SHORT COMMUNICATION

Vector species composition and malaria infectivity rates in Mkuzi, Muheza District, north-eastern Tanzania

E.J. KWEKA1,2,3, A.M. MAHANDE1,2, W.M.M. NKYA1,2, C. ASSENGA2, E.E. LYATUU3, E.NYALE3, F.W. MOSHA1,2, S.B. MWAKALINGA1,2,3 and E.A. TEMU3.
1Joint Malaria programme, P.O. Box 2228, Moshi, Tanzania
2Kilimanjaro Christian Medical Centre, P.O. Box 3010, Moshi Tanzania
3Tropical Pesticides Research Institute, P.O. Box 3024 Arusha, Tanzania
4Centre for Medical Parasitology, University of Copenhagen, Denmark
5Institute of Tropical Medicine, Nagasaki University, Nagasaki, Japan

Abstract: Entomological surveys were conducted in Mkuzi village in Muheza District, north-eastern Tanzania from April to September 2003. The objectives were to determine the species composition and infectivity rates of mosquitoes in Mkuzi village. Mosquito collection was done using CDC light trap and pyrethrum spray catch (PSC) techniques. The light trap: spray catch ratio was 2.2:1. A total of 2157 mosquitoes were collected (light trap=1483; PSC=674). Anopheles gambiae s.s. accounted for 56.7% (N=1224) of all mosquitoes collected. Other species were An. funestus complex (19.2%) and Culex quinquefasciatus (24.1%). The mosquito density per room was 74.15 and 33.7 for light trap and PSC techniques, respectively. A total of 1637 Anopheles mosquitoes were tested for circumsporozoite protein by Enzyme linked Immunosobent Assay (ELISA). The overall infectivity rate for circumsporozoite protein for P. falciparum in Anopheles mosquitoes was 21.14% (346/1637). Species-specific infectivity rates were 22.7% (278/1224) in An. gambiae s.s. and 0% (0/80) for An. funestus for An. parensis. Blood meal analysis indicated that 92.3% of An. gambiae s.s., 88.9% of An. funestus s.s., 64.5% of An. rivulorum and 67.7% of An. parensis had taken blood meal from human hosts. In conclusion, malaria transmission in Mkuzi area of Muheza district is mainly by the highly anthropophagic An. gambiae s.s. and An. funestus s.s. More studies are needed to identify the seasonal variation of species composition and transmission dynamics in this village.

Key words: mosquito, anthropophagy, sporozoite, Anopheles gambiae, An. funestus, malaria, Tanzania

Malaria is the leading cause of morbidity and mortality in Tanzania. Health facility data indicates that about 19% of all hospital deaths are due to malaria (Kitua, 2003). The lowlands of Muheza district in north-eastern Tanzania has been classified as an area of malaria holoendemic (Mboera & Magesa, 2001). Malaria is the one of the most prevalent severe infectious disease and remains the major cause of the human mortality and morbidity in Mkuzi village, Muheza district (Alilio et al., 2004). In this area of north-east Tanzania malaria is mainly transmitted by Anopheles gambiae s.s. and An. funestus (Mboera & Magesa, 2001). An. rivulorum and An. marshalli have also been identified as vectors of malaria in Muheza district (Magesa et al., 1991; Wilkes et al., 1996).

Information of mosquito species composition, abundance and dynamics are important in designing appropriate malaria control strategies. It was the aim of this study to identify the malaria vector species and their infectivity rates in Mkuzi village of Muheza District in northern east Tanzania.

The study was conducted at Mkuzi village about 10 km from Muheza township in north-east Tanzania. Mkuzi village comprises of four sub villages, Mkuzi, Maweni, Kweka and Daisaama. The village has homogenous characteristics in vegetations and house style.

Mosquitoes were collected using CDC light traps and pyrethrum spray catch (PSC) techniques. Five houses were selected for either CDC light trap or spray catch technique in each hamlet. Light traps were hung at the foot-end (30 cm high) of sleeping person under untreated bednets (Mboera et al., 1998). Person sleeping in the room was asked to set the trap and switch on and off at 18:00hr and 06:00hr, respectively. The houses selected were of similar size and type. For PSC technique five houses were also randomly selected in each hamlet. Spraying with 0.4% crude pyrethrum mixed in 99.6% kerosene was done between 06:00hr and 07:30hr. After 10 minutes, mosquitoes knocked down on white sheets were collected and preserved in petridishes with wet cotton and Whatman filter paper.

Mosquitoes collected were identified using morphological key (Gillies & de Meillon, 1968; Gillies & Coetzeet, 1987). Female anopheles mosquito were
kept in dry silica gel and stored at 4°C. Enzyme linked immunosorbent assay (ELISA) was used to detect the circumsporozoite protein for *Plasmodium falciparum* in mosquitoes collected (Wirtz *et al.*, 1987). Identification of the sibling species for *An. gambiae* was performed as described by Scott *et al.* (1993) while that of *An. funestus* complex was done by using Polymerase Chain Reaction (PCR) test (Koekemoer *et al.*, 2002). Blood meal from freshly blood fed mosquitoes caught by spray catch were smeared onto filter paper and stored at 4°C for later identification of bloodmeal source by precipitin test (Bray *et al.*, 1984).

A total of 2157 mosquitoes were collected of which 68.8% (N=1483) were collected by light trap and 31.2% (N=674) by pyrethrum spray catch technique. Of the collected mosquitoes, 56.7% (N=1224) were *An. gambiae* s.l.; 19.2% (N=413) were *An. funestus* s.l. and 20.3% (N=520) were *Culex quinquefasciatus*. The light trap: pyrethrum spray catch ratio was 2.2:1. The mosquito density per room was 74.2 and 33.7 for light trap and pyrethrum spray catch, respectively.

All *An. gambiae* s.l were identified to belong to the *An. gambiae* s.s. group. *Anopheles funestus* sibling species was composed of *An. funestus funestus* 68.5% (N=283), *An. rivulorum* 19.4% (N=80) and *An. parensis* 12.1% (N=50) (Table 1). A total of 1637 mosquitoes were tested for circumsporozoite protein, 1224 were *An. gambiae* s.s. and 413 were *An. funestus* s.l. Of the total *Anopheles* mosquitoes, 346 were found to be positive for *P. falciparum*. *An. gambiae* s.s. accounted for 27.7% (278/1224) while *An. funestus* 24.0% (N=68/283) of the total anopheline mosquitoes. None of the *An. rivulorum* or *An. parensis* was infected with *P. falciparum*. The overall anopheline sporozoite rate was 21.14% (346/1637) (Table 2). The difference in sporozoite rates between *An. gambiae* s.s and *An. funestus* was not statistically significant (t = 0.316, df = 5, P = 0.765). Identification of the blood meal source showed that, 92.3% of *An. gambiae* s.s., 88.9% of *An. funestus*, 64.5% of *An. rivulorum* and 67.7% of *An. parensis* had taken blood meal from human hosts.

**Table 1: Anopheles species composition collected at Mkuzi area in Muheza District**

<table>
<thead>
<tr>
<th>Species complex</th>
<th>Species</th>
<th>No</th>
<th>%</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Anopheles gambiae</em> s.l.</td>
<td><em>An. gambiae</em> s.s.</td>
<td>1224</td>
<td>100</td>
</tr>
<tr>
<td><em>Anopheles funestus</em> s.l.</td>
<td><em>An. funestus</em> funestus</td>
<td>283</td>
<td>68.5</td>
</tr>
<tr>
<td></td>
<td><em>An. rivulorum</em></td>
<td>80</td>
<td>19.4</td>
</tr>
<tr>
<td></td>
<td><em>An. parensis</em></td>
<td>50</td>
<td>12.1</td>
</tr>
</tbody>
</table>

**Table 2: Sporozoite rates of *An. gambiae* s.s. and *An. funestus* in Mkuzi area, Muheza District**

<table>
<thead>
<tr>
<th>Species</th>
<th>No. examined for sporozoite</th>
<th>No. infected</th>
<th>% infected</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>An. gambiae</em> s.s</td>
<td>1224</td>
<td>278</td>
<td>22.7%</td>
</tr>
<tr>
<td><em>An. funestus</em></td>
<td>283</td>
<td>68</td>
<td>24.0%</td>
</tr>
<tr>
<td><em>An. rivulorum</em></td>
<td>80</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td><em>An. parensis</em></td>
<td>50</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td><strong>1637</strong></td>
<td><strong>346</strong></td>
<td><strong>21.14%</strong></td>
</tr>
</tbody>
</table>
Discussion

An. gambiae s.s and An. funestus sibling species were the major malaria vectors in Mkuzi village in Muheza district of north-eastern Tanzania. An. gambiae s.s existed in higher proportion than An. funestus sibling species. In the coastal part of Tanzania An. gambiae s.s and An. funestus s.l have been identified to be major vectors of malaria (Mnzava & Kilama, 1986; Temu et al., 1998). The infectivity rates of the two species are among the highest recorded in the areas (Mboera & Magesa, 2001). In the current study, light trap caught more Anopheles mosquitoes than the spray catch techniques. This indicate that majority of the mosquitoes collected were host-seeking than resting.

Like in our study, Gillies (1964a) did not find sporozoite infected An. rivulorum in a sample of 147 mosquitoes. However, Wilkes et al. (1996) found 0.5% (5/1022) of the An. rivulorum were infected with malaria sporozoites in a study in villages around Muheza town. Our results showed that An. gambiae s.s and An. funestus are highly anthropophilic. Blood meal analysis indicated that An. gambiae s.s and An. funestus s.s. In addition over two-thirds of An. rivulorum and An. parensis had taken blood meals from human hosts. This high degree of human blood preference is likely to contribute to high malaria prevalence among residents in this area irrespective of the availability of cattle and other domestic animals. Similarly, Gillies (1964b) found mixed feed to account for less than 0.5% of the blood meals tested. In his study on host-preference in An. gambiae in Muheza. Our study was however, limited by the fact that it only collected indoor bitting/resting mosquitoes and only covered part of the year. A longitudinal study is likely to provide more information on the distribution and variation of the parameters studied throughout the year.

Acknowledgements

We acknowledge the village leaders and villagers for giving cooperation during the study. Mr. Aza Kimamo and Manaseh Nkya are acknowledged for mosquitoes collection while Mr. Frank Mnango for assistance in specimen transportation. This study received financial support from Danish International Development Agency.

References


