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QWeCI

Quantifying Weather and Climate Impacts on Health in Developing Countries

D1.1a – Report on current climate controls on selected infectious disease in Africa, based on database analysis and projection

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1) Introduction

The aim of QWeCI deliverable D1.1.a was to ascertain the potential effects of changes in climate upon selected infectious diseases of Africa. Initially, the work-package partners needed to decide which infections would be of greatest interest to the QWeCI project, and after discussion the short-list included Malaria, Rift Valley Fever and the tick-borne diseases Theileriosis, Babesiosis, Anaplasmosis, Tick-bite Fever and Cowdriosis. Work-package partners were apportioned specific diseases which they were to work on as a part of the work-package.

Information exported from the ENHanCEd Infectious Diseases (EID2) database was used to ascertain the names of vector species involved in the transmission of the chosen African diseases, and the geographical range of each of these vector species. The names of these vectors, along with the names of the diseases and the pathogens which cause them and any associated acronyms and synonyms were then used to undertake semi-automated literature searches to identify literature which potentially contained evidence for the effects of climate drivers upon some aspect of the chosen African diseases.

Work-package partners were provided with links to the literature identified by the searches and they examined each of these papers in order to write a review of the effects of climate upon each disease or set of diseases.

2) Methodologies

a) *ENHanCEd Infectious Diseases database to ascertain vector species of each disease*

The effects of climate upon disease were to be examined by utilising resources which were set up for a previous project, the ERA NET funded ENHanCE project. The main resource used was a unique database, the ENHanCEd Infectious Diseases (EID2) database [1], which contains information on both the pathogens of all animals (not including fish), including mankind, and their occurrence not just in Europe, but around the globe. The EID2 is a relational database which was created using s#arp architecture version 2.0 [2] within Visual Studio 2010. The database was designed via classes using domain driven design. As of June 2012, it consists of 38 tables and 31 C# classes. Its core is the NCBI Taxonomy database [3] which provides a hierarchal structure based on the phylogenetic tree to information on each host, vector or pathogen (here-after referred to as 'organism') node, such that outputs can be obtained for organisms and higher taxonomic groups (for instance Flaviridae, Ruminantia). The information on each organism node includes evidence of alternative names or synonyms, which were mostly provided as a part of the information from the NCBI Taxonomy database. Where it was felt that these were not specific enough, we were able to annotate these names and this information is also stored within the EID2 structure. If phylogenetic information for an organism had not previously been included within the NCBI Taxonomy database, they could be added artificially into the EID2 structure at the correct place within the phylogenetic tree. Further information about each organism, such as their taxonomic rank (genus, species etc) or their taxonomic division for pathogens (algae, bacteria, fungi, helminths – including thorny-headed worms and pentastomids, protozoa, viruses - including prion agents) has then been stored using a series of statements which are linked into the classes. These statements can be created using semi-automated methods such as data-mining of meta-data held within the NCBI Taxonomy database or the NCBI Nucleotide database [4], or they can be nominated by an individual using evidence from a publication. Data on publications described within PubMed [5] is also held as a part of the EID2, with papers included based upon the organisms which they describe, and abstract information available for recently published papers.

The EID2 is available in a web-based format and is publically accessible (after user registration), on the world-wide web. It serves as a portal for pathogen information, allowing interrogators to look at organism data in the context of the evidence available within PubMed or NCBI databases. http://www.zoonosis.ac.uk/EID2/

b) *Host-pathogen and organism-country information within EID2*

Specific information on pathogens affecting a certain host (termed a 'host-pathogen interaction') or pathogens occurring within a country (an 'organism-country interaction') was mined from meta-data

held within the NCBI Nucleotide database [4] and added to the EID2. The last update from the Nucleotide database was undertaken in December 2011. A further source of information utilised for organism-country interactions came from automated searches of the PubMed database [5] and the NCBI MeSH library [6]; when the name of an organism and the (minor subject) MeSH term for a country co-occurred within a certain number of publications, an assumption was made about the occurrence of that organism within that country.

c) *Testing the validity of automatically mined organism-country information in EID2*

The threshold number of papers in which to infer a pathogen-location interaction from automated searches of the PubMed database [5] and the NCBI MeSH library [6] was investigated using two different approaches.

i) *Positive predictive value approach*

The positive predictive value (PPV) of a test for whether papers showed a 'true' relationship between a pathogen and country MeSH term was established. This involved using a sub-sample of papers stratified according to the pathogen and continent on which the MeSH term country was located, after which papers were selected for inclusion in PPV calculation using a random number generator. Differences in the likelihood of a truly positive assumed relationship (not previously described using NCBI Nucleotide database metadata; [4]) arising as a result of pathogenic status or taxonomic division were examined using a generalised linear model with binomial errors and logit link function.

ii) *Binomial regression modelling approach*

A generalised linear model (GLM) with binomial errors and logit link function was used to ascertain the likelihood of an assumed pathogen-country interaction being correct. The outcome variable within the model was if a pathogen-country interaction had been reported in metadata from the NCBI Nucleotide database for at least one Nucleotide sequence. The explanatory variable was the number of papers from a PubMed search in which a pathogen and country MeSH term had co-occurred. Non-linear relationships in the data were investigated using generalised additive modelling (GAM) and inclusion of polynomial terms or piecewise regression functions in GLMs. The break points within the piecewise regression functions were explored using an iterative process where the break increased from the minimum in discrete steps representing the number of papers. Significantly improved GLM model fits were established by comparing models using Chi-squared analysis; the final GLM model was ascertained using deviance residuals with the smallest value being the best fit. The final GLM model included log10(n+1) transformation of the covariate. Further to the piecewise GLM analysis, linear spline models were also tested, again exploring breaks using an iterative process, as this technique would smooth the regression lines together rather than allowing the model to fit multiple separate lines in order to explain the data.

d) *Semi-automated literature searches*

Included within the literature searches were each pathogen/disease/vector name, a MeSH term for Africa [6] to limit the literature collated to the African region, and a climate term from a list of climate terms which had been finalised after discussion with work-package partners (table 1). All pathogen/disease/vector names were run in literature searches with all climate terms, and the searches period was limited to the years 1900-2010 inclusive. The bibliographic index used for literature searches was the PubMed database [5], and searches were undertaken using the title and abstract fields.

Table 1. Climate driver terms used within semi-automated literature searches of PubMed.

absolute humidity	dry seasonal	maximum summer temperature	sea level pressure
AD (Atlantic Dipole)	dry spell	maximum temperature	sequential days with rain
aerosol/s	dust	maximum wind speed	sequential days without rain
air temperature/s	dusty	maximum winter temperature	shortwave radiation
altered rainfall pattern/s	elevated temperature/s	mean annual temperature	small rainfall event
altitude	ENSO (El Nino Southern Oscillation)/El Nino/El Niño/La Nina/La Niña	mean summer temperature	SOI (Southern Oscillation Index)
ambient temperature/s	extreme weather	mean temperature	saturation vapour pressure
AMO (Atlantic Multidecadal Oscillation)	flood	mean wind	short rains
AMOC (Atlantic Meridional Overturning Circulation)	flooding	mean wind speed	soil moisture
annual rainfall	fog	mean winter temperature	solar flux
annual temperature variation	freezing	microclimate	southern oscillation
AO (Arctic Oscillation)	freezing level	minimum relative humidity	squall
AA0 (Antarctic Oscillation)	freezing point	minimum summer temperature	squall line
arid climate	frost	minimum temperature	storm
break cycle	heatwave/ heat wave	minimum wind speed	summer rainfall
changes in climate	heavy rain	minimum winter temperature	summer temperature/s
climate	heavy rainfall	MJO (Madden Julian Oscillation)	TAD (Tropical Atlantic Dipole)
climate change	high night-time temperature/s	Monsoon	temperature seasonality
climate condition/s	high rainfall	Monsoon onset	THC (ThermoHaline circulation)
climate driver	high summer temperature/s	NAO (North Atlantic Oscillation)	thermometer
climate variable/s	high temperature/s	NDVI (Normalised Difference Vegetation index)	total annual rainfall
climate variance	higher temperature/s	night-time temperature	total summer rainfall
climate-driver	humid	NOI (Northern Oscillation Index)	total winter rainfall
climatic condition/s	humidity	PNA (Pacific North American Index)	turbidity
coldwave/ cold wave	hurricane	PDO (Pacific Decadal Oscillation)	upper temperature/s
convection	ice day	precipitation	vapour pressure
convective rainfall	increased temperature/s	precipitation seasonality	vapour pressure deficit
cool temperature/s	IOD (Indian Ocean Dipole)	pre-monsoon	warm temperature/s
cooler temperature/s	IPD (Indian Pacific Dipole)	QBO (Quasi Biennal Oscillation)	warm years
cyclone	LAI (Leaf Area index)	radiosonde	warmer temperature/s
day-degrees	large rainfall event	radio sonding	weather station
days of temperature	light rain	rain	wet conditions
daytime temperture	light rainfall	rainfall	wet season
decreased temperature/s	long rains	rain-gauge	wind
dew point	longwave radiation	rainy season	wind speed
dew point temperature	low night-time temperature/s	relative humidity (RH)	windy
diurnal range	low rainfall	runoff	winter rainfall
drizzle	low summer temperature/s	salinity	winter rainy day/s
drought	low temperature/s	SAM (Southern Anular Mode)	winter temperature/s
dry	lower temperature/s	satellite	XBT
dry conditions	maximum relative humidity	saturation deficit	

3) Results

a) *ENHanCEd Infectious Diseases database to ascertain vector species of each disease*

A list of 158 names of pathogens, potential vectors and disease names was used for the literature searches. This included 7 bacteria species or genus, 45 flies, 20 protozoans, 84 ticks and 2 viruses.

b) *Testing the validity of automatically mined organism-country information in EID2*

i) *Positive predictive value approach*

If there was no direct evidence available from the NCBI Nucleotide database, a threshold (t) of five papers from PubMed in which a pathogen name and MeSH term for a country co-occurred within a paper was used as evidence of pathogen occurrence. This was based upon a preliminary study in which papers had been stratified according to the pathogen and the continent to which they were linked via a MeSH term for a country. The evidence within papers was then checked to ascertain true evidence of a pathogen occurring within a MeSH term country. This allowed the calculation of the PPV of the test (1-((1-PPV)^t)). The PPV for each paper was 0.95 (SE=0.05), and so a threshold of 5 papers was chosen which would mean that we could be 99.9% certain of a 'true' relationship. The likelihood of an assumed relationship between a pathogen and a MeSH term country being true was not affected by pathogenic status (P=0.393) or taxonomic division (P>0.05).

ii) *Binomial regression modelling approach*

Having explored GAM results and a fifth order polynomial term within GLMs, a log10(n+1) transformation of the explanatory variable within a final binomial regression model included a piecewise function with two breaks. The regression results suggest that the number of papers identified using PubMed is positively related to the likelihood of a pathogen-country interaction having been reported in the NCBI Nucleotide database, but the significance and characteristics of this relationship change dependent upon the number of PubMed papers (Overall results, df=5,3223, P<0.001). The breaks points for lines were between 2 and 3 papers and 6 and 7 papers, with the likelihood of Nucleotide evidence increasing as PubMed papers change from 3-6, to 1-2, to 7 and above. The alternative linear spline model explained slightly less of the residual deviance in the model (3974.8 as opposed to 3970.7, respectively) and thus less of the variation between data points; however, it too suggested two breaks points with similar differences in the characteristics of each section of the regression line.

c) *Semi-automated literature searches*

The 25,754 individual literature searches undertaken returned a total of 2889 rows of data which potentially describe the effect of a single climate driver upon a pathogen, vector species or disease. This included 2031 rows for Malaria, 262 rows for Rift Valley Fever, and 596 rows for tick-borne diseases.

4) Bibliography for introduction, methodologies and results sections

1. University of Liverpool (2011) The ENHanCEd Infectious Diseases database (EID2). National Centre for Zoonosis Research, http://www.zoonosis.ac.uk/eid2
2. Inc. CI (2009) S#arp Architecture Indiana, https://github.com/sharparchitecture/Sharp-Architecture
3. National Center for Biotechnology Information USNLoM (2012) The NCBI Taxonomy database homepage, http://www.ncbi.nlm.nih.gov/Taxonomy/
4. National Center for Biotechnology Information USNLoM (2012) The NCBI Nucleotide database homepage, http://www.ncbi.nlm.nih.gov/nuccore
5. Anon. PubMed, Bethesda, Maryland, US, http://www.ncbi.nlm.nih.gov/pubmed/ National Center for Biotechnology Information (NCBI), National Library of Medicine (NLM).
6. National Center for Biotechnology Information USNLoM (2012) The NCBI Medical Subject Headings (MeSH) database homepage, http://www.ncbi.nlm.nih.gov/mesh

5) Results of the literature reviews including integral bibliographies

a) ***Review of the effects of climate drivers upon Malaria in Africa***

i) *Introduction*

Malaria affects large parts of Africa and Asia and is responsible for nearly 800,000 deaths annually. Despite interventions resulting in reduction in global malaria mortality in the last 10 years [WHO, 2010], much concern still exists that in regions where malaria is either endemic, seasonal or has been present in the recent past, climate change might affect its presence and/or prevalence. In most African countries, more than 75% of cases are due to *Plasmodium falciparum*, whereas in

most other countries with malaria transmission, other, less virulent plasmodial species predominate. Almost all malarial deaths are caused by *P. falciparum* (WHO, 2008).

In Ghana, malaria is the most frequent cause of morbidity and mortality and constitutes approximately 40% of all out-patient department diagnosis across the country (Koram, 2003).

Malaria kills an African child every thirty seconds with 90% of all malaria deaths occurring in Sub-Saharan Africa (www.rbm.who.int. History of malaria). Malaria, apart from its public health importance, is also of economic significance (Gallup and Sachs, 2001).

Ecological studies in many areas of Africa show that altitude and bioclimatic structures have an important impact on vector distribution (Mwagangi et al 2007). Temperature, rainfall, relative humidity and altitude are the four major factors affecting the presence and abundance of anopheles mosquitoes in any given area (Maxwel et al 2003). This review discusses the effects of environmental factors such as altitude and topography as well as climatic factors such as rainfall, ambient and water temperature, and relative humidity that influences the dynamics of the vector population and vectorial capacity of the main Afro-tropical vectors involved in malaria transmission. Notably *Anopheles arabiensis*, *An. gambiae* s.s. and *A. melas* of the *An. gambiae* complex. Others are; *A. funestus*, *A. nili* and *A. pharoensis*.

ii) A. gambiae s.s

1) *Ecological requirement*

The *A. gambiae* Giles complex comprises six named species, one unnamed species and several 'incipient' species. It includes two of the most effective vectors and a third minor vector of malaria parasites in Africa (Gillies & Coetze, 1987, Hunt et al. 1998). The breeding habitats of these species, notably *A. gambiae* s.s. *A. arabiensis*, and *A. Melas*, are generally similar with slight variations. The larvae of *A. gambiae* are commonly found in clear, sunlit pools of water in small depressions such as foot or hoof prints, the edges of bore holes and burrow pits, roadside puddles formed by tire tracks, irrigation ditches and other man-made shallow water bodies [Mutuku et al 2007]. They have also been found breeding in polluted water rich in organic matter [Keating et al 2004,Castro et al 2010], in large bodies of water such as flood plains, and in pools of water along lake shores especially when there are fluctuations in water level as occurs in Lake Victoria in Kenya [Minakawa et al 2008]. Environmental alterations due to deforestation, swamp reclamation mainly for agriculture, excavation of sand and building stones, brick making and vegetation clearance may lead to an increase in larval habitats [Carlson et al 2004]. Grass growing in the larval habitats seems to be an additional requirement, since habitats with grass growing in them have been found to have more larvae than habitats with other vegetation types or open habitats [Imbahale et al 2011], Fillinger and others [2004]. These observations suggest that grass protects mosquito larvae from being swept or flushed away by running water [Paaijmans et al 2007]. Grass could also be convenient in offering newly emerged adult and gravid mosquitoes a shaded resting site. Consequently, this may lead to an increase in mosquito-human contact, eventually leading to an increase in malaria transmission.

2) *Altitude and temperature and rainfall*

As altitude increases, temperature declines. Development and survival of *A. gambiae* and its parasite are critically dependent on the ambient temperature; as the temperature drops so does the risk of infection. Models focusing on the impact of temperature on parasite development time in the vectors, assume a highland zone with malaria vectors, but without malaria transmission. Such zones would be prone to epidemics if temperatures temporarily increase and permit sporogony in the existing vector population.

The primary effect of increasing altitude is a log-linear reduction in vector abundance and, to a lesser extent, a reduction in the proportion of infective mosquitoes [Bodker et al., 2003]. Along an altitude transect in the Usambara mountains in Tanzania, Bodker et al (2003) observed that between a village at 300m altitude with temperature of 20.2 and 30 ^{0}C (Min & Max), and a highland village at 1700m with temperatures between 11.7 (Min) and 20.6^{0}C (Max), there was a reduction of >1000-fold in malaria transmission intensity. Below 16 °C, the aquatic stages of tropical *Anophe-*

les fail to develop or take a long time to develop (24 days) [Koenraadt et al., 2006], for instance in the cold temperatures of the highlands. Adult mosquitoes breed locally in the highlands [Bodker et al 2003] or they are dispersed from the lowlands [Koenraadt et al 2006].

Whichever way breeding occurs, highland malaria transmission is maintained at extraordinarily low vector densities. This is because, *A. gambiae* s.l can avoid extreme temperatures by resting in more favourable microclimates; for example, inside occupied houses the temperatures can be 3-6.5 °C warmer than outside [Bodker et al 2003]. Paaijmans et al (2007) showed that the mean daily water temperatures (in small, medium and large pools preferred by *A. gambiae*) in the highlands were generally higher than the mean air temperature, which eventually led to rapid development times. Koenraadt et al., (2006) observed *A. gambiae* s.s. was a better survivor than *A. arabiensis*.

Several authors have reported malaria transmission in the highlands of East Africa being maintained by *A. gambiae* s.s. A sporozoite rate of up to 10% has been reported for *A. gambiae* at high altitudes from 1000m to >1500m in Tanzania (Mboera et al 2006). Shililu et al (1998) in the highlands of western Kenya observed entomological inoculation rates (EIRs) of 29.2 infective bites per person per year due to *A. gambiae* s.s with a sporozoite rate of 6.3%. It is known that in the highlands, low temperatures prevented parasite development in mosquitoes during the cool season rains; highland transmission is therefore limited to the warm dry season when vector densities were low. It goes without saying that in the event of climate change, when the highlands experience elevated temperatures, malaria epidemics would be expected.

3) *Humidity and rainfall*

For a period of two years, Imbahale et al (2011) studied the ecology of *A. gambiae*, *A. arabiensis* and *A. funestus* in the highland villages of western Kenya. The area had altitudes ranging from 1,520-1,560 m, characterized by the cold and undulating hills that often form basin-shaped valleys that are prone to flooding, offering excellent mosquito breeding habitats. They observed that peaks in relative humidity coincided with higher amounts of rainfall and led to increases in larvae density in the following month. Cross correlation analysis showed that with no time lag, weekly rainfall significantly led to high densities of early instars in both temporary and permanent habitats. With a two-week time lag, early instars increased in density with increased rainfall, while late instars increased with a three-week time lag in both permanent and temporary habitats. Overall average, weekly temperatures of $>19^0$C and relative humidity >80% was optimal.

Similar to the larval abundance dynamics, the relative proportion of *A. gambiae* s.s. in the adult population peaked shortly after the onset of the rainy season, while *A. arabiensis* is the more dominant species during the dry season [Awolola et al., 2002]. A comparable differentiation can be observed on a spatial scale with *A. arabiensis* occurring in the more arid areas of Africa [Gillies and Coetzee, 1987]. On a finer spatial scale, adult *A. gambiae* s.s. were collected more frequently in the foothills of western Kenya, while *A. arabiensis* was more abundant on the plains that received less rain [White, 1972]. This difference has been explained by the different sensitivities of *A. gambiae* s.s. and *A. arabiensis* towards humidity conditions [Coz, 1973].

Increases in rainfall has been found to significantly correlate with an increase in number of larval *A. gambiae* s.l. habitats and the number of female *A. gambiae* s.l. collected from CDC-light traps housed following a one week time lag. The one week lag most likely reflect the time it takes to colonize habitats plus the time for eggs to develop into adults. It has also been observed that both larval and adult populations show a significant increase in the proportion of *A. gambiae* s.s. within the mixed population of *A. gambiae* s.s. and *A arabiensis* over time. The ratio of rainfall over precipitation/potential evapo-transpiration (P/PE), indicative of the humidity conditions in the area, is the driving force of this increase (Konraadt et al 2004).

iii) Anopheles arabiensis

A. arabiensis and *A. gambiae* are the principal vectors of malaria in sub-Saharan Africa, but in some areas, such as the Great Rift Valley in East Africa, *A. arabiensis* is the predominant malaria vector species (Minakawa et al. 2002). *A. arabiensis* is better adapted to dry environments than *A.*

gambiae [Lindsay et al. 1998]. *A. arabiensis*, when compared to *A. gambiae*, is described as a zoophilic, exophagic and exophilic species [White 1972]. However, it is also known to have a wide range of feeding and resting patterns, depending on geographical location [Gillies and Coetzee et al 1987]. This behavioural plasticity allows *A. arabiensis* to adapt quickly to counter indoor IRS control, where suitable genotypes occur [Coluzzi et al 1979].

1) *Ecological requirement*

A. arabiensis is considered a species of dry, savannah environments and sparse woodland [Coetzee et al 2000], yet it is known to occur in forested areas, but only where there is a history of recent land disturbance or clearance [Coetzee et al 2000]. Its larval habitats are similar to those of *A. gambiae*: generally small, temporary, sunlit, clear and shallow fresh water pools [Gimnig et al 2001], although *A. arabiensis* is able to utilize a greater variety of locations than *A. gambiae*, including slow flowing, partially shaded streams [Shililu et al 2003] and a variety of large and small natural and man-made habitats. It has been found in turbid waters [Gimnig et al 2001, 2000] and, on occasion, in brackish habitats [Bøgh et al 2003]. It readily makes use of irrigated rice fields, where larval densities are related to the height of the rice, peaking when the plants are still relatively short and then dropping off substantially as the rice plants mature [Mutero et al 2000, Mwangangi et al 2007, Dolo et al 2000]. *A. arabiensis* rapidly colonize rice fields where land use land cover change occurs (Dolo et al 2000).

2) *Altitude and temperature*

As a general rule, temperature decreases with increasing altitude and temperature is a key determining factor in malaria transmission. *A. arabiensis* seems by far to be the most ubiquitous in its reported distribution. Okara et al (2010) found *A. gambiae* in several habitats in Kenya; 'along the coast, across Western Kenya and central Kenya including the arid areas of the North West in Turkana district. The ubiquitous extent of *A. arabiensis* in both urban and rural settings has important implications for the broader success of vector control approaches promoted in Kenya (Okara et al 2010). The distribution of *A. arabiensis* is concentrated in the lower rainfall zones, which represent the drier savannah areas.

A. arabiensis is a vector that predominantly rests outdoors with a general preference for biting animals, which may have implications for the expansion of IRS into areas where transmission intensity is high and demands accelerated attacks on the vectorial capacity. There are also suggestions that this sibling species of the *A. gambiae* complex is beginning to dominate over *A. gambiae* in recent years, coincidental with expanded ITN coverage across East Africa.

3) *Physico chemical characteristics of habitat*

Ovipositing female mosquitoes are known to choose among water bodies based on cues such as temperature, light, water depth, turbidity, and presence of competitors [Lee 1991]. A number of workers have documented the effects of temperature on the development and relative abundance of rice land mosquito larvae [Lacey and Lacey 1990]. The influence of environmental covariates in the abundance of *A. arabiensis* mosquitoes, in the central province of Kenya has been examined [Mwagangi et al 2007]. Larval abundance was found to be highest between the transplanting and vegetative stages. Water temperatures at the experimental plots were highest during these stages of the rice growth cycle. However, when the rice was at the reproductive stage, water temperatures declined subsequently and so does the larval density.

Water turbidity is an important parameter associated with the abundance of *A. arabiensis* larvae in the habitats. Most larvae are collected from water with either clear or low turbidity. Gimnig et al. (2001) found increasing *A. gambiae* s.l. larvae densities with increasing turbidity. Robert et al. (1998) found a clear-water preference by *A. arabiensis* breeding in wells in urban Dakar. A study by Ye-Ebiyo et al. (2003) found that the production of *A. arabiensis* was favoured in moderately turbid water, although excessive turbidity limited the production of larvae. Water that is turbid from particles not edible by *Anopheles* sp. larvae, could disfavour the production of larvae, whereas water that is turbid from food particles represents a very suitable habitat [Mwagangi et al 2007]. Appli-

cation of fertilizer to rice paddies reduces turbidity of the habitat and thus, is an important cue for mosquito oviposition and consequent increasing larval densities.

Other important factors for the abundance of anopheline mosquito larvae in the habitats were pH and conductivity. In rice agro ecosystems, pH and conductivity have been shown to be important factors affecting larval abundance [Case and Washino 1975]. Fertilizer application increases pH and conductivity, which result in a rise in larval abundance due to greater oviposition by the gravid *Anopheles* mosquitoes. Nitrogenous fertilizers have been documented to increase Anopheline and culicine larvae densities in rice agro ecosystems [Mutero et al. 2004b]. pH was key factor associated with an increase in Anopheline larval abundance observed by Mwagangi et al 2007.

4) *Altitude*

A. arabiensis is one of the principal vectors of malaria in throughout sub-Saharan Africa often occurring sympatrically with *A gambiae* s.s,. However, in some areas, such as the Great Rift Valley in East Africa, *A. arabiensis* is the predominant malaria vector species (Minakawa et al. 2002). Nanjom et al 2003 also found *A. arabiensis* to be the principal vector responsible for malaria transmission in Ethiopia and Eritrea, also known as the horn of Africa. These countries have similar highland topographies and high elevation characterized by unique mountainous areas, rugged plateaus and interspersed with towering mountains and deep chasms. Hot and humid low lands and semi-desert areas. With average elevation of 2000 m above sea level and scarce rainfall, this confirms that *A. arabiensis* is better adapted to dry environments than *A. gambiae* (Lindsay et al. 1998).

Observations of Imbahale et al (2011) from Fort Ternan in western Kenyan highlands, indicate that *A. arabiensis* comprised 71% of *A. gambiae* s.l. collected. This is the highest proportion of this species that has ever been recorded in the highlands of western Kenya. Fort Ternan has average weekly air temperature of >19°C and an average maximum relative humidity of >80% providing conducive conditions for malaria transmission. However, the valleys in Fort Ternan are narrow with steep slopes, causing a rapid drainage of water unless human activities create or construct water-retaining structures. The presence of *A. arabiensis* in Fort Ternan can be attributed to the slow changes in land use, such as deforestation, that leads to changes in micro-climatic conditions favouring the survival of this species. The air temperatures found were lower than the corresponding water temperatures in the sampled habitats, a factor that seems to favour the existence of *A. arabiensis* in high altitude areas.

5) *Ambient temperature and flooding*

A. arabiensis is the single malaria-transmitting vector found in the desert-flanked Dongola Reach of the Nile River in Northern State of Sudan and the island of La Reunion. The flooding of the Nile and changes in ambient temperature determines the spatial changes in *A. arabiensis* density [Dukeen et al 1986]. The Nile reaches its highest levels in September coinciding with the lowest density of *A. arabiensis*. As the river level falls, suitable breeding sites form, but low winter temperatures delay the resurgence in mosquito numbers. By March, the river level is down almost to its minimum, but the temperature has not yet reached the summer maxima resulting in the peak of *A. arabiensis* density. A month later the temperatures are much higher and mosquito numbers drop to an intermediate level which is mostly sustained throughout the summer until the flood [Dukeen et al 1986, Ageep et al 2009].

iv) Anopheles funestus

A. funestus is a member of the Funestus subgroup [Garros et al 2005], which includes *A. aruni*, *A. confusus*, *A. funestus*, *A. parensis* and *A. vaneedeni*. The members of this subgroup exhibit important variation in their biology and behaviour, especially in regard to malaria vectorial capacity and are only morphologically distinguishable during certain stages in their development [Cohuet et al 2003]. However, only *A. funestus* is regarded as an important vector of malaria from in this subgroup [Coetzee et al 2004].

Some *A. funestus* were collected during the study period. However, this species is known to thrive well in hot and humid environments as opposed to the hot and dry conditions [Taylor et al 1993, Munga et al 2006]. It is also possible that lack of suitable long-lasting habitats preferred by this

species may partly account for the low densities witnessed in the current study [Ijumba et al 2002]. However, *A. funestus* complex appeared to be more important at 1,000 m. Here, the high rainfall probably provided perennial breeding in the permanent pools formed by a stream running through the middle of the village.

1) *Altitude and ecological requirements*

A. funestus is present in most of tropical Africa, and is the second most important vector of malaria. Abundant in open savannah but also in highlands up to 2,000m, the characteristic breeding site is a large deep and permanent pool of water shaded by vegetation, but mosquitoes also breed in swamps, lakeshores, streams, ponds, floating vegetation, low grass and rice, provided optimum breeding conditions persist. A typical *A. funestus* larval habitat is a large, permanent or semi-permanent body of fresh water with emergent vegetation, such as swamps, large ponds and lake edges. Larvae have been found in shaded and sunlit environments and Gillies & de Meillon [1968] concluded that A. funestus uses emergent vegetation as a refuge against predation while the shading it casts, or the presence of shade from overhanging plants, is of lesser importance. In some areas, *A. funestus* larvae, as with *A. arabiensis*, are associated with rice cultivation (e.g. Madagascar, Mali) [Carnevale et al 1999]. Where they are found, their favoured environmental conditions are very different to those of *A. arabiensis*. *A. funestus* replaces *A. arabiensis* in a successive temporal process during rice plant growth, exhibiting higher densities in older, maturing fields compared to the preceding open conditions preferred by *A. arabiensis* [Carnevale et al 1999]. *A. funestus* is considered to be highly anthropophilic [Duchemin et al 2006], which led Charlwood et al. [1996] to propose that *A. funestus* may have been the first Anopheline species to specialize on biting humans, surmising that its preferred larval sites (permanent water bodies in savannah-like environments) are likely to have been areas where humans first settled.

v) Anopheles melas

There is relatively little contemporary information about the behaviour of *A. melas*, perhaps because it is generally considered to be a vector of lesser importance, specifically where it occurs in sympatry with *A. gambiae* or *A. arabiensis*.

A study of the species composition of the *A. gambiae* complex in different vegetation zones in Ghana reveals the predominance of *A. gambiae* with a local presence of *A. melas* in areas with brackish water along the southern coast (Appawu et al. 1994). Bryan et al. (1987) studied the bionomics of sympatric populations of *A. melas* and *A. gambiae* in Gambia, western Africa and reported that the distribution of *A. melas* was limited to the vicinity of breeding sites associated with mangrove swamps, and it was less anthropophilic and more exophilic than *A. gambiae*. However, Awolola et al. (2002) reported that both *A. gambiae* and *A. melas* were anthropophagic in south-western Nigeria. *A. melas* was reported to be present all year long and consisted of 36.9% of the mosquito population found in the holo-endemic area of coastal Lagos, south-western Nigeria, (Awolola et al 2002). In this area *A. melas* was reported to be predominantly anthropophagic with 1.9% of them infected with *P. falciparum*. *A. melas* contributed significantly to the malaria transmission in this area, and was actually found to be the main vector that maintained transmission of *P. falciparum* during the dry season in Coastal Nigeria (Awolola et al 2002). Bogh et al 2003, sampled mosquito larvae and pupae in specific habitats in the flooded alluvial soils bordering the river in the central region of rural Gambia, during the rainy seasons of 1996 and 1997. The largest numbers of larvae were found during September, one month after the peak rains. *A. melas* (Theobald) was the dominant species (81.5%), followed by *A. gambiae* sensu stricto (Giles) (18.0%). *A. melas* coexisted with *A. gambiae* s.s. often but whereas *A. melas* were found in water with a salinity of up to 72% sea water (25.2 g NaCl l(-1)), *A. gambiae* s.s. only occurred in water with up to 30% sea water (10.5 g NaCl l(-1)). *A. melas* larvae were found in association with plant communities dominated by sedges and grasses (*Eleocharis* sp., *Paspalum* sp., *Sporobolus* sp.) and sea-purslane *Sesuvium portulacastrum* (L.) and the presence of cattle hoof prints, as reported by Diop and others (2002) in an entomological study of villages located in the Delta's Saloum (Senegal). This study allowed a better understanding of the contribution of *A. melas* to malaria transmission in mangrove swamp in Senegal. They observed that two villages (Djifere and Diakhanor) located be-

tween the sea and the river, are colonized entirely by *A. melas*. However, during the rainy season and at the beginning of the dry season, *A. melas* and *A. arabiensis* are sympatric. But the ratio of *A. melas*/*A. arabiensis* increases towards the coast, where *A. melas* exclusively predominates. They observed that when *A. melas* is predominant, endophagy, endophily and anthropophily are very marked. During the period of sympatry, *A. arabiensis* is responsible for the transmission and when it is absent, *A. melas* is the vector. Transmission occurs from July to March with a maximum at the beginning of the dry season. In the villages of the mangrove swamp, its prolongation until the middle of the dry season is due to *A. melas*.

Bryan (1983). *A. melas* has a comparably lower sporozoite rate than either *A. arabiensis* or A*. gambiae* (e.g. 0.35% compared to 3.5% for *A. gambiae* in The Gambia) [Bryan 1983, White et al 1974], yet in coastal areas where it can occur in very high densities it is still a problematic vector of malaria. Tuno et al (2010) reported that *A. melas* is highly dominant on the western coast of Ghana. And that *A. melas* showed high human blood rates in indoor resting mosquito samples despite the availability of a range of hosts. Tuno et al 2010 observed that, the exophily of *A. melas* (also reported by Bryan et al. (1987) is due to the year-around higher humidity in coastal areas and the people's habit of more frequent outdoor sleeping along the coast. It was thus concluded that the blood feeding behaviour of *A. melas*, and their successive resting behaviours may be largely influenced by environmental factors in addition to their inherent characteristics.

i) *Ecological requirements*

A. melas is commonly associated with brackish water and can utilize saline environments that other species, for example, *A. gambiae*, cannot tolerate [Bogh et al 2003], yet does not appear to require brackish water for larval stage development [Gelfand et al 1955]. It is generally restricted to coastal areas [Gelfand et al 1955] but has been found up to 150 km inland along the Gambia River, where salt water can intrude great distances (up to 180 km) upriver [Bryan et al 1897]. The density fluctuations of *A. melas* are closely associated with tidal changes rather than seasons, for example, Gelfand [1955] identified a peak in adult numbers 11 days after spring tides. The larvae of this species are associated with salt marsh grass (Paspalum spp.) and mangroves, but only trees of the genus *Avicenna*, which include white, grey and black mangrove, and not those from the genus *Rhizophora* ('true' or red mangrove spp.) [Muirhead-Thomson et al 1948]. These positive and negative associations with mangroves are thought to be strongly influenced by the predominant soil type associated with the different tree genera. *A. melas* preferentially oviposits on damp ground at low tide, rather than in open water, where the eggs are able to survive some degree of desiccation until the tides rise again, and appears to prefer the poorly drained, peaty-like soil common to Avicenna forests compared to the sandy, gravelly or smooth, fibrous peat soils common to the *Rhizophora* stands. Giglioli [1965] surmised, that this behaviour guarantees that the larvae will have sufficient time to complete their larval development and pupate in the less saline, relatively permanent waters of the new tide before it begins to recede and the water either becomes too salty, or dries out completely.

vi) Anopheles nili *complex*

A. nili is one of the most important vectors of human malaria in the equatorial forest domain of central Africa. It occurs in sympatry with *A. moucheti* along river networks where their immature stages are usually found at the edge of large rivers or islands within. These mosquitoes are found in forest villages and have a broad distribution from Nigeria to Uganda, with *A. nili* extending its range in the savannas of Western and Eastern Africa (Gillies and De Meillon, 1968). *A. nili* is largely exophilic and feeds on a variety of vertebrates, yet with a high proportion of blood meals taken on humans. Despite the public health importance of both *A. nili* and *A. moucheti* [Awono-Ambene et al., 2004; Antonio-Nkondjio et al., 2006], the *A. nili* complex has been generally overlooked in African vector studies despite being described as a highly efficient vector [Manguin et al 2008]. Amongst members of the complex, *A. nili* is considered the most important vector, although *A. carnevalei* and *A. ovengensis* are implicated as secondary vectors of *P. falciparum* in Cameroon [Antonio-Nkondjio et al 2006,].

1) *Ecological requirements*

Recent investigations of the ecological requirements of *A. nili* in Cameroon, a country in Central Africa at the core of the species range, showed that lotic rivers exposed to sunlight, with vegetation or debris were the best predictors of *A. nili* larval abundance [Antonio-Nkondjio et al 2009] and that habitats characterized by high water vapour pressure and rainfall, as typically observed in forest-savannah transition areas were of highest quality for the development of the species [Ayala et al 2009]. *A. nili* however, is scarce in deep forest environments, where it is replaced by other members of the group, namely *A. carnevalei* and *A. ovengensis* [Awone-Ambene et al 2009, Antonio-Nkondjio et al 2009]. Larvae of all members of the *A. nili* complex are found in vegetation at the edges of fast flowing streams and rivers [Manguin et al 2008]. However, *A. ovengensis* and *A. carnevalei* appear to be restricted to areas of deep forest, whereas *A. nili* is more abundant along rivers in degraded forest and savannah [Antonio-Nkondjio et al 2009]. A comprehensive survey of the river systems across Cameroon found *A. nili* larvae associated with sunlit sites whereas *A. carnevalei* larvae were more commonly found in shaded areas [Antonio-Nkondjio et al 2009].

2) *Human biting behavior and vectorial capacity*

A. nili is considered to be strongly anthropophilic and will readily bite both indoors and out [Antonio-Nkondjio et al 2006 and, 2002]. Others have described biting patterns that exploited the behaviour of their human hosts [Carnevale & Zoulani 1975], biting outdoors in the early evening when people are socializing, and then continuing to bite indoors once people move inside, with peak feeding occurring after midnight [Antonio-Nkondjio et al 2002]. The resting habits of *A. nili* are also described as 'variable' [Gillies et al 1968]. Krafsur [1870], in a lowland region of western Ethiopia, rarely found *A. nili* resting indoors despite the high densities found biting indoors, are indicative of exophilic behaviour. Conversely, Antonio-Nkondjio et al. [2006] examined populations across Cameroon and reported *A. nili* overwhelmingly resting indoors (466 females), with only one female captured in an outdoor shelter. In the same study they found no *A. carnevalei* females resting indoors or in outdoor shelters whereas all resting *A. ovengensis* captured were found indoors. Conversely, Awono-Ambene et al. [2004] stated that *A. ovengensis* was rarely found resting indoors and concluded it had 'exophilic habits'.

3) Climatic and environmental factors and malaria transmission

Adja et al [2011], observed in southern forested area of Cote d'Ivoire, that the most common malaria vectors were *A. nili* s.s. that helps maintain a high level of malarial transmission during the dry season. *A. nili* was present throughout the year and sustained malaria transmission all year round with the *P. falciparum* sporozoite rate reaching 2.4%. The estimated EIR for *A. nili* was very high i.e. 210 infective bites /person-year. *A. nili* has also been found to play a major role in malarial transmission in some villages in a forested area of Cameroon (Carnevale et al., 1992). *A. nili* (s.l.) can be said to be a very efficient vector of *P. falciparum*.

Carnevale et al 1992 reported from the villages near Sanaga river, in the forest zone of south Cameroon, that, *A. nili* is the main species of mosquito regularly found biting man inside houses. Its densities are related to the flow level of the river. It is also the main malaria vector in terms of intensity and seasonal duration of transmission. The yearly malaria inoculation rate due to *A. nili* alone is 104 infective bites/man, varying between 3 infective bites/man in October and 20 in March.

vii) Anopheles pharoensis

The range of *A. pharoensis* extends throughout the Afrotropical Region, except the central rainforest area, spreading into the Palaearctic Region along the Nile up to the Mediterranean coast.

1) Ecological requirements

A. pharoensis is found in marshes, ponds, rice fields, lake shores, swamps, old water lands and often extensive wet season flooding and floating vegetation. The highest densities of *A. pharoensis* are associated with large vegetated swamps, where the main larval habitat is characterized by floating plants such as *Pistia* and *Potamogeton*.

2) *Human biting behavior and transmission potential*

A. pharoensis is weakly anthropophilic, and it bites humans and animals indoors or outdoors, resting outdoors after feeding. Females will enter houses and bite man, but prefer domestic animals. They feed from dusk to dawn with a peak at about 01:00 (Gillies and deMeillon 1968). The malaria vector status of *A. pharoensis* is well established in Egypt (Barber & Rice, 1937), but uncertain in Africa south of the Sahara, despite several records of sporozoite-positive specimens (Gillies & De Meillon, 1968; Gillies & Coetzee, 1987). These contrasting views on the vector role of *A. pharoensis* might be correlated with the existence of different sibling species, as suggested by Miles et al. (1983) from polytene chromosome studies on material from different African localities. Egyptian vector populations of *A. pharoensis* are characterized by the chromosomal Xu inversion, whereas the alternative standard arrangement X+"allows the recognition of markedly zoophilic and exophagic non-vector *A. pharoensis*. Both karyotypes occur in sub-Saharan Africa, where apparent variations in the biting behaviour of *A. pharoensis* lead to a puzzling situation when analyzing its role as a vector, particularly in areas where most of the malaria transmission is due to *A. funestu.s* and *A. gambiae* s.1. The finding of five CS-positive specimens, their distribution in time and the scarcity of other malaria vectors, strongly support the involvement of *An. pharoensis* in the maintenance of meso-endemic *P. falciparum* malaria in the Senegal River delta.

3) *Rainfall, irrigation and malaria transmission*

In the Ziway area of central Ethiopia where irrigation schemes have improved the lives of the people, Kibret et al (2010) found that the abundance of *A. pharoensis* was significantly higher than that of *A. arabiensis* during the dry irrigated period of the year. They also observed that canal leakage pools, irrigated fields and irrigation canals were the major breeding habitats. Larval and adult abundance of the malaria vectors, *A. pharoensis*, was higher in the irrigated than in the non-irrigated village throughout the period of study. *P. falciparum* sporozoite infection rates of 0.66% were determined in *A. pharoensis* in the irrigated village. Peak biting activities of *A. pharoensis* occurred before 22:00 h, which is a source of concern that the effectiveness of ITNs may be compromised as the mosquitoes feed on blood before people go to bed. The area receives between 700 and 800 mm of annual rainfall, with the main rains from June to September and short rains in April and May. The mean annual temperature is 20^0C. Malaria transmission in Ziway is generally unstable and seasonal, with peak transmission between September and November, immediately after the main rainy season and a secondary transmission period between April and May in the short rainy season. *P. falciparum* is the most prevalent malaria parasite, responsible for 60–70% of malaria cases, followed by P*. vivax* (Abose et al. 1998b). However, there are increasing levels of malaria prevalence in the dry season as a result of *A. pharoensis* breeding all year round in the irrigation area.

viii) Plasmodium falciparum

1) *Altitude, temperature and humidity*

At 17°C, parasites develop but not rapidly enough to cause an epidemic. On the other hand, temperatures ≥20^0C are sufficient to catalyze an epidemic. External ambient air temperatures of 17°C may correspond to indoor temperatures of around 20°C, i.e. those experienced by the parasite within the indoor-resting vector. *P. falciparum* fails to develop between 16°C and 19°C (Mollneaux et al 1988). This is the temperature at high altitudes with an average elevation of 2000m above sea level. Importantly, inhabited houses can be warm enough to allow the parasite to develop, even if it is too cold for development in an unoccupied house or outside. Moreover, in an occupied house the relative humidity may stabilize at around 60%, which fevers mosquito survival; outside relative humilities may vary considerably (12- 80%).

Although the greatest increase was recorded at the highest elevation where the impact of cold nights were dramatically reduced by 6.5^0C due to higher indoor temperatures. At this elevation, houses were generally more draft-proof and often had ceilings as an adaptation to the cool climate (29% had ceilings at 1,700 m compared with 0.3% in the other villages). We only detected sporozoites in *A. gambiae* s.l. and *A. funestus* complex indicating that the major highland vectors were the same as those in the plains. Sporozoite rates in *A. gambiae* s.l. declined from 300 m to 800 m (April-June) suggesting that decreasing temperatures increased parasite development time, the

first time a systematic decrease has been documented along a temperature transect in Africa. (Bodker et al 2003) observed that in the highlands, low temperatures prevented parasite development in mosquitoes during the cool season rains, and highland transmission was therefore limited to the warm dry season when vector densities were low.

ix) Plasmodium malariae

P. malariae is a parasitic protozoon that causes malaria in humans. It is closely related to *P. falciparum* and *P. vivax* which are responsible for most malarial infection. While found worldwide, it is a so-called "benign malaria" and is not nearly as dangerous as that produced by *P. falciparum* or P*. vivax*. *P. malariae* causes fevers that recur at approximately three-day intervals (a quartan fever), longer than the two-day (tertian) intervals of the other malarial parasites, hence its alternate names quartan fever and quartan malaria.

1) *Epidemiology and geographic distribution*

P. malariae is the one of the least studied species that infects humans, in part because of its low prevalence and milder clinical manifestations compared to the three other species. It is widespread throughout sub-Saharan Africa, much of Southeast Asia, Indonesia, on many of the islands of the western Pacific and in areas of the Amazon Basin of South America [Westling et al 1997]. In endemic regions, prevalence ranges from less than 4% to more than 20%, [Bruce et al 2006], but there is evidence that *P. malariae* infections are vastly underreported [Mohapatra et al 2008].

x) Plasmodium ovale

P. ovale is a species of parasitic protozoa that causes tertian malaria in humans. It is closely related to *P. falciparum* and *P. vivax*, which are responsible for most malaria. It is rare compared to these two parasites, and substantially less dangerous than *P. falciparum*. *P. ovale* has recently been shown by genetic methods to consist of two subspecies, *P. ovale curtisi* and *P. ovale wallikeri* [Sutherland et al 2010]. Ovale malaria produces a tertian fever clinically similar to that of vivax malaria but somewhat less severe. It exhibits relapses for the same duration as is seen with vivax malaria throughout the tropics, but it tends to appear in isolated pockets and at relatively low frequency compared to *P. falciparum* or *P. vivax*. Chloroquine resistant *P. malariae* has been reported from southern Sumatra, Indonesia [Maguire et al., 2002].

1) *Epidemiology and geographical distribution*

Microscopically confirmed *P. ovale* is exceedingly rare in eastern Indonesia, New Guinea, and the Philippines but is relatively common in West Africa (Hombhange, 1998). While it is frequently said that *P. ovale* is very limited in its range being limited to West Africa [Faye et al 1998], the Philippines, eastern Indonesia, and Papua New Guinea, and to discrete areas of the western pacific [Baird and Hoffman 2004]. It has been reported from Bangladesh [Fuehrer et al 2010], Cambodia and India [Snounou et al 1993], Thailand and Vietnam [Gleason et al 1970]. The reported prevalence is low (<5%) with the exception of West Africa, where prevalences above 10% have been observed.

xi) Plasmodium vivax

P. vivax infection is called benign tertian or vivax malaria. Red blood cells infected with *P. vivax* are enlarged and when properly stained with Giemsa often show stippling on the erythrocyte membrane, known as schuffners dots. All stages of the parasite are present in the peripheral circulation, single infections of invaded erythrocytes are characteristic; gametocytes appear simultaneously with the first asexual parasites. The duration of the viability of the sexual stages appears to the less than 12 hours. *P. vivax* produces the classic relapsing malaria initiated from hypnozoite in the liver that have resumed development after a period of latency. Relapses can occur at periods ranging from every few weeks to a few months for up to five years after the initial infection, the specific periodicity of the relapses is a characteristic of the geographic strain of the parasite. Vivax malaria also has recrudescence due to persistent circulating parasites.

Vivax malaria also constitutes an important burden on public health throughout most of the tropical and many subtropical or temperate latitudes. Although less often fatal, this infection causes a se-

verely debilitating disease with frequent and sometime multiple episodes of relapse. Moreover, recent reports reveal cases of severe malaria caused by *P. vivax* [Andrade et al. 2010c] display patterns of inflammation and immunopathology similar to those seen in severe *P. falciparum* malaria cases. These findings suggest that different *Plasmodium* species can trigger strikingly similar host responses that can result in severe disease with significant risk of severe disease and death caused by the same spectrum of syndromes typically linked to *P. falciparum* malaria [Genton et al., 2008].

1) *Epidemiology and geographical distribution*

P. vivax accounts for 65% of malaria cases in Asia and South America. *P. vivax* is uncommon in sub-Saharan Africa, but common in South Asia and Central America, and is predominant in South America. It can also be found in mainly in Latin America, and in some parts of Ethiopia. *P. vivax* can cause death due to splenomegaly (a pathologically enlarged spleen), but more often it causes debilitating – but non-fatal – symptoms [Lindsay et al 2006].

2) *Endemic and epidemic malaria*

Important, and rarely appreciated, endemic and epidemic malaria need different approaches to their control and prevention. Endemic malaria needs ongoing routine measures, whereas the control of epidemic malaria relies on measures being applied in the right place at the right time. This is particularly important where resources to tackle the disease are limited. Developing epidemic malaria early warning and response approaches that includes seasonal forecasts and climate monitoring, as well as vulnerability assessment, case surveillance and response planning holds promise not only in Africa but for use beyond Africa in malarial areas of Asia and Latin America (Hellmuth et al. 2007).

Malaria bibliography

Adja AM, N'goran K, Koudou, Dia1 G, Fontenille K, and Chandre: Contribution of Anopheles funestus, An. gambiae and An. nili (Diptera: Culicidae) to the perennial malaria transmission in the southern and western forest areas of Coˆ te d'Ivoire. 2011. Annals of Tropical Medicine & Parasitology, 105 (1) 13–24

Ageep TB, Cox J, Hassan MM, Knols BGJ, Benedict MQ, Malcolm CA, Babiker A, El Sayed BB: Spatial and temporal distribution of the malaria mosquito Anopheles arabiensis in northern Sudan: influence of environmental factors and implications for vector control. Malar J 2009, 8:123.

Antonio-Nkondjio C, Kerah CH, Simard F, Awono-Ambene P, Chouaibou M, Tchuinkam T, Fontenille D: Complexity of the malaria vectorial system in Cameroon: contribution of secondary vectors to malaria transmission. 2006, J Med Entomol, 43:1215-1221

Antonio-Nkondjio C, Ndo C, Costantini C, Awono-Ambene P, Fontenille D, Simard F: Distribution and larval habitat characterization of Anopheles moucheti, Anopheles nili, and other malaria vectors in river networks of southern Cameroon. 2009. Acta Trop, 112:270-276.

Awono-Ambene H, Kengne P, Simard F, Antonio-Nkondjio C, Fontenille D: Description and bionomics of Anopheles (Cellia) ovengensis (Diptera: Culicidae), a new malaria vector species of the Anopheles nili group from south Cameroon. J Med Entomol 2004, 41:561-568

Awolola, TS, Okwa O, Hunt RH, Ogunrinade AF, Coetzee M: Dynamics of the malaria-vector populations in coastal Lagos, south–western Nigeria. Annals of Tropical Medicine and Parasitology, 2002 96 (1): 75-82(8)

Ayala D, Carlo Costantini, Ose K, Kamdem GC, Antonio-Nkondjio C, Agbor JP, Awono-Ambene P, Fontenille D, Simard F: Habitat suitability and ecological niche profile of major malaria vectors in Cameroon. Malar J 2009, 8:307.

Baird JK, Hoffman SL). "Primaquine therapy for malaria". 2004. Clin. Infect. Dis. 39 (9): 1336–45. DOI:10.1086/424663. PMID 15494911.

Bødker R, Akida J, Shayo D, Kisinza W, Msangeni HA, Pedersen EM, Lindsay SW: Relationship Between Altitude and Intensity of Malaria Transmission in the Usambara Mountains, Tanzania. 2003. J. Med. Entomol. 40(5): 706-717

Bøgh C, Clarke SE, Jawara M, Thomas CJ, Lindsay SW. Localized breeding of the Anopheles gambiae complex (Diptera: Culicidae) along the River Gambia, West Africa. Bull Entomol Res. 2003. 93(4):279-87.

Bryan JH, Petrarca V, Di Deco MA, Coluzzi M: Adult behaviour of members of the Anopheles gambiae complex in the Gambia with special reference to An. melas and its chromosomal variants. Parassitologia 1987, 29:221-249.

Bryan JH: Anopheles gambiae and A. melas at Brefet, The Gambia, and their role in malaria transmission. 1983. Ann Trop Med Parasitol, 77:1-12.

Bruce, M. C.; Macheso, A.; Galinski, M. R.; Barnwell, J. W: "Characterization and application of multiple genetic markers for Plasmodium malariae". 2006. Parasitology 134 (5): 637–650. DOI:10.1017/S0031182006001958. PMC 1868962. PMID 17140466Dia I,

Carlson JC, Byrd BD, Omlin FX: Field assessments in western Kenya link malaria vectors to environmentally disturbed habitats during the dry season. BMC Public Health 2004, 4:33

Carnevale P, Le Goff G, Toto JC, Robert V: Anopheles nili as the main vector of human malaria in villages of southern Cameroon. Med Vet Entomol 1992. 6(2):135-8.

Carnevale P, Guillet P, Robert V, Fontenille D, Doannio J, Coosemans M, Mouchet J: Diversity of malaria in rice growing areas of the Afrotropical region. Parassitologia 1999, 41:273-276

Carnevale P, Zoulani A: Agressivité d'Anopheles nili (Theobald), 1904 à l'intérieur et à l'extérieur des maisons. Cahiers ORSTOM, Entomol Med Parasitol 1975, 13:69-73.

Case TJ, Washino RK: Correlates of mosquito larval densities and survivorship in some northern California rice fields. 1975. Proc Calif Mosq Control Assoc 43:155.

Castro MC, Kanamori S, Kannady K, Mkude S, Killeen GF, Fillinger U: The importance of drains for the larval development of lymphatic filariasis and malaria vectors in Dar Es Salaam, United Republic of Tanzania. 2010. PLoS Neglect Trop Dis, 4:e693.

Charlwood, J.D., Edoh, D: Polymerase chain reaction used to describe larval habitat use by Anopheles gambiae complex (Diptera: Culicidae) in the environs of Ifakara, Tanzania. 1996. J. Med. Entomol. 33, 202–204

Colin A Malcolm, Badria El Sayed, Ahmed Babiker, Romain Girod, Didier Fontenille, Bart GJ Knols, Abdel Hameed Nugud, Mark Q Benedict; Field site selection: getting it right first time around Malar J 2009, 8(Suppl 2):S9

Coetzee M, Craig M, le Sueur D: Distribution of African malaria mosquitoes belonging to the Anopheles gambiae complex. Parasitol Today 2000, 16:74-77.

Coluzzi, M. et al. (1979) Chromosomal differentiation and adaptation to human environments in the Anopheles gambiae complex. Trans. R. Soc. Trop. Med. Hyg. 73, 483–497

Mboera et al Tanzania Health Res Bull 2006; 8(1) 22-7

Coz, J: Les mécanismes d'isolement génétique dans le complexe Anopheles gambiae Giles. Cah. ORSTOM 1973.Ent. Méd. 11, 41–56.

Diop A, Molez JF, Konaté L, Fontenille D, Gaye O, Diouf M, Diagne M, Faye O: Role of Anopheles melas Theobald (1903) on malaria transmission in a mangrove swamp in Saloum, Senegal. 2002. Parasite. 9(3):239-46.

Dolo G, Briet OJT, Dao A: The relationship between rice cultivation and malaria transmission in the irrigated Sahel of Mali, West Africa. 2000. Cah Agricultures 9: 425.

Duchemin JB, Tsy JM, Rabarison P, Roux J, Coluzzi M, Costantini C: Zoophily of Anopheles arabiensis and An. gambiae in Madagascar demonstrated by odour-baited entry traps. Med Vet Entomol 2001, 15:50-57.

Dukeen MYH, Omer SM: Ecology of the malaria vector Anopheles arabiensis Patton (Diptera: Culicidae) by the Nile in northern Sudan. Bull Entomol Res 1986, 76:451-467.

Fillinger U, Sonye G, Killeen GF, Knols BG, Becker N: The practical importance of permanent and semi-permanent habitats for controlling aquatic stages of Anopheles gambiae sensu lato mosquitoes: operational observations from a rural town in western Kenya. Trop Med Int Health 2004, 9:1274-1289.

Gallup J and Sachs J. The Economic burden of Malaria. Am. J. Trop. Med. Hyg. 64(1,2) S, 85-96 (2001)/

Gelfand HM: Anopheles gambiae Giles and Anopheles melas Theobald in a coastal area of Liberia, West Africa. Trans R Soc Trop Med Hyg 1955, 49:508-527.

Gimnig JE, Ombok M, Kamau L, Hawley W. 2001. Characteristics of larval anopheline (Diptera: Culicidae) habitats in western Kenya. J Med Entomol 38:282–288.

Gillies MT, De Meillon B: The Anophelinae of Africa South of the Sahara (Ethiopian Zoogeographical Region) 1968 . The South African Institute for Medical Research. 1968 (2).

Gillies, M.T. and Coetzee, M. (1987) A Supplement to the Anophelinae of Africa South of the Sahara. Publ. S. Afr. Inst. Med. Res. No. 55

Gleason NN, Fisher GU, Blumhardt R, Roth AE, Gaffney GW "Plasmodium ovale malaria acquired in Viet-Nam". (1970). Bull. World Health Organ. 42 (3): 399–403. PMC 2427544. PMID 4392940

Hellmuth M.E, Moorhead A, Thomson M.C, and Williams J. (eds) 2007. Climate Risk Manaegment in Africa: Learning from Practice. International Research Institute for Climate and Society (IRI). Columbia University, New York, USA.

Hunt, R.H. et al. (1998) The Anopheles gambiae complex: a new species from Ethiopia. Trans. R. Soc. Trop. Med. Hyg. 92, 231–235

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

Imbahale SI, Paaijmans KP, Mukabana WR, Lammeren RV, Giheko AK, Willem Takken: A longitudinal study on Anopheles mosquito larval abundance in distinct geographical and environmental settings in western Kenya. 2011. Malar J 10:81

Keating J, Macintyre K, Mbogo CM, Githure JI, Beier JC: Characterization of potential larval habitats for Anopheles mosquitoes in relation to urban land-use in Malindi, Kenya. Int J Health Geogr 2004, 3:9.

Kibret S, Alemu Y, Boelee E, Tekie H, Alemu D, Petros B: The impact of a small-scale irrigation scheme on malaria transmission in Ziway area, Central Ethiopia 2010. Tropical Med Int Health 15 (1): 41–50

Koenraadt CJM, Githeko AK, Takken W: The effects of rainfall and evapotranspiration on the temporal dynamics of Anopheles gambiae s.s. and Anopheles arabiensis in a Kenyan village Acta Tropica 90 (2004) 141–153

Koram K. A. Malaria Chemotherapy in Ghana: Current situation, challenges and prospects (2003) unpublished.

Lacey LA, Lacey CM. 1990. The medical importance of riceland mosquitoes and their control using alter- natives to chemical insecticides. J Am Mosq Control Assoc 6:1–93.

Lee SJ.. Major factors affecting mosquito oviposition. 1991. Chin J Entomol 6:23–35.

Lindsay SW, Parson L, Thomas CJ: Mapping the ranges and relative abundance of the two principal African malaria vectors, Anopheles gambiae sensu stricto and A. arabiensis, using climate data. 1998. Proc. R. Soc. Lond. 265, 847–854.

Maxwell CA, Chambo W, Mwaimu M, Magogo F, Carneiro IA, Curtis CF. Variations in malaria transmission and morbidity with altitude in Tanzania and with introduction of alphacypermethrin treated nets. Malar J 2003;2:28.

Manguin S, Carnevale P, Mouchet J, Coosemans M, Julvez J, Richard- Lenoble D, Sircoulon J: Biodiversity of malaria in the world Montrouge, France: John Libbey Eurotext; 2008.

Minakawa N, Sonye G, Dida GO, Futami K, Kaneko S: Recent reduction in the water level of Lake Victoria has created more habitats for Anopheles funestus. Malar J 2008, 7:119.

Mohapatra, P. K.; Prakash, A.; Bhattacharyya, D. R.; Goswami, B. K.; Ahmed, A.; Sarmah, B.; Mahanta, J. Detection & molecular confirmation of a focus of Plasmodium malariae in Arunachal Pradesh, India. 2008. The Indian journal of medical research 128 (1): 52–56. PMID 18820359

Mollneaux L. The epidemiology of human malaria as an explanation of its distribution, including some implications for its control. In: Wernsdorfer WH, McGregor I, eds. Malaria: principles and practice of malariology, vol. 2. New York, Churchill Livingstone, 1988: 913- 998.

Munga S, Minakawa N, Zhou G, Mushinzimana E, Barrack OJ, Githeko AK, Yan G: Association between landcover and production of malaria vectors in the western Kenyan highland. Am J Trop Med Hyg 2006, 74:69-75.

Mutuku FM, Alaii JA, Bayoh MN, Gimnig JE, Vulule JM, Walker ED, Kabiru E, Hawley WA: Distribution, description, and local knowledge of larval habitats of Anopheles gambiae s.l. in a village in western Kenya. 2006. Am J Trop Med Hyg, 74:44-53

Mutero CM, Ng'ang'a PN, Wekoyela P, Githure J, Konradsen F. 2004b. Ammonium sulphate fertilizer increases larval populations of Anopheles arabiensis and culicine mosquitoes in rice fields. Acta Trop 89: 187–192.

Muirhead-Thomson RC: Studies on Anopheles gambiae and An. melas in and around Lagos. Bull Entomol Res 1948, 38:527-558.

Mwangangi J, Shililu J, Muturi E, Weidong G, Mbogo C, Kabiru E. Dynamics of immature stages of Anopheles arabiensis and other mosquito species (Diptera: Culicidae) in relation to rice cropping in a rice agro-ecosystem in Kenya. J Vector Ecol 2007;32:6–22.

Mwangangi JM, Muturi EJ, Shililu JI, Muriu S, Jacob B, Kabiru EW, Mbogo CM, Githure JI, Novak RJ: Environmental covariates of Anopheles arabiensis in a rice agro ecosystem in Mwea, Central Kenya: J. Am. Mosq control Assoc, 23(4):371-377. 2007.

Nyanjom SRG, Chen H, Gebre-Michael T, Bekele E, Shililu J, Githure J, Beier JC, Yan G: Population Genetic Structure of Anopheles arabiensis Mosquitoes in Ethiopia and Eritrea, 2003. Journal of Heredity:94(6):457–463

Okara RM, Sinka ME, Minakawa N, Mbogo CM, Hay SI, Snow RW: Distribution of the main malaria vectors in Kenya 2010. Malar J, 9:69

Paaijmans KP, Wandago MO, Githeko AK, Takken W: Unexpected high losses of Anopheles gambiae larvae due to rainfall. PLoS ONE 2007, 2:11.

Robert V, Awono-Ambene HP, Thioulouse J: Ecology of larval mosquitoes, with special reference to Anopheles arabiensis (Diptera: Culcidae) in market- garden wells in urban Dakar, Senegal. 1998 J Med Entomol 35:948–955.

Snounou G, Viriyakosol S, Jarra W, Thaithong S, Brown KN (April 1993). "Identification of the four human malaria parasite species in field samples by the polymerase chain reaction and detection of a high prevalence of mixed infections". Mol. Biochem. Parasitol. 58 (2): 283–92. DOI:10.1016/0166-6851(93)90050-8. PMID 8479452

Shiliu et al: Seasonal density, sporozoite rate and EIR of An gambiae and funestus in the high altitude sugar cane growing zone western Kenya. (1998) 3 (9) 706-71

Taylor CE, Toure YT, Coluzzi M, Petrarca V: Effective population size and persistence of Anopheles arabiensis during the dry season in West Africa. Med Vet Entomol 1993, 7:351-357.

Tuno N, Kjaerandsen J, Badu K, Kruppa T: Blood-Feeding Behavior of Anopheles gambiae and Anopheles melas in Ghana, Western Africa. 2010. J. Med. Entomol. 47(1): 28-31

Westling J, Yowell CA, Majer P, Erickson JW, Dame JB, Dunn, BM: Plasmodium falciparum, P. Vivax, and P. Malariae: A Comparison of the Active Site Properties of Plasmepsins Cloned and Expressed from Three Different Species of the Malaria Parasite. 1997. Experimental Parasitology 87 (3): 185–193. DOI:10.1006/expr.1997.4225. PMID 9371083.

White GB: The Anopheles gambiae complex and malaria transmission around Kisumu, Kenya. Trans R Soc Trop Med Hyg 1972, 66:572-581.

White GB, Rosen P: Comparative studies on sibling species of Anopheles gambiae Giles complex (Dipt: Culicidae). II. Ecology of Species A and B in savanna around Kaduna, Nigeria, during transition from wet to dry season. Bull Entomol Res 1973, 62:613-625.

World Health Organization (WHO): World Malaria Report 2008. Pp. 10. Retrieved 17-08-2009.

World Health Organization (WHO): World Malaria Report 2010. Geneva, Switzerland 2010.http://www.who.int/malaria

www.rbm.who.int. History of Malaria

Ye-Ebiyo Y, Pollack RJ, Kiszewski A, Spielman A: Enhancement of development of larval Anopheles arabiensis by proximity to flowering maize (Zea mays) in turbid water and when crowded. 2003. Am J Trop Med Hyg 68:748–752.

b) **Review of the effects of climate drivers upon Rift Valley Fever in Africa**

i) *Introduction*

Rift Valley fever (RVF) is an acute fever causing viral disease that affects domestic animals (such as cattle, buffalo, sheep, goats, and camels, among others), and humans. RVF is most commonly associated with mosquito-borne epidemics during years of unusually heavy rainfall events. The RVF virus, a member of the genus *Phlebovirus* in the family *Bunyaviridae*, is responsible for the disease. RVF was first reported among livestock by veterinary officers in Kenya in the early 1900s.

Numerous epidemic/epizootic outbreaks have been reported periodically in many African countries during the past 30 years, including Egypt in 1977 (Meegan 1979, Hoogstraal et al., 1979) and in 1993 (Arthur et al. 1993); Mauritania in 1987 (Jouan et al., 1988, Digoutte and Peters 1989), 1993 (Zeller et al., 1997), and 1998 (Nabeth et al., 2001); and Somalia and Kenya in 1997-1998 (Woods et al. 2002). The virus has been recently located for the first time outside of the African continent, in Saudi Arabia and Yemen during 2000-2001 (Miller et al., 2002, Jupp et al., 2002).

ii) *RVF carrying vectors in Senegal*

In Senegal, many mosquito species (Fontenille et al.1995; Diallo et al., 2000) as well as humans and livestock (Wilson et al., 1994; Thonnon et al., 1999) have been found to be infected with the RVF virus.

After the RVF outbreak of 1987, entomological studies were conducted in Senegal from 1991 to 1996 to identify the sylvatic vectors of the virus. During the rainy season in 1993 and for the Barkedji site in the Ferlo region, viruses were carried by *Aedes vexans* and by *Ae. ochraceus*. Using CO2-CDC light traps (from October to November 1993), they were sampled in the vicinity of three temporary ponds, and cattle watering holes. In November, a virus was sampled from one sheep. In 1974 and 1983, the virus had also been isolated from *Ae. dalzieli* (Fontenille et al., 1998; Sall, 2001).

In 1998, following the re-emergence of RVF virus in southeastern Mauritania and in the Diawara region, an entomological survey was undertaken at the northern border of Senegal to assess the extent of the virus circulation. During this study (Diallo et al., 2000), the virus was isolated for the first time from *Culex poicilipes*.

In Senegal, the epidemiological role of the mosquitoes species involved in RVF transmission cycle (*Aedes sp*. and *Culex sp*.) is peculiar. The environmental maintenance of the virus is mainly due to so-called 'vertical transmission' (Wilson, 1994) while *Culex sp*. mosquitoes amplify the phases of the virus cycle (Diallo, 2000; Ndione et al, 2003 ; Ndione et al, 2005; Ndione et al, 2008).

Although all of the above vectors differ from those in East and South Africa (Meegan, 1988), they all use the same type of breeding sites and feed on cattle and sheep (Fontenille et al., 1998; Ba et al., 2006).

iii) *RVF and rainfall in Senegal*

Linthicum et al. (1999), by using the Normalized Difference Vegetation Index (NDVI) as a proxy for rainfall (Davies et al., 1985; Anyamba and Tucker, 2005; Tucker and Nicholson, 1999) have highlighted possible linkages between rainfall and Rift Valley Fever (RVF) epidemics. Anyamba et al. (2001) have also studied relationships between RVF occurrence, inter-annual variability of the warm phase of El Niño-Southern Oscillation (ENSO), and excess rainfall over Kenya (Linthicum et al., 1999). Kelly-Hope and Thomson (2008), GEO (2010a, 2010b) produced a comprehensive review related to infectious diseases and climate drives.

In West Africa, more precisely over Senegal and southern Mauritania, RVF epidemics (Diallo et al., 2005), do not seem to follow the same relationships as that over East Africa. The spatio-temporal distribution of discrete rainfall events (such as squall-lines) during the rainy/summer monsoon season (contrary to the seasonal amount of total rainfall over East Africa) appears to be the confounding parameter for mosquitoes' production (Ndione et al., 2003). In accordance with Bâ et al. (2005), Mondet et al. (2005a, b), Ndione et al. (2008), rainfall frequency (including intra-seasonal variability) is a key factor modulating *Ae*. *vexans* population abundance (Figures 1and 2). Interestingly enough, rainfall events seem to have very little effect on the *Cx*. *poicilipes* abundance (Bâ et al., 2005).

Figure 1: Rainfall, ponds levels and daily abundance of *Aedes vexans arabiensis* females in Barkedji region (Ferlo, Senegal) during the 2002 and 2003 rainy seasons (Mondet et al., 2005)

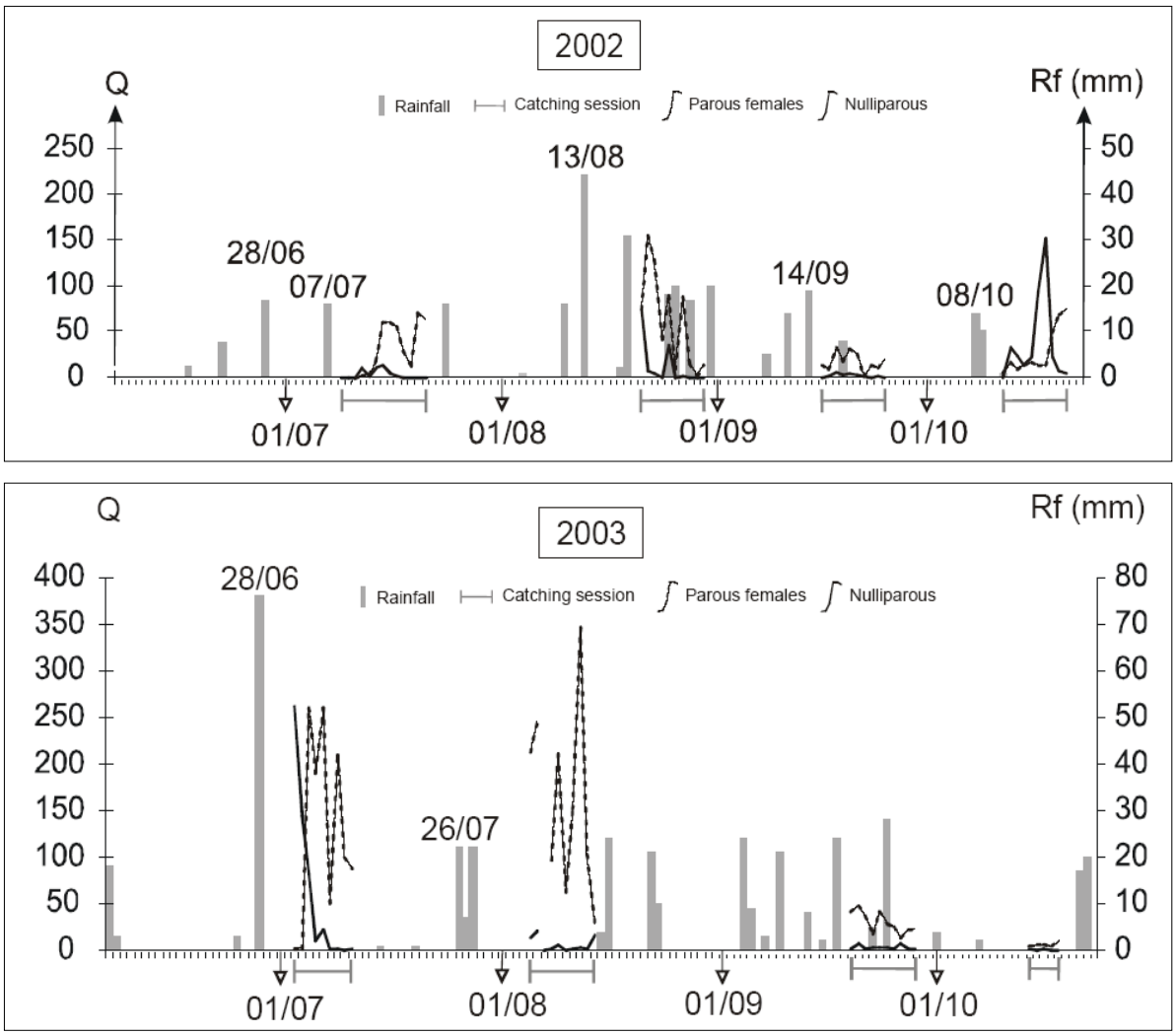
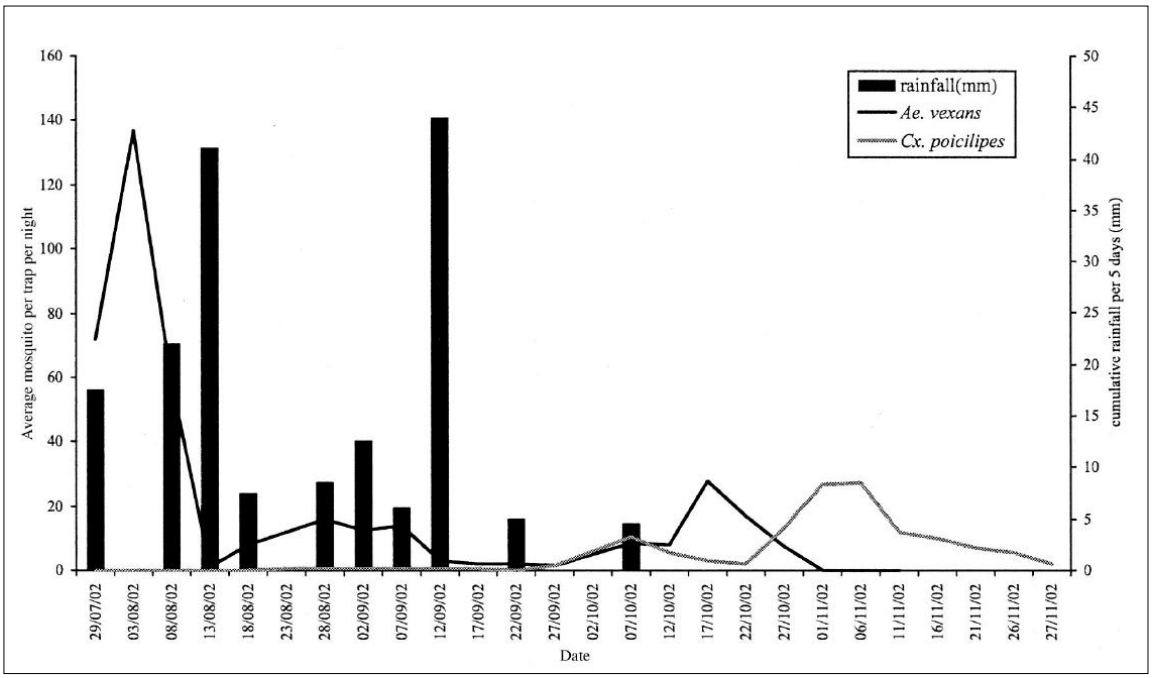


Figure 2: Population dynamics of *Ae*. *vexans* and *Cx*. *poicilipes* in Niakha ground pool in **2**002 (Bâ et al, 2005).



This is particularly true for the *Ae. vexans* mosquitoes whose eggs are often laid along the edges of the ponds. When the time lag between two rainfall events is large enough (10-to-15 days), the number of eggs present along the already dried-up ponds' edges becomes quite important. Intense rainfall events (i.e., more than 20 mm, as produced by squall-lines), trigger powerful mechanisms for enhanced hatching (Mondet et al., 2005a and b). Recently, modelling results by Porphyre et al. (2005) linking ponds' dynamics, discrete rainfall events, and mosquitoes' abundance involved with RVF, have been successfully implemented.

Finally, a better understanding of the biological mechanisms driving RVF would contribute to the development of early warning systems (EWS) in a constantly changing climate and environment. Health information systems (HIS), agencies and organizations, decisions makers and other national stakeholders over West Africa will thus have a panoply of additional products in support of appropriate measures to apply in regions under threat.

Rift Valley Fever bibliography

Anyamba A., Linthicum K.J., Tucker C.J., 2001. Climate-disease connections: Rift Valley Fever in Kenya, Cad Saude Publica, 17(suppl): 133-140.

Anyamba, A., & Tucker, C. J. (2005). Analysis of Sahelian vegetation dynamics using NOAA-AVHRR NDVI data from 1981–2003. Journal of Arid Lands, 63, 569−614.

Arthur R.,M.S. El Sharkawy, S. E. Cope, B. A. Botros, S. Oun, J. C. Morrill, R. E. Shope, R. G. Hibbs, M. A. Darwish, I.Z.E. Imam. 1993. Recurrence of Rift Valley fever in Egypt. Lancet 342: 1149Ð1150.

Ba Y., Diallo D., Kebe C.M.F., Dia I., Diallo M., 2005. Aspects of bioecology of two Rift Valley Fever virus vectors in Senegal (West Africa): Aedes vexans and Culex poicilipes (Diptera: Culicidae), Journal of Medical Entomology, 42(5): 739-750.

Ba Y., Diallo D., Dia I., Diallo M., 2006. Comportement trophique des vecteurs du virus de la fièvre de la vallée du Rift au Sénégal : implications dans l'épidémiologie de la maladie, Bulletin de la Société Pathologique Exotique, 99(4): 283-289.

Davies F.G., Linthicum K.J., James A.D., 1985. Rainfall and epizootic Rift valley fever.Bulletin of the World Health Organisation, 63(5): 941-943.

Diallo M., Lochouarn L., Ba K., Sall A.A., Mondo M., Girault L., Mathiot C., 2000. First isolation of the Rift Valley fever virus from Culex poicilipes (Diptera: Culicidae) in nature, American Journal of Tropical Medicine and Hygiene, 62: 702-704.

Digoutte J.-P., Peters C.J., 1989. General aspects of the 1987 Rift Valley fever epidemic in Mauritania. Research in virology, 140: 27-30.

Fontenille D., Traore-Lamizana M., Zeller H.G., Mondo M., Diallo M., Digoutte J.-P., 1995. Rift valley fever in western Africa: isolations from Aedes mosquitoes during an interepizootic period, American Journal of Tropical Medicine and Hygiene, 52(5): 403-404.

Fontenille D., Traore-Lamizana M., Diallo M., Thonnon J., Digoutte J.-P., Zeller H.G., 1998. Nouveaux vecteurs de la fièvre de la vallée du Rift en Afrique de l'Ouest. Emerging Infectious Diseases, 4: 289-293.

GEO, 2010a. GEO Task US-09-01a- Critical Earth Observation Priorities, Final Report, 80p.

GEO, 2010b. GEO Task US-09-01a- Critical Earth Observations Priorities. Health Societal Benefit Area: Infectious Diseases, 160p.

Jouan A., Le Guenno B., Digoutte J.-P., Philippe B., Riou O., Adam F., 1988. An RVF epidemic in Southern Mauritania, Annales de l'Institut Pasteur / Virologie, n°139, pp. 307-308.

Jupp P.G., Kemp A., Grobbelaar A., Leman P., Burt F.J., Alahmed A.M., Al Mujalli D., Al Khamees M., Swanepoel R., 2002. The 2000 epidemic of Rift Valley fever in Saudi Arabia: mosquito vector studies. Medical and Veterinary Entomology,1: 245-252.

Kelly-Hope L., Thomson M.C., 2008. Climate and Infectious Diseases. In Seasonal Forecasts, Climatic Change and Human Health, Health and Climate, Series Advances in Global Change Research, Vol. 30(I): 31-70, Thomson M.C., Garcia-Herrera R., Beniston M. (Eds.) 234 p.

Lacaux J.-P., Tourre Y.-M., Vignolles C., Ndione J.-A., Lafaye M., 2007. Ranking Ponds from High-Resolution Remote Sensing: application to Rift Valley Fever Epidemics in the Ferlo Region (Senegal). Remote Sensing of Environment, 106: 66-74.

Linthicum K.J., Assaf A., Compton J.T., Kelley P.W., Myers M.F., Peters C.J., 1999. Climate and satellite indicators to forecast Rift Valley Fever epidemics in Kenya. Science, 285: 397-400.

Meegan J.M., Hoogstraal H., Moussa M.I., 1979. An epizootic of Rift valley fever in Egypt in 1977.Vetenary Record, 105(6): 124-5.

Meegan J.M., Bailey C.H., 1988. Rift valley fever. Arboviruses Epidemiolgy and Ecology (ed. T.P. Monrath), CRC Press, Boca Raton, 51-76.

Miller B.R., Godsey M.S., Crabtree M.B., Savage H.M., Al-Mazrao Y., Al-Jeffri M.H., Abdoon A.M., Al-Seghayer S.M., Al-Shahrani A.M., Ksiazek T.G., 2002. Isolation and genetic characterization of Rift Valley fever virus from Aedes vexans arabiensis, Kingdom of Saudi Arabia. Emerging Infectious Disease, 8: 1492-1494.

Mondet B., Diaïté A., Ndione J.-A., Fall A.G., Chevalier V., Lancelot R., Ndiaye M., Ponçon N., 2005a: Rainfall patterns and population dynamics of Aedes (Aedimorphus) vexans arabiensis, Patton 1905 (Diptera: Culicidae), a potential vector of Rift Valley Fever virus in Senegal. Journal of Vector Ecology, 30: 102-106.

Mondet B., Diaïté A., Fall A.G., Chevalier V., 2005b. Relations entre la pluviométrie et le risque de transmission virale par les moustiques : cas du virus de la Rift Valley Fever (RVF) dans le Ferlo (Sénégal). Environnement, Risques et Santé, vol. 4, n°2, pp. 125-129.

Nabeth P., Kane Y., Abdalahi M.O., Diallo M., Ndiaye K., Ba K., Schneegans F., Sall A.A.,Mathiot C., 2001.Rift Valley fever outbreak in Mauritania in 1998: seroepidemiologic,virologic, entomologic, and zoologic investigations.Emerging infectious diseases, Nov-Dec. 7(6):1052-1054.

Ndione J.-A., Besancenot J.-P., Lacaux J.-P., Sabatier P., 2003. Environnement et épidémiologie de la fièvre de la vallée du Rift (FVR) dans le bassin inférieur du fleuve Sénégal. Environnement, Risques et Santé, vol. 2, n°3, pp. 176-182.

Ndione J.-A., Bicout D., Mondet B., Lancelot R., Sabatier P., Lacaux J.-P., Ndiaye M., Diop C., 2005. Conditions environnementales associées à l'émergence de la fièvre de la vallée du Rift dans le delta du fleuve Sénégal en 1987. Environnement, Risques et Santé, vol. 4, n° 2, S5-S10.

Ndione J.-A., Diop M., Lacaux J.-P., Gaye A.Th., 2008. Variabilité intrasaisonnière de la pluviométrie et émergence de la fièvre de la vallée du Rift (FVR) dans la vallée du fleuve Sénégal : nouvelles considérations, Climatologie, vol. 5, pp. 83-97.

Porphyre T., Bicout D.J., Sabatier P., 2005. Modelling the abundance of mosquito vectors versus flooding dynamic. Ecological modelling, 183(2-3): 173-181.

Sall B., 2001. Épidémio-surveillance de la FVR au Sénégal : objectifs, méthodologie, résultats obtenus. In Lefèvre P.C., éd., Séminaire sur la surveillance épidémiologique et le contrôle de la fièvre de la vallée du Rift en Afrique de l'Ouest, FAO, Dakar, pp. 17-19.

Thonnon J., Picquet M., Thiongane Y., Lo M., Sylla R., Vercruysse J., 1999. Rift valley fever surveillance in the lower Senegal river basin: update 10 years after the epidemic. Tropical Medecine and International Health, 4: 580-585.

Wilson M.L., Chapman L.E., Hall D.B., Dykstra E.A., Ba K., Zeller H.G., Lamizana M.T., Hervry J.-P., Linthicum K.J., Peters J., 1994. Rift valley fever in rural northern Senegal: human risk factor and potential vectors. American Journal of Tropical Medicine and Hygiene, 50(6): 663-675.

Woods C.W., Karpati A.M., Grein T., McCarthy N., Gaturuku P., Muchiri E., Dunster L., Henderson A., Khan A.S., Swanepoel R., Bonmarin I., Martin L., Mann P., Smoak B.L., Ryan M., Ksiazek T.G., Arthur R.R., Ndikuyeze A., Agata N.N., Peters C.J., 2002. An outbreak of Rift Valley fever in Northeastern Kenya, 1997-1998. Emerging Infectious Diseases, 8: 138-144.

Zeller, H. G., D. Fontenille, M. Traore´-Lamizana, Y. Thiongane, and J. P. Digoutte. 1997. Enzootic activity of Rift

Valley fever virus in Senegal. Am. J. Trop. Med. Hyg. 56: 265Ð272.

iii) **Review of the effects of climate drivers upon tick-borne diseases of Africa**

A review document was not delivered by the relevant work-package partner.

This was due to the resignation and departure from the University of Pretoria, to take up a new post, of the expert in tick borne diseases.