Supplementary data

**Figure legends**

Supplementary Figure 1. Phylogenic trees describing the relationships of the pvs25 and Pks25 alleles detected in this study compared to sequences available in Genbank. The evolutionary history was inferred by using Maximum Likelihood method based on the Tamura-Nei model. Number of substitutions per site is indicated by the scale bar. Bootstrap values were calculated for 1000 replications. Phylogenetic analysis was conducted by using MEGA6.06. Scale bar indicates nucleotide substitutions per site.

**Table**

Supplementary Table 1 Results of the collection, dissections and PCR processing of *Anopheles dirus* mosquitoes caught by human landing catch in the study area

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Year | Period | No. caught | No. night | Biting density\* | No. dissected | No. sporozoites | % |
| 2008 | Jan to Dec | 2120 | 724 | 2.9 | 2119 | 22 | 1.0 |
| 2009 | Jan to Dec | 2856 | 676 | 4.2 | 2848 | 32 | 1.1 |
| 2010 | Jan to Feb | 667 | 140 | 4.8 | 666 | 16 | 2.4 |
| Jan 2008 to Feb 2010 | | 5643 | 1540 | 3.7 | 5633 | 70 | 1.2 |

\*Biting density, average human-biting density (No. of caught / No. of caught person-night)