GENETIC POLYMORPHISIM AND NATURAL SELECTION IN THE C-TERMINAL 42-kDa REGION OF MEROZOITE SURFACE PROTEIN-1 IN *PLASMODIUM FALCIPARUM* MYANMAR ISOLATES

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Background

214 million

There were 214 million new cases of malaria worldwide in 2015.

Source: WHO Facts from World malaria report 2015

438 000

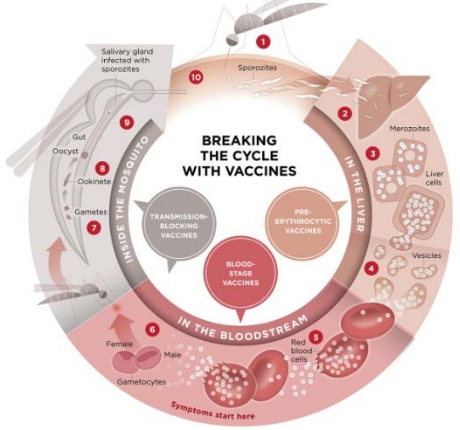
There were 438 000 deaths caused by malaria in 2015.

Source: WHO Fact sheet on malaria

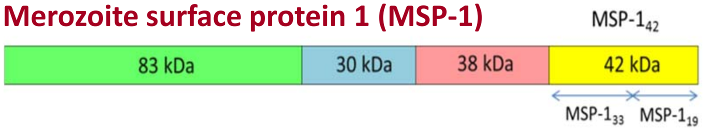
57 countries

Between 2000 and 2015, 57 countries achieved reductions in new malaria cases of least 75%.

Source: WHO Facts from World malaria report 2015



Merozoite surface protein 1 (MSP-1)

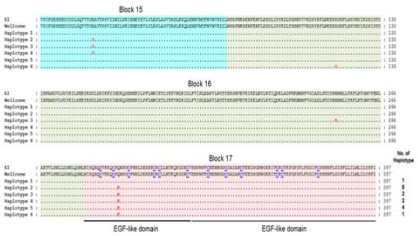


Analyze genetic polymorphism and the effect of natural selection in PfMSP-1$_{42}$ among Myanmar *P. falciparum* isolates

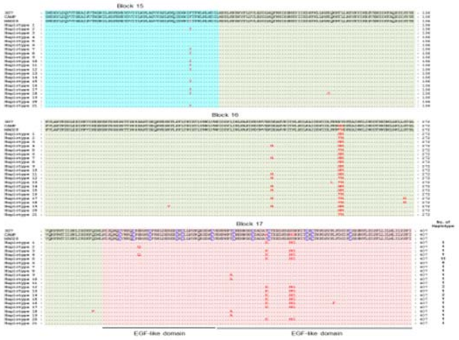
Results

A total of 33 different haplotypes, including K1, 3D7, and RO33 allele types, were identified in Myanmar PfMSP-1$_{42}$

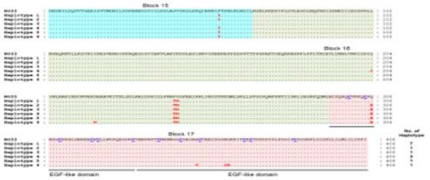
K1 allele types



3D7 allele types



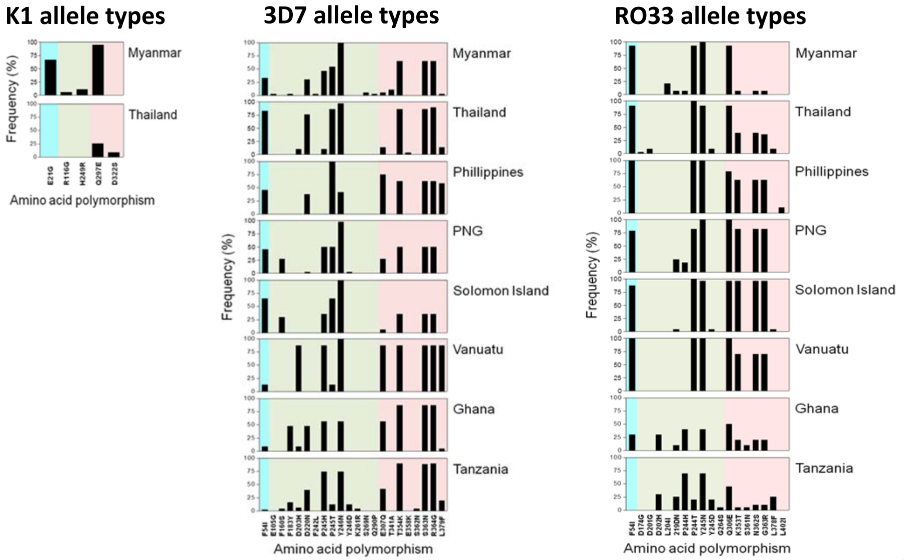
RO33 allele types



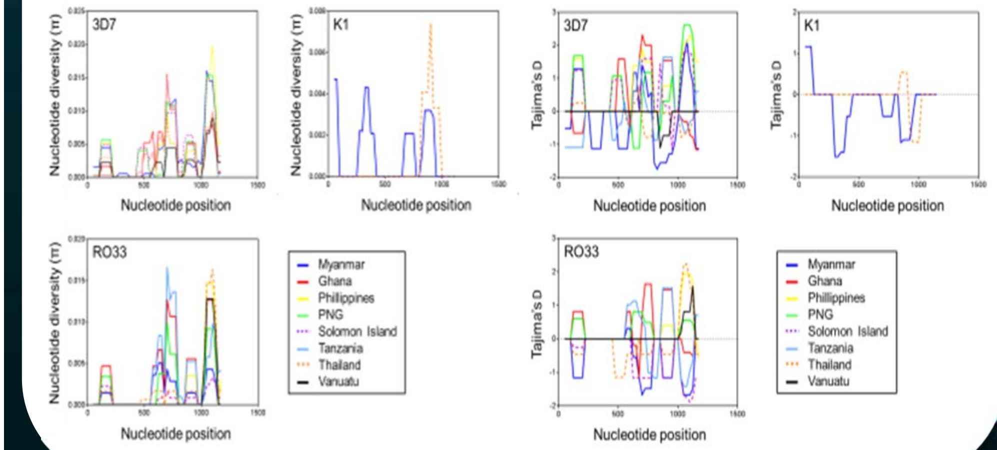
Myanmar PfMSP-1$_{42}$ is under natural selection

Allele type	Fragment	K	H	Hd ± SD	π ± SD	dS-dN	Tajima's D	Fu and Li's D	Fu and Li's F
K1	Block 15	0.4706	2	0.471 ± 0.082	0.0021 ± 0.0004		1.1662 (P>1.10)	0.6669 (P>0.10)	0.9102 (P>0.10)
	Block 16	0.6405	4	0.477 ± 0.134	0.0010 ± 0.0004		- 1.3474 (P>0.10)	- 0.7011 (P>0.10)	- 1.0078 (P>0.10)
	Block 17	0.3203	3	0.307 ± 0.132	0.0009 ± 0.0004		- 1.0963 (P>0.10)	- 0.5522 (P>0.10)	- 0.7978 (P>0.10)
	Full	1.4314	6	0.765 ± 0.080	0.0012 ± 0.0003	0.0012	- 1.0067 (P>0.10)	- 0.5129 (P>0.10)	- 0.7495 (P>0.10)
3D7	Block 15	0.6036	4	0.536 ± 0.066	0.0031 ± 0.0005		0.5012 (P>0.10)	0.7802 (P>0.10)	0.8101 (P>0.10)
	Block 16	1.8799	8	0.769 ± 0.043	0.0027 ± 0.0004		- 0.6520 (P>0.10)	- 2.0169 (P>0.10)	- 1.8602 (P>0.10)
	Block 17	1.8168	6	0.632 ± 0.072	0.0053 ± 0.0006		0.2351 (P>0.10)	- 0.2023 (P>0.10)	- 0.0785 (P>0.10)
	Full	4.3003	21	0.902 ± 0.040	0.0035 ± 0.0003	- 0.0028	-0.1839 (P>0.10)	-1.6252(P>0.10)	- 0.9915(P>0.10)
RO33	Block 15	0.1429	2	0.143 ± 0.119	0.0007 ± 0.0006		- 1.1552 (P>0.10)	- 1.3975 (P>0.10)	- 1.5239 (P>0.10)
	Block 16	0.7912	4	0.571 ± 0.132	0.0012 ± 0.0004		- 1.2220 (P>0.10)	- 1.4143 (P>0.10)	- 1.5541 (P>0.10)
	Block 17	0.5714	3	0.275 ± 0.148	0.0017 ± 0.0011		- 1.7976 (P>0.10)	- 2.2738 (P>0.10)	- 2.4488 (P>0.10)
	Full	1.5055	6	0.736 ± 0.109	0.0012 ± 0.0004	- 0.0015	- 1.7962 (P<0.05)	- 2.2693 (P<0.05)	- 2.4505 (P<0.05)

Myanmar PfMSP-1_{42} showed similar, but not identical amino acid changes to global PfMSP-1_{42}



Global PfMSP-1_{42} showed similar nucleotide diversity across the gene, but different patterns of natural selection



Conclusions

- Myanmar PfMSP-1_{42} showed similar amino acid polymorphism patterns compared to those from other global PfMSP-1_{42}, but not identical.
- The global PfMSP-1_{42} was under a complicated influence of natural selection, in which either balancing selection or purifying selection occurs in each population, depending on the allele types and geography.
- Our results extend our understanding of the genetic nature of the global PfMSP1_{42} population and have significant implication for the development of PfMSP1_{42}-based vaccine.

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