

ELECTRONIC APPENDIX

This is the Electronic Appendix to the article

Selection strength and hitchhiking around two anti-malarial resistance genes

by

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Electronic appendices are refereed with the text; however, no attempt is made to impose a uniform editorial style on the electronic appendices.

SUPPORTING MATERIAL

Table S1. Primer used to amplify microsatellites on Chromosome 4. The positions of oligo sequences are shown in the published sequence of strain 3D7 parasites (Gardner *et al.* 2002). Names marked with asterisks indicate those markers used in the construction of the *P. falciparum* genetic map (Su *et al.* 1999). Three oligos are shown for each microsatellite marker. The first two oligos were used in the first round of amplification (for Laos samples only), while the second two were used in the second round of amplification (for samples from both Laos and Thailand). PCR conditions were as described previously (Anderson *et al.* 1999).

Locus	Primer Sequences	Position in Chr 4		Repeat Structure		Distance from <i>dhfr</i> (kb)
		start	end	(AT) _n	Other	
d_217	ACTACCATATTTATGCCTCT AGAATTTTTAGGGATTAAG TGTGTATCCTTTCTAATATATCG	217085	217265	16		-537.32
d_294	ACAATAAATAAGGCTCTATCA ACTTTTCGAGTGTCTTGTAG GAACAATATTTTCATATATATAATGC	294317	294498	17		-460.09
d_391	TTTAACACACATATAAGGTACA GATTTTAGTTCTGGTCGTAT TAAAGTGATTGTCATTTTTG	391076	391211	13		-363.33
d_613	ATGAACGTTCTATATTGAGT TCTTTATACGAAAATGAAAA CATATAGTGAAAAGACTAAAAA	613129	613332	14		-141.28
C4M39*	AATGGTATGAACGTGATTCA AAAGTAGTCATTGTAATAGC AAGTAGTCATTGTAATAGC	665618	665777	19	A ₂₉	-88.79
C4M40*	GCATTGTGCTTATGTATGAG GTAGCTGTCCGTTTCGAC CAAAAAGAAGAAAAGGGGAAT	696730	696873	14	(ATTT) ₈	-57.68
d_75_0	TTAGTGACAGTGAACAGGTA AAATTTTCAAATCCAATTAC ATCCATGTATATCGAGTTCT	724795	724944	14		-29.61
d_100_1	TTCTACGAATTATTTTTCCA ACAAGTTAAAAGACGAAACA AATAATAGGACACAGAAAATGT	749922	750119	12		-4.49
d_100_4	TAATATTATCCTTTCTGCAA ACAAAAAGAAAATCATCAAA GTCAATAATTTCTGCATCAT	750228	750412	14	A ₂₀ , (ATTT) ₇	-4.18
d_100_8	ACAGTTATAAGATTAATGCAA ACTGATGAAATTGTAAATGA	750540	750739	16		-3.87
d_103_4	ATTGAAACTAGCTCAACAAA	753190	753404	15		-1.22

	TTATAAGATTCCCATAGACA AAGTGAGTAAATATGAATGTGC					
d_104_5	ATATTCCAACATTTTCAAGA ATTTTTGCTTTCAACCTTAC TTTTTACTAGCCATTTTTGT	754308	754479	15		-0.1
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dhfr		754408	756234			
d_106_5	TATGAACAAATGATGACAAA ATTCATGTTCAAGTAAAAA	756254	756429	16		0.2
d_106_8	TAAAGAAGGCATAATTTTCA CATTGAGATAAATAAGTGTTC	756649	756756	17		0.52
d_110_3	CACATATAAATAAATATATCTCGAA TAAATAACCCAAAATCATGT ACCTCTTGAAGTATCATTTTT	760083	760284	18	A ₃₂	4.05
d_112_2	TTGTTTTTGTTAAGTTGTTT GAATATGACACAAATTAGTAGG TTTTTCCTATCTATCATATTGTT	761994	762104	15		5.87
C3M35*	GGAAATATATATCATACTTGG TTTTTGGTGTGCGTTATTTTT TTCATGTGTAAATATAATAAAGTGA	795928	796146	22	(ATTT) ₉	39.91
C4M28*	TTCTACCTATAAGTGTCAAG GGTTAACTAATGCGTATTTAA TGTGAGGCAAAGGGAAAATC	805219	805398	19	A ₂₀ (ATTT) ₆	49.16
C4M15*	GGAATACTCCAAAGGTAATAA GGATATAAAAAATAGGGTTAG TCCCGAAGAAGAAGTTGTCA	877111	877261	21		121.03
d_937	TATTGGATGTCATATTTCAA GCGTTAAAGCATACTAAAT GATATTTCAAATTGGTTACA	937168	937326	15		181.09
d_994	ACTTCTAATATATCATGTAGTATGG TCATATATGCAATGAGAAATA ATAGAAATACTTCCTTCTGAT	994633	994779	12	A ₁₅ (AT) ₇	238.55
d_1055	CAAAATAACGTTTTACTTGA CAAAATTGATATATGCACAC TTCATTGTTTTAATTAGCAT	1055828	1055950	16		299.72

Table S2. Primer used to amplify microsatellites on Chromosome 4. The positions of oligo sequences are shown in the published sequence of strain 3D7 parasites (Gardner *et al.* 2002). Names marked with asterisks indicate those markers used in the construction of the *P. falciparum* genetic map (Su *et al.* 1999). Three oligos are shown for each microsatellite marker. The first two oligos were used in the first round of amplification (for Laos samples only), while the second two were used in the second round of amplification (for samples from both Laos and Thailand). PCR conditions were as described previously (Anderson *et al.* 1999).

Locus	Primer Sequences	Position in Chr 7		Repeat Structure		Distance from <i>dhfr</i> (kb)
		start	end	(AT) <i>n</i>	Other	
CH7_27663	TACATATTTTTGGTTTTTCC AATAATTTTGTTAACACATCG AATGTATCTATCCATTTTATACTT	27663	27991	20		-279.9
CH7_94734	AGTATTAATTATCACTATCCAATT GATAAAGAAGTCGTTTCATGTT CATATGATAAAGAAGTCGTTTC	94734	94846	17		-213.08
CH7_118715	GGAAGAAGCCTTAGATAAAA TTTATAAGGCACACATGAAT GTACATCTTATGGAAGAAGC	118715	118885	14		-189.041
CH7_152697	ATTTATCTATCGCCTTTGTT TGATAAATCATCTGGAACAT ATGTGTGATAAATCATCTGG	152697	152898	17		-155.028
CH7_176413	AATTGTCCAAACAAATAAAA TGATAGGATAAGTTTTTGAA CTCTTAAAATTGTCCAAACA	176413	176587	13		-131.339
CH7_203615	AAAAATATAAATTCATGTGC GGATTTATAATATTCAAAGGA TTATTTAAGATGACTTTTGTAAG	203615	203741	20		-104.185
CH7_228136	ATTTGTTTTATTTTTCACC AAAAGCTGTCAATTTTAAAT CATTGATCCATTTATGATT	228136	228236	11		-79.69
CH7_252695	CGTTTAGTTTTAGAATGCA TTTTATTATGTATACGTGTGT AAGACCGTTTAGTTTTAGAAT	252695	252821	16		-55.105
CH7_278503	TATGTACCCTCAAGTAGACC ATTTATTCATTCCTTTTGT TAGGCATATTCCTTTTATT	278503	278658	10		-29.268
3E7*	AAGAATGAAAGTATTTTATAGC CCCCTTCAAAAAGGAAATAACAC TGCGTAAATTTGATGTAAT	296911	297093	15		-10.833

CH7_303313	GTCAATTTTATTTTGTCT ATACAATTTGGGTGAAA GGTGTCAATTTTATTTGTT	303313	303544	11	-4.382
CH7_304928	TAAAAAGCACCTTATTCATT AAATCGAATTTATTTATCG AATTTCTACTAGTATCATAAACA	304928	305112	15	-2.814
pfcr		307926	311020		
CH7_311610	AATTCATACTGTGTCAAAGG ACCTATTTATCAAAACACCA TAGAAATGAGAAGAAGCAAA	311610	311773	22	0.59
CH7_321409	CGGTATGATTATAATTTGAGA ACATTTAAGAAAAACCCATT GCTCACATCATTCTAACAT	321409	321614	(ATT)12	10.389
CH7_334596	ATCCATACTGCAAAAATAAA TAAATGGAAAGGAGTTTGTA TTAATCCATACTGCAAAAAT	334596	334788	15	23.576
CH7_350596	CACAATCAAATAAAGGAAAG TTTTGTTTGGTACATTTTTC AAACACAATCAAATAAAGGA	350596	350797	11	39.576
CH7_389962	TGTGTTTGTGTATAGACATTTT TGTTTAATGGAATAACAAAAA AATTTGCTACATCCACATT	389962	390069	15	78.942
CH7_414109	TCAGAAATTTTACTTGACC AAAATAACTGTTTTCTTTCT CCATACCATTAATTTGGTT	414109	415067	11	103.089
CH7_441903	ATACCCATGGTTACTACTAAA AGATTGAACGAAAAATATCA ATGCACTGAACAATCTTTAT	441903	442040	11	130.883
CH7_465082	ACGACAAGAAGTAAAACAAA AAAAATAGATAACTAACAATATGC AAAGAACGACAAGAAGTAAA	465082	465246	13	154.062
CH7_503929	TCGAAACTAATGAAAAATTG TTTTGGTTATATTACTTGCA GCTCCATTTAATCGAAACT	503929	504090	15	192.909
CH7_552849	TTATGTTTTCATCGTTTTCT TGTCATATTTGTGAAAGTCA TGTGATTATGTTTTGATCG	552849	553036	19	241.829
CH7_626325	AAACAAAAAGGTACACACAC ACTGTTTCAGGTAATACACG TCCCTTCTAAAAAGTTTACAT	626325	626544	13	315.305

CH7_699177	CTCTTTTTCTTTCTCTTTT ACGACGGTATGAAATAAATA TTC AATGGTAATAAATCGAG	699177	699415	21	388.157
CH7_779523	TTGTAATGTTGTCATGTTGT CCGTTTATATATTCAGCTTG TGATATTTTAAGGAATCGAC	779523	779693	10	468.503

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