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Malaria entomological profile in Tanzania from 1950 to 2010: a review of mosquito distribution, vectorial capacity and insecticide resistance

BILALI KABULA[1,2,3], YAHYA A. DERUA[1], PATRICK TUNGU[1], DENNIS J. MASSUE[1], EDWARD SAMBU[1], GRADES STANLEY[4], FRANKLIN W. MOSHA[2] and WILLIAM N. KISINZA[1]
[1]*National Institute for Medical Research, Amani Research Centre, Muheza, Tanzania*
[2] *Kilimanjaro Christian Medical College, Moshi, Tanzania*
[3] *National Institute for Medical Research, Tukuyu Research Centre, Tukuyu, Tanzania*
[4]*National Institute for Medical Research, Head Quarters, Dar es salaam, Tanzania*

Abstract: In Sub Saharan Africa where most of the malaria cases and deaths occur, members of the *Anopheles gambiae* species complex and *Anopheles funestus* species group are the important malaria vectors. Control efforts against these vectors in Tanzania like in most other Sub Saharan countries have failed to achieve the set objectives of eliminating transmission due to scarcity of information about the enormous diversity of *Anopheles* mosquito species and their susceptibility status to insecticides used for malaria vector control. Understanding the diversity and insecticide susceptibility status of these vectors and other factors relating to their importance as vectors (such as malaria transmission dynamics, vector biology, ecology, behaviour and population genetics) is crucial to developing a better and sound intervention strategies that will reduce man-vector contact and also manage the emergency of insecticide resistance early and hence a success in malaria control. The objective of this review was therefore to obtain the information from published and unpublished documents on spatial distribution and composition of malaria vectors, key features of their behaviour, transmission indices and susceptibility status to insecticides in Tanzania. All data available were collated into a database. Details recorded for each data source were the locality, latitude/longitude, time/period of study, species, abundance, sampling/collection methods, species identification methods, insecticide resistance status, including evidence of the kdr allele, and *Plasmodium falciparum* sporozoite rate. This collation resulted in a total of 368 publications, encompassing 806,273 Anopheles mosquitoes from 157 geo-referenced locations being collected and identified across Tanzania from 1950s to 2010. Overall, the vector species most often reported included *An. gambiae* complex (66.8%), *An. funestus* complex (21.8%), *An. gambiae s.s.* (2.1%) and *An. arabiensis* (9%). A variety of sampling/collection and species identification methods were used with an increase in molecular techniques in recent decades. Only 32.2% and 8.4% of the data sets reported on sporozoite analysis and entomological inoculation rate (EIR), respectively which highlights the paucity of such important information in the country. Studies demonstrated efficacy of all four major classes of insecticides against malaria vectors in Tanzania with focal points showing phenotypic resistance. About 95% of malaria entomological data was obtained from north-eastern Tanzania. This shows the disproportionate nature of the available information with the western part of the country having none. Therefore it is important for the country to establish entomological surveillance system with state of the art to capture all vitally important entomological indices including vector bionomics in areas of Tanzania where very few or no studies have been done. This is vital in planning and implementing evidence based malaria vector control programmes as well as in monitoring the current malaria control interventions.

Keywords: malaria, mosquito, vectorial capacity, sporozoite, inoculation rate, insecticide resistance, Tanzania

Background

Malaria is the world's most prevalent vector borne disease caused by infection with a protozoan parasite of the genus Plasmodium. The disease is transmitted through bites from infected female mosquitoes of the genus Anopheles (WHO, 2010). The burden of malaria in Tanzania is high, yet little is known about the distribution of Anopheles mosquitoes that are vectors of the disease, how the species interact, overlap or differ across the country (WHO, 2010). Knowledge of the geographical distribution of the different species, their ecological parameters, role in transmission, and susceptibility to insecticide-based interventions is critical if malaria is to be controlled and eliminated in the next decade.

Vector control is a major component of the global strategy for malaria control which aims to prevent parasite transmission mainly through interventions targeting adult anopheline vectors (WHO, 2005). Insecticide treated nets (ITNs) and indoor residual spraying (IRS) are the cornerstone of malaria

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control programmes (WHO, 2010). High coverage with either of these interventions can result in a dramatic reduction in malaria associated morbidity and mortality (Lengeler, 2004; Pluess *et al.,* 2010).

From 2009, Tanzania embarked on countrywide free distribution of long lasting insecticide treated nets (LLINs) to cover all sleeping spaces and indoor residual spraying (IRS) to epidemic prone districts. This aims at attaining LLINs/ITNs universal coverage by 2013 (MOHSW, 2008). By mid 2011 more than 26 million LLINs had been distributed countrywide (MoHSW, 2011). However, the widespread development of resistance to pyrethroid insecticides in malaria vectors, recorded from West Africa (Chandre *et al.,* 1999a & 1999b**;** Etang *et al.,* 2003) East Africa (Vulule *et al.,* 1994; Ranson *et al.,* 2000) and South Africa (Hargreaves *et al.*, 2000) raises concern over the sustainability of ITNs/LLINs and IRS for malaria control. Both public health and agricultural use of pyrethroids may contribute to the development of resistance in mosquito populations. In Kenya, the use of permethrin-treated net was associated with reduced permethrin susceptibility in *An. gambiae* s.s. (Vulule *et al.,* 1994) while in South Africa indoor spraying with deltamethrin resulted in pyrethroid resistance in *An. funestus* (Hargreaves *et al.*, 2000). Agricultural use of pyrethroids, primarily in cotton-growing areas, has contributed to selection for resistance in *An. gambiae* s.s. in West Africa (Chandre *et al.,* 1999a,b; Etang *et al.,* 2003). It is unclear how resistance will affect the level of malaria control achieved by ITNs, as this may vary with the molecular mechanism(s) of resistance present in the vector population (Chandre *et al.,* 2000). However, the potential threat posed by development of resistance in vector populations has long been recognized (Curtis *et al*., 1998).

Malaria vectors are remarkably stable in a wide range of bio-ecological and seasonal conditions and hence appear to be very flexible both in exploiting new man-made environments and their response to malaria control activities (Colluzzi, 1984). This adaptability to environmental changes, leading to marked contrasts in vector bionomics, has lead to the development of various levels of vectorial efficiency for the populations of *Anopheles* species in heterogeneous environments within the same locality. Therefore this adaptability of *Anopheles* mosquitoes to environmental changes has become a very important factor in the epidemiology of malaria (Toure *et al*., 1994). Environmental heterogeneities have arisen mainly as a result of human activities which acts as a means of constant evolutionary challenge as they provide a source of climatic and environmental change to which anthropophilic anopheles mosquitoes have to respond by developing a highly dynamic vector-host relationship. This has eventually resulted into continuous change in both spatial and temporal patterns of malaria. Information on the distribution of malaria vector species in different bio-ecological locations is therefore important for understanding the epidemiology of malaria and in planning control measures that incorporate vector control approaches. In Tanzania, only limited scientific data exist on the link between bio-ecological zones and the distribution of malaria vectors (Mnzava & Kilama, 1986).

Several maps of malaria vector spatial distributions in Africa have been produced, however, most are at continental or sub-regional scale with limited specific data available for further use by national programmes and researchers aiming to better understand the epidemiology of the disease (Lindsay *et al.,* 1998; Coetzee *et al.,* 2000; MARA, 2005). This review therefore was carried out to establish and obtain the status of malaria vector bionomics /establishing the malaria entomological profile in Tanzania from historical data. Specifically, the study sought to (i) review the malaria vector species and their geographical distribution; (ii) determine the documented malaria transmission indices; and (iii) understand the susceptibility status of malaria vectors to insecticides used for vector control in the country. This review will provide an essential baseline on the known profile of malaria vectors and will be an important resource for malaria control and research programmes in the country.

Methodology

Data were obtained from both published documents (journal articles, thesis/dissertations as well as book chapters) and unpublished documents (technical reports). These were collected from research institutions, universities or through the MEDLINE search. Therefore when searching articles online we used *malaria vector species/distribution, anopheles, entomological inoculation rate (EIR), sporozoite rate, human blood*

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index, insecticide resistance status and Tanzania as search terms, and combinations thereof. All articles with information on Anopheles were included.

Each document was assigned a specific identification number and its information entered/recorded into a specific data collection form. For each article the following information was recorded: the locality, latitude and longitude, time/period of study, year project was initiated, species, number of specimens recorded, collection method (animal baits, human baits, indoor/outdoor resting collections, bednet trap, exit traps, human landing catches, and pyrethrum spray catches), stage of collection (adult or larval), morphological identification method (cytogenetic analysis of polytene chromosome, cross mating, morphology), molecular identification method, insecticide resistance status, insecticide tested, presence or absence of the kdr allele, *P. falciparum* sporozoite rate, EIR, human blood index (HBI) and the reference. Only articles containing information related to the objective of this study were included in the final analysis.

The locations (i.e. mosquito collection sites) were geo-referenced using the latitude and longitude coordinates obtained by crosschecking the names with the Directory of Cities and Towns in the World (2011) databases. In some sites the locations/coordinates were obtained from the research articles, as provided by the authors, while in some others these were obtained from the internet sources. Degree/minutes/seconds were converted into decimal degrees. It is acknowledged that there are limitations in using geographical coordinates obtained retrospectively. All the relevant information was entered into Microsoft Access database provided by WHO African Region and data analysis was performed using SPSS (Version 15 for Windows, SPSS Inc., Chicago, IL). All data were mapped using the geographical information systems software ArcGIS 9.2 (ESRI, Redlands, CA). The overall studied areas and species distributions of the main Anopheles species were mapped. Obtained data were also tabulated as far as necessary.

Results and Discussion

Data type and source

The reviewed documents presented in this paper were journal publications, technical reports and theses published between 1950 and 2010. A total of 368 documents were collected and reviewed. Of these 92 (25%) were from longitudinal studies and 276 (75%) cross-sectional studies (Table 1). From the information collected, it is evident that 95% of the data set was obtained from north-east and eastern Tanzania. This shows the disproportionate nature of the available information with the western part of the country having none (Figures 1, 2).

Table 1: Data source by year of publication

Data source/ Year	1950-60	1961-70	1971-80	1981-90	1991-2000	2001-10	Total	%
Technical reports	5	9	23	26	13	25	101	27.4
Journal	15	36	28	47	58	51	235	63.9
Thesis /Book chapters	3	5	9	5	8	2	32	8.7
Total	23	50	60	78	79	78	368	

The malaria entomological data are biased to the areas where the health research institutions are based i.e. north, north-east and east. From early 1960s to 1985 all research activities on malaria vectors were almost concentrated in Tanga and Kilimanjaro Regions with some few in Manyara, Zanzibar and Dodoma. Later after 1985 there was an expansion of the research works towards the central, western and southern parts of the country (Figure 2).

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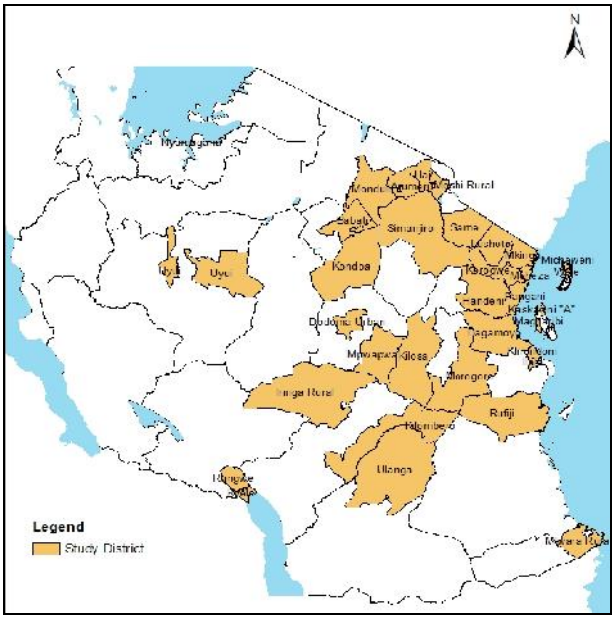

Figure 1: Distribution of the entomological studies by district in Tanzania (1965-2010)

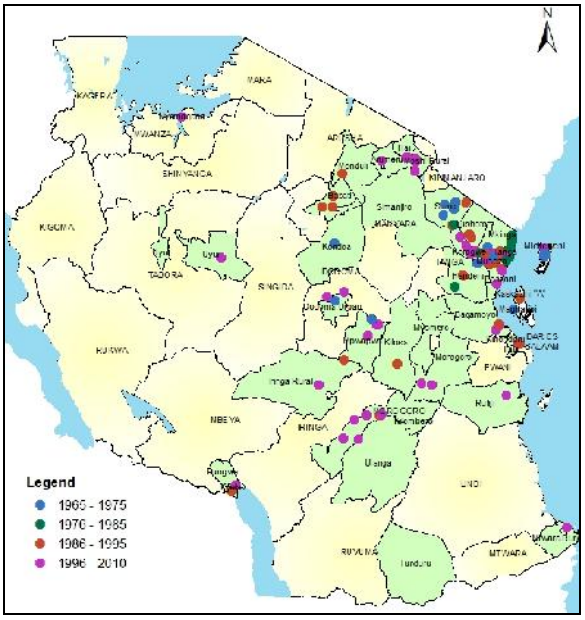

Figure 2: Distribution of entomological studies by year of publication

Malaria vector species and distribution

A total of 806,273 Anopheles mosquitoes from 157 geo-referenced locations across Tanzania were collected and identified between 1950s and 2010. However some publications did not state how many mosquitoes were collected / identified and therefore were not included in this figure. Overall, the vector species most often reported included *An. gambiae* complex (66.8%), *An. funestus* complex (21.8%), *An. gambiae s.s.* (2.1%) and *An. arabiensis* (9%). Other species (0.2%) included *An. coustani, An. leesoni, An. parensis, An. quadriannulatus, An. merus, An. marshallii* and *An. rivulorum. (*Gillies and Wilkes, 1965 ; Balirwa, 1975; Lines *et al.,* 1987; Magesa *et al.,* 1991; Wilkes *et al.,* 1995; Mboera *et al.,* 1997, 2010*;* Temu *et al*., 1998; Malima, 1999*;* Braimah *et al.,* 2005; Kulkarni *et al.,* 2006a*;* Kigadye *et al*., 2010*).*

Majority of the articles indicated the occurrence of *An. gambiae* s.l., and *An. funestus* across the studied areas of the country (Figure 3). Results reported from various articles show that the most abundant malaria vectors are the *An. gambiae* complex, *An. funestus* complex, *An. gambiae s.s.* and *An. arabiensis* with these vectors existing in sympatry in most locations (Biro, 1987; Charlwood *et al.,* 1998; Mboera, 2000; Mboera *et al*., 2010; Ijumba *et al.,* 2002). No article reported on how the M & S molecular forms of the *gambiae s.s* are distributed in the country. *Anopheles merus were* reported *to* dominate the mangrove and coastal part of the country (Bushrod, 1981; Mnzava & Kilama, 1986; Shiff *et al*., 1995; Temu *et al.,* 1998; Kigadye *et al.*, 2010) (Figure 4). Studies also indicated the presence of *An. funestus* s.s. and *An. rivulorum* among the *An. funestus* group. However the *An. funestus* s.s was predominantly found in all studied sites (Wilkes *et al.,* 1995; Koekemoer *et al.,* 2002; Temu *et al.,* 2007). *An. rivulorum* has been identified as a vector of malaria in some studies in Muheza, Tanzania (Malima, 1999; Wilkes *et al*., 1996). *A. funestus*, *A. rivulorum*, *A. leesoni* and *A. parensis.* One study reported the presence *A. funestus*, *A. rivulorum*, *A. leesoni* and *A. parensis* in sympatry in coastal Tanzania (Temu *et al.,* 2007). All these four members of the *A. funestus* group were found to be positive for *Plasmodium falciparum* though the rate was higher in *A. funestus* which was also found to be predominantly anthropophagic (Temu *et al.,* 2007). The role of *A. rivulorum*, *A. leesoni* and *A. parensis* in malaria transmission was not established and the Temu *et al.* (2007). Similar to the observations by Temu *et al.* (2007), in a recent study by Kweka *et al*. (2010) none of the 80

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collected *An. rivulorum* was found infected with malaria sporozoite. The sympatric occurrence of the same four members of *A. funestus* group has also been reported in other parts of Africa (Kamau *et al.,* 2003; Awolola *et al.,* 2005).

The total number of mosquitoes collected is under represented as the numbers of mosquitoes collected were not available in some studies. As the species abundance was not specified in some studies, the totals for each species was carried out independently and did not interfere with any of the calculations reported here. Clearly, research on the composition and distribution of the *An. funestus* group and *An. gambiae complex* is important, as they are important vectors contributing to the transmission of malaria in the country. We have recorded little research work being done on *An. funestus* from 2000. One main reason may be that this vector is refractory to colonization, and very difficult to find in the field, and its larvae are very difficult to find at high densities due to their tendency to stay submerged for long periods (Gillies & De Meillon, 1968). New techniques for egg laying and colonizing which will facilitate research opportunities in the future need to be developed.

The main methods of collecting Anopheles mosquitoes included adult collections (94.7%) and larval collections (1.3%), while a 1.3% used larval and adult collections combined. Adult collections were made primarily from pyrethrum spray catches (PSC) (12%), human landing catches (HLC) (10%), indoor resting (IR) collections (17%), CDC light trap (7%) and exit trap collections (ETC) (3%). Most collections (51%) were made using a combination of methods e.g. net catch/human bait, pyrethrum spray catch/exit trap, human landing catch/pyrethrum spray catch, pyrethrum spray catch/human bait traps / pit traps, pyrethrum spray catch/ indoor resting (IR) collections / pit trap, pyrethrum spray catch/CDC light trap/human landing catch. Larval collections were made from potential breeding sites, which included gutters, abandoned road sides, standing waters, vehicle tracks, tires, shallow wells, ponds, swamps, drains, rivers, small streams, irrigation ditches, hoof prints, domestic containers and empty cans. Some collections were made using a combination of larval and adult collection methods, e.g. pyrethrum spray catches/larval, indoor resting collections/larval, human landing catches/exit trap and indoor resting/human landing catch/pyrethrum spray catches/larval collections. We have noted the great variability in the reporting of the mosquito sampling and collection methods used over time. For example, PSC, HLC, IR, CDC light and ETC were the methods most frequently used either singly or in combination for adult mosquito collections. Surprisingly, the expensive and labour intensive method of the HLC (Sikulu *et al.,* 2009) is still being used in the country which is probably due to a lack of a suitable substitute for this important metric. However, recent tent traps have been tested and calibrated to the HLC and their use as an alternative tool is being tried in different locations across Africa (Sikulu *et al.,* 2009). The variability in the use of different sampling and collection methods calls for simpler and more standardized methods; the value of this has been previously emphasized (Hay *et al*., 2000; Kelly-Hope & McKenzie, 2009).

The methods of species identification were cytogenetic analysis of polytene chromosome (8.6%), enzyme electrophoresis (6.6%), PCR (7.9%), cross-mating technique (1.3%), cytogenetic analysis together with multilocus protein electrophoresis (11.3%) and cytogenetic analysis together with PCR (2%). Morphological identification was the most used (63.6%) method of identification in studies carried out in Tanzania. Cytogenetic analysis of polytene chromosome dominated from 1970s to early 1990s when PCR took over as the species identification method. Earlier studies used more cross mating techniques (Odetoyinbo & Davidson, 1968), morphological (Gillies & Wilkes, 1965; Davis *et al.,* 1995) and cytogenetic methods (Gillies & Wilkes, 1965; White *et al.,* 1972). For species identification, however, by the 2000s cross mating techniques and cytogenetic methods were nonexistent (Okorie *et al.,* 2011). In recent decades the emphasis has shifted to molecular techniques including PCR assays that target specific regions of repeat gene families, such as the ribosomal RNA (rRNA) gene family. A diagnostic assay for the identification of the *An. gambiae* complex based on IGS and ITS sequence differences was developed and applied routinely (Scott *et al.,* 1993). Similar techniques were also developed for *An. funestus s.l.* (Koekemoer *et al.,* 2002) along with more advancements allowing the simultaneous identification the *An. gambiae* complex species and *An gambiae* s.s. M and S molecular forms (Fanello *et al.,* 2002).

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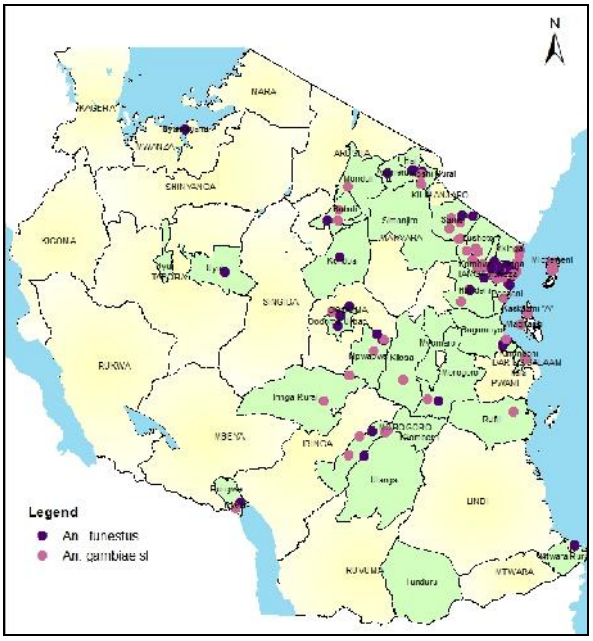

Figure 3: Distribution *of An. gambiae* s.l. and *An. funestus* in Tanzania

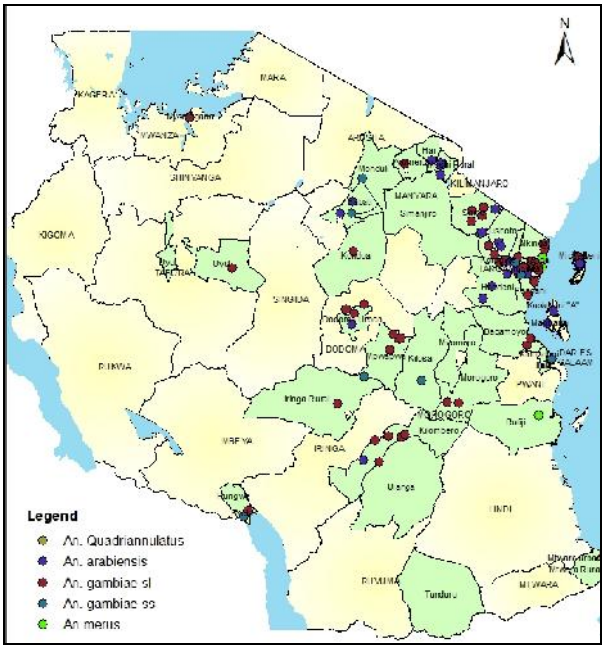

Figure 4: Distribution of *An. gambiae* complex in Tanzania

Malaria transmission indices

The proportion of Anopheles mosquitoes found to be carrying Plasmodium sporozoites, usually called the 'malarial sporozoite rate', has often been used as a measure of mosquito infectivity (Mboera & Magesa, 2001; Bass *et al.,* 2008). This shows the infection status of a mosquito and therefore giving the indication of the intensity of malaria transmission in a given locality. Detection of human-specific *Plasmodium* species in the mosquito host is one of the principal components in malaria vector control and monitoring programmes (Bass *et al.,* 2008). This parameter is extremely important for choosing and targeting malaria control interventions. Indeed, protective efficacy of vector control measures should be dependent on the initial intensity of malaria transmission.

Traditionally, determining mosquito infectivity has for many years based on dissection and visual assessment of glands using a microscope. However, this requires skilled personnel, is time consuming and does not determine the *Plasmodium* species present. It has, therefore, been largely superseded by more rapid immunological and molecular approaches (Bass *et al.,* 2008). The malaria sporozoite rate has been investigated in various areas of Tanzania (Mboera, 2000). In this review however, only 32.2% of the data sets reported on sporozoite analysis and transmission. Microscopic dissection (49.5%) and ELISA analysis (50.5%) were the methods reported for estimating sporozoite infectivity with noted increase in the use of ELISA in past two decades. The overall sporozoite rate reported varied according to *Anopheles* species and area of the study. The sporozoite rate in *Anopheles gambiae* ranged from 0 -11.8%. The sporozoite infection rate in *An. arabiensis* reported ranges from 0.01–11.1% and 0.29%-11.8% in *An. funestus* (Tables 2, 3). The highest sporozoite rate of 25% in *Anopheles gambiae* was reported by Mnzava (1991) in Muheza.

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Table 2: Sporozoite rate (%) in *Anopheles funestus* in Tanzania

Year of Publication	Sporozoite Rate (%)	Reference
1968	1.3	Freyvogel & Kihaule (1968).
1970	1.68	White *et al.* (1970)
1972	1.62	White *et al.* (1972)
1987	11.1	Matola *et al*. (1987)
1989	0.29-2.78	Mnzava *et al.* (1989)
1991	1.9-9.8	Magesa *et al.* (1991)
1995	2.1	Hoc & Wilkes (1995)
1996	6.9	Wilkes *et al.* (1995)
1998	2.6	Maxwell *et al.* (1998)
1998	4.4	Charlwood *et al.,* (1998)
1998	6	Temu *et al.* (1998)
2002	0.82-1.2	Ijumba *al.* (2002)
2003	0.48	Drakeley *et al*. (2003)
2003	2.5-5.2	Bodker *et al.* (2003)
2006	0.8-0.9	Kulkarni *et al.* (2006)
2007	2.3	Mboera *et al.* (2007, 2010)

Although the sporozoite rates found in *An. gambiae* and *An. funestus* in north-eastern Tanzania, showed a marked decline between the mid-1930s and the mid-1970s, then rising in the again in 1980s and 1990s (Mboera, 2000; Mboera & Magesa, 2001). The fall and rise in mosquito infectivity was attributed to the widespread use of antimalarial drugs (chloroquine), which initially tended to reduce the infectivity of patients for mosquitoes, and the subsequent development of resistance to these drugs in the malarial parasites (Mboera & Magesa, 2001). As a result of widespread use artesunate combination therapy (ACT) in the country, a similar declining trend of the sporozote rate (as of 1970s) is expected be observed. However due to scarcity of information on transmission this change could not be registered in this review. In recent years, there has been a decreasing trend in the number of publications reporting on transmission. There is need therefore to revitalize more work on this area which is important in assessing the impact of malaria control interventions.

Similarly, only 8.4% of the reviewed studies estimated the entomological inoculation rate (EIR), highlighting the paucity of such important information in Tanzania (Temu *et al.,* 1998; Ijumba *et al.,* 2002; Bodker *et al.,* 2003; Kulkarni *et al.,* 2006a). "Available EIRs value ranges from 0.03-299.3 infective bites per person per year for *An. funestus* (Temu *et al.,* 1998; Ijumba *et al.,* 2002; Bodker *et al.,* 2003; Kulkarni *et al.,* 2006a; Mboera *et al.,* 2007, 2010); 2.0 – 6241 for *An. arabiensis (*Mnzava 1991; Temu *et al.,* 1998; Ijumba *et al.,* 2002; Kulkarni *et al.,* 2006a); 0.05 - 1022 for *An. gambiae* s.s. *(*Mnzava 1991; Temu, *et al.,* 1998; Bodker, *et al.,* 2003); 18.3 for *An. merus* (Temu, *et al.,* 1998) and 0.01 – 2181.7 for *An. gambiae* s.l. (Temu, *et al.,* 1998; Bodker, *et al.,* 2003; Mboera *et al.,* 2007, 2010)."

Mosquitoes feed from a range of different host vertebrates. Some species have developed a characteristic host preference, feeding preferentially from humans, mammals other than human and birds. Host selection by mosquitoes is a result of a combination of intrinsic preferences modulated by intrinsic factors (Mboera, 2000). Host preferences and therefore the feeding preference of the mosquito can be assessed by analyzing the blood meal origin of the mosquito (Tempelis, 1975; Noutcha & Anumdu 2009). This has led to the estimation of the degree of degree of anthropophily through the human blood index (HBI). Several studies in Tanzania have documented the host preference of malaria vectors (Temu *et al.,* 1998; Ijumba *et al.,* 2002; Bodker *et al.,* 2003; Kulkarni, *et al.,* 2006a). The documented Human Blood Index (HBI) for *An. funestus*, *An. arabiensis* and *An. gambiae* ranged from 45-100%, 47.9-73.9% and 67-100% respectively (Temu *et al.,* 1998; Ijumba *et al.,* 2002; Bodker *et al.,* 2003; Kulkarni *et al.,* 2006; Mwanziva *et al.,* 2010). The HBI values above suggest a relatively higher anthropophagic tendency to malaria vector

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population in Tanzania. As the country is scaling up the malaria interventions, with speculations that mosquitoes are changing the feeding preference, there is need to investigate further on mosquito feeding pattern and host preferences.

Table 3: Sporozoite rate (%) in *Anopheles gambiae complex* in Tanzania

Year of publication	Sporozoite Rate (%)	Reference
1966	3.19	Pringle (1966).
1968	1.2	Freyvogel & Kihaule (1968)
1970	4.85	White *et al.* (1970)
1972	0.32-4.23	White *et al.* (1972)
1973	3-6	Bushrod & Magayuka (1973)
1987	11.8	Matola *et al.* (1987)
1989	0.58-1.36	Mnzava *et al.* (1989)
1991	8.7-9.5	Lines *et al.* (1991)
1991	5.2-10	Magesa *et al.* (1991)
1991	2.5-25	Mnzava (1991)
1995	9	Hoc & Wilkes (1995)
1995	2.8	Davis *et al.* (1995)
1997	11.5	Hogg & Hurd (1997)
1997	7.4	Mboera *et al.* (1997)
1998	7.3-9.8	Temu *et al.* (1998)
1998	5.9	Maxwell *et al.* (1998)
1998	2.5	Charlwood *et al.* (1998)
2002	0.01-0.12	Ijumba *et al.* (2002)
2003	0.39	Drakeley *et al.* (2003)
2003	0.7- 4.9	Bodker *et al.* (2003)
2006	0.5-11.1	Kulkarni *et al.* (2006a)
2007	3.4	Mboera *et al.* (2007, 2010)

Insecticide resistance

Only five studies reported data on insecticide resistance for malaria vectors in Tanzania (Mnzava, 1991; Kulkarni *et al.,* 2006b, 2007; Matowo *et al.,* 2010; WHO/GATES VBC project unpublished report). Of these, two were from countrywide surveys, while the rest were localized. The species most tested for insecticide resistance were *An. gambiae* s.l (Kulkarni *et al.,* 2007; B. Kabula *et al*., unpublished) and *An. arabiensis* (Kulkarni *et al.,* 2006; Matowo *et al.,* 2010). The insecticides tested were permethrin, deltamethrin, Lambacyhalothrin and DDT. The first countrywide survey that conducted in 2004/5 indicated that all mosquito species were full susceptible to pyrethroids and DDT (Kulkarni *et al.,* 2007). The second country wide survey was conducted in and 2008/9. Similarly the result from this survey indicated continued susceptibility of the local mosquito population to pyrethroids and DDT in most of the sites with some focal areas with noted phenotypic resistance (B. Kabula *et al.,* unpublished). The biochemical basis of permethrin resistance in *An. arabiensis* from Lower Moshi, with elevated levels of mixed function oxidases and ß-esterases has been registered (Matowo, *et al.,* 2010). A low frequency of West African *kdr* (L104F) *was detected in* Moshi (Kulkarni *et al.,* 2006b).

While studies have demonstrated efficacy of all four major classes of insecticides against malaria vectors in Tanzania (Kulkarni *et al.,* 2007), with focal points with phenotypic resistance (B. Kabula *et al.,* unpublished), there is no room for complacency. Continuous monitoring of this efficacy is imperative for timely deployment of effective resistance management tactics when resistance is recognized. Similarly, the presence of the West African *kdr* mutation at low frequency in this East African population of *An. arabiensis*

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has implications for the spread of the *kdr* gene across the African continent, therefore close monitoring of resistance is essential.

Conclusion and recommendations

The current review has evidently and clearly shown a very scarcity and skewed of malaria entomological data in the country. The data has evidently shown that about 95% of malaria entomological data were obtained from studies carried out in north-eastern and eastern Tanzania. This shows the disproportionate nature of the available information with the western part of the country having none. The data obtained from only part of the country has been extrapolated as platform for malaria vector control interventions in the country. This extrapolation may not always be true thus leading to the implementation of the decision made on the basis of the wrong information. This may be the reason for the failure of several malaria vector control interventions to achieve the set objectives of eliminating transmission.

Similarly, only 32.2% and 8.4% of the data sets reported on sporozoite analysis and EIR respectively, which highlights the paucity of such important information in the country. This review and other studies in the country have shown that malaria prevalence rates, parasite densities and entomological inoculation rates vary from one area to another (Mboera, 2000; Mboera *et al*., 2010; 2011). This means that our malaria control interventions are most probably not on evidence based information. Malaria vector distribution in Tanzania is also not exhaustively understood as most studies were done in the north-eastern and eastern part of the country. This calls for an urgent need of establishing an entomological surveillance system with state of the art to capture all vitally important entomological indices including vector bionomics representing the less exploited/unexploited parts of the Tanzania. This will hopefully provide more information on entomological data particularly in areas where the information are scanty. There is also need for regular updating of the current malaria entomological profile for appropriate decision making and proper intervention strategies for malaria vector control in the country.

Authors' contributions

Bilali Kabula organized and coordinated the review, organized data and wrote the first and subsequent drafts of the manuscript. Yahya Derua, Patrick Tungu, Denis Masue and Edward Sambu performed the review. Grades Stanley organized data and produced maps. Franklin Mosha and William Kisinza contributed to the writing and proof-reading of the manuscript. All authors have seen and contributed to revisions of the manuscript.

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