Assembling a geo-coded inventory of Anopheline (Diptera: Culicidae) species occurrence in Africa

Robert W Snow, David Kyalo, Punam Amratia, Abdisalan M Noor, Maureen Coetzee

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1. Introduction

Botha De Meillon highlighted in 1939 that "*Malaria in South Africa, as elsewhere in the world, is an entomological disease. Its epidemiology only becomes clear when knowledge of its entomology has been elucidated*" [1]. This obvious statement is as relevant today as it was over 70 years ago. All national malaria strategies across sub-Saharan Africa implement interventions aimed at reducing human exposure to infectious malaria vectors. These include insecticide treated nets, applications of residual insecticides on household walls, or the targeting of larval stages of vectors to reduce vector abundance, survival and/or human-feeding frequency. However, the distribution of vector compositions linked to their intrinsic behavioural bionomics and their resistance to insecticides remains largely unknown, or under-emphasized, when planning vector control at national scales.

2. Historical inventories of malaria vectors and early maps

The first global inventory of the Genus Anopheles (Diptera: Culicidae) malaria vectors was published in 1901 and reproduced in 1903 and 1910 [2]. Sir Rickard Christophers updated this inventory in 1924 for the purposes as he described it "*as a necessary preliminary to studying the geographical distribution of species, has been published in the belief that, as a handy means of reference to known species with their correct names, it would be useful to medical men and others*" [3]. In 1929, an assembly of reported locations of vectors from published and unpublished sources from the beginning of the 1900s, was developed as lists per country, location names and for the first time shown on regional maps [4]. This was updated for the Africa region in 1938, providing bibliographic sources, locations, taxonomic keys for adult mosquitoes stages and more details on bionomics by the Natural history Museum, London [5] and repeated for larval stages in 1952 [6]. During the Second World War, the US Sanitary Department developed a separate inventory [7].

The most definitive catalogue of recorded Anopheline species for the Africa region was published in 1968 by Mick Gillies and Botha de Meillon, updating earlier work [8] and capturing a wealth of published and unpublished observations from across the continent, linked to spatial grids of their distributions (Figure 1). This geo-referenced catalogue was accompanied by comprehensive notes on the species role in malaria transmission and bionomics [9]. Updated inventories of Anopheline distributions were published in 1972 [10] and 1987 [11].

National entomological reconnaissance formed an important part of activities mounted at aggressive control and elimination during the first 60 years of the last century. These were often assembled as hand drawn vector species distribution maps from routine surveys or compilations of national research and surveillance. The most notable sub-regional assemblies of available information on anopheline malaria vectors was undertaken during the 1950s for Central Africa (Chad, Central African Republic, Congo, Gabon) [12] and the West African region (Figure 2) [13].

Figure 1: Location representation of information on Anophelines up to 1960s: distributions and range of Left *An funestus* and Right *An gambiae* [9]

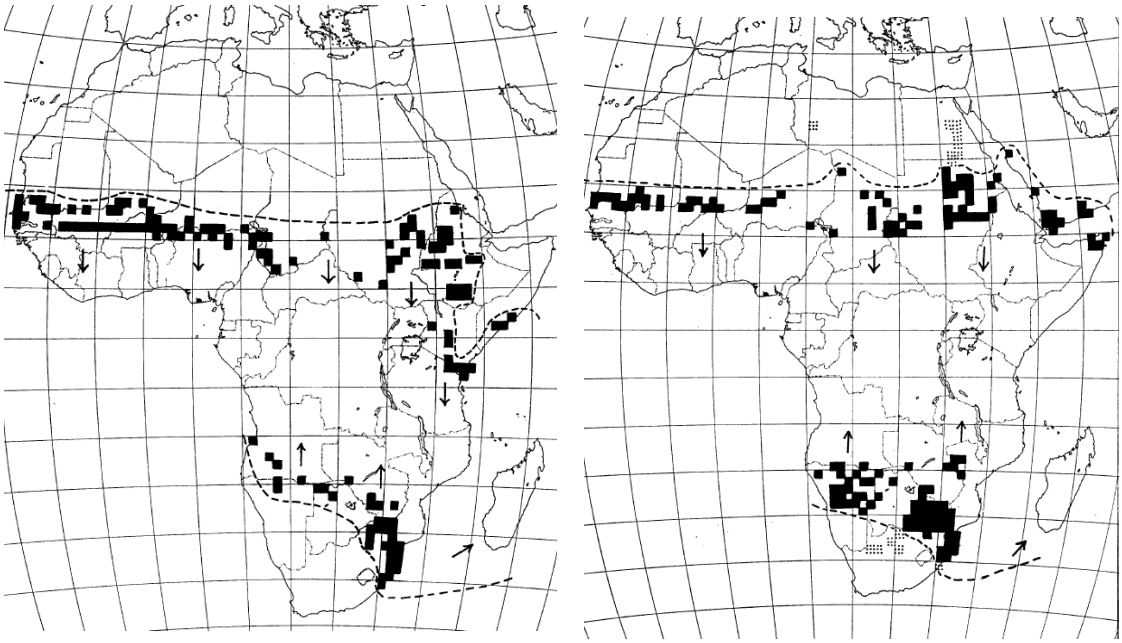
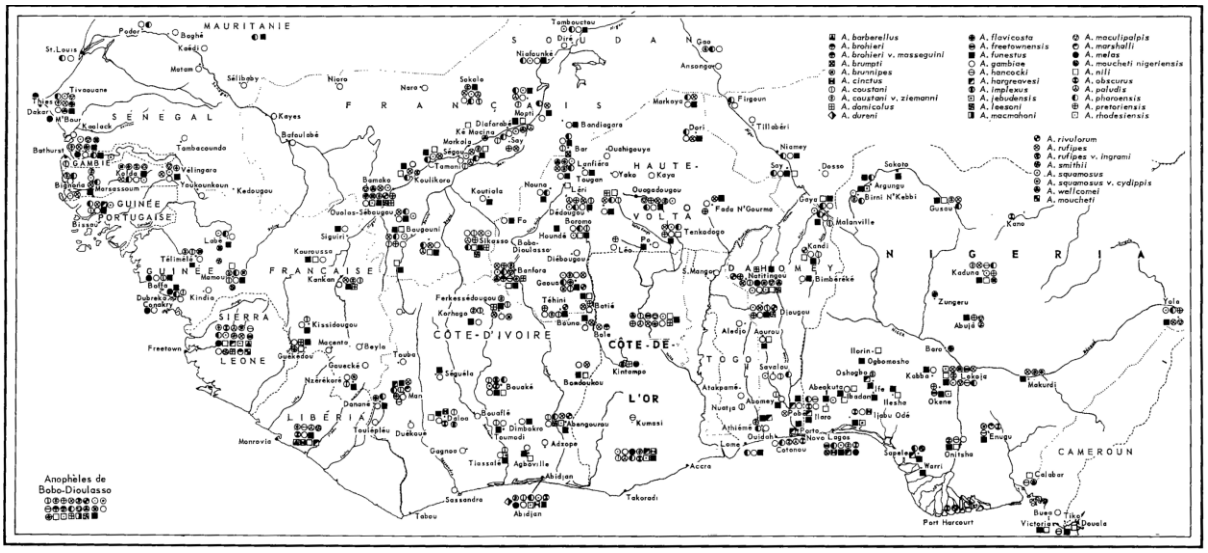


Figure 2: Anopheline species distributions in West Africa [13]

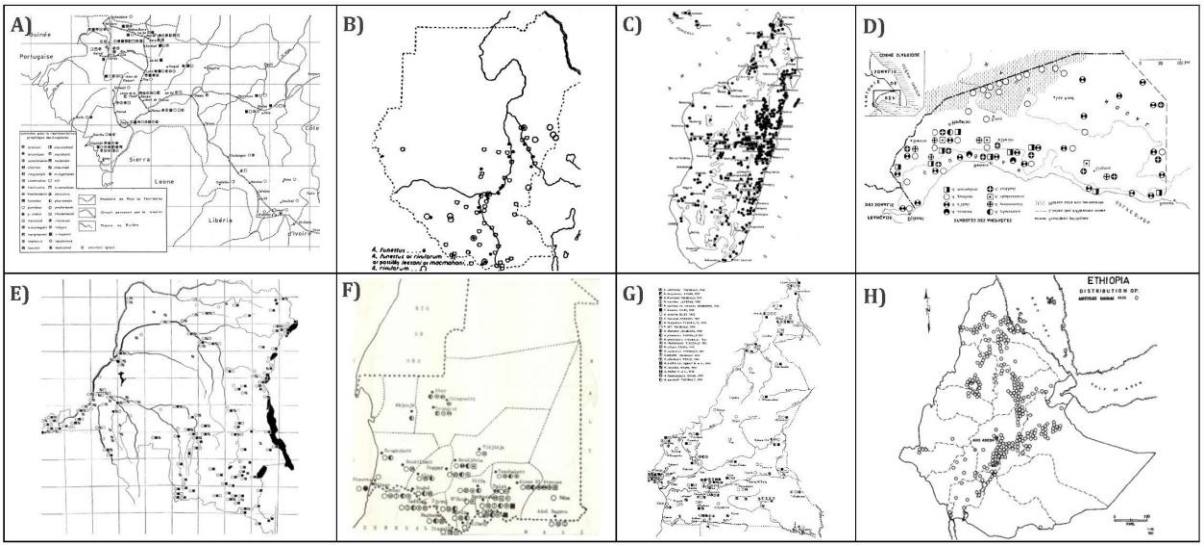


Some of the earliest national inventories of malaria vector species on the African continent, and its islands, were compiled in Algeria [14], Cape Verde [15], Democratic Republic of Congo (DRC) [16], Egypt [17], Eritrea [18], Ethiopia [19,20], Kenya [21,22], Gabon [23], Liberia [24], Mauritius [25], Mozambique [26,27], Nigeria [28], Rwanda and Burundi [29], South Africa [30-33], Sudan [34], Zambia [35] and Zanzibar [36,37].

During the 1950s and 1960s, efforts to compile national inventories of primary and secondary vectors of malaria provided important descriptions of the distributions and ranges of anophelines in countries preparing for pre-elimination or national control. These referenced national inventories included those developed for Angola [38], Burundi and Rwanda [39], Cameroun [40], Congo [41], Côte-d'Ivoire [42], DRC [43,44], Ethiopia [45], Guinea [46], Liberia

[47], Libya [48], Madagascar [49], Mali [50], Mauritania [51], Morroco [52], Nigeria and Cameroon [53,54], The Gambia [55], Sao Tome & Principe [56], Somalia [57], Tunisia [58] and Zanzibar [59]. Many of these national inventories provided maps showing distributions of anopheline species (Figure 3) and covered many of the secondary vectors of malaria and other species within the anophelinae family.

Figure 3: A) Guinea (all Anopheline species)[46]; B) Sudan (exampled with *An coustani, An ziemanni, An obscurus and An symesi*) [34]; C) Madagascar (*An mascarensis*) [49]; D) Somaliland (*An azaniae, An d'thali, An gambiae, An macmahoni, An pharoensis, An pretoriensis, An rhodesiensis, An turkhudi*) [60]; E) DRC (all Anopheline species)[44]; F) Mauritania (*An melas, An gambiae, An rufipes, An pharoensis, An d'thali, An pretoriensis, An funestus, An demeilloni, An rhodesiensis*) [61]; G) Cameroon (all Anopheline species) [13]; H) Ethiopia (*An gambiae*) [45]



During the Global Malaria Eradication era descriptions of the anopheline vectors, shown as sub-national distributions, were regarded as important preludes to the attack phases of control and notably the likely impact of indoor residual house-spraying. The surveillance of malaria vectors continued in Africa where elimination was pursued (e.g. North Africa and the islands) but entomological reconnaissance for malaria control became a forgotten public health science during the 1970s and 1980s across much of sub-Saharan Africa [62].

3. The revival of geo-coded vector databases

In 1996, the Mapping Malaria Risk in Africa collaboration was launched [63-66] to assemble, geo-code and map malaria parasite and vector surveys undertaken across Africa south of the Sahara. The initiative focused only on documenting records of the sibling species of the *Anopheles gambiae* complex and *An. funestus* s.l. resulting in 2535 geo-referenced records of anopheline malaria vectors from reports of surveys undertaken between 1920 and 2004. This was a milestone collaboration, managed by scientists across the Africa region, and started a renaissance in the assembly of empirical malaria information as geo-coded inventories.

The African Network for Vector Resistance (ANVR) was established in 2000, and amongst its objectives was the important goal of improving dissemination of resistance data [67]. Over

the next 10 years, a database was developed to store the results of resistance monitoring activities by ANVR members. This database has now been integrated for open access with the launch of IRBase [68-70]. This database is linked to a spatial display platform and by 2014 contained information from 4,084 susceptibility data points for 1,505 locations using recommended WHO methods from 54 countries worldwide between 1954 and 2012 [70].

Two initiatives started in 2005, aiming to extend work started by MARA/ARMA, globally for malaria vectors under the Malaria Atlas Project (MAP) [71,72], and a wider disease vectors initiative to create a global geo-coded repository of vectors of chagas, dengue, leishmaniasis and malaria called the Disease Vectors Database [73,74]. The MAP repository focussed only on peer-reviewed published reports of dominant vector species (for Africa the complexes of *An. gambiae*, *An. funestus*, *An. nili* and *An. moucheti*) resulting in 4,234 site-location reports for the African continent from surveys undertaken between 1984 and 2010. The Disease Vectors Database included "secondary" vectors, many of which are not true vectors of malaria (*An. coustani*, *An. paludis*, *An. hancocki*, *An. marshallii*, *An. pharoensis* and *An. rufipes*) [73, 75][1].

The MosquitoMap initiative [76] was launched as part of the Walter Reed Bioinformatics Unit's systematic catalogue of Culicidae, based at the Smithsonian Institution, made publically available in 2009. This portal was transformed to cover a broader range of insect vectors in 2012 and is a comprehensive on-line digital archive of species locations allowing for mapped distributions, linked to the Walter Reed bionomics descriptions and provides users with some abilities to develop web-based ecological niche models of vector distributions [77-79]

Other useful on-line resources include VectorBase, that focuses on descriptions of bionomics and gene libraries of many disease vectors [80] and the Vector-Borne Disease Network (VecNet) [81], established in 2011 with an original aim to provide information necessary for modelling approaches to elimination scenario planning [82].

A common feature of the more recent on-line global or regional vector species location databases is that they are often a) a poor representation of the entire historical reference material for any given country; b) do not capture important unpublished reports from national control agencies and research partners; and c) do not always cover the secondary vectors reported in countries. For example, in the DRC, the MARA and MAP databases report only 4 and 20 site locations respectively for Dominant Vector Species (DVS) of the *An. gambiae* and *An. funestus* complexes. Some countries have recognised the importance of updating inventories of anopheline distributions, notably where regional compendia are incomplete for country purposes. Examples of these more contemporary national inventories are found in the Cote d'Ivoire [83], DRC [84], Eritrea [85], Kenya [86], Madagascar [87], Mali [88-90], Niger [91], Nigeria [92], Senegal [93], Tanzania [94] and countries concerned about re-introduction of malaria following elimination, Morocco [95], Egypt [96] and Reunion [97].

[1] It is no longer possible to connect to this online database

4. General purpose of INFORM vector data assembly

Investments have already been made over the last 20 years to develop regional and global species occurrence maps and databases for malaria. We have embarked on the present data assemblies with this in mind, and it is not the intention of INFORM to replicate, duplicate or replace previous or current efforts to maintain these digital repositories of data. Rather, the ambition is to capture as much historical, contemporary unpublished data and the full range of anopheline species as geo-coded digital inventories linked to original PDF materials for distribution to national malaria control programmes across Africa. These geo-coded bibliographic resources are often not available at country-levels for further interrogation, analysis or identifying information gaps. Following the broader principles of INFORM [98], we hope these databases and digital libraries, will be owned, updated and shared by national programmes to provide a more informed basis for future vector control activities.

We have not focussed on the important assemblies of information related to resistance, these data have been carefully curated, geo-coded and validated by the IRBase initiative [68,70] and we encourage national programmes and their research partners to share data with this network.

The range of countries we have included in our searches of possible malaria vectors include island and mainland territories that have never supported malaria transmission, islands that have eliminated malaria and North African countries that have since the 1960s systematically reduced the extent and finally eliminated malaria. As such we have made efforts to locate literature and reports on vector species compositions in Lesotho and the Western Sahara (previously Spanish Morocco); the African offshore islands of the Chagos Islands, Mascarene archipelago (British Indian Ocean Territory), the Seychelles archipelago (Mahé, Praslin, La Digue, Aride and outer islands), Tromelin Island (French Overseas Territory), Saint Helena (Atlantic Ocean British Overseas Territory), the Aldabra Island group (Aldabra, Assomption, Cosmoledo and Astove), Canary Islands (Tenerife, Grand Canaria, Lanzarote, Feuteventura, La Palma, Gomera, Hierro) that have not supported malaria transmission; Reunion and Mauritius that have eliminated malaria; and Morocco, Algeria, Tunisia, Libya and Egypt that have largely eliminated malaria since the late 1960s. Understanding the malaria vector species range, even with territories free of malaria, provides a basis to understand the receptive, “potential” risks of malaria, and a more complete understanding of the ecological range of vector species.

Throughout we have used as a basis for delineating national boundaries provided under UN sponsored boundary digital processing [99]. The boundary anomalies, and how we treat these, have been described in the accompanying working paper [100; Section 5.3].

5. Data assembly methods

Methods used by us to identify sources of information have been opportunistic, cascaded approaches and do not adhere to methods proposed for systematic reviews or meta-analysis [101], as a reliance only upon peer-reviewed materials would result in the exclusion of valuable, rich unpublished data sources at country-levels. We have used personal contacts, casual references to surveys in ministry of health reports, searches of archives and more

traditional peer-reviewed publication searches to track down possible sources of anopheline vectors survey data from across the continent. The following sections attempt to articulate the approaches taken to locate information.

5.1. Data searches

We began our searches for original reference sources using the bibliographies provided in earlier inventories published between 1929 - 1987 [4-6, 9-11]. These regional inventories were updated with citations to reports assembled as part of national or sub-regional inventories developed during the 1950s and 1960s (see above). Original reports not available on-line through journal digital repositories or HINARI [102], were located at libraries in Antwerp, Paris, Lisbon, London and the archives of the Ministry of Health in Arusha, Tanzania and Nairobi, Kenya. Two additional and notable sources for unpublished materials were identified through reviews of colonial medical administration annual reports from across Africa published between 1910 and 1955 and reports of the World Health Organization made following consultants country visits or quarterly reporting of pilot malaria elimination projects during the 1960s and 1970s. Full details of European and African regional library archive searches are provided elsewhere [100].

Online electronic databases were used as one means of identifying peer-reviewed, published data on Anopheles species locations, most notably those published since the 1980s, including: PubMed [103]; Google Scholar [104]; the Armed Forces Pest Management Board – Literature Retrieval System [105]; the World Health Organization Library Database [106]; and the Institute de Recherché pour le Development on-line digital library service [107]. Regional journals, including the large number of national medical, public health and parasitological journals, were not identified readily from the above sources but titles and abstracts were available on African Journals Online (AJOL) [108].

In all digital electronic database searches for published work the free text keywords "*Anopheles*" and "*country-name*" were used. We avoided using specialised Medical Subject Headings (MeSH) terms in digital archive searches to ensure as wide as possible search inclusion. Searches were supplemented through routine weekly notifications from Malaria World [109], the Roll Back Malaria news alert service [110], the Environmental Health at USAID malaria bulletins [111] and Santé Tropicale for Francophone country national and regional journals including Medecine D'Afrique Noire [112].

All publications were cross-referenced using the bibliographies for additional sources that may have been missed or that may correspond to unpublished or 'grey' literature, not controlled by commercial publishers. Finally, we compared our search findings with those of MAP and MARA to check if we had omitted published materials.

Doctoral and masters theses undertaken with entomological components were sourced from local university libraries in the faculties of zoology, medicine or related biological sciences in Kenya, Tanzania, Senegal, Mali, Sudan, Mozambique, UK, Belgium and France. National and international malaria congresses and conference proceedings were also reviewed for abstracts that contained information on species identifications at specific localities. These

two sources were very opportunistic and it is expected that a wealth of information is available across university departments in Africa, not captured by us.

In addition to formal searches of on-line resources and library archives, we also contacted entomologists working across Africa, within research institutes or as part of National Malaria Control programmes, to investigate the possibilities of unpublished survey reports. In recent years, following the scaled introduction of indoor residual house-spraying, countries have established more rigorous malaria vector surveillance, providing a new rich source of species location data.

5.2. Organization of the database

The basic principle of the database was to ensure a site-specific inventory. As such, multiple reports from the same site were collapsed to a single entry, with all citations to that site referenced to that site. Invariably, multiple authors of published material report on the same surveys or aspects of entomological work from the same site across a period of several years. Individual reports vary in the stages of vector sampled and the precision methods used to distinguish species and sibling species of complexes. In such cases, all sampling, vector stage and species identification methods were recorded across surveys. We have included more than once individual survey sites only if these could be uniquely separated by at least 10 complete years[2]. Often, where sites were part of longitudinal surveillance this resulted in sometimes decade long periods of enquiry. In addition, multiple reports cited works by other entomologists at the same sites, these were also captured during the data abstractions, labelled op cit "authors" in the event that original reports could not be located.

5.3. Species identification

Throughout the data assembly we have only recorded the reported presence of a species as Y where this was described during a survey. We only recorded absence as N when the report specified its absence during the survey. Therefore the database contains information predominantly of species presence.

A perennial problem with assemblies of vector inventories over time are the ambiguities in taxonomy. These improve with time as part of detailed mosquito systematics and improvements in morphological keys. With an expansion in the use of genetic differentiation techniques from the late 1960s, species and sibling species differentiation has improved. The default methods for species identification today are those provided by Polymerase Chain Reaction (PCR). Improving species identification has resulted in difficulties in attributing species reports to revised classes.

Africa is home to the most effective and efficient vectors of human malaria: *An. gambiae* Giles complex and *An. funestus* Giles Group [9,113]. The earliest descriptions of the *An. gambiae* complex referred to a single species, *An. costalis*, during the first decade of the last century. Following the Liverpool School visit to The Gambia in 1902, this species was named *An. gambiensis* Giles. The salt-water breeding, mainly coastal sibling species (*An. melas*

[2] For national reviews and inventories of survey data we have often assumed that reports of vector occurrence summarised has been undertaken within the previous decade if no specific survey date was provided.

Ribbands and *An. merus* Dönitz) were confirmed as sibling species of the gambiae complex in the 1940s through observations on salinity tolerance and slight morphological variations from freshwater breeding *An. gambiae* [114-116].

Cross-mating, hybridization methods distinguished three fresh-water breeding species of *An. gambiae* (A-C) in the 1960s [117-119]. A morphologically unique sibling was identified in the mineral springs of the Semliki National Park, Bwamba district, Uganda, and named *An. bwambae* White (previously species D). It appears to be restricted to this area only and probably a secondary vector when sympatric with *An. gambiae* s.s. [120,121]. The zoophilic *An. quadriannulatus* A and *An. quadriannulatus* B were described as sibling-species of the *An. gambiae* complex (previously species C) in the early 1980s but not regarded as vectors of malaria within their geographic ranges of southern Africa and Ethiopia [113,122]. *An. quadriannulatus* B from Ethiopia was later renamed *An. amharicus* Hunt, Wilkerson & Coetzee sp. n. [123,124] while the name *An. quadriannulatus* was retained for the southern African form. Chromosomal investigations of species A and B were undertaken in the late 1960s and this led to the ability to distinguish between *An. gambiae sensu stricto* and *An. arabiensis* [125].

Differentiation of *An. gambiae* s.s. was first recognised in the 1980s based on five chromosomal forms: 'Mopti', 'Bamako', 'Savanna', 'Forest' and 'Bissau' [88,126,127]. Two of these forms were later genetically distinguished as *An. gambiae* s.s. S form (Savanna/ Bamako) and M form (Mopti) [128,129]. In 2013, the "M form" was re-named *An. coluzzii* Coetzee & Wilkerson sp. n [124]. This degree of taxonomical transition makes it hard to describe the location of members of the *An. gambiae* complex over time.

In the database we have recorded the gambiae complex to as much detail as possible from the reports - *An. gambiae s.l* (if only complex mentioned), *An. gambiae* s.s. (Species A when possible to differentiate from *An. arabiensis* (Species B) and saltwater breeding varieties), *An. gambiae* S form (when indicated as Savannah or Bamako or S forms) and *An. colluzzi* (when indicated as M form or Mopti form). *An arabiensis*, *An. melas*, *An. merus* and *An*. *bwambae* were all recorded separately where information allowed. *An. quadriannulatus* was recorded under other species notes. Throughout our data extractions we have simply recorded what is available from each report, updating earlier reports with cross-mating or chromosomal analyses undertaken during the 1960s and 1970s at the same sites during the same time intervals of the complex descriptions [for example 118,130,131]. In certain locations, where subsequent surveys proved the absence of *An. gambiae s.s* and only *An. arabiensis* presence we have coded the presence of *An. arabiensis* as bracketed [Y].

Far from being easier, the *An. funestus* complex has taxonomic complexity similar to that of *An. gambiae.* The *An. funestus* group originally consisted of nine species: the major African malaria vector *An. funestus s.s*. and eight minor or non-vectors (*An. aruni*, *An. parensis*, *An. vaneedeni*, *An. confusus*, *An. rivulorum*, *An. leesoni*, *An. brucei* and *An. fuscivenosus* [9,11]. Subsequent studies on the systematics of the group resulted in a reclassification of the group with *An. funestus*, *An. aruni*, *An. parensis*, *An. confusus, An. vaneedeni* and *An. funestus-like* (described in Malawi) being grouped together as members of the "*An. funestus* subgroup"; *An. rivulorum*, *An. rivulorum-like*, *An. brucei* and *An. fuscivenosus* form their own subgroup; and *An. leesoni* has been grouped with the Asian *Anopheles minimus* subgroup [132-135].

Among the funestus group, *An. funestus* s.s. is a significant vector in the transmission of malaria [133]; *An. rivulorum* has been recently implicated in transmission in Tanzania and might contribute as a secondary vector to transmission elsewhere [136,137]; all other species in this group are not implicated malaria transmission. Despite morphological similarities between the members of the funestus group and other groupings described above, we have presumed that when *An. funestus* is mentioned in reports this invariably refers to *An. funestus* s.s. When *An. rivulorum* has been mentioned specifically we have indicated this as Y within the database under its own column. Where other members of the funestus group have been specified these have been recorded under other species notes.

In 1951, De Meillon provided a list of other anopheline species found infected with the malaria parasite occurring under natural conditions in Africa [138]. He further classified these as primary (*An. gambiae* and *An. funestus* groups), secondary (implicated in transmission in restricted areas and where exhibiting an endophilic nature) and tertiary (where uncertainty existed on source of plasmodia, vectors were short-lived and mostly exophilic). The list of secondary vectors included *An. brunnipes* (mainly in DRC), *An. hancocki*, *An. hargreavesi*, *An. moucheti moucheti*, *An. nili*, *An. pharoensis* and *An. rufipes*. Examination of over 8,000 specimens during the 1950s from across West Africa confirmed the likely roles of these vectors and showed almost no sporozoite infections or oocyst development in the "tertiary" species, and significant infection rates among De Meillon's "secondary" vectors [139].

As might be expected, our most detailed understanding of the infectivity rates, bionomics and biology of anophelines in Africa is for the gambiae and funestus groups. Far less is known about the roles, behavior and importance for control of "secondary" vectors. Since the 1950s this has improved marginally for several vector groups. *An. moucheti* is an important vector in equatorial forests in Central and West Africa [140-143]. This vector was originally divided into three morphological forms *An. moucheti moucheti* (type form), *An. moucheti bervoetsi* and *An. moucheti nigeriensis* [144]. However, recent classifications recognizes *An. moucheti* and *An. bervoetsi* as formal species while *An. moucheti nigeriensis* is considered as a morphological variant within *An. moucheti* [142,143]. The *An. nili* complex comprises four formal species, *An. nili* s.s, *An. somalicus*, *An. carnevalei* and *An. ovengensis* [145,146]. *An. somalicus*, has never been incriminated in human malaria transmission, however the three other members are highly anthropophilic and are important vectors of malaria within their geographical range from most of West, Central and East Africa mainly populating humid savannas and degraded rainforest areas [147,148]. Both *An. moucheti* and *An. nili* we regard as dominant vectors and in recording their presence information have specified under other species notes the species compositions where reported.

One additional vector, not previously considered as a primary/secondary vector is *An. mascarensis,* found uniquely on the islands of Madagascar, Comoros and Mayotte, and we consider an important secondary vector across its island niche [149,150].

The lists provided by De Meillon and Holstein of dominance of vectors in relation to malaria transmission did not include those found predominantly in North Africa. Vectors in this sub-region have been previously reviewed, including bionomics and infectivity rates, and the following are regarded as primary vectors within their ecological niches *An. labranchiae* and

An. sergentii and An. multicolor; while we regard *An. pharoensis* (for this sub-region) as a secondary vector [95,96,151-156].

Vectors for which there remains some ambiguity regarding their specific roles in malaria transmission across the wider Africa region, despite isolated reports of sporozoite infectivity rates, likely longevity and irregular human feeding, include *An. d'thali* [157], *An. coustani* and *An*. *ziemanni* [158], *An. flavicosta*, *An. squamosus*, *An. brunnipes*, *An. rufipes* [159-161], *An. brunnipes*, *An. hargreavesi*, *An. marshalii* var. gibbinsi [162], *An. algeriensis, An. maculipennis* (within the Africa region) and *An. hispanolia* [154]; also see for broader coverage of bionomics [9,151,156]. All these species we regard as incidental, unimportant vectors of malaria. We have reported what was stated in the reports and often left these uncorrected as taxonomic differentiation has improved and re-classifications have occurred with time, for example we record *An. salbaii* where this was stated but *An. hervyi* for the same species after its re-classification, we are also uncertain about earlier descriptions of *An. mauritanius* viz-a-viz *An coustani*.

In summary, we regard the following classifications as primary and secondary vectors and all other Anophelinae as either incidental vectors in rare circumstances or confirmed non-vectors of malaria. Given the taxonomic difficulties described earlier and their changes with time we regard all *sensu lato* complex descriptions as referring to one of the primary vectors within their respective groups

Primary within their ecological range

An. gambiae s.l.
- *An. gambiae s.s* (all molecular forms)
- *An. coluzzii*
- *An. arabiensis*
- *An. melas*
- *An. merus*

An. funestus s.s
An. nili s.l
- *An. nili s.s*
- *An. carnevalei*
- *An. ovengensis*

An. moucheti s.l.
- *An. moucheti moucheti*
- *An. moucheti nigeriensis*

An. labranchiae
An. sergentii
An. multicolor[3]

[3] *An. multicolor* has been an important, although weak, vector in the southern provinces of Tunisia, Oases in Algeria and Fezzan region of Libya [163]

Secondary within their ecological range

An. hancocki
An. pharoensis[4]
An. mascarensis
An. rivulorum
An. bwambae

5.4 Sampling and species identification methods

For each record we documented whether adults or larvae were sampled, a summary of methods used to sample vectors (for example animal bait catches, bed net traps, CDC light traps, human landing catches, human bait catches[5], indoor resting searches, pyrethrum spray catches, exit traps, outdoor bait traps, Ifakara tent traps, monks word traps, larval searches or larvae reared to adults)[6]. If there were no details available then "unknown" was recorded, often the case from national reviews of previous unpublished data. We also recorded the methods used to identify species, whether by morphological keys, cross-mating, Polymerase Chain Reaction (PCR), Chromosome Banding Sequences, DNA probes or enzyme electrophoresis.

When a site was sampled more than once within an overlapping time period or re-sampled using more definitive species identification techniques all reference sources were included and all methods of vector sampling and identification included in the respective columns.

5.5. Survey locations

Data geo-coding, defining a decimal longitude and latitude for each survey location, was a particularly demanding task. Mosquito systematics, however, often report longitude and latitude of survey locations and detailed descriptions of survey sites. More recent use of Global Positioning Systems (GPS) during survey work does enable locations of vector surveys to be defined with greater precision. To position each survey location where longitudes and latitudes were not available in the original survey reports we have used a variety of digital resources, amongst which the most useful were Microsoft Encarta Encyclopedia (Microsoft, 2004) and Google Earth (Google, 2009). Other sources of digital place name archives routinely used included GEOnet Names Server of the National Geospatial-Intelligence Agency, USA [167]; Falling Rain Genomics' Global Gazetteer [168]; Alexandria Digital Library prepared by University of California, USA [169]; African Data Sampler [170]; MapCarta [171];

[4] Note, despite a poor vector of malaria there has been recent evidence that in the face of ITN use on Senegal River this vector has increased its importance [164], it contributes to transmission in irrigations schemes in Kenya [165] and remains a potential vector in Egypt. However, there are two genetically different forms - in north Africa/Saharan countries versus southern Africa [166]

[5] It was not always clear if human landing and human bait catches were different, the latter could include sampling subjects protected by specially constructed bed nets that served as traps

[6] Keys to the coding abbreviations used for each sampling method are provided in the country-specific databases provided to national malaria control programmes.

Maplandia [172]; Global geodatabase-cities [173]; Open Street Map [174]; VMAP0 [175]; IslamicFinder [176].

Across Africa a number of national digital, GPS confirmed, place-name gazetteers exist for populated places, health facilities or schools. These are increasing in number, precision and coverage. These were obtained on request from national census bureau's, ministries of education and health and NGO partners and proved to be valuable locating communities in Burkina Faso, Kenya, The Gambia, Mozambique, Madagascar, Somalia, Malawi, Mauritania, Ghana, Niger, Namibia, Senegal, Somalia, South Africa, Tanzania, Uganda, Zambia and Zanzibar.

Several reports that had summarized national data did not provide village or community names but locations and species identifications were shown on maps. Here we have extracted the locations and have labelled them district point 1, 2 etc. If mapped presentations were of a high enough resolution we were able to locate the village names using Google earth underlying the shown location.

All coordinates were subjected to a final check using second level administrative boundary Global Administrative Units Layers (GAUL) spatial database developed and revised in 2008 by Food and Agriculture Organization (FAO) of the United Nations [99,177]. The spatial selection tool in ArcGIS 10.1 (ESRI, USA) was used to verify points whether along the coastline were located on land as defined by GAUL 2008. The Global lakes and Wetlands (GLWD) database developed by the World Wildlife Fund [178] was used to ensure inland points were positioned on land and not water bodies. Here we aimed to identify survey coordinates that fell slightly off the coastline, located on the river or in incorrect administrative units, every anomaly was re-checked and re-positioned using small shifts in combination with Google Earth.

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