SUPPLEMENTAL MATERIALS

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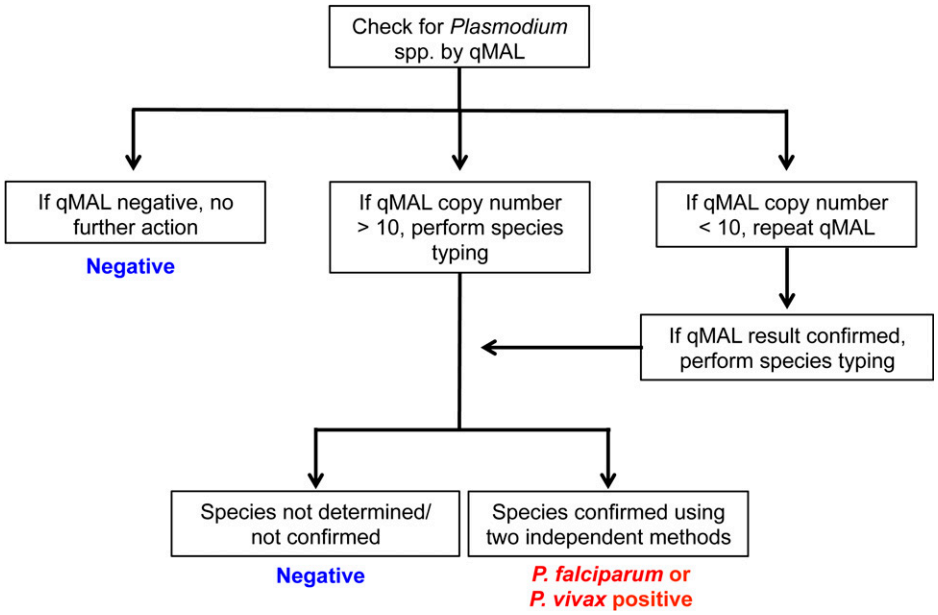
Nested single-species polymerase chain reaction. Single-species nested polymerase chain reaction (PCR) was used to detect the presence of *Plasmodium falciparum*, *Plasmodium vivax*, *Plasmodium ovale*, *Plasmodium malariae*, and *Plasmodium knowlesi*. The primary PCR used two genus-specific primers corresponding to the 18S rRNA, P1F: 5′-ACG ATC AGA TAC CGT CGT AAT CTT-3′ and P2R: 5′-GAA CCC AAA GAC TTT GAT TTC TCA T-3′ (expected size of PCR product is around 140–160 bp). The nested PCR was then performed using P1F and a species-specific reverse primer, *P. falciparum* 5′-CAA TCT AAA AGT CAC CTC GAA AGA TG-3′, *P. malariae* 5′-AAG GAA GCT ATC TAA AAG AAA CAC TCA T-3′, *P. ovale* 5′-ACT GAA GGA AGC AAT CTA AGA AAT TT-3′, *P. vivax* 5′-CAA TCT AAG AAT AAA CTC CGA GAG GAA A-3′, or *P. knowlesi* 5′-CTG AAG GAA GCA ATC TAA GAG TTC-3′ (expected size of PCR product is 110 bp).

Genotyping *P. vivax* parasites. The multiplex primary PCR was done in a total volume of 15 μL, containing 4 μL genomic DNA, 7.5 μL 2× Gotaq® Green Master Mix (Promega, Madison, WI), 0.6 μL each primer (0.2 μM), and 1.1 μL nuclease free water. Primers: *msp1*F3_PF 5′- GGA GGA CAT AAG CTA CCT GCT C-3′, *msp1*F3_PR 5′- GTT GTT ACT TGG TCT TCC TCC C-3′, MS2_PF 5′- AGC ACG ACC AAC AAG AGA GG-3′ and MS2_PR 5′- TGG GGA GAG ACT CCC TTT TC-3′. For the individual nested PCRs, 1 μL primary PCR product was used. The forward primers for the nested PCRs were labeled with fluorescent dyes: VIC for *msp*1F3 and 6FAM for MS2. Primers: *msp1*F3_NF 5′-VIC-CAA GCC TAC CAA GAA TTG ATC CCC AA-3′, *msp1*F3_NR 5′-ATT ACT TTG TCG TAG TCC TCG GCG TAG TCC-3′, MS2_NF 5′-6FAM-GAG CTA GCC AAA GGT TCA ACA-3′, and MS2_NR 5′-TGG GGA GAG ACT CCC TTT TC-3′. Cycling conditions were as follows: initial denaturation 95°C for 1 minute, then 35 cycles (primary PCR) or 25 cycles (nested PCR), with 30 seconds denaturation at 95°C, 45 seconds annealing at 59°C, and 1 minute extension at 72°C plus a final extension of 5 minutes at 72°C. Final products were subjected to capillary electrophoresis using the Genescan Service at Macrogen (Seoul, Korea) (ABI3730XL capillary analyzer) with results analyzed using Peak Scanner v1.0 (Applied Biosystems, Foster City, CA).

***CYP2D6* genotyping.** The CYP2D6 genotyping assay is able to identify the following alleles: normal function *1, *2, *35; decreased function *9, *10, *17, *29, *41; loss of function *3, *4, *5, *6, *7, *8, *11, *15; and duplications. The CYP2D6 alleles were scored as follows: loss of function alleles, 0; decreased function alleles, 0.5; and normal function alleles, 1. Duplicated alleles were assigned two times the appropriate score. The predicted phenotypes were assigned according to the rule-base system of the Luminex xTAG CYP2D6 Kit v3: poor metabolizer phenotype was assigned to two loss of function alleles; intermediate metabolizer was assigned to two decreased function alleles, or a loss of function allele with a decreased function allele; extensive metabolizer was assigned to two normal function alleles, or one normal function allele with one decreased or loss of function allele; ultrarapid metabolizer was assigned when there was duplication of normal function alleles.[1]

SUPPLEMENTAL REFERENCE

1. Vanwong N, Ngamsamut N, Hongkaew Y, Nuntamool N, Puangpetch A, Chamnanphon M, Sinrachatanant A, Limsila P, Sukasem C, 2016. Detection of CYP2D6 polymorphism using Luminex xTAG technology in autism spectrum disorder: CYP2D6 activity score and its association with risperidone levels. *Drug Metab Pharmacokinet 31:* 156–162.



SUPPLEMENTAL FIGURE 1. Flow-chart used for detection and classification of malaria infections during the 9-month follow-up period.