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Supplementary appendix

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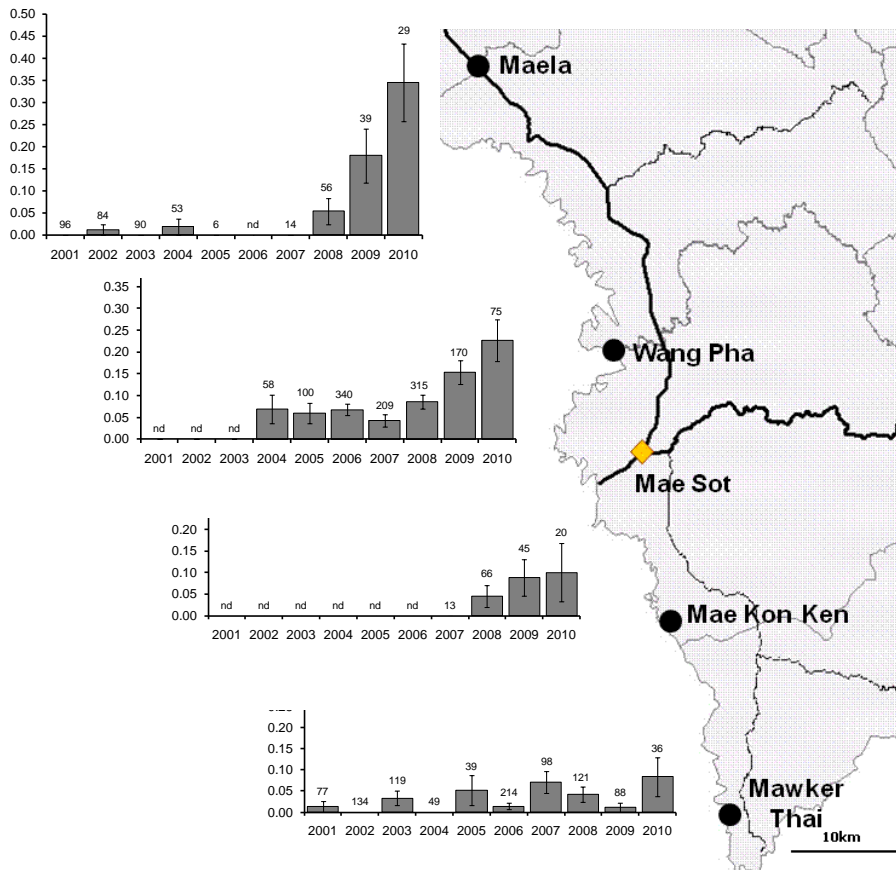
APPENDIX MATERIAL

Emergence of artemisinin-resistant malaria on the western border of Thailand: a longitudinal study

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Appendix 1. Geographical variation in $t_{1/2} P$. The section of the Thai-Myanmar border containing the four study clinics is shown, with bar charts showing changes in the proportions of slow clearing parasites ($t_{1/2} P \geq 6.2$ hrs) from 2001-10. Years in which no patients were treated are marked “nd”. There is a sharp rise in proportions of slow clearing parasites in clinics north of Maesot between 2008-10.

MAL13-2158308	TTATTTTGTGTTGAATATATATCAACTCTTTGATGCATGTTCTGAAATTTTAAAGTAA[A/T]CTTTTTTTTTTTTATTCATGTCAATTTTCTGTCCAGTTCGTTTCATATATGATTTTGCA	13	2158308	A	0.26
MAL13-2570163	TATTAATTTAAAAGAATTTTTGAGTTCAAAAAAAGTATTTCATCTAAATTTGATTTTC[A/C]ATTATTGATTTAAAACATTTGATCAGAACAGTTCCTAGAGAAATTTAAATATTCATTATCT	13	2570163	A	0.46
*MAL14-990875	AGTAGTGTCTATAACAACATGCATCATAATATAAATCATCAAGAAAATTA[T/C]AGAAATCAAAACAGCTATAGCCACTTTTCGGTCAATGGTAGCTATATCGA	14	990875	G	0.32
MAL14-1199184	TACAGTATATACTTTAAATATCTGTACCAAGGTAGATAAAAAATCTTCATATATATATGT[A/T]CCATTAGTTCGAACTTTATGTATTTCTGGACAATATTCACACTCCTATCCTTAATTTTA	14	1199184	A	0.38
MAL14-1458321	TAGTTGAATATGCTGAAGAGGTAGAATTAAGAAGAAGGTTGAAAAACATTTATGGGAG[A/G]AAAAGTTAATATGACAGAGAATCCGAGTGTTTTACATACAGCTTTAAGAATACCCATAGA	14	1458321	G	0.45
MAL14-1757546	AGAGGTACATATTAATAGATTTTTTAAATGAAAAATAGTAATAAAAAAATGTAACGCATG[A/G]TGATAGTGTATTACCAATGGTAATGAAACGGACGCGAAAAAATGTTGATGAGAATAA	14	1757546	A	0.32
MAL14-1853537	ATATGCTCGTATATCATTCAAAAATTAAGATGCATGATTATATCTGTAATAAGATGAGT[A/G]ACATTTATAAATACACAATTCAAATTTTTTAACATTTCAACAGGACTATTATTCAGGTAT	14	1853537	A	0.36
MAL14-3017684	ACACATCCAGAGGAGAGTATTTTCATCTTGAATAAGTCAATCCGTTAAACATTTCTGAAGAG[A/T]AGATCTATCTTTCTTTATCCAATAAAACATTTTCTCTCGGTTTCATATCATGAAGCGG	14	3017684	T	0.37
MAL14-3124926	TGTGAAGAAGAAAAGAATTAATGGGAGCAGCTGGAGGAAGATATGTCGAAGAAGAGGTA[C/G]AGGGAGCAGTTGGAGGAAGAAATGTTGATGAAGAGGTAGAGGGAGCAGTTGGAGGAAGAA	14	3124926	C	0.34

Appendix 3. Age structure of patient population

Age category (yrs)	Frequency	Percent
<5	666	20.8
5-15	1109	34.63
≥15	1427	44.57
Total	3202	100

Appendix 4. Multiple regression analysis of t1/2P, stratified by location. Locations (from North to South) are Maela (MLA), Wang Pha (WPA), Mae Khon Ken (MKK) and Mawker Thai (MKT). The influence of patient age, prior malaria exposure, gender and sampling date on log t1/2P were examined using least squares regression in (A) all samples and (B) only patients with clearance data showing a good fit to a linear model ($r^2 \geq 0.8$). In both analyses sampling date strongly influences t1/2P in three of the four locations (black shading, white text). Significance of associations with patient age, gender and malaria exposure do not fall below $p=0.025$ and fail to reach Bonferroni corrected table-wide significance levels ($0.05/16=0.003$) in both analyses.

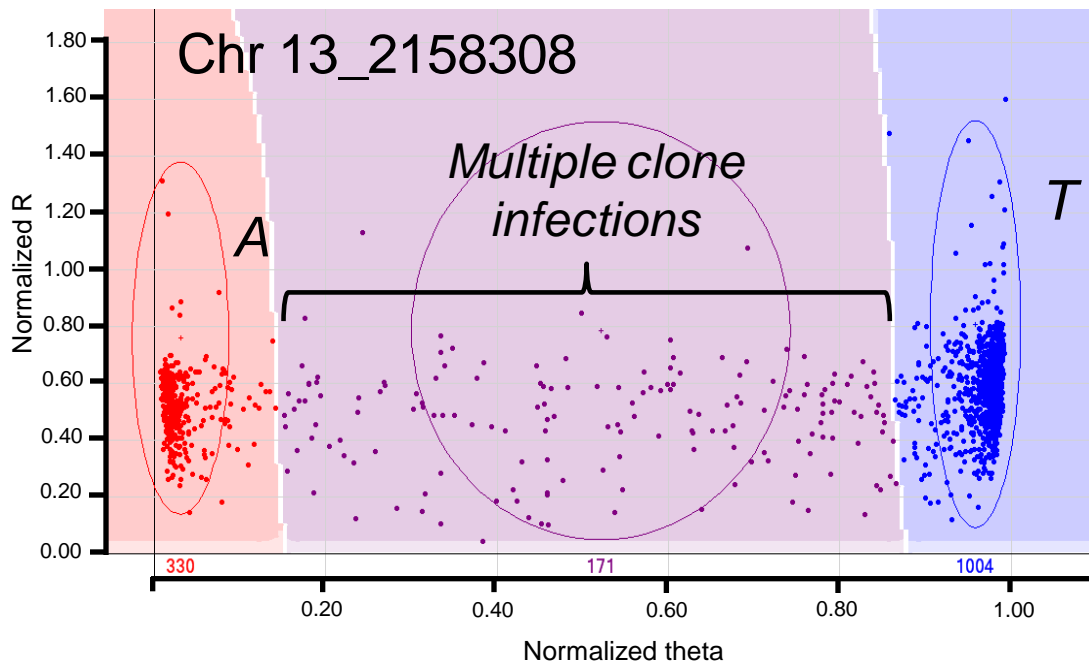
(A) t1/2P measures calculated from slopes with $r^2 > 0.8$ only

	MLA	n=433	WPA	n=1244	MKK	n=141	MKT	n=931
	F	p	F	p	F	p	F	p
Admission Date	82.834	8.9E-20	12.678	3.7E-04	0.943	0.332	14.123	1.7E-04
Age (yrs)	1.440	0.230	2.686	0.101	0.232	0.630	0.005	0.944
Malaria exposure ¹	0.016	0.899	2.457	0.117	0.287	0.592	4.512	0.034
Gender	3.301	0.069	0.639	0.424	1.827	0.176	0.748	0.387

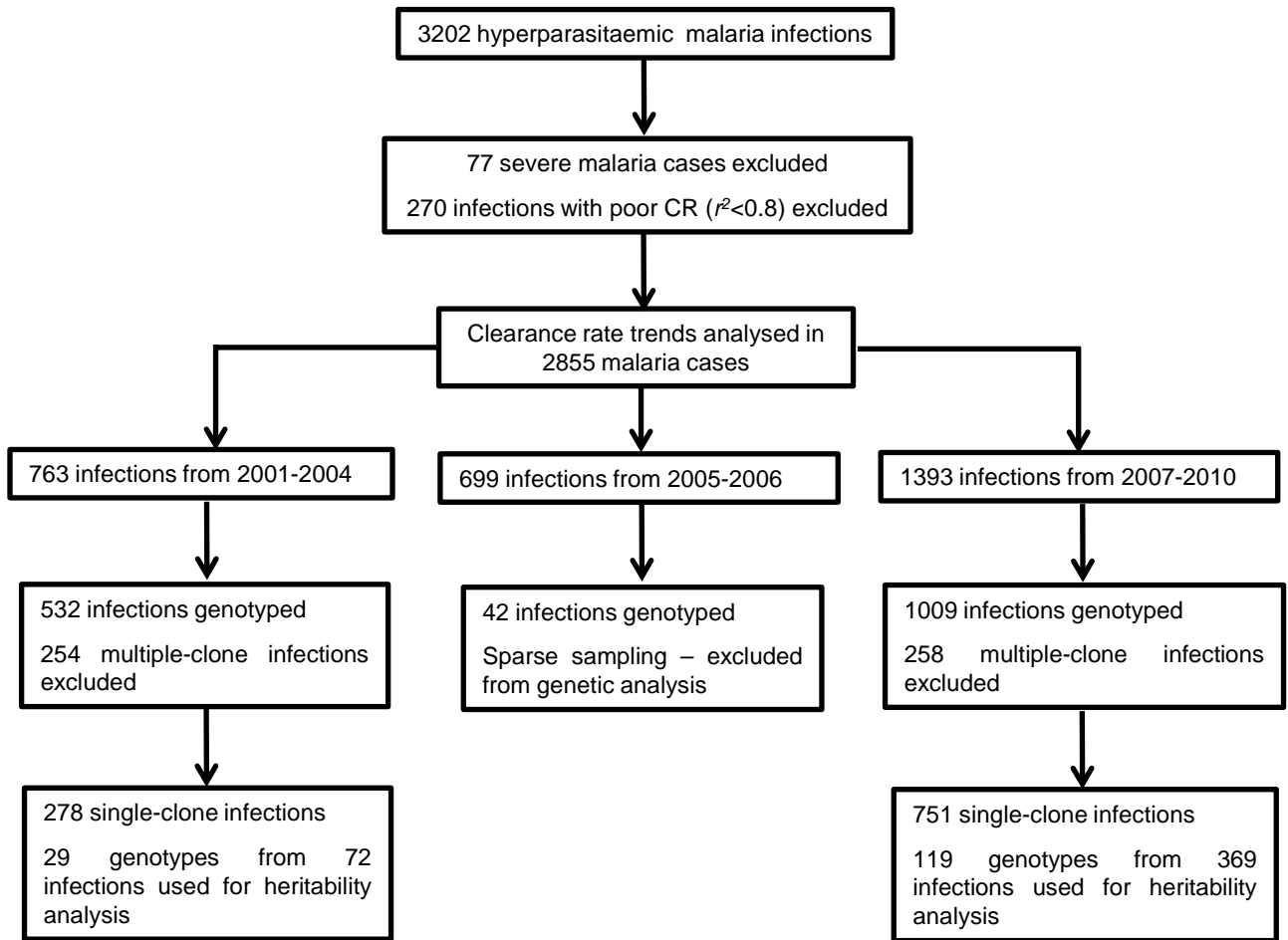
(B) All data

	MLA	n=444	WPA	n=1346	MKK	n=150	MKT	n=1038
	F	p	F	p	F	p	F	p
Admission Date	79.154	5.7E-19	13.430	2.5E-04	0.292	0.589	13.572	2.3E-04
Age (yrs)	1.722	0.189	1.121	0.290	0.441	0.507	0.341	0.559
Malaria exposure ¹	0.003	0.956	4.086	0.043	0.255	0.614	3.945	0.047
Gender	5.006	0.025	0.661	0.416	2.605	0.107	0.028	0.867

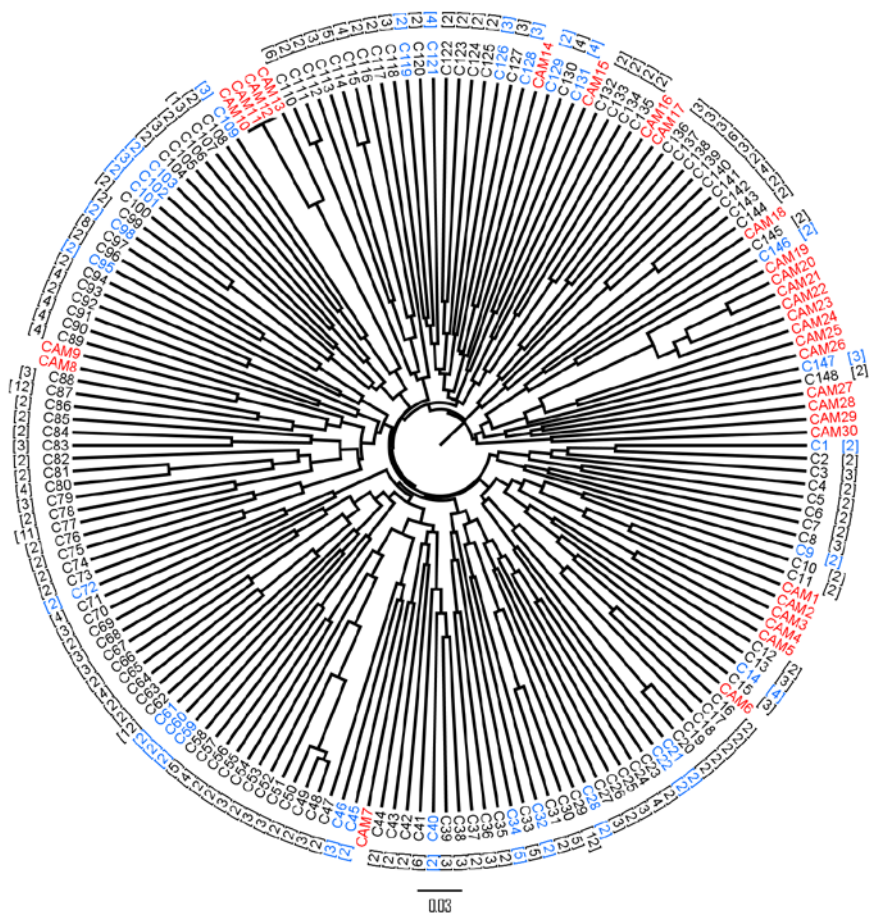
¹Malaria exposure was defined by a documented malaria episode prior to the current episode.



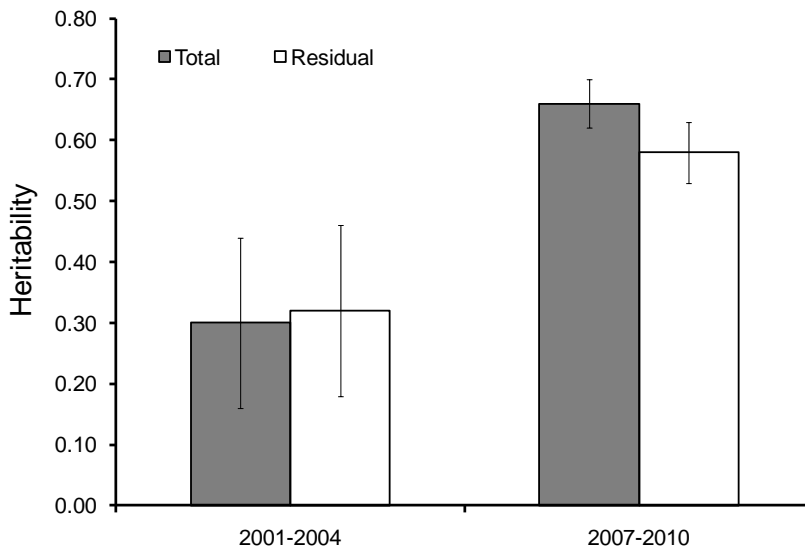
Appendix 5. Genotyping data for one SNP. A typical SNP graph for the A/T SNP on chromosome 13, position 2158308, showing clustering of samples based on their genotypes. Genotype calls are made based on the normalized ratio of fluorescence intensity signals for the “A” and the “B” allele in the sample. The X-axis shows Norm Theta values, which correspond to the composition of the “B” allele in each sample. Multiple-clone infections are easily identified and were excluded from CR heritability analysis.



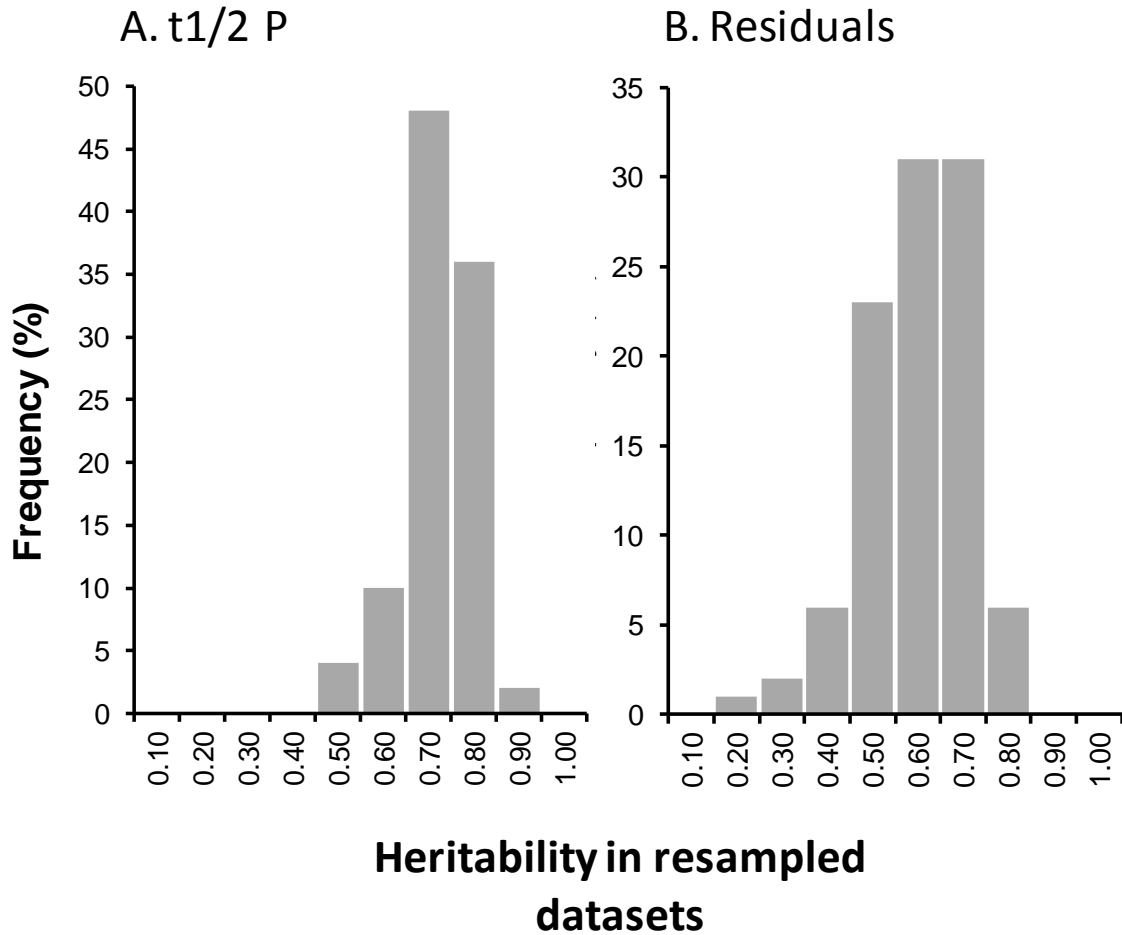
Appendix 6. Sampling breakdown for epidemiology and genetic analyses. Exclusion criteria are detailed in the text. The flow chart details how parasites with identical 93-locus genotypes infecting multiple patients were identified in the data set.



Appendix 7. Genetic relatedness among parasites. The tree shows the relatedness among 148 93-locus parasite genotypes infecting 441 patients. Blue genotype labels indicate infections collected between 2001 and 2004, black labels those collected from 2007-2010, while red labels show 30 infections from Cambodia. The numbers of patients infected with each genotype are shown in square brackets.



Appendix 8. Change in heritability of clearance rates on the Thai-Myanmar border. The proportion of variation in $t_{1/2} P$ that is due to parasite genetic factors (heritability) is shown for 2001-4 and 2007-10 time windows. Grey bars show heritability of $t_{1/2} P$, while white bars show heritability analysis of residuals after removing effects of significant covariates. The error bars are 1 SD. The increase in heritability observed between 2001-4 and 2007-10 periods were tested by permutation (Appendix 9) and were significant for both $t_{1/2} P$ ($p < 0.01$) and residuals ($p = 0.04$).



Appendix 9. Permutation-based comparison of heritability in 2001-4 and 2007-10. In 2001-4, 29 groups of patients are infected with indistinguishable parasite genotypes, while in 2007-10, there were 119 groups. We randomly resampled 250 patients from 2007-10 generating samples containing on average 29 parasite genotypes infecting >1 patient. This resampling exercise provides a direct comparison with the 2001-4 period. Heritability estimates from 100 resampled 2007-10 datasets (range=0.48-0.85 exceeded that observed in 2001-4, demonstrating that the observed increase in H^2 is significant ($p < 0.01$). For residuals (following removal of effects of covariates) all but 4 resampled datasets exceeded H^2 values for 2001-4 ($p = 0.04$). These analyses are shown below. The frequency distribution shows H^2 values from 100 resampled 2007-10 datasets for A. $t_{1/2}P$ measures and B. residuals.