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Mosquitoes composition, abundance and distribution in swampy and flooded shoreline habitats of Lake Baringo, Kenya, during a period of extreme flooding (2012-2013)

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Abstract

Mosquito ecology is influenced by wetness in the environment. In 2011-2014, a rise in waters of Lake Baringo resulted in unprecedented flooding that inundated over 88km² of the shoreline. A longitudinal study carried out from October 2012-October 2013 assessed mosquito abundance and diversity in two habitats. A total of 386,624 mosquitoes were captured, 89% from flooded shoreline and 11% from swampy habitat. Family Culicinae constituted 10 genera. *Mansonia* dominated the catches with 98% from flooded shoreline and swampy habitat 2%. Genetic sequences of *Aedes albopictus* species was identified and reported for the first time in the basin. Diversity index was higher in swampy habitat (Simpson Diversity Index=0.56), compared to flooded shoreline (Simpson diversity index =0.13). Future recurring floods will result in drastic changes of the ecology and could lead to emergence and re-emergence of more species.

Keywords: extreme flooding, flooded shoreline, swamps, mosquito, diversity, Lake Baringo

1. Introduction

Mosquitoes are well known vectors of human pathogens, including arboviruses and are considered to be the main vectors of killer diseases such as malaria, Rift Valley Fever, Dengue haemorrhagic fever, Yellow Fever, West Nile Fever and Chikungunya Fever [1]. According to a report by WHO [2], malaria transmitted by mosquitoes is currently responsible for 1.4% of global disease burden, with the vast majority of burden from among children in sub-Saharan Africa. Flooding from either heavy rains, Elnino, or artificially induced floods mostly result in creation of several ecotope layers in a habitat that promote the proliferation of mosquitoes including distribution and breeding [3]. Lake Baringo basin has diversity of habitats whose composition of fauna and flora is influenced by human activities, environmental changes and that are affected differently by floods. The basin has severally experienced outbreaks of diseases such as Rift Valley Fever (RVF), mostly attributed to Elnino/Southern Oscillation phenomenon (ENSO) rains causing flooding [4]. The notable Elnino floods in Lake Baringo occurred in 1997-1998 [5] and 2006-2007 [6] resulting in livestock and human death. However, other than floods resulting from heavy rains, an extreme and unprecedented flooding occurred in 2011-2014 in Lake Baringo basin and was associated with changes in earth geological factors that contributed into rise of lake waters and submerged farms along the lake shores [7]. This extreme flooding phenomenon is rare and is said to be a 50 year cycle with previous recorded occurrence from the Lake Baringo drainage basin having occurred in 1901 and 1963 [5, 8]. The phenomenon affected the mosquito dynamics in the region and from different habitats. In a study by Lutomiah [9] carried out in Lake Baringo basin, it was reported that mosquitoes of the genus *Mansonia* dominates the swampy areas. According to Paula [3], flooding at initial stages results in a decrease of mosquitoes of genus *Mansonia* from a habitat, but after a few weeks, the population goes up due to emergence of macrophytes. The prolonged floods can also result in loss of diversity with excess nutrients causing eutrophication effects [10]. This study, which commenced in October 2012 and ended in October 2013, therefore sought to understand probable changes that take place during periods

of an unprecedented extreme flooding in an ecology.

2. Materials and methods

2.1 Site and location of study area

Lake Baringo basin is located in Baringo County, on the floor of the central arm of the Great Rift Valley in Kenya and at an altitude of 950m above sea level. The basin is located at latitudes 00°28'N and 00°32'N and longitudes 36°58'60E and 36°00'E. It consists of plains, swamps and undulating flat land along the lake shores that is prone to flooding. Two study sites were selected to represent two habitats occurring in the Lake Baringo basin; flooded lake shoreline and swampy habitat. The flooded lake shoreline included several villages with Ngambo selected to represent the rest because of its accessibility and Kapkuikui to represent swampy areas that lies along Liboi plains.

2.2 Sampling of mosquitoes

This study was a longitudinal research covering 12 months from October 2012 - October 2013. Twelve mosquito trapping sites were identified in the study area with six sampling sites for each habitat. Sampling was carried out once a month for the 12 months consistently at night and daytime. Two CDC light traps were used in the field at daytime, two at night and two more within homesteads the site of the trap was separated from each other by a distance of approximately 300 to 500 metres, and coordinates taken. Trapping in daytime was from 3pm to 6pm with CDC traps baited with iced carbon dioxide in an insulated container. At night, trapping was done from 6pm to 6am. Dry iced Carbon dioxide and illuminating light from CDC trap was used to attract mosquitoes. After the trapping period, the mosquito cages were labelled with a unique identification barcode before transporting to the field laboratory for chilling and sorting into different genus and sexes.

2.3 Treatment of mosquito samples in the field

All chilled insect samples in the cage were placed on a white background surface where mosquitoes were separated from non-mosquitoes. The mosquitoes were then sorted into different sexes and genus based on morphological identification features as outlined by Edwards [11] and Rueda [12]. Females of the same genus were counted and put together into pools of 50 individuals or less. All sorted mosquitoes were stored in nitrogen cylinders awaiting extraction of the nucleic acid components. The data of genus, sexes and GPS coordinates was entered into a Microsoft Excel® spreadsheet. The diversity was calculated using Simpsons and Shannon Weaner Indices of Diversity.

3. Results and Discussion

3.1 Spatial variation in mosquito composition and distribution

During the sampling period of 12 months from October 2012 - October 2013, a total of 386,624 mosquito individuals were captured belonging to two families, Anopheline and Culicinae. Family Anopheline comprised of only one genus, *Anopheles* while Culicinae comprised of 10 genera: *Mansonia*, *Coquillettidia*, *Culex*, *Ficalbia*, *Aedomyia*, *Aedes*, *Theobaldia*, *Uranotaenia*, *Orthopodomyia*, *Hodgesia*, and 8 species identified morphologically and 14 unidentified (Table 1). Mosquitoes of genus *Hodgesia* were caught from swampy habitat only, while those of genus *Orthopodomyia* inhabited

flooded shoreline. The genus *Aedes* had the highest number of species with 3 confirmed species and 4 unidentified species distributed across the two habitats. *Culex* was similarly diverse with 3 confirmed species and 4 unidentified species. *Mansonia* had only 3 species while the other genera were each represented by one species.

With the study recording a total of 386,624 mosquito individuals, this is probably the highest number of genera caught in a single study conducted in the Lake Baringo basin. The abundance averaged monthly 32,218 catches. In this study, the catches were recorded in entire period of study during the wet and dry season. It leaves no doubts that this was among a few studies that have reported such remarkable high catches when compared with other reported catches. A study by Ondiba [13] had a total catches of 9,729 in the lake basin (lowland area) averaging monthly catches of 811 individual mosquitoes.

The high number of mosquito genera [12] from Lake Baringo basin could not simply be attributed to normal seasonal changes, but also to prolonged wetted changes in the flooded lake shoreline. In a study carried out during the El Niño floods of 2006 - 2007 by Sang [6], nine genera were reported from all habitats of the basin. A study by Ondiba [13] found a lesser number of eight genera while Ajamma [14] recorded only seven genera from studies carried out in 2012.

Table 1: List of mosquito species identified found in Lake Baringo basin, Kenya, during periods of heavy flooding, November 2012 to November 2013

Family	Genera	Species
Anopheline	Anopheles	<i>Anopheles gambiae</i> s.s. complex <i>Anopheles arabiensis</i>
Culicinae	Aedes	<i>Aedes aegypti</i> <i>Aedes lineatopennis</i> <i>Aedes albopictus</i> <i>Aedes spp</i> (unidentified) (4)
	Culex	<i>Culex pipens quinquefasciatus</i> <i>Culex pipiens pipiens</i> <i>Culex tritaeniorhynchus</i> <i>Culex spp</i> (unidentified) (3)
	Ficalbia	<i>Ficalbia spp</i> (unidentified) (1)
	Aedeomyia	<i>Aedeomyia spp</i> (unidentified) (1)
	Mansonia	<i>Mansonia uniformis</i> <i>Mansonia africana</i>
	Coquillettidia	<i>Coquillettidia spp</i> (unidentified) (1)
	Theobaldia	<i>Theobaldia spp</i> (unidentified) (1)
	Uranotaenia	<i>Uranotaenia spp</i> (unidentified) (1)
	Orthopodomyia	<i>Orthopodomyia spp</i> (unidentified) (1)
	Hodgesia	<i>Hodgesia spp</i> (unidentified) (1)

3.2 Spatial abundance and dominance of mosquitoes

Individual mosquitoes captured from flooded lake shoreline consisted of 89% of the total number of individual mosquitoes trapped with 11% of population harboured in swampy habitat throughout the sampling period. The catches of mosquitoes from the flooded lake shoreline and swampy habitat was significantly different at $t(23)=2.07$, $p=0.0056$.

Mosquitoes of genus *Mansonia* were the dominant species in the larger Lake Baringo basin (85%) with 98% coming from flooded lake shoreline habitat and 2% from swampy habitat. The catches of genus *Mansonia* from flooded and swampy habitat was significantly different at $t(13) =2.06$, $p=0.01$. On the other hand, genus *Aedes* formed 0.3% of total mosquito catches from the basin with 98% of the individuals caught

from swampy habitat. *Culex* dominated the swampy habitat mosquito community and constituted 11% of the overall population, with 64% of the total from swampy habitat and 35.4% from flooded lake shoreline.

Mosquitoes of genus *Mansonia* are usually found in areas with water, macrophytes and are shaded. In this study, flooded lake shoreline habitat provided favourable breeding and resting sites resulting in *Mansonia* high abundance within the basin compared to other genera. This was due to the changes in the lake shoreline habitat with more grounds submerged and an increase in emergent vegetation where the genus could oviposit and develop into adults. The unprecedented floods that submerged lake shoreline habitat created a conducive environmental and physio-chemical conditions of the water and substrate that favoured proliferation of genus *Mansonia*. While sampling the same lake basin during heavy rains caused by the Elnino in 2006, Sang ^[6] reported the genus dominating with about 87%, with the highest proportion from swampy habitat. However, Ajamma ^[14] while sampling the same area for a longer period of three years, found the genus dominating with a lower proportion of 57.9%. The high abundance of genus *Mansonia* should be of interest in that, most of its species are incriminated in transmission of arboviruses such as RVF as reported by Tantely ^[15].

Mosquitoes of *Aedes* species were rare in the flooded lake shoreline indicating that the environment was not favourable for growth to the genus. Environmental variables among them precipitation and temperature have a substantial impact on mosquito population growth, through the activation of their breeding sites ^[16]. A change in the abiotic factors and pH of the water including substrate in the habitat would therefore affect the breeding sites of mosquitoes of *Aedes* species and abundance. In flooded lake shoreline habitat, the flood waters caused deterioration of the mosquito ecology as floods prolonged and inundated the vegetation. In this ecology, floods washed animal waste which continued to degrade and release dissolved nutrients into water further polluting the ecology. This made the habitat less favoured for most of the mosquito species to oviposit and develop into adults. According to Shamsuzzaman ^[17], most of *Aedes* species of mosquitoes require at first fresh water from rains, and that have collected in tree holes, containers and swamps to breed before developing into adults.

In contrast, swampy habitat supported large diverse genera and species of mosquito life in high numbers with *Culex* abundance at 64%, *Aedes* 98%, *Coquilletidia* 53%. These genera play a critical primary and secondary role in transmission of arboviruses. Their presence highlight the high potential risk of infection with mosquito-borne viruses particularly in this habitat. The frequent precipitation, slow flowing springs, water holes, vegetation and dense grass in the swampy habitat accorded numerous breeding sites for different genera in the study period.

The high number of mosquito genera necessitated genomic sequencing. This was in order to identify species of mosquitoes that could not be identified using morphological key. The Next Generation Sequencing (NGS) was able to amplify nucleotide sequences from pooled mosquito DNA libraries that suggested presence of *Aedes albopictus* in the Lake Baringo basin. This species of mosquito had not been reported in the study area and Kenya prior to this study and more studies are needed. The finding of this species confirms

the richness of the Lake Baringo basin ecology in terms of mosquito diversity, the threat from emerging vectors and that probably more species inhabit the ecology than is documented.

4. Conclusion

From these study, it is concluded that during the extreme unprecedented flooding:-

1. The mosquito distribution, abundance and diversity from the flooded lake shoreline habitat was the most affected by the unprecedented flooding of Lake Baringo basin.
2. Lake Baringo basin was infested by diverse mosquito species totalling to 11 species with mosquitoes of genus *Mansonia* been dominant with an abundance of 84% catches, *Culex* (11%) and *Anopheles* (3%).
3. The flooded lake shoreline experienced loss of mosquito diversity during the extreme unprecedented flooding

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