gephebase.org/search-criteria?/and+Experimental Evidence=" mapping+"#gephebase-summary-title"="">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; 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 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, Dihydropteroate synthase (pvdhps), Multidrug resistance protein 1 (pvmdr1), PVX_084940, PVX_101445) (<a +5855+"and+trait="Xenobiotic" and+grouphaplotypes='true#gephebase-summary-title"' href="https://www.gephebase.org/search-criteria?/or+Taxon ID=" resistance="">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

With strong evidence of recent selection in western Thailand. The signal of selection encompasses multiple genes such that we cannot be certain of the specific gene under selection. A noteworthy candidate also observed in selective sweeps in South America