IKONOS-DERIVED MALARIA TRANSMISSION RISK IN NORTHWESTERN THAILAND

Ratana Sithiprasasna[1], Donald M Ugsang[2], Kiyoshi Honda[2], James W Jones[1]
and Pratap Singhasivanon[3]

[1]Department of Entomology, US Army Medical Component, Armed Forces Research Institute of Medical Sciences, Bangkok; [2]Space Technology Applications and Research Program, Asian Center for Research on Remote Sensing, Asian Institute of Technology, Pathum Thani; [3]Department of Tropical Hygiene, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand

Abstract. We mapped overall malaria cases and located each field observed major malaria vector breeding habitat using Global Positioning System (GPS) instruments from September 2000 to October 2003 around the three malaria-endemic villages of Ban Khun Huay, Ban Pa Dae, and Ban Tham Seau, Mae Sod district, Tak Province, Thailand. The land-use/land-cover classifications of the three villages and surrounding areas were performed on IKONOS satellite images acquired on 12 November 2001 with a spatial resolution of 1 x 1m. Stream network was delineated and displayed. Proximity analysis was performed on the locations of the houses with and without malaria cases within a 1.5 km buffer from *An. minimus* immature mosquito breeding habitats, mainly stream margins. The 1.5 km used in our proximity analysis was arbitrarily estimated based on the *An. minimus* flight range. A statistical *t*-test at 5% significance level was performed to evaluate whether houses with malaria cases have higher proximities to streams than houses without malaria cases. The result shows no significant difference between proximity to streams between houses with malaria cases and houses without malaria cases. We suspect that the actual flight range of *An. minimus* may be greater than 1.5 km. The *An. minimus* larval habitat deserves more detailed investigation. Further studies on human behavior contrary to that required for adequate malaria control among these three villages are also recommended.

INTRODUCTION

Malaria transmission is associated with location since the disease is focused around specific mosquito breeding sites and can be transmitted within certain distances from them. There is also a clustering of people with malaria parasites and clinical symptoms at particular locations. In low endemicity areas, the level of malaria risk may vary between households because of their location and other characteristics that affect contact between humans and vectors. Information on the distribution of malaria on the ground can permit controls to be targeted towards the foci of transmission and the locations of high malaria risk. Such targeting can greatly increase the effectiveness of control measures. Exclusion of these locations can cause the failure of control measures. Computerized mapping and management of location data using Geographical Information Systems (GIS) and remote sensing can assist the targeting of control measures against malaria at the focal and household levels, leading to effective control.

Control of malaria in Thailand presents a significant challenge. Targeting the populations at greatest risk can increase the effectiveness of interventions. Risk of malaria, as measured by parasite prevalence, estimated annual malaria incidence, and risk of clinical illness, has been shown to increase with mosquito exposure (Trape *et al,* 1992, 1993; Thompson *et al,* 1997; Staedke *et al,* 2003). Some data suggest that parasite prevalence (Thomas and Lindsay, 2000) and clinical illness (Clarke *et al*, 2002) are less common in more frequently exposed children, possibly due to acquired immunity. GPS and GIS technology coupled with clinical data can be

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Correspondence: Pratap Singhasivanon, Department of Tropical Hygiene, Faculty of Tropical Medicine, Mahidol University, 420/6 Rajvithi Road, Bangkok 10400, Thailand.
Tel: 66 (0) 2644-7483
E-mail: tmpsh@mahidol.ac.th

used to identify geographic areas at greatest malaria risk (Carter *et al*, 2000). In this study, GPS and GIS were used to map the location of households in three villages in northwestern Thailand in Mae Sot district, Tak Province: Ban Khun Huay, Ban Pa Dae, and Ban Tham Seau. The three Karen villages are located about 20 km east of the city of Mae Sot near the Myanmar border. We examined the relationship between the location of the residence and the incidence of clinical episodes of malaria.

This study is part of a longitudinal study described elsewhere (Sithiprasasna *et al*, 2003 a,b). *An. minimus* has been implicated as a vector for malaria based on the detection of sporozoites using ELISA for *P. falciparum* and *P. vivax*. The vectorial capacities and entomological inoculation rates were calculated. *An. dirus* was encountered rarely and probably played little part in transmission in these three villages during the study period. Information obtained provided on nightly biting activity, parity rate, infectivity, and adult and larval bionomics. Spatial and temporal comparisons were displayed on different satellite images, including the Normalized Difference Vegetation Index data from the National Oceanographic and Atmospheric Administration satellites (NOAA/NDVI), the LANDSAT satellite Thematic Mapper and the IKONOS satellite in a GIS. We sampled 291 bodies of water for *Anopheles* larvae around the three malaria-endemic villages and modeled surface slope and wetness indices to identify the extent and

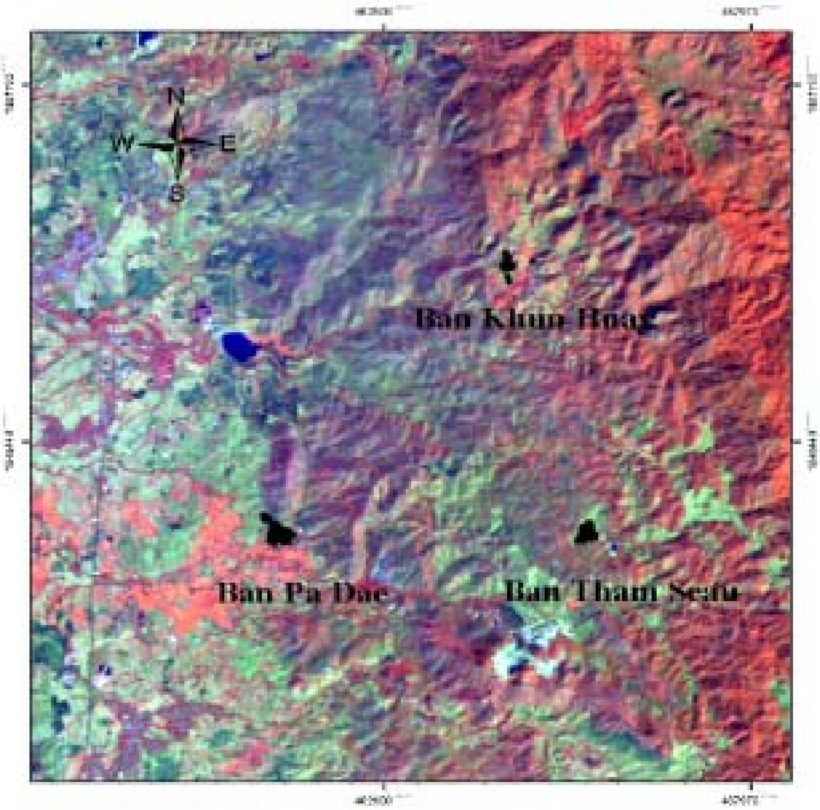

Fig 1–Locations of each house (black dot) in three villages utilizing Global Positioning System data overlaid on LANDSAT 5 Thematic Mapper data dated 22 January 1999 (band combination 4, 5, 2).

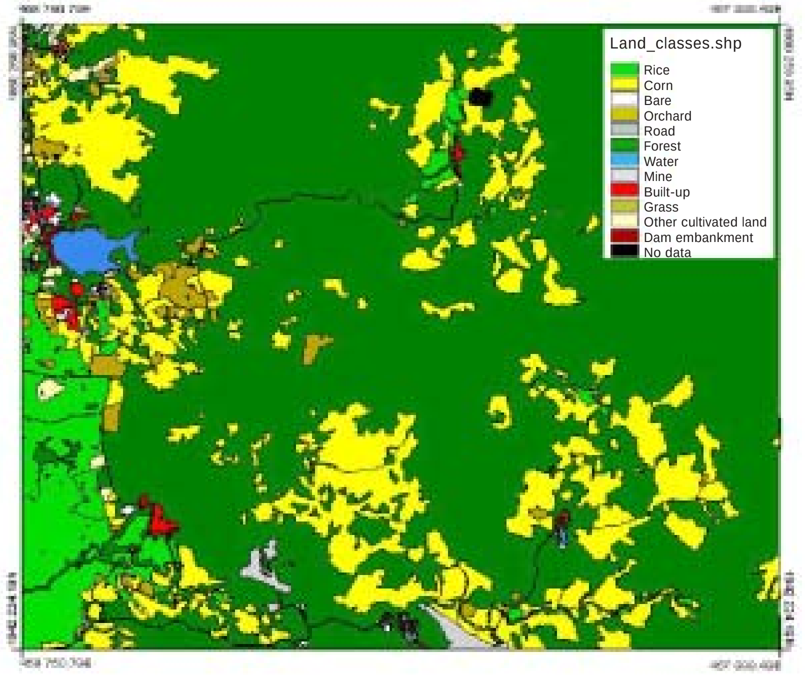

Fig 2–Classified IKONOS image showing land-use/land-cover of the study area.

spatial pattern of potential breeding habitats of the major malaria vectors *An. dirus, An. maculatus, An. minimus*, and *An. sawadwongporni* by digitizing base topographical maps of the study site.

Malaria is a complex disease. Its severity is a function of the interaction between the *Anopheles* mosquito vector, the parasite, the host, and the environment. Different mosquito species have different habitat preferences, such as rice fields, plantations, forests, forest fringes, and foothills. Many of these features can be identified on satellite images (Sithiprasasna *et al*, 2003a,b). Immature stages of mosquitos are found in a variety of aquatic habitats, but larval surveys are expensive, time-consuming, and cumbersome. As an alternative to the traditional ground-based survey approach to vector surveillance, this study used a combination of remote sensing (RS) and GIS technologies to develop landscape predictors of anopheline abundance, which is considered an indicator of potential human vector contact and malaria transmission risk. Satellite data can be used to map the extent and condition of environmental factors pertinent to malaria transmission over space and time.

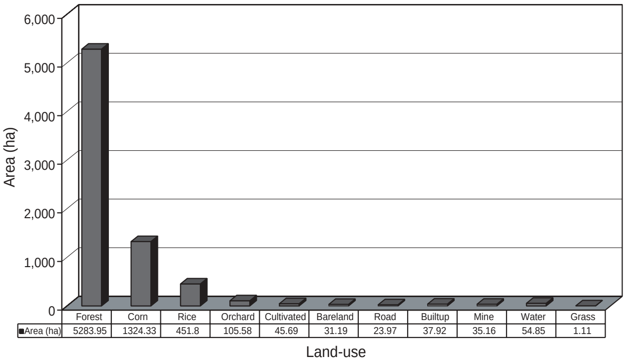

Fig 3–Land-use/land-cover and their respective total area in hectares.

Passive instruments on satellites measure only radiation (reflected light or emitted energy), therefore observations include the vegetation index, surface temperature, and cloud temperature. These are used to determine the ecological conditions on the ground and assess information regarding ecological variables relevant to malaria control. Low spatial resolution satellite data, such as from NOAA (National Oceanographic and Atmospheric Administration) and Meteosat, are available at a scale and frequency of observation which can cover a large area. NOAA satellite data are commonly used to monitor changing ecological conditions over multiple years since data are available from 1981 to the present (Linthicum *et al,* 1999; Anyamba *et al,* 2002). High spatial resolution satellite data (such as LANDSAT, IKONOS) can provide up-to-date detailed spatial mapping which can be used as a source of spatial baseline mapping (Pope *et al*, 1992; Sithiprasasna *et al,* 2003a,b). Fine spatial resolution data acquired by remote sensing has been used in several studies to estimate adult mosquito numbers (Beck *et al*, 1994, 2000; Rejmankova *et al*, 1995; Roberts *et al*, 1996; Sithiprasasna *et al*, 2003a,b). We adopted this approach to estimate variations in cases in geographical area. This allowed us to examine variation in the relationship between exposure and infection. The spatial resolution is important because the user must determine which data are appropriate for a particular application. IKONOS, with a high resolution of 1 m (pixel size of 1 by 1 m), and LANDSAT Thematic Mapper, with a high spatial resolution of 30 m (pixel size of 30 by 30 m), can be used to map objects in detail and characterize land use in an area. Recent developments in the access of remotely sensed vegetation and weather data, and their analysis along with other data sources within a GIS, have opened new possibilities in malaria stratification, monitoring, and early warning.

MATERIALS AND METHODS

Study area

Mosquitos were collected in 3 villages in Mae Sot district, Tak Province (Fig 1). Ban Khun Huay, Ban Pa Dae, and Ban Tham Seau are Karen villages, located about 20 km east of the city of Mae Sot near the Myanmar border with Thailand.

Mosquito collection

Adult mosquito collections were conducted monthly from August 2001 to December 2003 on human bait made between 18 00 and 06 00 hours. All anopheline mosquitos were captured and the time of collection recorded. All collections were conducted using a standard method to permit temporal and spatial comparisons between collections and statistical evaluation. All mosquitos were tested for *P. falciparum* and *P. vivax* CS antigen using the enzyme-linked immunosorbent assays (ELISA). Larval collections were made in and around the study area to determine the types and abundance of habitats where anophelines occur. Geographical coordinates for all larval habitats were recorded using a Trimble GPS GeoExplorer III. Mosquito larvae were reared to adults, and identified as to species.

Satellite data

LANDSAT Thematic Mapper, (dated 22 January 1999) with a spatial resolution of 30 x 30 m, and IKONOS images, (dated 12 November 2001) with a spatial resolution of 1 x 1 m, of the three villages and surrounding area were acquired and used in GIS using ERDAS (2002) and ENVI (2000) software.

Thematic maps were generated using ArcGIS 8.3 (ESRI, 2001-2002) software. RS-based GIS included spatial and temporal data in the form of geographic coverage and descriptive information in the form of relational databases associated with the mapped features.

Land-use/land-cover classification

Visual interpretation of the IKONOS images was based on the results of a ground survey and other ancillary data. A to-

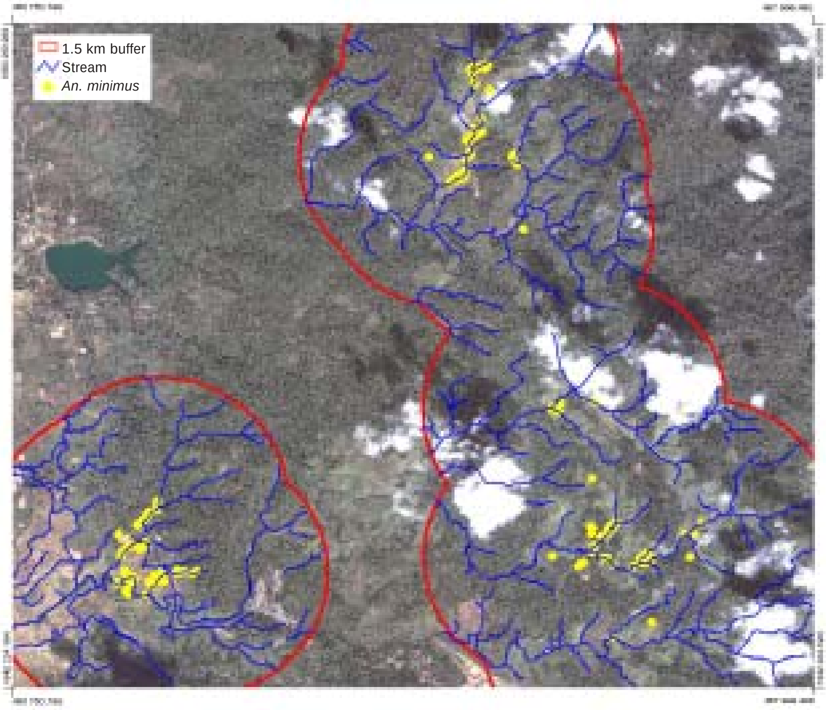

Fig 4–Stream network within 1.5 km buffer of *An. minimus* larval habitats displayed in yellow dots.

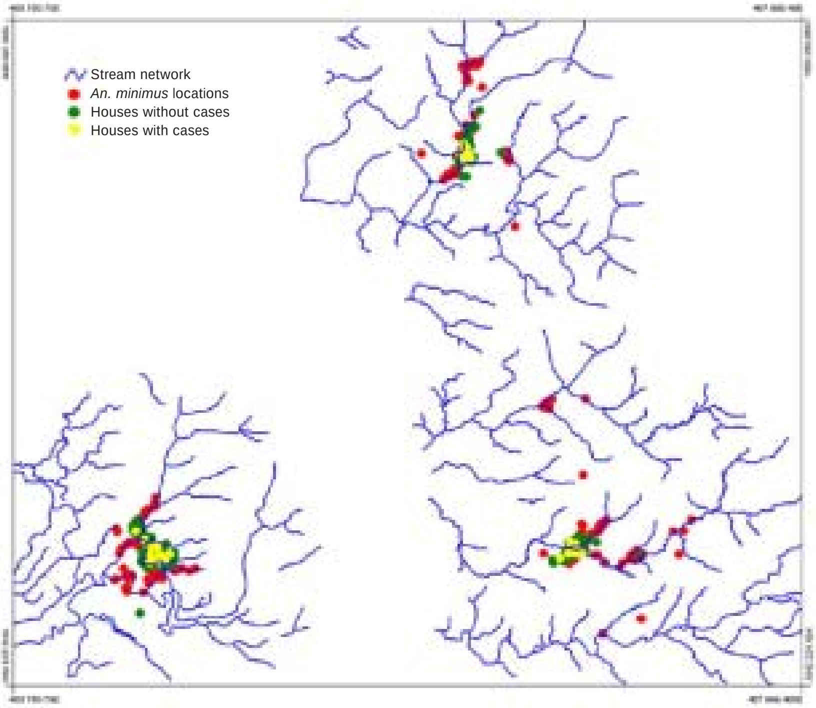

Fig 5–Stream network (blue line) with locations of *An. minimus* larval habitats displayed in red dots, houses with no malaria patients displayed in green dots, and houses with malaria patients displayed in yellow dots.

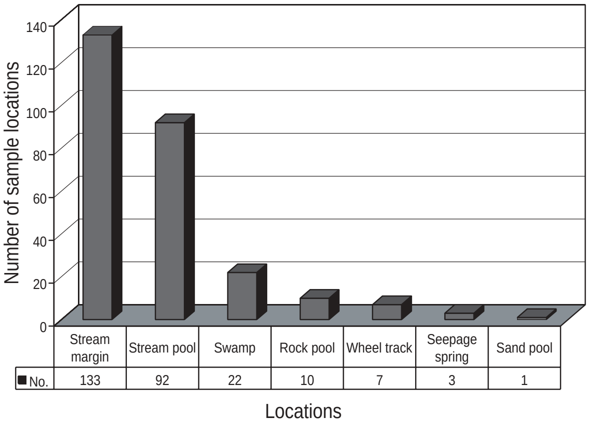

Fig 6–Types of *An. minimus* larval habitats.

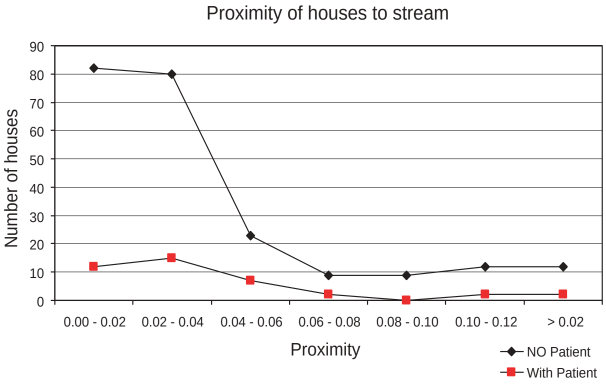

Fig 7–Proximity of houses with and without malaria cases to stream.

tal of 27 ground-truth sampling locations were made, covering Ban Khun Huay, Ban Pa Dae, and Ban Tham Seau villages. The IKONOS image was imported to ArcGIS and, at a minimum display scale of 1: 5,000, land-use/land-cover classes were screen digitized. Within built-up areas, digitizing details were increased to a scale of 1: 2,000 or larger.

Stream network delineation

Streams in the study area are the breeding habitats of the major malaria-transmitting vector, *An. minimus* (Sithiprasasna *et al*, 2003a). Delineating stream networks was important in mapping the locations of these potential breeding sites. One-arc second (30 meters) Shuttle Radar Topography Mission (SRTM) data of the study area was imported into ArcGIS as a grid file. Using the hydrological modeling extension of ArcGIS, the stream network was extracted from the SRTM grid file. The extracted stream network was edited using the IKONOS image as a base map. Editing was done within a 1.5 km buffer zone of the locations where *An. minimus* larvae were collected (Figs 4-5).

Proximity analysis

The edited stream network shapefile in ArcGIS was imported to ENVI 3.4 image processing software as an ENVI vector file and rasterized with a pixel size of 5 x 5 m. The resulting raster stream network was used as an input to calculate proximity to streams. Proximity was calculated by 1/(R*R), where R is the distance from the target pixel (center of the window) to other pixels in the window. Proximity is normalized in the window, which means that if all pixels in the window are streams, proximity becomes 1. A window size of 1.5 by 1.5 km was used based on the estimated mosquito flight range.

RESULTS

Locations of Ban Khun Huay, Ban Pa Dae, and Ban Tham Seau are displayed on LANDSAT data in Fig 1. Visual interpretation was performed to classify the pan-sharpened IKONOS image into land-use/land-cover classes (Fig 2). Fig 3 showed the dominant land-use of the study area as forest (71.45%), followed by corn (17.91%). Large tracts of what were formerly tree-covered hills and slopes are now cultivated for corn production. Forest to corn land-use conversion was prevalent in Ban Khun Huay and Ban Tham Seau. Other forest areas are converted to orchard plantations (banana, fruit trees, teak, etc). Areas converted to rice fields comprised 6.2% of the total. In Ban Khun Huay and Ban Tham Seau, rice areas are located in small valleys, where streams serve as a source of water for irrigation. Large tracts of rice fields are found in Ban Pa Dae. Other than a large water reservoir, water bodies were found in small ponds and in running streams. Fig 4 showed stream network (blue line) within 1.5 km buffer of *An. minimus* larval habitats (yellow dots) with locations of Ban Khun Huay (in the middle of yellow dots at top), Ban Pa Dae (at bottom left) and Ban Tham Seau (at bottom right) displayed on a 100 km^2 true color

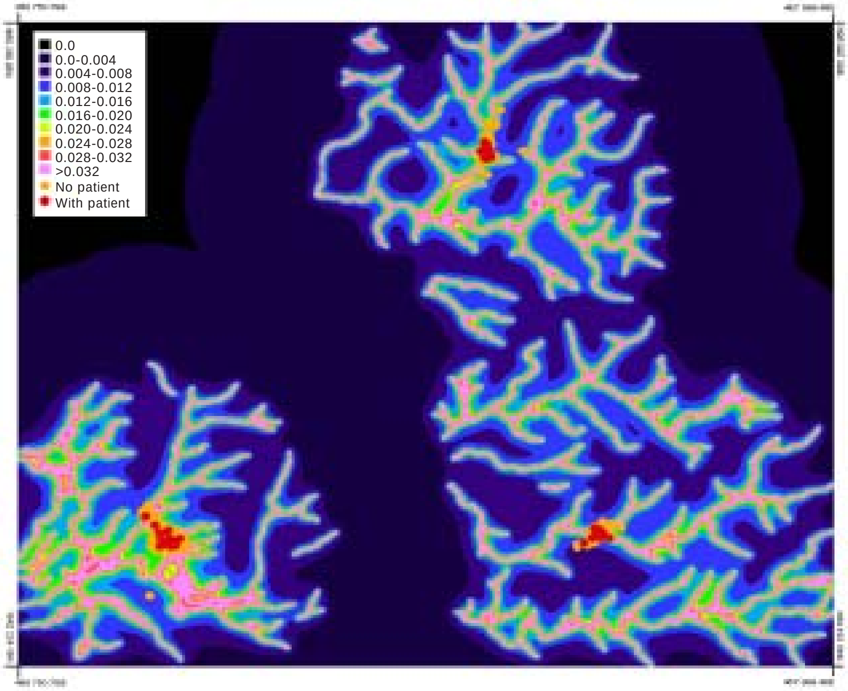

Fig 8–Proximity to stream showing the locations of houses with and without malaria cases.

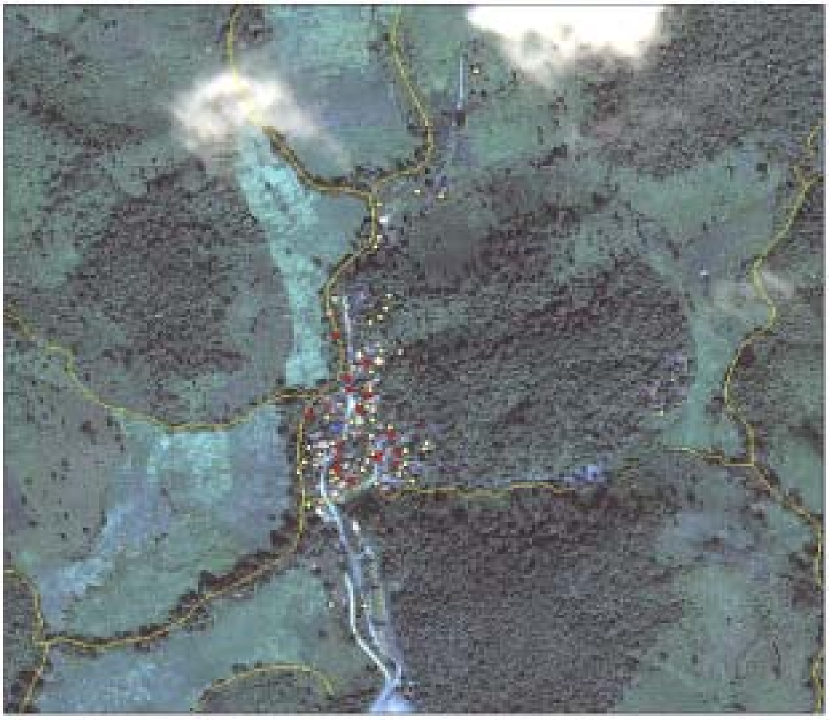

Fig 9–Thematic map showing locations of houses by Global Positioning System overlaid on IKONOS (spatial resolution 1 by 1 m) dated 12 November 2001 displayed in true color of Ban Khun Huay with malaria patients in red dots and without malaria patients in yellow dots. Stream network is displayed in yellow lines.

of IKONOS satellite image. Stream network with locations of *An. minimus* larval habitats displayed in red dots, houses with no malaria patients displayed in green dots, and houses with malaria patients displayed in yellow dots, were displayed in Fig 5. *An. minimus* larvae were observed in 268 locations. Of this total, 84% of the specimens were collected from stream margins and stream pools (Fig 6). The remaining 16% of the samples were collected from swamps, rock pools, wheel tracks, seepage springs, and sand pools. The proximities of streams to houses with and without malaria cases were summarized (Fig 7). Locations of houses with and without malaria cases were overlaid on the proximity image (Figs 8-11). A statistical test at 5% significance level was performed to evaluate whether houses with malaria cases have higher proximities to streams than houses without malaria cases. The results show no significant difference in proximity means between the 2 groups (Table 1).

DISCUSSION

There are many studies of malaria transmission and proximity to vector larval habitats, since this disease is focused around specific mosquito breeding sites. Malaria risk in a number of countries increases with proximity to larval habitats including: Uganda (Staedke *et al*, 2003), Senegal (Trape *et al*, 1992, 1993), Mozambique (Thompson *et*

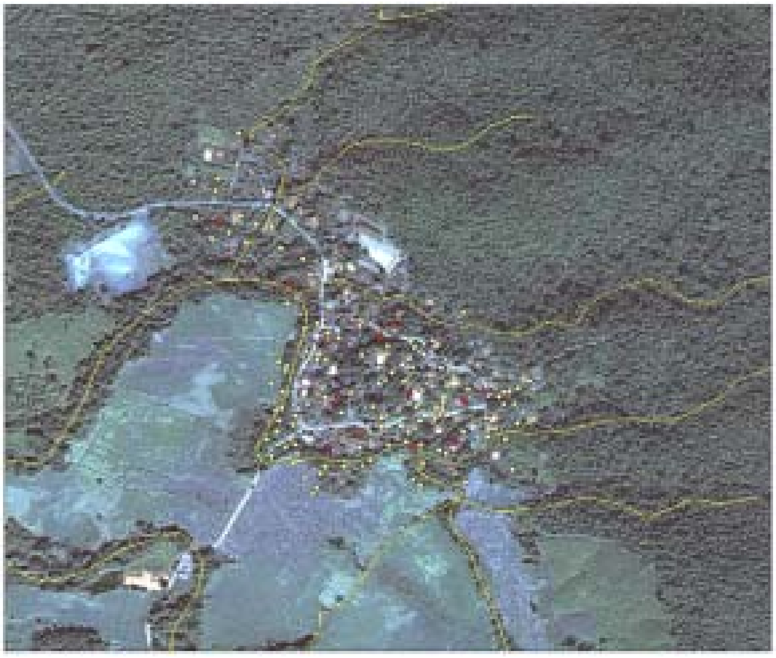

Fig 10–Thematic map showing locations of houses by Global Positioning System overlaid on IKONOS (spatial resolution 1 by 1 m) dated 12 November 2001, displayed in true color, of Ban Pa Dae, with- malaria patients in red dots and without-malaria patients in yellow dots. Stream network is displayed in yellow lines.

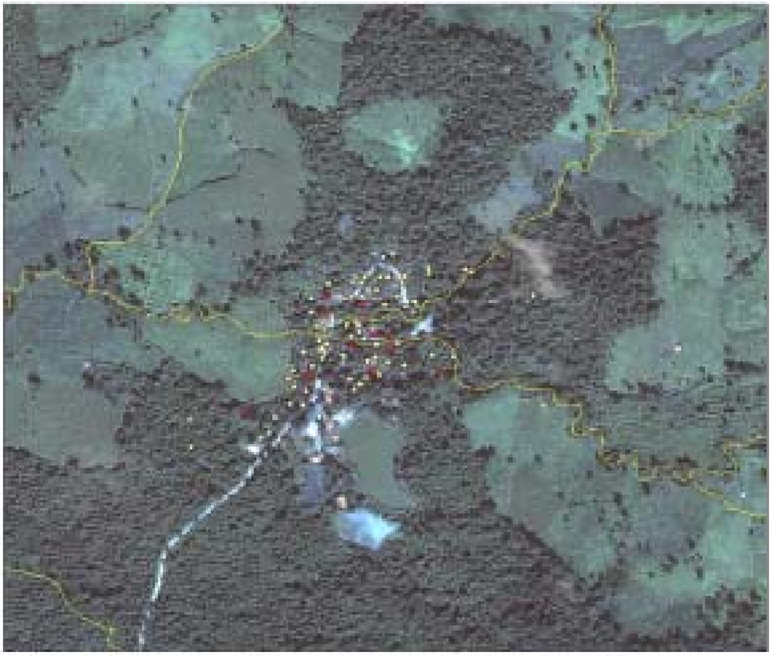

Fig 11–Thematic map showing locations of houses by Global Positioning System overlaid on IKONOS (spatial resolution 1 by 1 m) dated 12 November 2001, displayed in true color, of Ban Tham Seau, with-malaria patients in red dots and without-malaria patients in yellow dots. Stream network is displayed in yellow lines.

al, 1997), Gambia (Thomas and Lindsay, 2000; Clarke *et al*, 2002), Uganda (Njama *et al*, 2003), and Sri Lanka (Gunawardena *et al*, 1998; Van Der Hoek *et al*, 1998, 2003; Konradsen *et al*, 2003).

In our study, in order to determine the type and abundance of habitats where *An. minimus* occurs, larval surveys and collections were made within a 0.5-1 km radius around each village. We observed a high proportion of larvae close to human settlements. The 1.5 km used in our proximity analysis was arbitrarily estimated based on the *An. minimus* flight range. Since we could not find any significant difference in malaria risk and proximity to streams when we compared houses with malaria cases and houses without malaria cases, we suspect that the actual flight range *An. minimus* may be greater than 1.5 km. We suggest that the *An. minimus* larval habitat deserves a more detailed investigation. Further studies on human behavior contrary to that required for adequate malaria control, including: 1) failure to use mosquito nets, insect repellents, house-spraying; 2) delay in seeking treatment; and 3) failure to comply with prescribed drug regimens, are recommended for these three villages.

The identification of foci of malaria transmission requires methods of locating vector breeding sites, recording mosquito densities, rates of sporozoites and oocysts, human malaria case incidence rates, and locating and characterizing houses and the domestic environment. Locations are greatly assisted by the use of hand-held, satellite-dependent GPS. RS also provides high-reso-

Table 1

Statistical *t*-test (two-samples assuming unequal variances) of proximity to streams.

	n	Mean	Standard deviation	*t*	p-value
Houses with no malaria patient	227	0.040	0.032	0.203	0.420
Houses with malaria patient	40	0.039	0.032		

lution images that reveal patterns of vegetation and other environmental features and conditions on the ground. All forms of geographical data can be assembled using computer-assisted management of spatial information, such as GIS. These can be applied to national malaria control programs. Once developed, GIS can be exported to the regional or local levels in order to target more precisely limited resources for sustainable malaria control. The major objective in the application of GIS to malaria control is the mapping of the distribution of malaria risk, where possible, down to the household level. GIS can also be used to generate predictive models of malaria risk and transmission in specific situations and locations. In studies in Belize and Mexico, RS and GIS were used to develop predictive models for the presence and abundance of malaria vectors in rural villages and houses (Rejmankova *et al,* 1995, 1998; Beck *et al*, 1994; Roberts *et al*, 1996). The distance between villages and mosquito larval habitats was an important parameter in the predictive models (Rejmankova *et al*, 1995). The satellite data were used to locate specific types of vector breeding sites (Sithiprasasna *et al*, 2003b). The GIS was then used to examine the relationships between breeding sites and distances to human habitations. Predictive models for two of the three vectors in Belize have proved particularly accurate (Lindsay *et al*, 1991; Rejmankova *et al*, 1995).

Properly used, GPS, RS, and GIS could allow the location and quantification of malaria risk to be determined in a more accurate, time and cost-effective way. Affordable hardware and software for using GIS and RS are now available. These systems are valuable tools, allowing information on malaria transmission and malaria risk to be processed and used to guide the management of malaria control campaigns.

REFERENCES

Anyamba A, Linthicum KJ, Mahoney R, Tucker CJ, Kelley PW. Mapping potential risk of Rift Valley fever outbreaks in African savannas using vegetation index time series data. *Photogrammet Engineer Remote Sens* 2002; 68: 137-45.

Beck LR, Rodriguez MH, Dister SW, *et al*. Remote sensing as a landscape epidemiologic tool to identify villages at high risk for malaria transmission. *Am J Trop Med Hyg* 1994; 51: 271-80.

Beck LR, Lobitz BM, Wood BL. Remote sensing and human health: new sensors and new opportunities. *Emerg Infect Dis* 2000; 6: 217-27.

Carter R, Mendis K, Roberts D. Spatial targeting of interventions against malaria. *Bull WHO* 2000; 78: 1401-11.

Clarke SE, Bogh C, Brown RC, Walraven GE, Thomas CJ, Lindsay SW. Risk of malaria attacks in Gambian children is greater away from malaria vector breeding sites. *Trans R Soc Trop Med Hyg* 2002; 96: 499-506.

ENVI software version 3.4, ENVI user's guide. Boulder, Colorado: ENVI Research Systems, 2000.

ERDAS software version 8.5 of ERDAS IMAGINE tour guide, field guide, and virtualGIS. Atlanta, GA: ERDAS, 2002.

ESRI. ArcGIS 8.3 of ArcMap, ArcCatalog, ArcToolbox and spatial analyst user's guide. Redlands, CA. 2001-2002.

Gunawardena DM, Wickremasinghe AR, Muthuwatta L, *et al*. Malaria risk factors in an endemic region of Sri Lanka, and the impact and cost implications of risk factor-based interventions. *Am J Trop Med Hyg* 1998; 58: 533-42.

Konradsen F, Amerasinghe P, Van Der Hoek W, Amerasinghe F, Perera D, Piyaratne M. Strong association between house characteristics and malaria vectors in Sri Lanka. *Am J Trop Med Hyg* 2003; 68: 177-81.

Lindsay SW, Wilkins HA, Zieler HA, Daly RJ, Petrarca V, Byass P. Ability of *Anopheles gambiae* mosquitos to transmit malaria during the dry and wet seasons in an area of irrigated rice cultivation in The Gambia. *J Trop Med Hyg* 1991; 94: 313-24.

Linthicum KJ, Anyamba A, Tucker CJ, Kelley PW, Myers MF, Peters CJ. Climate and satellite indicators to forecast Rift Valley fever epidemics in Kenya. *Science* 1999; 285: 397-400.

Njama D, Dorsey G, Guwatudde D, *et al.* Urban malaria: primary caregivers' knowledge, attitudes, practices and predictors of malaria incidence in a cohort of Ugandan children. *Trop Med Int Health* 2003; 8: 685-92.

Pope KO, Sheffner EJ, Linthicum KJ, *et al*. Identification of central Kenyan Rift Valley fever virus vector habitats with Landsat TM and evaluation of their flooding status with airborne imaging radar. *Remote Sens Environ* 1992; 40: 185-96.

Rejmankova E, Roberts DR, Pawley A, Manguin S, Polanco J. Predictions of adult *Anopheles albimanus* densities in villages based on distances to remotely sensed larval habitats. *Am J Trop Med Hyg* 1995; 53: 482-8.

Rejmankova E, Pope KO, Roberts DR, *et al*. Characterization and detection of *Anopheles vestitipennis* and *Anopheles punctimacula* (Diptera: Culicidae) larval habitats in Belize with field survey and SPOT satellite imagery. *J Vector Ecol* 1998; 23: 74-88.

Roberts DR, Paris JF, Manguin S, *et al*. Predictions of malaria vector distribution in Belize based on multispectral satellite data. *Am J Trop Med Hyg* 1996; 54: 304-8.

Sithiprasasna R, Linthicum KJ, Liu GJ, Jones JW, Singhasivanon P. Some entomological observations on temporal and spatial distribution on malaria vectors in three villages in North-western Thailand using a Geographic Information System (GIS). *Southeast Asian J Trop Med Public Health* 2003a; 34: 505-16.

Sithiprasasna R, Linthicum KJ, Liu GJ, Jones JW, Singhasivanon P. Use of GIS-based spatial modeling approach to characterize the spatial patterns of malaria mosquito breeding habitats in North-western Thailand. *Southeast Asian J Trop Med Public Health* 2003b; 34: 517-28.

Staedke SG, Nottingham EW, Cox J, Kamya MR, Rosenthal PJ, Dorsey G. Proximity to mosquito breeding sites as a risk factor for clinical malaria episodes in an urban cohort of Ugandan children. *Am J Trop Med Hyg* 2003; 69: 244-6.

Thompson R, Begtrup K, Cuamba N, *et al*. Malaria Project: a temporal and spatial study of malaria transmission and disease in a suburban area of Maputo, Mozambique. *Am J Trop Med Hyg* 1997; 57: 550-9.

Thomas CJ, Lindsay SW. Local-scale variation in malaria infection amongst rural Gambian children estimated by satellite remote sensing. *Trans R Soc Trop Med Hyg* 2000; 94: 159-63.

Trape JF, Lefebvre-Zante E, Legros F *et al*. Vector density gradients and the epidemiology of urban malaria in Dakar, Senegal. *Am J Trop Med Hyg* 1992; 47: 181-9.

Trape JF, Lefebvre-Zante E, Legros F, *et al*. Malaria morbidity among children exposed to low seasonal transmission in Dakar, Senegal and its implications for malaria control in tropical Africa. *Am J Trop Med Hyg* 1993; 48: 748-56.

Van Der Hoek W, Konradsen F, Dijkstra DS, Amerasinghe PH, Amerasinghe FP. Risk factors for malaria: a microepidemiological study in a village in Sri Lanka. *Trans R Soc Trop Med Hyg* 1998; 92: 265-9.

Van Der Hoek W, Konradsen F, Amerasinghe PH, Perera D, Piyaratne MK, Amerasinghe FP. Towards a risk map of malaria for Sri Lanka: the importance of house location relative to vector breeding sites. *Int J Epidemiol* 2003; 32: 280-5.