Parasitol Res (2008) 102:1329–1335
DOI 10.1007/s00436-008-0914-7

ORIGINAL PAPER

Blood-feeding patterns of *Culex quinquefasciatus* and other culicines and implications for disease transmission in Mwea rice scheme, Kenya

Ephantus J. Muturi · Simon Muriu · Josephat Shililu · Joseph M. Mwangangi · Benjamin G. Jacob · Charles Mbogo · John Githure · Robert J. Novak

Received: 6 December 2007 / Accepted: 29 January 2008 / Published online: 23 February 2008

Abstract Studies were conducted in Mwea Rice Scheme, Kenya during the period April 2005 and January 2007 to determine the host-feeding pattern of culicine mosquitoes. Mosquitoes were collected indoors and outdoors and tested for human, bovine, goat, and donkey blood meals by an Enzyme-Linked Immunosorbent Assay. A total of 1,714 blood-engorged samples comprising *Culex quinquefasciatus* Say (96.1%), *Culex annulioris* Theobald (1.8%), *Culex poicilipes* Theobald (0.9%), *Aedes cuminsi* Theobald (1.0%), *Aedes taylori* Edwards (0.1%), and *Mansonia africana* Theobald (0.1%) were tested. Except for *A. taylori*, in which the single blood meal tested was of bovine origin, the other species fed mostly on both bovine (range 73.3–100%) and goats (range 50–100%). Donkeys were also common hosts for all species (range 19.4–23.5%) except *A. taylori* and *M. africana*. *C. quinquefasciatus* was the only species containing human blood meals (0.04), and indoor collected populations of this species had significantly higher frequency of human blood meals (9.8%) compared with outdoor-collected populations (3.0%). Mixed blood feeding was dominant among culicine species comprising 50.0%, 73.3%, 73.5%, 80.6%, and 94.1% of the samples for *M. africana*, *C. poicilipes*, *C. quinquefasciatus*, *C. annulioris*, and *A. cuminsi*, respectively. Ten mixed blood meal combinations including a mixture of all the four hosts were observed in *C. quinquefasciatus*, compared to one blood meal combination for *M. Africana*, and two combinations for *C. poicilipes*, *C. annulioris*, and *A. cuminsi*. Mixed bovine and goat blood meal was the most common combination among the five culicine species followed by a mixture of donkey, bovine, and goat blood meals. We conclude that culicine species in Mwea are least likely to be vectors of lymphatic filariasis due to their high "preference" for livestock over human hosts, but they present an increased risk for arbovirus transmission particularly Rift Valley Fever virus, in which domestic animals serve as amplification hosts.

E. J. Muturi (✉) · B. G. Jacob · R. J. Novak
Department of Medicine,
William C. Gorgas Center for Geographic Medicine,
University of Alabama at Birmingham,
206C Bevill Biomedical Research Building,
845 19th Street South,
Birmingham, AL 35294, USA
e-mail: emuturi@uab.edu

S. Muriu · J. Shililu · J. M. Mwangangi · J. Githure
Human Health Division,
International Centre of Insect Physiology and Ecology,
Nairobi, Kenya

J. M. Mwangangi · C. Mbogo
Centre for Geographic Medicine Research-Coast,
Kenya Medical Research Institute,
Kilifi, Kenya

Introduction

The subfamily Culicinae is a diverse group of mosquitoes comprised of many genera that differ in both their biology and behavior. This group is also known to contain important vectors of lymphatic filariasis (LF) and several arboviruses notably Rift Valley Fever (RVF) virus, dengue fever, yellow fever, West Nile Virus (WNV), Japanese encephalitis, and many others (White 1989; Gubler 1996). In Africa, where one-third of the global burden of LF occurs, *Culex quinquefasciatus* Say is known to be one of the major vectors (Thompson et al. 1996; Mwandawiro et al. 1997; Bogh et al. 1998). In addition, several species of *Aedes* and *Culex* are known to transmit yellow fever,

RVF, and dengue viruses and have been involved in major outbreaks of these diseases in several African countries (Gubler 2004; Diallo et al. 2005; Rynn 2007). Understanding the potential risk of different culicine species in disease transmission and development of appropriate early warning systems and vector-control strategies is therefore urgently required in order to minimize the burden of culicine-borne diseases.

Blood-feeding patterns are considered one of the most important components of disease transmission. This information makes it possible to estimate the degree of human–vector contact and to understand the role of a given species in disease transmission cycle, both of which are critical for vector-control measures (Garret-Jones et al. 1980). Several factors including host preference, host availability, host density, and host irritability are known to influence blood feeding by mosquitoes (Washino and Tempelis 1983). These factors play a significant role in determining the epidemiological significance of a particular mosquito species. Species with a narrow host range such as *Anopheles gambiae* Giles *s.s.*, *Anopheles funestus* Giles and *C. quinquefasciatus* are considered important vectors of both malaria and Bancroftian filariasis and those that switch between hosts are considered important in arbovirus transmission (Chandler et al. 1975b). Other studies have shown that diversion of host-seeking mosquitoes can reduce the risk of disease transmission (Burkot 1988; Reuben et al. 1992). In view of this concept, zooprophylaxis is considered a potential tactic to control mosquito-borne diseases (Arunachalam et al. 2005; Mahande et al. 2007).

In rice-growing areas of the African continent, high populations of vector mosquitoes are known to co-exist (Chandler et al. 1975a; Snow 1983; Lacey and Lacey 1990; Muturi et al. 2006). Although this does not necessarily translate to increased malaria transmission (Ijumba and Lindsay 2001), existing evidence do indicate that rice cultivation increases the risk of lymphatic filariasis (Hunter 1992; Thompson et al. 1996; Appawu et al. 2001) as well as epidemic arbovirus transmission (Fontenille et al. 1998; Diallo et al. 2005). Surprisingly, most studies in irrigated areas focus mainly on malaria vectors at the expense of other mosquito species (Ijumba et al. 2002; Dolo et al. 2004). Therefore, substantial information is available on the blood-feeding patterns of malaria vectors in these areas (Chandler et al. 1975b; Ijumba et al. 2002; Dolo et al. 2004), but little is known about the feeding patterns of other mosquito species. A study in the rice-growing area of the Kano Plain, Kenya, reported that *Mimomyia mediolineata* Theobald and *Mimomyia splendens* Theobald fed mainly on amphibians and occasionally on man, while *Uranotaenia balfouri* Theobald and *Mimomyia hispida* Theobald fed mainly on amphibians and cattle (Boreham et al. 1975). Further studies in the same area found that *Coquillettidia karandalaensis* Wolfs, *Culex poicilipes* Theobald, and *Culex univittatus* Theobald were highly ornithophilic species (Chandler et al. 1976) while *Mansonia uniformis* Theobald, *Mansonia africana* Theobald, *Culex antennatus* Becker, *C. univittatus*, *Aedes circumluteolus* Theobald, and *Aedes ochraceus* Theobald had preference for human and cattle hosts (Chandler et al. 1975b). Apart from these studies, knowledge on the feeding pattern of culicine mosquitoes in African rice agroecosystems is scanty. Because environmental factors are known to influence mosquito-feeding patterns (Washino and Tempelis 1983), it is often impossible to compute a general estimate of feeding patterns to be used throughout a species distribution range. The current study examined the blood-feeding pattern of six culicine species in Mwea Rice Irrigation Scheme in Central Kenya. This area was recently hit by a Rift Valley Fever virus epidemic (Centers for Disease Control 2007).

Materials and methods

Study area

The studies were conducted in Mwea Rice Irrigation Scheme in central Kenya, 100 km north-east of Nairobi. The study area has been described in detail by Mutero et al. 2004, Mwangangi et al. 2006, and Muturi et al. 2007. The Mwea Rice Irrigation Scheme covers an area of approximately 13,600 ha with forty villages and 150,000 people in 2,500 households. More than 75% of the land in each village is under rice cultivation with the remaining area being used for subsistence farming and human habitation. Four villages, Rurumi, Karima, Kiuria, and Kangichiri, were randomly selected for this study. Cattle, goats, and chickens are the main domestic animals found in all four study sites. Donkeys are also found in each of the sites but in low numbers. The majority of houses are mud-walled with iron roofing and unscreened eaves and windows. Seventeen known culicine species occur in the area with *C. quinquefasciatus* as the dominant species (Muturi et al. 2006). There is no data implicating any of the 17 culicine species with disease transmission in the area but they are considered potential vectors of arboviruses. The recent report of Rift Valley Fever virus cases in the area serves to confirm this claim (Centers for Disease Control 2007). *C. quinquefasciatus* is also considered a potential vector of Bancroftian filariasis together with *Amopheles arabiensis* (the main malaria vector in the area; Muturi et al. 2006, 2008).

Mosquito collection

Adult mosquito collections were conducted biweekly between April 2005 and January 2007. Indoor-resting

mosquitoes were collected using the pyrethrum spray catch (PSC) method (World Health Organization 1975) and outdoor populations were collected by Centers for Disease Control (CDC) miniature light traps (J.W. Hock Ltd, Gainesville, FL, USA). The mosquitoes in each study site were collected in twenty randomly selected houses (0700–1100 h) and six light trap stations (1800–0700 h). A detailed explanation of the sampling strategy has been described elsewhere (Muturi et al. 2006).

Laboratory processing

All culicine mosquitoes collected by PSC and CDC light traps were transported to the laboratory and sorted by sex and species using morphological characteristics as described by Edwards (1941). The females were further classified into their respective blood-feeding stages (unfed, blood-fed, semi-gravid, and gravid) by examining their abdomen under a dissecting microscope (World Health Organization 1975). All blood-fed mosquitoes from each collection were preserved in labeled vials containing anhydrous calcium sulphate (drierite).

Blood meal identification

Samples of blood-fed mosquitoes were cut transversely between the thorax and the abdomen using a sterile scalpel for each sample. The posterior portions containing the blood meal were placed individually in labeled vials. The abdomen of each mosquito was ground in 50 μl of phosphate-buffered saline (PBS) with subsequent addition of 950 μl of PBS and then stored at −20°C. Blood meals were identified by a direct enzyme-linked immunosorbent assay (ELISA) using anti-host (IgG) conjugates (Kirkegaard and Perry, Gaithersburg, MD) against human, bovine, donkey, and goat (Beier et al. 1988). All blood meal samples were first screened for human and bovine blood meals and later for goat and donkey blood meals. Positive controls included serum for each host tested, and different combinations human, bovine, goat, and donkey serum mixtures in PBS. Negative controls comprised ground male mosquitoes in PBS. This setup ensured that the samples were monitored for any possible cross reaction.

Statistical analyses

Data were analyzed using SPSS version 11.5 statistical package (SPSS, Inc., Chicago, IL). Because there was no significant site-to-site variation in mosquito-feeding pattern, the data for the four villages was pooled before analysis. Chi-square test was used to compare the difference in human blood index (HBI) between indoor and outdoor-collected *C. quinquefasciatus* mosquitoes.

Results

A total of 6,122 blood-fed mosquitoes were collected indoors and outdoors during the study period. These comprised *C. quinquefasciatus* (6,047), *C. annulioris* Theobald (36), *C. poicilipes* (17), *A. cuminsi* Theobald (17), *A. taylori* Edwards (two) and *M. africana* (three). From this total, 1,714 samples were tested for blood meal sources. These included 1,648 *C. quinquefasciatus*, 31 *C. annulioris*, 15 *C. poicilipes*, 17 *A. cuminsi*, one *A. taylori*, and two *M. africana*. The single blood meal specimen for *A. taylori* was of bovine origin, whereas one of the two specimens of *M. africana* was of bovine origin and the other was a mixture of bovine and goat. Blood meal sources for the other species were from at least three of the four hosts tested, with bovine and goats as the most common hosts (Table 1). All the four hosts were found to be sources of *C. quinquefasciatus* blood meals with proportions of 86.2%, 72.5%, 18.9%, and 3.9% for bovine, goats, donkeys, and human blood meals, respectively. The proportion of indoor collected *C. quinquefasciatus* containing human blood meals was 9.8% and significantly higher than 3.0% for outdoor-collected populations (χ^2=21.863, df=1, P<0.05). The other species; *C. poicilipes*, *C. annulioris*, and *A. cuminsi* had taken their blood meals from all hosts except humans. The proportion of bovine, goat, and donkey blood meals, respectively, was 73.3%, 73.3%, and 13.3% for *C. poicilipes*, 90.3%, 80.6%, and 19.4% for *C. annulioris*, and 94.1%, 100%, and 23.5% for *A. cuminsi*. These species had taken their blood meals outdoors rather than indoors (Table 1). The positive controls for our ELISA analysis did not show any evidence of cross reaction.

With exceptions of *A. taylori*, in which the single blood meal sample was identified to be from a single host, and *M. africana*, where one of the two samples tested was a mixture of bovine and goat, the largest proportion of the blood meals for all of the other species were from more than one host. The percentage of mixed blood meals ranged from 73.3% (11 of 15) of the samples for *C. poicilipes* to 94.1% (16 of 17) of the samples for *A. cuminsi* (Table 2). Overall, only 26.2% of the blood meal samples were from a single host.

The various combinations of mixed blood meals obtained from different mosquito species are shown in Table 3. *C. quinquefasciatus* was found to have ten different combinations of mixed blood meals. The dominant mixed blood meal combination for this species was a mixture of goat and bovine (75.5%). Other common combinations were donkey, bovine, and goat mixtures (18.4), donkey and bovine mixtures (1.9%) and donkey and goat mixtures (1.5%). Five *C. quinquefasciatus* specimens had a mixture of all four hosts. Two blood meal

Table 1 Blood-feeding pattern of six culicine species in Mwea Rice Scheme, Kenya

Species	Location	# Tested	Human (%)	Cow (%)	Donkey (%)	Goat (%)
C. quinquefasciatus	Indoors	204	20 (9.8)	108 (52.9)	52 (25.5)	90 (44.1)
	Outdoors	1444	44 (3.0)	1312 (90.9)	260 (18.0)	1104 (76.5)
	Overall	1648	64 (3.9)	1420 (86.2)	312 (18.9)	1194 (72.5)
C. poicilipes	Indoors	5	0 (0.0)	3 (60.0)	0 (0.0)	3 (60.0)
	Outdoors	10	0 (0.0)	8 (80.0)	2 (20.0)	8 (80.0)
	Overall	15	0 (0.0)	11 (73.3)	2 (13.3)	11 (73.3)
C. annulioris	Indoors	8	0 (0.0)	5 (62.5)	1 (12.5)	5 (62.5)
	Outdoors	23	0 (0.0)	23 (100)	5 (21.7)	20 (87.0)
	Overall	31	0 (0.0)	28 (90.3)	6 (19.4)	25 (80.6)
A. cuminsi	Indoors	1	0 (0.0)	1 (100.0)	0 (0.0)	1 (100.0)
	Outdoors	16	0 (0.0)	15 (93.8)	4 (25.0)	16 (100.0)
	Overall	17	0 (0.0)	16 (94.1)	4 (23.5)	17 (100.0)
A. taylori	Indoors	0	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
	Outdoors	1	0 (0.0)	1 (100.0)	0 (0.0)	0 (0.0)
	Overall	1	0 (0.0)	1 (100.0)	0 (0.0)	0 (0.0)
M. Africana	Indoors	0	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
	Outdoors	2	0(0.0)	2 (100.0)	0 (0.0)	1 (50.5)
	Overall	2	0(0.0)	2 (100.0)	0 (0.0)	1 (50.5)
Total		1714	64 (3.7)	1478 (86.2)	324 (18.9)	1248 (72.8)

combinations; bovine and goat mixtures and donkey, bovine and goat mixtures were found in *C. poicilipes* and *C. annulioris*. Bovine and goat was the dominant combination for both species accounting for 81.8% and 76.0% of mixed blood meals for *C. poicilipes* and *C. annulioris*, respectively. *A. cuminsi* had two mixed blood meal combinations; bovine and goat mixtures (75%), and donkey, bovine, and goat mixtures (25.0%).

Discussion

Our study demonstrated the highly zoophilic nature of culicine mosquitoes collected at the Mwea, Kenya study sites. With the exception of *C. quinquefasciatus*, which fed on humans at low frequency, the other species fed on livestock, mainly on cattle and goats and less frequently on donkeys. Bogh et al. (1998) reported a human blood index (HBI) of 0.9 for indoor collected *C. quinquefasciatus* along the Kenyan coast. In western Kenya, the HBI for indoor and outdoor-collected *C. quinquefasciatus* was 0.88 and 0.23, respectively (Beier et al. 1990). Our HBI results for this species were 0.10 and 0.03, respectively for indoor and outdoor-collected populations, and therefore many times lower than in the western or coastal regions of Kenya. We did not conduct a census of domestic animals, but a quick observation revealed that cattle and goats were more common than donkeys and therefore more likely to be encountered by host-seeking mosquitoes. Chicken, dogs, cats, wild birds, and rodents were also present but lack of resources could not allow us test them as sources of mosquito blood meals. These animals are known to be important sources of blood meals for mosquitoes in the area (Kamau et al. 2003) and should be included in future studies. Importantly, we neither found any negative samples in our blood meal analysis nor evidence for cross reaction. However, it is possible that many blood meals were a mixture of identified and unidentified hosts. Moreover, out of the 17 culicine species known to occur in the area, blood-fed samples were only obtained for six species and all except one species had very few representatives. We are therefore cautious in interpretation of these results and recommend the need for further studies to establish the blood-feeding behavior of the diverse culicine species occurring in similar areas and their potential in disease transmission.

C. quinquefasciatus and *A. arabiensis* Patton are known to occur in higher densities in the study area compared with

Table 2 Proportion of different culicine species that had taken their blood meals from single or multiple hosts in Mwea Rice Scheme, Kenya

Species	Single host	Multiple hosts	Total
Culex quinquefasciatus	436 (26.5)	1,212 (73.5)	1,648
Culex poicilipes	4 (26.7)	11 (73.3)	15
Culex annulioris	6 (19.4)	25 (80.6)	31
Aedes cuminsi	1 (5.9)	16 (94.1)	17
Aedes taylori	1 (100.0)	0 (0.0)	1
Mansonia africana	1 (50.0)	1 (50.0)	2
Total	449 (26.2)	1,265 (73.8)	1,714

Table 3 Mixed blood meal combinations among culicine mosquitoes in Mwea Rice Scheme, Kenya

Blood meal combinations	*C. quinquefasciatus*	*C. poicilipes*	*C. annulioris*	*A. cuminsi*	*M. africana*
Bovine, goat	914 (75.5)	9 (81.8)	19 (76.0)	12 (75)	1 (100.0)
Donkey, goat	18 (1.5)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
Human, bovine	6 (0.5)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
Human, donkey	9 (0.7)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
Donkey, bovine	23 (1.9)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
Donkey, bovine, goat	223 (18.4)	2 (18.2)	6 (24.0)	4 (25.0)	0 (0.0)
Human, bovine, goat	12 (1.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
Human, donkey, goat	1 (0.1)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
Human, donkey, bovine	1 (0.1)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
All four hosts	5 (0.4)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
Total	1212 (100.0)	11 (100.0)	25 (100.0)	16 (100.0)	1 (100.0)

adjacent non-irrigated areas (Muturi et al. 2006). Because of the greater biting nuisance associated with these vectors, most people in irrigated areas sleep under bed nets and use other mosquito-control tactics that force mosquitoes to seek alternative hosts (Ijumba and Lindsay 2001; Ijumba et al. 2002; Mutero et al. 2004). This may partly account for significantly lower HBI for culicine mosquitoes in the study area as compared with the non-irrigated areas of western or coastal Kenya. However, although the HBI for indoor collected *C. quinquefasciatus* was significantly higher than that of outdoor-collected population, it is difficult to tell whether a human blood meal was taken indoors or outdoors. Our data suggested that most individuals of this species entered the house after feeding outdoors on domestic animals. It is therefore likely that some or possibly all of the indoor collected mosquitoes had obtained human blood meals outdoors.

The low anthropophily observed for culicine mosquitoes in the present study could be both beneficial and detrimental to disease transmission. On the positive side, it may disfavor transmission of Bancroftian filariasis by *C. quinquefasciatus* through loss of significant number of worms to the wrong host, or by failing to pick up enough parasites that can sustain transmission. Generally, filariasis transmission is very inefficient because there is no parasite multiplication in the mosquito and continuous exposure to many infective bites is required (Bockarie et al. 2002). It has been estimated that as many as 15,500 infective bites by *C. quinquefasciatus* are required to produce a patent human infection (Hairston and De Meillon 1968). Such infective bites are unlikely to be obtained when the human-biting rates are low. The commonness of cattle and goat feeding by mosquito species in the current study may also reduce transmission of arboviruses that may require amplification in other domestic animals or in wild animals or birds. For instance, pigs play an important role in pre-epizootic amplification of Japanese encephalitis (JE) virus in southeast Asian countries that experience JE epidemics (Peiris et al. 1992) while cattle are considered dead-end hosts (Ilkal et al. 1988). Japanese encephalitis prevalence is therefore high in areas where the pig population is higher relative to that of cattle (Colless 1959; Pennington and Phelps 1968; Mitchell et al. 1973) and low in areas where the cattle populations outnumbers that of pigs (Reuben et al. 1992). Marsupials also have been reported to divert host-seeking mosquitoes away from pigs thereby impeding establishment of JE virus (van den Hurk et al. 2003). On the negative, these mosquito species presents a high risk of Rift Valley Fever (RVF) virus transmission. This virus is transmitted by *Aedes* species to domestic animals including cattle, goats, sheep, and camels where virus amplification occurs leading to propagation into various *Culex* species that spread the virus (McIntosh 1972). The feeding pattern for the species in Mwea therefore present an ideal condition for RFV, and efforts should be made to establish the risk factors of the disease in similar areas and to develop sustainable mosquito surveillance and control systems.

Our findings demonstrated that nearly all the species examined fed on multiple hosts within a single gonotrophic cycle. *C. quinquefasciatus* had the greatest number of mixed blood meal combinations and was the only species containing mixed blood meals from all of the four hosts tested. Mixed feeding within the same gonotrophic cycle is common among mosquitoes and its epidemiological significance has been greatly debated (Garret-Jones et al. 1980; Burkot 1988). Arunachalam et al. (2005) suggested that multiple feeding may favor or disfavor disease transmission depending on whether the vector feeds on potential hosts or dead-end hosts. For instance, cattle feeding by malaria vectors may reduce malaria transmission through loss of certain number of sporozoites in non-human hosts (Hadis et al. 1997). Like wise, multiple feeding of JE vectors on dead-end hosts such as cattle and goat may divert mosquitoes from potential hosts such as pigs and birds resulting in reduced JE transmission (Arunachalam et al. 2005). In contrast, multiple feeding on potential hosts such

as cattle and goats, as observed in our study, may enhance amplification and transmission of RVF. These findings illustrate that domestic animals can be both the cause of an increase in the disease and the avenue through which it could be reduced. It is therefore essential to understand how domestic animals may impact on different mosquito-borne diseases before adopting zooprophylaxis as a disease-control strategy in similar areas.

In conclusion, our study has demonstrated the "preference" of domestic animals over humans by six culicine species. The study has shown that these mosquitoes have a tendency to feed on multiple hosts within the same gonotrophic cycle. Our findings demonstrate the great potential of these species to transmit RVF virus in similar areas. We recommend the need for sustained surveillance and control of these species in order to minimize the risk. More importantly, the potential role of domestic animals in arbovirus epidemiology should be evaluated before incorporating zooprophylaxis as part of mosquito-borne disease-control tactic.

Acknowledgements We are grateful to Prof. Christian Borgemeister, Director General, International Centre of Insect Physiology and Ecology for his strong support in this project. We acknowledge the technical support provided by James Wauna, Peter Barasa, Enock Mpanga, Peter M. Mutiga, William Waweru, Nelson Maingi, Martin Njigoya, Paul K. Mwangi, Christine W. Maina, Gladys Karimi, Irene Kamau, Nicholus Gachoki, and Naftaly Gichuki. We thank Mr. Raphael Wanjogu of the National Irrigation Board for providing us with laboratory space to conduct the study. This research was supported by NIH/NIAID grant # U01A1054889 (Robert Novak).

References

Appawu AM, Dadzie SK, Baffoe-Wilmot A, Wilson DM (2001) Lymphatic filariasis in Ghana: entomological investigation of transmission dynamics and intensity in communities served by irrigation systems in the Upper East Region of Ghana. Trop Med Int Health 6:511–516

Arunachalam N, Samuel P, Hiriyan J, Rajendran R, Dash A (2005) Short report: Observations on the multiple feeding behavior of *Culex tritaeniorhynchus* (Diptera: Culicidae), the vector of Japanese encephalitis in Kerala in Southern India. Am J Trop Med Hyg 72:198–200

Beier JC, Perkins PV, Wirtz RA, Koros J, Diggs D, Gargan TP, Koech DK (1988) Blood meal identification by direct enzyme-linked immunosorbent assay (ELISA), tested on *Anopheles* (Diptera: Culicidae) in Kenya. J Med Entomol 25:9–16

Beier JC, Odago W, Onyango F, Asiago C, Koech D, Roberts C (1990) Relative abundance and blood feeding behavior of nocturnally active culicine mosquitoes in Western Kenya. J Am Mosq Contr Assoc 6:207–212

Bockarie M, Tavul L, Kastens W, Michael E, Kazura JW (2002) Impact of untreated bednets on prevalence of *Wuchereria bacrofti* transmitted by *Anopheles farauti* in Papua New Guinea. Med Vet Entomol 16:116–119

Bogh C, Pedersen E, Mukoko D, Ouma J (1998) Permethrin-impregnated bednet effects on resting and feeding behavior of lymphatic filariasis vector mosquitoes in Kenya. Med Vet Entomol 12:52–59

Boreham PF, Chandler JA, Highton RB (1975) Studies on the feeding patterns of mosquitoes of the genera *Ficalbia*, *Mimomyia*, and *Uranotaenia* in the Kisumu area of Kenya. Bull Entomol Res 65:69–74

Burkot T (1988) Non-random host selection by anopheline mosquitoes. Parasitol Today 4:156–161

Centers for Disease Control (2007) Rift valley fever outbreak—Kenya, November 2006–January 2007. CDC 56:73–76

Chandler J, Highton R, Hill M (1975a) Mosquitoes of the Kano plain, Kenya 1. Results of indoor collections in irrigated and nonirrigated areas using human bait and light traps. J Med Entomol 12:504–510

Chandler JA, Boreham PF, Highton RB, Hill M (1975b) A study of the host selection pattern of the mosquitoes of the Kisumu area of Kenya. Trans R Soc Trop Med Hyg 69:415–425

Chandler JA, Highton RB, Boreham PF (1976) Studies on some ornithophilic mosquitoes (Diptera: Culicidae) of the Kano Plain, Kenya. Bull Entomol Res 66:133–143

Colless D (1959) Notes on the culicine mosquitoes of Singapore. VII. Host preferences in relation to the transmission of disease. Ann Trop Med Parasitol 53:259–267

Diallo M, Nabeth P, Ba K, Sall AA, Mondo M, Girault L, Abdalahi MO, Mathiot C (2005) Mosquito vectors of the 1998–1999 outbreak of Rift Valley Fever and other arboviruses (Bagaza, Sanar, Wesselsbron and West Nile) in Mauritania and Senegal. Med Vet Entomol 19:119–126

Dolo G, Briet OJT, Dao A, Traore SF, Bouare M, Sogoba N, Niare O, Bagayogo M, Sangare D, Teuscher T, Toure YT (2004) Malaria transmission in relation to rice cultivation in the irrigated Sahel of Mali. Acta Trop 89:147–159

Edwards F (1941) Mosquitoes of the Ethiopian region. III. Culicine adults and pupae. British Museum (Nat. Hist.), London

Fontenille D, Traore-Lamizana M, Diallo M, Thonnon J, Digoutte J, Zeller H (1998) New vector of Rift Valley Fever in West Africa. Emerg Infect Dis 4:289–293

Garret-Jones C, Boreham PF, Pant CP (1980) Feeding habit of Anophelines (Diptera:Culicidae) in 1971–1978, with reference to the human blood index: a review. Bull Entomol Res 70:165–185

Gubler D (1996) The global resurgence of Arboviral diseases. Trans R Soc Trop Med Hyg 90:449–451

Gubler DJ (2004) The changing epidemiology of yellow fever and dengue 1900 to 2003: full circle? Comparative Immunology. Microb Infect Dis 27:319–330

Hadis M, Lulu M, Makonnen Y, Asfaw T (1997) Host choice by indoor-resting *Anopheles arabiensis* in Ethiopia. Trans R Soc Trop Med Hyg 91:376–378

Hairston NG, De Meillon B (1968) On the inefficiency of transmission of *Wuchereria bancrofti* from mosquito to human host. Bull World Health Organ 38:935–941

Hunter J (1992) Elephantiasis: a disease of development in north-east Ghana. Social Sc Med 35:627–649

Ijumba J, Lindsay S (2001) Impact of irrigation on malaria in Africa: paddies paradox. Med Vet Entomol 15:1–11

Ijumba J, Mosha F, Lindsay S (2002) Malaria transmission risk variations derived from different agricultural practices in an irrigated area of northern Tanzania. Med Vet Entomol 16:28–38

Ilkal M, Dhanda V, Rao B, George S, Mishra A, Prasanna Y, Gopalakrishna S, Pavri K (1988) Absence of viraemia in cattle after experimental infection with Japenese encephalitis virus. Trans R Soc Trop Med Hyg 82:628–631

Kamau L, Koekemoer LL, Hunt RH, Coetzee M (2003) *Anopheles parensis:* the main member of the *Anopheles funestus* (Diptera: Culicidae) species group found resting inside human dwellings in Mwea area of central Kenya. J Am Mosq Control Assoc 19:130–133

Lacey L, Lacey C (1990) The medical importance of riceland mosquitoes and their control using alternatives to chemical insecticides. J Am Mosq Contr Assoc 6:3–93

Mahande A, Mosha F, Mahande J, Kweka E (2007) Feeding and resting behaviour of malaria vector, *Anopheles arabiensis* with reference to zooprophylaxis. Malaria J 6:100

McIntosh B (1972) Rift Valley Fever. 1. Vector studies in the field. J South Afr Vet Assoc 43:391–395

Mitchell CJ, Chen P, Boreham P (1973) Host-feeding patterns of four *Culex* species in an endemic area of Japanese encephalitis. Bull World Health Organ 49:293–299

Mutero C, Kabutha C, Kimani V, Kabuage L, Gitau G, Ssennyonga J, Githure J, Muthami L, Kaida A, Musyoka L, Kiarie E, Oganda M (2004) A transdisciplinary perspective on the links between malaria and agroecosystems in Kenya. Acta Trop 89:171–186

Muturi J, Shililu J, Jacob B, Githure J, Gu W, Novak R (2006) Mosquito species diversity and abundance in relation to land use in a riceland agroecosystem in Mwea, Kenya. J Vector Ecol 31:129–137

Muturi EJ, Mwangangi J, Shililu J, Muriu S, Jacob B, Mbogo C, Githure J, Novak R (2007) Evaluation of four sampling techniques for the surveillance of *Culex quinquefasciatus* (Diptera: Culicidae) and other mosquitoes in African rice agro-ecosystems. J Med Entomol 44:503–508

Muturi J, Muriu S, Shililu J, Mwangangi J, Jacob B, Mbogo C, Githure J, Novak R (2008) Effect of rice cultivation on malaria transmission in central Kenya. Amer J Trop Med Hyg 78:270–275

Mwandawiro C, Fujimaki Y, Mitsui Y, Katsivo M (1997) Mosquito vectors of Bancroftian filariasis in Kwale district Kenya. East Afri Med J 74:288–293

Mwangangi JM, Muturi EJ, Shililu J, Muriu S, Jocob B, Kabiru EW, Mbogo CM, Githure J, Novak R (2006) Survival of immature *Anopheles arabiensis* (Diptera: Culicidae) in aquatic habitats in Mwea rice irrigation scheme, central Kenya. Malaria J 5:114

Peiris JSM, Amerasinghe FP, Ratnayke C, Karunaratne S, Tsai T (1992) Japanese encephalitis in Sri Lanka—the study of an epidemic: vector incrimination, porcine infection and human disease. Trans R Soc Trop Med Hyg 86:307–313

Pennington N, Phelps C (1968) Identification of the host range of *Culex tritaeniorhynchus* mosquitoes on Okinawa, Ryuku Islands. J Med Entomol 5:259–267

Reuben R, Thenmozhi V, Samuel P, Gajanana A, Mani T (1992) Mosquito blood feeding patterns as a factor in the epidemiology of Japanese encephalitis in southern India. Amer J Trop Med Hyg 46:654–663

Rynn C (2007) A review of the 1992–1993 Yellow Fever outbreak in Kenya and future management options. J Rural Trop Public Health 6:40–44

Snow W (1983) Mosquito production and species succession from an area of irrigated rice fields in The Gambia, West Africa. J Trop Med Hyg 86:237–245

Thompson D, Malone J, Harb M, Faris R, Huh O, Buck A, Kline B (1996) Bancroftian filariasis distribution and diurnal temperature differences in the southern Nile delta. Emerg Infect Dis 2:234–235

van den Hurk F, Johansen C, Zborowski P, Paru R, Foley P, Beebe N, Mackenzie J, Ritchie S (2003) Mosquito host-feeding patterns and implications for Japanese encephalitis virus transmission in northern Australia and Papua New Guinea. Med Vet Entomol 17:403–411

Washino R, Tempelis C (1983) Mosquito host bloodmeal identification: methodology and data analysis. Ann Rev Entomol 28:179–201

White GB (1989) Lymphatic filariasis. WHO: Geographical distribution of arthropod-borne diseases and their principal vectors. WHO/VBC/89., pp 23–35

World Health Organization (1975) Manual on Practical Entomology in Malaria, part II. Methods and Techniques. WHO, Geneva