

Mosquitoes of Northwestern Uganda

J.-P. Mutebi,^{1,4} M. B. Crabtree,¹ R. C. Kading,² A. M. Powers,¹ J. P. Ledermann,¹ E. C. Mossel,¹ N. Zeidner,¹ J. J. Lutwama,³ and B. R. Miller¹

¹Centers for Disease Control and Prevention (CDC), 3156 Rampart Road, Fort Collins, CO 80521 ²Department of Microbiology, Immunology and Pathology, Colorado State University, Fort Collins, CO 80523 ³Department of Arbovirology, Uganda Virus Research Institute (UVRI), P.O. Box 49, Entebbe, Uganda and ⁴Corresponding author, e-mail: JMutebi@cdc.gov

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Abstract

Despite evidence of arbovirus activity in northwestern Uganda (West Nile Sub-region), there is very limited information on the mosquito fauna of this region. The only published study reported 52 mosquito species in northwestern Uganda but this study took place in 1950 and the information has not been updated for more than 60 yr. In January and June 2011, CO₂ baited-light traps were used to collect 49,231 mosquitoes from four different locations, Paraa (9,487), Chobe (20,025), Sunguru (759), and Rhino Camp (18,960). Overall, 72 mosquito species representing 11 genera were collected. The largest number of distinct species was collected at Chobe (43 species), followed by Paraa (40), Sunguru (34), and Rhino Camp (25). Only eight of the 72 species (11.1%) were collected from all four sites: *Aedes (Stegomyia) aegypti formosus* (Walker), *Anopheles (Cellia) funestus* group, *Culex (Culex) decens* group, *Cx. (Culex) neavei* Theobald, *Cx. (Culex) univittatus* Theobald, *Cx. (Culiciomyia) cinereus* Theobald, *Cx. (Oculeomyia) poicilipes* (Theobald), and *Mansonia (Mansonioides) uniformis* (Theobald). Fifty-four species were detected in northwestern Uganda for the first time; however, these species have been detected elsewhere in Uganda and do not represent new introductions to the country. Thirty-three species collected during this study have previously been implicated in the transmission of arboviruses of public health importance.

Key words: Mosquito, species composition, Uganda, Paraa, Chobe

Between the mid-1930s and the early 1970s, a considerable amount of information on species composition, biology, and ecology of mosquitoes was compiled in Uganda (Smithburn et al. 1941, Smithburn and Haddow 1944, Haddow 1946, Smithburn and Haddow 1946, Smithburn et al. 1946, Haddow et al. 1948, Haddow and Mahaffy 1949, Haddow and van Someren 1950, Haddow et al. 1951, Smithburn and Haddow 1951, Dick and Haddow 1952, Gillett 1972). This entomological information was gathered in conjunction with epidemiological investigations of yellow fever (YF) conducted by the Yellow Fever Research Institute (currently the Uganda Virus Research Institute) in Entebbe. The primary aim was to study the epidemiology of YF in eastern Africa. Serologic surveys in the West Nile sub-region of Uganda detected very few YF-immune human sera (Sawyer and Whitman 1936, Mahaffy et al. 1946). YF-immune sera were detected close to the northern and the western borders of the province (close to forested or wooded areas) while none were found in the vast majority of the territory in the middle and the east (Mahaffy et al. 1946) suggesting an absence of yellow fever virus (YFV) transmission in most of West Nile sub-region. As a result of these findings, the epidemiological investigations were diverted to areas with higher YF activity which led to cessation of the associated entomological studies.

Lumsden and Buxton (1951) conducted additional epidemiological investigations in the West Nile sub-region of Uganda. The primary aim was to gain more information on the maintenance and transmission of YFV in an area with an extended dry season. Similar to previous studies (Sawyer and Whitman 1936, Mahaffy et al. 1946), the few YF antibody-positive human sera were mostly from males residing close to forested areas. In contrast, eight out of 27 (36%) monkey sera were positive for YF-antibodies which suggested that YF was endemic to the West Nile sub-region and maintained in transmission cycles involving monkeys. Lumsden and Buxton (1951) also conducted an entomological survey in the West Nile sub-region in an effort to incriminate the endemic YF vectors. During this study, 52 different species of mosquitoes were collected and identified. This study represents the only documented account of the mosquitoes of northwestern Uganda. In 2008, the US Centers for Disease Control and Prevention (CDC) and Uganda Virus Research Institute (UVRI) initiated an arbovirus surveillance program in Uganda with the primary aim of screening for and describing arboviruses of public health and veterinary importance. This study provided the opportunity to update the species composition of the mosquito fauna of northwestern Uganda. In this manuscript, we describe and discuss

mosquito species composition at four locations in northwestern Uganda and the public health implications of our findings.

Materials and Methods

Study Sites

Mosquitoes were collected at four study sites: Paraa and Chobe in Murchison Falls National Park (MFNP), Sunguru Village and Rhino Camp, Arua District, in the West Nile sub-region (formerly West Nile District) of Uganda (Fig. 1). The typical vegetation and landscape for each study location are presented in Fig. 2.

Paraa ($2^{\circ}17'N$: $31^{\circ}34'E$) is located in the northwest section of MFNP approximately 15 miles south of Pakwach. Murchison Falls National Park ($3,840\text{ km}^2$) is at the northern end of the Albertine Rift Valley and extends from the northeastern shores of Lake Albert in the West to Karuma Township on the Victoria Nile in the East (Fig. 1). Paraa consists of open savannah grassland with a few isolated trees and thickets (Fig. 2A). Rainfall occurs from March to November; average rainfall at the study site is 878.2 mm per annum with a range of 592–1,210.2 mm (Monaghan et al. 2012). The mean annual temperature is 23.6°C with a range of 22.5 – 24.4°C (Monaghan et al. 2012). The altitude at the trap site is approximately 654m (2,145ft) above sea level.

Chobe, $2^{\circ}15'N$: $32^{\circ}08'E$, is located in the northeast section of MFNP on the northern side of the Victoria Nile, approximately seven miles west of Karuma Township (Fig. 1). The ecosystem of Chobe is mostly moist semi-deciduous forest (Fig. 2B) and the altitude approximately 637m (3,716ft) above sea level. Similar to Paraa, Chobe is characterized by one wet season from March to November and one dry season from December to February. The average annual precipitation at the study site is 980 mm (range 665–1,160 mm) and the average daily temperature is 22.2°C (range 21.3 – 22.7°C) (Monaghan et al. 2012).

Sunguru, $2^{\circ}48'N$: $30^{\circ}53'E$, is located in Arua district near the border with the Democratic Republic of Congo (Fig. 1). The area is mostly wooded grassland, sparsely inhabited (Fig. 2C), approximately 27 km south of the city of Arua and the altitude is

approximately 1,398 m (4,586 ft) above sea level. Similar to Paraa and Chobe, Sunguru is characterized by one wet season from March to November and one dry season from December to February. Mean annual rainfall is 1,675.4 mm (range 1,092–2,090 mm) and mean daily temperature is 21.3°C (range 20.5 – 21.9°C) (Monaghan et al. 2012).

Rhino Camp, $2^{\circ}58'N$: $31^{\circ}24'E$, is located approximately 32 km (20mi) east of the city of Arua in Arua District and adjacent to the Albert Nile (Fig. 1). It is at an altitude of approximately 634.6 m (2,082 ft) above sea level (Monaghan et al. 2012). Rhino Camp is primarily a wooded savanna grassland (Fig. 2D) characterized by an extended but light rainy season, from March to November, and a short but severe dry season from December to February. The average annual precipitation is 789.5 mm (range 517–1,044.4 mm) and average daily temperature is 26.2°C (range 25.1 – 26.8°C) (Monaghan et al. 2012). Both Sunguru and Rhino Camp are residential areas. Chobe and Paraa are part of the MFNP, which is a protected area without human settlements.

Mosquito Collections

Mosquitoes were captured by using CDC miniature light traps (Clarke Mosquito Control, Roselle, IL) with dry ice, as a source of carbon dioxide. Dry ice was placed in an insulated modified Igloo® drink cooler (John. W. Hock Company, Gainesville, FL) with a small outlet-hole in the bottom, and suspended above the trap. The traps were hung approximately 1 m from the ground between 4 and 6 p.m. and collected following morning between 8 and 10 a.m.

At Paraa, two collection trips were conducted from 19–22 January 2011, and 18–21 June 2011. Fifteen to 20 traps were used and all of them were hung on tree branches in thickets along trails near the student hostel and the museum approximately 1.2 km north of Paraa Safari Lodge. The traps were spaced approximately 100–300 m apart depending on availability of suitable sites, and sheltered from direct sunlight and wind.

Two collection trips were conducted at Chobe, 22–25 January 2011 and 21–24 June 2011. Fifteen to 20 traps were placed on the northern side of Chobe Safari Lodge approximately 0.8 km away

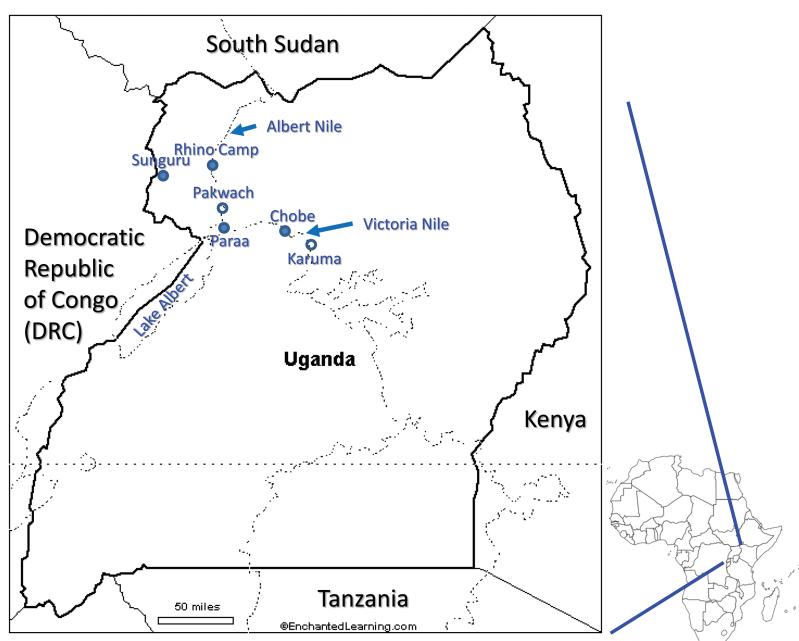


Fig. 1. A map of Uganda showing the locations of Chobe and Paraa in Murchison Falls National Park, Sunguru, and Rhino Camp.

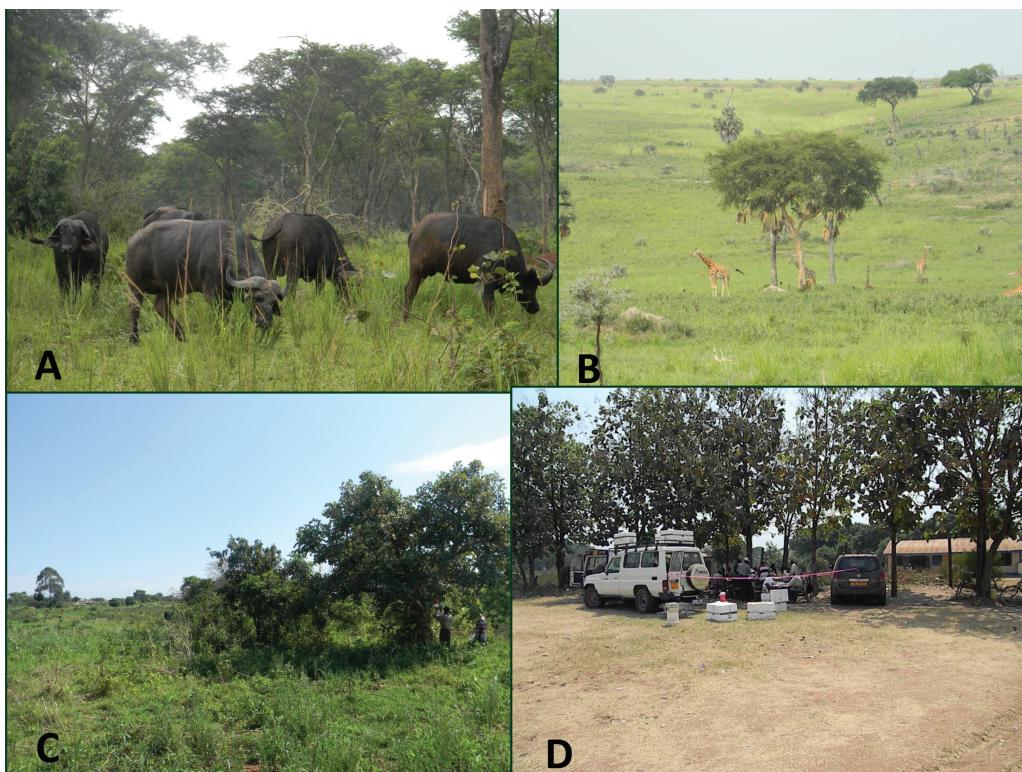


Fig. 2. Photographs illustrating the general vegetation and topology of each of the study sites (A) Chobe, (B) Paraa, (C) Sunguru, and (D) Rhino Camp.

from the Victoria Nile. All traps were hung in the forest approximately 50–100 m apart to minimize interference between the traps.

Two collection trips were conducted in Sunguru 13–15 January 2011 and 13–16 June 2011. Twenty traps were used, all of which were placed in homesteads or in vegetable gardens between homesteads. Traps were placed approximately 200–300 m apart to minimize interference.

One collection trip was conducted in Rhino Camp between 16 January and 19 January 2011. Twenty traps were used and all were placed 100–300 m apart in homesteads or in vegetable gardens between homesteads.

Mosquito Processing

Mosquitoes were collected each morning, chilled, separated from other arthropods and counted into labeled cryotubes. Small pieces of Kimwipes tissues (Kimberly-Clark Professional*, Roswell, GA) were included in the tubes to hold mosquito specimens in place and prevent them from rubbing against each other and losing morphological characters used in morphological identification. The tubed mosquitoes were kept frozen either on dry ice or in liquid nitrogen dry shippers and shipped frozen to the CDC laboratory in Fort Collins, CO, for processing. At the CDC laboratory, the mosquitoes were identified to species on the basis of morphological characters by using the keys of Edwards (1941), Jupp (1996), Gillies and DeMeillon (1968), Gilles and Coetzee (1987), and Huang (2004), and notes by Haddow et al. (1951), Gillett (1946), Corbet (1958), and Gillett (1972). Voucher specimens for each species were kept for future reference and for identification consultations. Mosquito taxa that demonstrated morphological variation across sites (*Coquillettidia* (*Coquillettidia*) *cristata* (Theobald), *Cq.* (*Coquillettidia*) *fuscofasciata* (Theobald)) as well as those representing a known species complex (*Anopheles*

(*Cellia*) *funestus* s.l. Gilles) were further characterized using molecular methods.

From the study areas included in this manuscript, four specimens of *Cq. cristata* were analyzed molecularly: two specimens collected in Chobe on 24 January 2011, and three collected in Sunguru on 15 January 2011. Additionally, one specimen of *Cq. fuscofasciata* from Chobe (25 January 2011), one from Kibale (20 June 2010), one from Lake Mburo (10 June 2010), two from Kitubulu, and one from Paraa (21 January 2011) were selected for molecular analysis. Additional specimens of both of these species collected in other parts of Uganda were analyzed simultaneously (data not shown). Eighteen specimens morphologically identified as *An. funestus* s.l. were analyzed molecularly. These mosquitoes included seven specimens from Sunguru, collected on 14 and 16 January 2011; eight specimens from Paraa collected between 19–21 January 2011 (7) and on 19 June 2011 (1); and three specimens from Chobe, collected on 24 January 2011.

For molecular characterization of the *Coquillettidia*, DNA was extracted from whole specimens frozen at -80°C using the DNA Investigator Kit (Qiagen Inc., Valencia, CA). The tissue extraction procedure was used with the following modifications: mosquitoes were mechanically homogenized in buffer ATL prior to the addition of proteinase K, and samples were lysed overnight at 56°C. For *An. funestus* s.l., extraction methods were the same except that a front leg was removed from mounted voucher specimens instead of homogenizing whole specimens.

From the *Coquillettidia*, two genetic markers were amplified for sequencing: an approximately 400 bp fragment of the mitochondrial NADH dehydrogenase subunit 4 (ND4) (Simon et al. 1994), and a 311 bp fragment of the mitochondrial cytochrome oxidase I (COI) (Vinogradova et al. 2003). *Anopheles funestus* s.l. specimens were analyzed using the species-specific multiplexed PCR described

by Koekemoer et al. (2002). Specimens were also screened with the additional primer for an *An. (Cellia) rivulorum* Leeson-like species reported by Cohuet et al. (2003). To resolve the identity of specimens from which no PCR amplification was obtained, additional arthropod-specific CO1 primer pairs were employed: C1-J-1718/C1-N-2191 (473 bp amplicon); C1-J-1859/TL-2-3014 (1155 bp amplicon) (Simon et al. 1994). All PCR amplifications were performed on a BioRad T-100 thermal cycler (BioRad Laboratories, Hercules, CA) using previously published amplification conditions (Simon et al. 1994). Amplicons were run on 1% agarose gels and products of the expected size were extracted and purified using a MinElute Gel Extraction Kit (Qiagen Inc., Valencia, CA). Purified amplicons were bidirectionally sequenced using the BigDye Terminator version 3.1 Cycle Sequencing Kit (Applied Biosystems, Foster City, CA) and analyzed on an ABI 3130 genetic analyzer (Applied Biosystems). Sequences were evaluated using the DNASTAR Lasergene core suite (Madison, WI), generating multiple sequence alignments and performing pairwise comparison of sequences within and between species using the ClustalW algorithm.

Diversity Indices

Species richness and species diversity were calculated for each location and collection period. Species richness was reported as the number of mosquito species at each location. Species diversity was estimated by calculating the Simpson Index (Simpson 1949). The Simpson index (D), which accounts for both species richness and the relative abundance of each species, was calculated as $D = n(n - 1)/N(N - 1)$, where n = the total number of mosquitoes of a particular species and N = the total number of mosquitoes of all species collected at each site. For simplicity, we also report Simpson's index of diversity ($1 - D$), which is interpreted as the greater the index, the greater the sample diversity. An index of 0 would indicate perfect homogeneity, whereas an index of 1 would indicate perfect heterogeneity.

Results and Discussion

The grand total of mosquitoes collected during the study was 49,231, of these, 20,025 were collected at Chobe, 18,960 at Rhino Camp, 9,487 at Para, and 759 at Sunguru (Table 1). The mosquitoes belonged to 11 genera and 72 species (Table 1). In total, 40,294 (81.6%) of the 49,393 specimen collected belonged to 2 genera *Coquillettidia* and *Mansonia* (Table 2). The number of genera varied from site to site; 10 were collected at Chobe, 9 at Para, 8 at Rhino Camp, and 7 at Sunguru (Tables 1 and 2). Six genera, *Aedeomyia*, *Eretmapodites*, *Lutzia*, *Mimomyia*, *Toxorhynchites*, and *Uranotaenia*, were not detected at all study sites (Table 2). The genus *Aedeomyia* was not detected in Chobe or Sunguru, *Eretmapodites* was only detected in Chobe and Para, the genus *Lutzia* was not detected in Rhino Camp, the genus *Mimomyia* was not detected in Sunguru, the genus *Toxorhynchites* was only detected in Chobe and the genus *Uranotaenia* was not detected in Para (Table 1). However, very few individuals of these genera were collected suggesting low population density or poor response to light traps.

The highest number of different species within a genus collected from each of the sites was from the genus *Culex*; 19 species, 14 species, 16 species, and 8 species collected at Chobe, Para, Sunguru, and Rhino Camp, respectively (Tables 2–6). Overall, the most diverse genera in the collections were *Culex* (24 species) and *Aedes* (16 species) (Table 2) as observed previously in western Uganda (Mutebi et al. 2012).

In Chobe, *Coquillettidia* species made up the largest proportion of individuals collected, whereas *Culex* species made up the largest

proportion of individuals collected at Para, and *Mansonia* species at Sunguru and Rhino Camp (Tables 2–6). *Mansonia* species made up by far the largest proportion of the total collection (24,268 mosquitoes/49.3%) (Table 2). The second and third most frequently collected species were in the genera *Coquillettidia* (16,026 mosquitoes) and *Culex* (5,894 mosquitoes), respectively (Table 2). *Coquillettidia* species were the most abundant species in Chobe which is a forest ecosystem; this same association was observed between *Coquillettidia* species and forest ecosystems in western Uganda (Mutebi et al. 2012) and in Zika forest (Kaddumukasa et al. 2014) (Table 2). In contrast, *Coquillettidia* species were relatively rare at all of the other study sites (Para, Sunguru, and Rhino Camp) (Table 2) which were predominantly open and/or wooded savannah grassland ecosystems. *Mansonia* species were abundant at all three sites adjacent to the River Nile (Chobe, Para, and Rhino Camp), and were the most abundant species at both Para and Rhino Camp (Table 2). This is likely due to the presence of papyrus swamps along the River Nile, which are excellent larval habitats for the three *Mansonia* species collected in the course of this study.

Overall, a total of 72 mosquito species were identified in northwestern Uganda (Table 1). The greatest species richness was detected at Chobe (43 species), followed by Para (40), Sunguru (34), and Rhino Camp (25) (Table 2). Of the 72 species, only eight (11.1%) were collected from all four sites: *Ae. (Stegomyia) aegypti formosus* (Walker), *An. funestus* group, *Cx. (Culex) decens* group, *Cx. (Culex) neavei* Theobald, *Cx. (Culex) univittatus* Theobald, *Cx. (Culiciomyia) cinereus* Theobald, *Cx. (Oculeomyia) poicilipes* (Theobald), and *Ma. (Mansonioides) uniformis* (Theobald) (Table 1). As noted before, there is a wide range of variation in species composition among different sites in Uganda despite relatively close proximity and similarity in climate and ecosystem (Mutebi et al. 2012, Mayanja et al. 2014). In the present study, Para, Sunguru, and Rhino Camp are all wooded grasslands and the sites are within 156 km (97mi) of each other; however, only 10 of the 72 species were collected from all three sites (Table 1).

Diversity indices for each collection are reported in Tables 3–6. On average, species diversity was highest in Sunguru (Simpson's Diversity Indices 1-D = 0.86 in January and 0.91 in June), followed by Rhino Camp (0.66 in January), Para (0.33 in January and 0.82 in June), and Chobe (0.28 in January and 0.17 in June) (Tables 3–6). While Chobe had the highest species richness (43 species) (Table 2), it was the least biologically diverse. This finding is due to *Ma. (Mansonioides) africana* (Theobald) and *Cq. (Coquillettidia) fraseri* (Theobald) comprising 84.8 and 91.1% of the January 2011 and June 2011 collections from this site, respectively (Table 3). Species diversity differed greatly at Para between the two sampling periods, ranging from 0.33 to 0.82 (Table 4). A similar temporal species diversity difference was observed in Sempaya in western Uganda (Mutebi et al. 2012). However, Sempaya is a tropical forest ecosystem, whereas Para is mostly open grassland. While the overall number of mosquitoes collected at Sunguru (Table 5) was very low, this location had the highest species diversity and the species diversity index was consistently high (0.91 and 0.86) during both seasons (Table 5). The diversity indices presented in this manuscript were calculated based on light trap collections. Light trap collections are biased toward mosquito species that are attracted to light and CO₂ and may not represent an accurate picture of complete species diversity at each location.

Mosquito Collections at Chobe

To our knowledge, this is the first documented account of the mosquito fauna of Chobe. In total, 20,025 mosquitoes were collected: 3,731

Table 1. Number of mosquito species and subspecies collected at four locations in northwestern Uganda in 2011

Genus	Subspecies	Species	Chobe	Paraa	Sunguru	Rhino Camp
<i>Aedes</i>	<i>Aedimorphus</i>	<i>albocephalus</i>		33		
		<i>alboventralis</i>	41			
		<i>cumminsii</i>	7			
		<i>stenoscutus</i>	3	1		
		<i>stokesi</i>	2			
		<i>tarsalis</i>	8			
		<i>spp</i>	1			
	<i>Diceromyia</i>	<i>furcifer</i>			1	
	<i>Mucidus</i>	<i>graham</i>		1		
	<i>Neomelaniconion</i>	<i>albothorax</i>		32		
		<i>circumluteolus</i>	2	42		
	<i>Stegomyia</i>	<i>aegypti aegypti</i>		44		
		<i>aegypti formosus</i>	83	164	4	1
		<i>metallica</i>		1		
		<i>simpsoni</i> group		1	1	
		<i>spp</i>	5	6		
<i>Aedes</i>						
<i>Aedomyia</i>	<i>Aedomyia</i>	<i>africana</i>				2
		<i>furfurea</i>	152	1		
<i>Anopheles</i>	<i>Anopheles</i>	<i>coustani</i>	13	5	56	
		<i>tenebrosus</i>		7		
		<i>ziemanni</i>		5		210
	<i>Cellia</i>	<i>funestus s.s.^a</i>	3	3	4	
		<i>funestus</i> group	46	119	5	627
		<i>gambiae</i> group	1	8		
		<i>gibbinsi</i>			11	
		<i>longipalpis</i>				32
		<i>maculipalpis</i>			3	
		<i>rivulorum</i>		200	2	609
		<i>rivulorum/demeilloni</i>		3		
		<i>theileri</i>				2
		<i>wellcomei</i>				2
		<i>wellcomei</i> ssp. <i>ugandae</i>	1			
<i>Anopheles</i>		species	5	77		370
<i>Coquillettidia</i>	<i>Coquillettidia</i>	<i>azurites</i>		185	14	128
		<i>cristata</i>	4		110	2
		<i>fraseri</i>	14905		61	
		<i>fuscopennata</i>	3	5		
		<i>maculipennis</i>	3		8	
		<i>metallica</i>	40	472		66
		species			20	
<i>Culex</i>	<i>Culex</i>	<i>antennatus</i>	308	775		65
		<i>decens</i> group	132	174	74	6
		<i>duttoni</i>	11	35	33	
		<i>mirificus</i>			1	
		<i>neavei</i>	271	299	2	278
		<i>ornatothoracis</i>	55			
		<i>perfuscus</i>	299	21		
		<i>pipiens</i>			12	
		<i>pipiens complex</i>		1		
		<i>quinquefasciatus</i>	1		14	
		<i>trifilatus</i>	1		23	
		<i>trifilatus</i> ssp. <i>aenescens</i>	6		23	
		<i>univittatus</i>	4	77	37	55
		<i>watti</i>	1			
	<i>Culiciomyia</i>	<i>cinerellus</i>		1		
		<i>cinereus</i>	8	6	90	4
		<i>nebulosus</i>	36	4	1	
	<i>Eumelanomyia</i>	<i>insignis</i>	5	1		9
		<i>rubinotus</i>			5	3
	<i>Kitzmilleria</i>	<i>moucheti</i>	1		1	
	<i>Oculeomyia</i>	<i>annulioris</i>	43	29	79	
		<i>annulioris</i> ssp. <i>consimilis</i>	3		1	
		<i>bitaeniorhynchus</i>	2	9		

Table 1. Continued

Genus	Subspecies	Species	Chobe	Paraa	Sunguru	Rhino Camp
<i>Culex</i>		<i>poicilipes</i>	1	13	1	2029
<i>Eretmapodites</i>		species	223	82	54	56
<i>Lutzia</i>	<i>Metalutzia</i>	<i>chrysogaster</i>	2	3		
<i>Mansonia</i>	<i>Mansonioides</i>	<i>tigripes</i>	45	3	2	
		<i>africana</i>	3,308	6,200		2,142
		<i>africana nigerrima</i>				583
		<i>uniformis</i>	69	160	2	10,582
<i>Mansonia</i>		species	11	178		1,033
<i>Mimomyia</i>	<i>Mimomyia</i>	<i>mimomyiaformis</i>	1	1		62
<i>Toxorhynchites</i>	<i>Toxorhynchites</i>	<i>brevipalpis</i>	1			
<i>Urantotaenia</i>	<i>Pseudoficalbia</i>	<i>mashonaensis</i>			2	1
		<i>nivipous</i>			1	
		<i>pallidocephala</i>	1			
		<i>alboabdominalis</i>				1
		<i>connali</i>			1	
Total			20,177	9,487	759	18,960
Grand Total			49,383			

^aIdentified using molecular methods (R Kading).

Table 2. Number of species and total number of individuals in the different genera collected at each study site

	Chobe	Paraa	Sunguru	Rhino Camp	Total
<i>Aedes</i>	8(304)	10(326)	3(6)	2(3)	16(639)
<i>Anopheles</i>	5(69)	8(427)	6(81)	6(1,852)	14(2,429)
<i>Coquillettidia</i>	5(14,955)	3(662)	4(213)	3(196)	6(16,026)
<i>Culex</i>	19(1,411)	14(1,527)	16(451)	8(2,505)	24(5,894)
<i>Eretmapodites</i>	1(2)	1(3)			1(5)
<i>Lutzia</i>	1(45)	1(3)	1(2)		1(50)
<i>Mansonia</i>	2(3,388)	2(6,538)	1(2)	3(14,340)	3(24,268)
<i>Mimomyia</i>	1(1)	1(1)		1(62)	1(64)
<i>Toxorhynchites</i>	1(1)				1(1)
<i>Urantotaenia</i>	1(1)		3(4)	2(2)	5(7)
Total	44(20,177)	40(9,487)	34(759)	25(18,960)	72(49,383)

in January 2011 and 16,294 in June 2011 (Table 3). Forty-four mosquito species in 10 genera were collected at this site (Tables 2 and 3). The largest number of species collected were in the genus *Culex* (19 species), followed by *Aedes* (7), *Coquillettidia* and *Anopheles* (5 species each), *Mansonia* (2), and 1 each in the genera *Eretmapodites*, *Lutzia*, *Mimomyia*, *Toxorhynchites*, and *Urantotaenia* (Tables 2 and 3). Twenty-eight and 32 species were collected in January 2011 and June 2011, respectively, and of these, only 17 (38.6%) were collected during both sampling periods (Table 3), suggesting seasonal variation in species composition. The most abundant species collected in January was *Ma. africana* (84.8%) and in June *Cq. fraseri* (91.1%) (Table 3). Interestingly, *Cq. fraseri* only made up 1.61% of the total collection in January and *Ma. africana* <1% of the collection in June, whereas both species are associated with the same larval habitats, swamps, and marshes (Hopkins 1952).

Mosquito Collections at Paraa

Similar to Chobe, this is the first documented account of the mosquitoes of Paraa. In total, 9,487 mosquitoes were collected at Paraa; 7,607 in January 2011 and 1,880 in June 2011. The collection included 40 species in nine genera (Tables 2 and 4). The most abundant species collected was *Ma. africana* which accounted for 65.4% of the total number of mosquitoes collected at this site (Table 1) followed by *Cx. (Culex) antennatus* (8.2%), *Cx. neavei* (3.2%), and *An. rivulorum* (2.1%) (Table 1). Similar to Chobe, the

majority of *Ma. africana* (99.8%) were collected in January 2011 and very few in June 2011 (0.2%). The most interesting finding at Paraa was the detection of *Ae. aegypti formosus* specimens that had specific abdominal ornamentation of *Ae. (Stegomyia) aegypti aegypti* (L) (scattered white scales on the first abdominal tergite and apical white scales on tergites 2 through 7) described by Huang (2004). To our knowledge, this is the first time a form of *Ae. aegypti formosus* with the same abdominal ornamentation as *Ae. aegypti aegypti* has ever been detected in Uganda; all other specimens examined to date clearly exhibited abdominal ornamentation typical of *Ae. aegypti formosus*.

Mosquito Collections at Sunguru

Similar to Chobe and Paraa, the mosquito fauna of Sunguru have not previously been described. In total, 759 mosquitoes belonging to seven genera, 32 species, and 2 subspecies were collected in Sunguru (374 in January 2011 and 285 in June 2011) (Tables 1 and 5). The most commonly captured species at this site were *Cq. cristata* (14.5%), *Cx. cinereus* (11.9%), *Cx. (Oculeomyia) annulioris* (Theobald) (10.4%), *Cx. (Culex) decens* group (Theobald) (9.7%), *Cq. fraseri* (8%), and *An. (Anopheles) coustani* (Laveran) (7.4%) (Table 1). There were variations in species composition between January 2011, when 23 species and one subspecies were collected, and June 2011, when 25 species and 2 subspecies were collected (Table 5). Five species: *An.*

Table 3. Mosquito species collected at Chobe, Murchison Falls National Park, Uganda, in January and June 2011

Genus	Subgenus	Species	Number collected (%)		
			Jan. 2011	June 2011	
<i>Aedes</i>	<i>Aedimorphus</i>	<i>alboventralis</i>		41	(0.25)
		<i>cumminsii</i>	3	(0.08)	4 (0.02)
		<i>stenoscutus</i>		3	(0.02)
		<i>stokesi</i>		2	(0.01)
		<i>tarsalis</i>	4	(0.11)	4 (0.02)
	<i>Neomelaniconion</i>	species	1	(0.03)	
		<i>circumluteolus</i>	2	(0.05)	
	<i>Stegomyia</i>	<i>aegypti formosus</i>	3	(0.08)	80 (0.49)
		species	1	(0.03)	
<i>Culex</i>	<i>Anopheles</i>	species	1	(0.03)	3 (0.02)
		<i>coustani</i>	13	(0.35)	
		<i>funestus s.s.^a</i>	3	(0.08)	
		<i>funestus group</i>	46	(1.23)	
		<i>gambiae s.l.</i>			1 (0.01)
	<i>Coquillettidia</i>	<i>wellcomei</i> ssp. <i>ugandae</i>	1	(0.03)	
		species			5 (0.03)
		<i>cristata</i>	2	(0.05)	2 (0.01)
		<i>Fraseri</i>	60	(1.61)	14,845 (91.11)
		<i>fuscofasciata</i>	2	(0.05)	1 (0.01)
<i>Culex</i>	<i>Culex</i>	<i>maculipennis</i>			3 (0.02)
		<i>metallica</i>	7	(0.19)	33 (0.20)
		<i>antennatus</i>	88	(2.36)	220 (1.35)
		<i>decens</i> group	16	(0.43)	116 (0.71)
		<i>duttoni</i>	1	(0.03)	10 (0.06)
	<i>Culiciomyia</i>	<i>neavei</i>	230	(6.16)	41 (0.25)
		<i>ornatothoracis</i>			55 (0.34)
		<i>perfuscus</i>	10	(0.27)	289 (1.77)
		<i>quinquefasciatus</i>			1 (0.01)
		<i>trifilatus</i>			1 (0.01)
<i>Culex</i>	<i>Eumelanomyia</i>	<i>trifilatus aenescens</i>			6 (0.04)
		<i>univittatus</i>			4 (0.02)
		<i>watti</i>			1 (0.01)
		<i>cinereus</i>			8 (0.05)
		<i>nebulosus</i>	2	(0.05)	34 (0.21)
	<i>Kitzmilleria</i>	<i>insignis</i>	1	(0.03)	4 (0.02)
		<i>moucheti</i>	1	(0.03)	
		<i>annulioris</i>	16	(0.43)	27 (0.17)
		<i>annulioris</i> ssp. <i>consimilis</i>	3	(0.08)	
		<i>bitaeniorhynchus</i>			2 (0.01)
<i>Culex</i>	<i>Mansonioides</i>	<i>poicilipes</i>	1	(0.03)	
		species	1	(0.03)	229 (1.39)
		<i>chrysogaster</i>			2 (0.01)
		<i>tigripes</i>			45 (0.28)
		<i>africana</i>	3,164	(84.80)	144 (0.88)
	<i>Mimomyia</i>	<i>uniformis</i>	36	(0.96)	33 (0.20)
		species	11	(0.29)	
		<i>mimomyiaformis</i>	1	(0.03)	
		<i>brevipalpis</i>			1 (0.01)
		<i>pallidocephala</i>	1	(0.03)	
Totals			3,731		16,294
Grand total		20,025			
D			0.72		0.83
1-D			0.28		0.17

Simpson's Diversity Index (D) and Simpson's Index of Diversity (1-D) for each collection trip are presented at the bottom of the table.

^aIdentified using molecular methods (R Kading).

coustani, *An. funestus* s.s., *Cx. (Culex) mirificus* Edwards, *Cx. (Kitzmilleria) moucheti* Evans, and *Cx. poicilipes* were only detected in January 2011. Eight species, *Ae. (Diceromyia) furcifer* (Edwards), *Ae. (Stegomyia) simpsoni* sl (Theobald), *Cq. (Coquillettidia) aurites* (Theobald), *Cx. neavei*, *Cx. (Culiciomyia)*

nebulosus Theobald, *Ma. uniformis*, *Uranotaenia (Pseudoficalbia) nivipous* Theobald, *Ur. (Uranotaenia) connali* Edwards and one subspecies *Cx. (Oculeomyia) annulioris* ssp. *aenescens* Edwards, were only detected in June 2011. The relative abundance of some species such as *An. coustani*, *Cq. cristata*, *Cx. (Culex) duttoni*,

Table 4. Mosquito species collected at Paraa, Murchison Falls National Park, Uganda, in January and June 2011

Genus	Subspecies	Species	Number collected (%)			
			Jan. 2011		June 2011	
<i>Aedes</i>	<i>Aedimorphus</i>	<i>albocephalus</i>	1	(0.01)	32	(1.70)
		<i>circumluteolus</i>	1	(0.01)		
		<i>stenoscutus</i>			1	(0.05)
		<i>graham</i>			1	(0.05)
		<i>neomelaniconion</i>			32	(1.70)
	<i>Stegomyia</i>	<i>albothorax</i>			41	(2.18)
		<i>circumluteolus</i>			44	(2.34)
		<i>aegypti aegypti</i>			154	(8.19)
		<i>aegypti formosus</i>	10	(0.13)		
		<i>metallica</i>			1	(0.05)
<i>Anopheles</i>	<i>Anopheles</i>	<i>simpsoni</i> group			1	(0.05)
		species	1	(0.01)	5	(0.27)
		<i>furfuraea</i>			1	(0.05)
		<i>coustani</i>	4	(0.05)	1	(0.05)
		<i>tenebrosus</i>	1	(0.01)	6	(0.32)
		<i>ziemanni</i>	1	(0.01)	4	(0.21)
		<i>funestus s.s.^a</i>	2	(0.03)	1	(0.05)
		<i>funestus</i> group	71	(0.93)	48	(2.55)
		<i>gambiae</i> group			8	(0.43)
		<i>rivulorum</i>	67	(0.88)	133	(7.07)
<i>Anopheles</i>	<i>Anopheles</i>	<i>rivulorum/demeilloni</i>	3	(0.04)		
		species	22	(0.29)	55	(2.93)
		<i>aurites</i>	179	(2.35)	6	(0.32)
		<i>fuscopennata</i>	5	(0.07)		
		<i>metallica</i>	336	(4.42)	136	(7.23)
		<i>antennatus</i>	41	(0.54)	734	(39.04)
		<i>decens</i> group	107	(1.41)	67	(3.56)
		<i>duttoni</i>	16	(0.21)	19	(1.01)
		<i>neavei</i>	112	(1.47)	187	(9.95)
		<i>perfuscus</i>	4	(0.05)	17	(0.90)
<i>Culex</i>	<i>Culex</i>	<i>pipiens</i> complex			1	(0.05)
		<i>univittatus</i>	42	(0.55)	35	(1.86)
		<i>cinereus</i>	3	(0.04)	3	(0.16)
		<i>cinerellus</i>	1	(0.01)		
		<i>nebulosus</i>			4	(0.21)
		<i>insignis</i>			1	(0.05)
		<i>annulioris</i>	22	(0.29)	7	(0.37)
		<i>bitaeniorhynchus</i>	7	(0.09)	2	(0.11)
		<i>poicilipes</i>	11	(0.14)	2	(0.11)
		species	37	(0.49)	45	(2.39)
<i>Eretmapodites</i>	<i>Eretmapodites</i>	<i>chrysogaster</i>			3	(0.16)
		<i>tigripes</i>			3	(0.16)
		<i>Metalutzia</i>				
		<i>Mansonioides</i>				
		<i>africana</i>	6190	(81.37)	10	(0.53)
		<i>uniformis</i>	132	(1.74)	28	(1.49)
		species	178	(2.34)		
		<i>Mimomyia</i>			1	
		<i>mimomyiaformis</i>				
		Totals	7607		1880	
Grand total		9,487				
D			0.67		0.18	
1-D			0.33		0.82	

Simpson's Diversity Index (D) and Simpson's Index of Diversity (1-D) for each collection trip are presented at the bottom of the table.

^aIdentified using molecular methods (Kading).

Cx. cinereus, *Cx. Quinquefasciatus*, and *Cx. annulioris* varied dramatically from January to June. These observations demonstrate seasonal variations for these species at this site. There was very little variation in the relative abundance of some species such as *Cq. fraseri*, *Cx. decens* group, *Cx. Univittatus*, and *Cx. pipiens* (Table 5). The majority (93%) of the members of the *Cx. pipiens* complex in the present study were detected in Sunguru (Table 1), which is approximately 60 miles from Omugo, the location where

WNV was first isolated from a febrile woman (Smithburn et al. 1940).

Mosquito Collections at Rhino Camp

This is the first description of the mosquito fauna of Rhino Camp. Only one collection was conducted at this location in January 2011 and it yielded 18,960 mosquitoes belonging to seven genera and 25 species (Table 1). The species most frequently captured were *Ma.*

Table 5. Mosquito species collected at Sunguru, Uganda, in January and June 2011

Genus	Subspecies	Species	Number collected (%)		
			Jan. 2011		June 2011
<i>Aedes</i>	<i>Diceromyia</i>	<i>furcifer</i>		1	(0.26)
	<i>Stegomyia</i>	<i>aegypti formosus</i>	1	(0.27)	3 (0.78)
<i>Anopheles</i>	<i>Anopheles</i>	<i>simpsoni</i> group		1	(0.26)
	<i>Cellia</i>	<i>coustoni</i>	56	(14.97)	
<i>Coquillettidia</i>	<i>Coquillettidia</i>	<i>funestus</i> s.s. ^a	4	(1.07)	
		<i>funestus</i> group	4	(1.07)	1 (0.26)
		<i>gibbinsi</i>	5	(1.34)	6 (1.56)
		<i>maculipalpis</i>	1	(0.27)	2 (0.52)
		<i>rivulorum</i>	1	(0.27)	1 (0.26)
<i>Culex</i>	<i>Culex</i>	<i>aurites</i>		14	(3.64)
		<i>cristata</i>	17	(4.55)	93 (24.16)
		<i>fraseri</i>	25	(6.68)	36 (9.35)
		<i>maculipennis</i>	2	(0.53)	6 (1.56)
		species	20	(5.35)	
<i>Culex</i>	<i>Culex</i>	<i>decens</i> group	37	(9.89)	37 (9.61)
		<i>duttoni</i>	2	(0.53)	31 (8.05)
		<i>mirificus</i>	1	(0.27)	
		<i>neavei</i>		2	(0.52)
		<i>pipiens</i>	10	(2.67)	2 (0.52)
		<i>quinquefasciatus</i>	14	(3.74)	
		<i>trifilatus</i>	23	(6.15)	
		<i>trifilatus</i> ssp. <i>aenescens</i>	20	(5.35)	3 (0.78)
		<i>univittatus</i>	15	(4.01)	22 (5.71)
		<i>cinereus</i>	2	(0.53)	88 (22.86)
<i>Lutzia</i>	<i>Lutzia</i>	<i>nebulosus</i>		1	(0.26)
		<i>rubinotus</i>	4	(1.07)	1 (0.26)
		<i>Kitzmilleria</i>	1	(0.27)	
		<i>Oculeomyia</i>	61	(16.31)	18 (4.68)
		<i>annulioris</i>		1	(0.26)
		<i>annulioris</i> ssp. <i>consimilis</i>			
		<i>poicilipes</i>	1	(0.27)	
		species	45	(12.03)	9 (2.34)
		<i>tigripes</i>	1	(0.27)	1 (0.26)
				2	(0.52)
<i>Mansonia</i>	<i>Mansonioides</i>	<i>uniformis</i>		1	(0.26)
		<i>mashonaensis</i>		1	(0.26)
<i>Uranotaenia</i>	<i>Pseudoficalbia</i>	<i>nivipous</i>		1	(0.26)
		<i>Uranotaenia</i>	<i>connali</i>		1 (0.26)
Totals			374		385
Grand total		759			
D			0.09		0.14
1-D			0.91		0.86

Simpson's Diversity Index (D) and Simpson's Index of Diversity (1-D) for each collection trip are presented at the bottom of the table.

^aIdentified using molecular methods (R Kading).

uniformis (55.8%), *Ma. africana* (11.3%), *Cx. poicilipes* (10.7%), *An. funestus* group (3.3%), *An. (Cellia) rivulorum* Leeson (3.2%), and *Ma. (Mansonioides) africana nigerrima* Theobald (Table 1).

Molecular Taxonomy Observations

Sequences for *Coquillettidia* species and *An. funestus* have been deposited in GenBank under accession numbers MG132070, and MG190073–MG190076.

Coquillettidia

ND4 sequences from *Cq. fuscopennata* and *Cq. cristata* were aligned and evaluated by pairwise comparison for this 400 bp amplicon. Pairwise distances within and between these two species from multiple geographic locations were not sufficient for differentiation at the species level. Identity among *Cq. fuscopennata* from different collection sites was 99.2–100%, whereas identity within *Cq. cristata* as

well as between *Cq. fuscopennata* and *Cq. cristata* was 97.1–100%. Unfortunately, ND4 sequences from other mosquitoes in the genus *Coquillettidia* are not represented on GenBank for comparison.

For the COI amplicon (using the primers of Vinogradova et al. 2003), mosquitoes morphologically identified as *Cq. cristata* from Chobe and Sunguru shared only 96.5% identity with each other, the same percentage identity observed between each of those specimens and *Cq. fuscopennata* from Lake Mburo, Kitubulu, and Kibale. Specimens collected from the same site were identical to each other. In comparison, the homologous COI sequences derived from *Cq. fuscopennata* collected from four different locations in Uganda (Sipi, Lake Mburo, Kitubulu, and Kibale) were identical to each other. Collectively, these molecular data suggest that there is some genetic structuring present within what we now consider morphologically as *Cq. cristata*, which should be investigated further.

The *Cq. cristata* specimens from Chobe and Sunguru were all morphologically identified as *Cq. cristata*. Specimens from both

Table 6. Mosquito species collected at Rhino Camp, Uganda, in January 2011

Genus	Subspecies	Species	Number col-
			lected (%)
			Jan. 2011
<i>Aedes</i>	<i>Stegomyia</i>	<i>aegypti formosus</i>	1 (0.01)
<i>Aedomyia</i>	<i>Aedomyia</i>	<i>africana</i>	2 (0.01)
<i>Anopheles</i>	<i>Anopheles</i>	<i>ziemanni</i>	210 (1.11)
	<i>Cellia</i>	<i>funestus</i> group	627 (3.31)
		<i>longipalpis</i>	32 (0.17)
		<i>rivulorum</i>	609 (3.21)
		<i>theileri</i>	2 (0.01)
		<i>wellcomei</i>	2 (0.01)
<i>Anopheles</i>		species	370 (1.95)
<i>Coquillettidia</i>	<i>Coquillettidia</i>	<i>aurites</i>	128 (0.68)
		<i>cristata</i>	2 (0.01)
		<i>metallica</i>	66 (0.35)
<i>Culex</i>	<i>Culex</i>	<i>antennatus</i>	65 (0.34)
		<i>decens</i> group	6 (0.03)
		<i>neavei</i>	278 (1.47)
		<i>univittatus</i>	55 (0.29)
	<i>Culicomyia</i>	<i>cinereus</i>	4 (0.02)
	<i>Eumelanomyia</i>	<i>insignis</i>	9 (0.05)
		<i>rubinotus</i>	3 (0.02)
	<i>Oculeomyia</i>	<i>poicilipes</i>	2,029 (10.70)
<i>Culex</i>		species	56 (0.30)
<i>Mansonia</i>	<i>Mansonioides</i>	<i>africana</i>	2,142 (11.30)
		<i>africana nigerrima</i>	583 (3.07)
		<i>uniformis</i>	10,582 (55.81)
<i>Mansonia</i>		species	1,033 (5.45)
<i>Mimomyia</i>	<i>Mimomyia</i>	<i>mimomyiaformis</i>	62 (0.33)
<i>Uranotaenia</i>	<i>Pseudoficalbia</i>	<i>mashonaensis</i>	1 (0.01)
	<i>Uranotaenia</i>	<i>alboabdominalis</i>	1 (0.01)
Grand total			18,960
D			0.34
1-D			0.66

Simpson's Diversity Index (D) and Simpson's Index of Diversity (1-D) for each collection trip are presented at the bottom of the table.

locations shared the same morphological property of having dark scales on the posterior corners of all tergites and mixed black and yellow scales on the sternites. These findings are in contrast to the description of Edwards (1941), which states that the abdomen of *Cq. cristata* matches that of *Cq. nigrithorax* in being wholly yellow with no darkening on the corners of the tergites. Considering these morphological variations among the *Cq. cristata* collected during this study and those described by Edwards (1941), and the divergent sequencing results at the COI locus, there appears to be some intraspecific genetic variation among *Cq. cristata* collected in different geographic locations that warrants further study. Unfortunately, no sequences from *Cq. cristata*, or the morphologically similar *Cq. nigrithorax*, exist in the Barcode of Life (COI) database, or on Genbank for further comparison.

Anopheles funestus s.l.

Eighteen specimens morphologically identified as *An. funestus* s.l. were also analyzed molecularly. These mosquitoes included seven specimens from Sunguru, collected on 14 and 16 January 2011; eight specimens from Paraai collected between 19 and 21 January 2011 (7) and on 19 June 2011 (1); and three specimens from Chobe, collected on 24 January 2011. From Paraai, six of the eight specimens

tested were determined by PCR and sequencing to be *An. rivulorum*. The remaining two specimens from that location had a >99% sequence similarity to *An. funestus* s.s. at the COI locus (top BLAST hit DQ287358); however, there was no amplification obtained from the multiplex assay which included an *An. funestus*-specific primer (Koekemoer et al. 2002). Similarly in Sunguru, four of seven specimens matched *An. funestus* s.s. by sequencing COI after obtaining no amplification with the multiplex assay. From Chobe, two of three specimens were also identified as most like *An. funestus* s.s. by sequencing the COI amplicon, but for which no amplification was obtained from the multiplex assay. The remaining specimen from Chobe was confirmed as *An. funestus* s.s. by multiplex PCR and sequencing of both the COI amplicon and the internal transcribed spacer region 2 (ITS2) amplicon derived from the multiplex assay. These results suggest that there are multiple cryptic species within the *An. funestus* species complex in addition to *An. funestus* s.s. and *An. rivulorum* present at our collection sites.

Spillings et al. (2009) reported similar results from specimens collected in Malawi, specifically, 61 of 63 specimens morphologically identified as *An. funestus* s.l. during that study did not amplify with the multiplex assay. Sequence analysis of ITS2 identified variations within the *An. funestus*-specific primer binding site, and demonstrated a sequence variation of 4.5% compared with *An. funestus* s.s. (Spillings et al. 2009). On the basis of further molecular, cytogenetic, and cross-mating evidence, those authors concluded that the *An. funestus*-like specimens represented a new member of the *An. funestus* complex (Spillings et al. 2009). Further phylogenetic analysis of members of the *An. funestus* species complex, including the *An. funestus*-like specimens from Malawi, was carried out by Choi et al. (2012, 2013). Based on results generated from both the ND5 and COI genes, Choi et al. (2012) suggested that the Malawi *An. funestus*-like specimens did indeed represent a distinct lineage from the other species in the *funestus* group, supporting the findings of Spillings et al. (2009). Choi et al. (2012) further described two clades of *An. funestus*-like specimens that emerged during their analysis, and noted that further study on this group of mosquitoes is necessary to resolve phylogenetic relationships within this group. Currently, *An. funestus*-like specimens have only been reported from Malawi. However, our results from Uganda are consistent with the Malawian studies, and may represent additional locations from which representatives of these novel *An. funestus*-like lineages are present. A multiple sequence alignment of COI sequences generated from *An. funestus* specimens from this study and reference *An. funestus* sequence AY423059, demonstrated that all of the *An. funestus* sequenced in this study share a COI genotype consistent with lineage 1 (Choi et al. 2013) except for one specimen (#3) from Sunguru. This specimen from Sunguru does not match the lineage 1 genotype and also differs at the locus associated with lineage 2 (Choi et al. 2013); however not enough genetic information for lineage 2 *An. funestus* is available on GenBank for more in-depth comparison. Further study on *An. funestus* complex mosquitoes in Uganda is warranted.

Potential Medical Importance

Of the 72 mosquito species collected in this study, 33 have been implicated in the transmission of arboviruses of public health importance (Table 7). This suggests that there is a high potential for maintenance and transmission of arboviruses in this region. Human serological surveys (Henderson et al. 1970) showed presence of antibodies against chikungunya, Sindbis, Bunyamwera, West Nile, Wesselsbron, Banzi, and Zika viruses in this region, which suggests that these viruses are endemic in the region. The presence of both

Table 7. Mosquito species collected in northwestern Uganda from which arboviruses of medical importance have previously been isolated

Genus	Subgenus	Species	Arbovirus(es)
<i>Aedes</i>	<i>Aedimorphus</i>	<i>albocephalus cumminsii</i>	MIDV ¹ , WNV ^{1,19} DENV-2 ^{1,5} , MIDV ^{1,3,5} , PGAV ^{1,5} , RVFV ^{1,2,5,20} , SHOV ^{1,3} , SPOV ^{1,4,5} , WSLV ^{1,5} , SINV ³ CHIKV ⁵
		<i>tarsalis</i>	MIDV ^{1,5} , PGAV ¹ , SHOV ^{1,5} , WSLV ^{1,5} , ZIKAV ^{1,5} , RVFV ^{2,17}
		<i>taylori</i>	DENV-2 ^{1,5,22} , YFV ^{1,5,6} , CHIKV ⁵ , ZIKAV ⁵ , ORUV ⁵
		<i>grahami</i>	CHIKV ⁵ , ZIKAV ⁵
		<i>albothorax</i>	WNV ^{1,5}
	<i>Stegomyia</i>	<i>circumluteolus</i>	BUNV ¹ , GERV ¹ , LEBV ¹ , MIDV ^{1,4} , PGAV ^{1,5} , RVFV ¹ , SHOV ¹ , SPOV ¹ , WSLV ^{1,4,5} , WNV ^{1,5,19}
		<i>aegypti</i>	CHIKV ^{1,5} , DENV-1 ¹ , DENV-2 ^{1,22} , DENV-3 ¹ , DENV-4 ¹ , DUGV ¹ , ORUV ^{1,5} , USUV ¹ , VEEV ¹ , WNV ^{1,5,19} , YFV ^{1,5,8,21} , ZIKAV ^{1,5,23} , SFV ⁵ , WSLV ⁵ , BBKV ⁵
		<i>metallicus</i>	YFV ^{5,6} , WSLV ⁵ , ZIKAV ⁵
		<i>simpsoni group</i>	YFV ^{6,13,14} , BBKV ⁵ , NRIV ⁵
		<i>coustani</i>	CHIKV ^{1,5} , PGAV ^{1,5} , WNV ^{1,19} , NRIV ⁵
<i>Anopheles</i>	<i>Anopheles</i>	<i>funestus complex</i>	BWAV ^{1,5,24} , CHIKV ^{1,5} , ONNV ^{1,5,9,15,16} , ORUV ^{1,5} , PGAV ^{1,5} , SFV ^{1,4} , WSLV ^{1,5} , TATV ⁵ , NDOV ⁵ , TATV ^{4,5}
		<i>gambiae s.l.</i>	BWAV ^{1,5} , CHIKV ¹ , ILEV ^{1,5} , MIDV ^{1,5} , ONNV ^{1,5,15,16} , ORUV ^{1,5} , ZIKAV ^{1,5} , TATV ⁵ , NRIV ⁵ , NDOV ⁵ , BGIV ⁵ , TATV ^{4,5}
<i>Coquillettidia</i>	<i>Coquillettidia</i>	<i>pharoensis</i>	SINV ¹ , WSLV ⁵ , NRIV ⁵ , BGIV ⁵
		<i>aurites</i>	USUV ¹ , TATV ^{4,5}
		<i>fuscopennata</i>	SINV ^{1,10} , CHIKV ¹⁰ , YFV ^{1,6}
		<i>maculipennis</i>	CHIKV ⁵
<i>Culex</i>	<i>Culex</i>	<i>metallica</i>	MIDV ^{1,5} , WNV ^{1,19} , BBKV ⁵
		<i>antennatus</i>	PGAV ¹ , WNV ^{1,5,19} , RVFV ^{2,20} , SINV ¹ , WSLV ⁵ , BBKV ⁵ , NRIV ⁵
		<i>decens group</i>	WNV ^{5,19} , CHIKV ⁵ , BBKV ⁵
		<i>neavei</i>	SPOV ^{1,4} , WNV ^{5,8,12,19} , SINV ⁸ , BBKV ⁵ KOUV ⁵
		<i>perfuscus</i>	ORUV ^{1,5} , USUV ^{1,5} , WNV ^{1,5,19} , WSLV ^{1,5} , SINV ⁵ , BBKV ⁵
		<i>pipiens</i>	JBEV ¹ , LACV ¹ , SFV ¹ , SLEV ¹ , TAHV ¹ , WEEV ¹ , WNV ¹⁹ , BANV ⁵ , BUNV ⁵
		<i>quinquefasciatus</i>	CHIKV ^{1,5} , EEEV ¹ , KUNV ¹ , MTBV ¹ , MURV ¹ , OROV ¹ , RRV ¹ , SLEV ¹ , SINV ¹ , VEEV ¹ , WANV ¹ , WEEV ¹ , WNV ^{1,5,19} , BBKV ⁵
		<i>univittatus</i>	SINV ^{1,25} , SPOV ¹ , USUV ^{1,5} , WSLV ¹ , WNV ^{1,5,19}
		<i>cinereus</i>	CHIKV ⁵ , MIDV ⁵ , BBKV ⁵
		<i>nebulosus</i>	MIDV ⁵ , BBKV ⁵ , BGIV ⁵
<i>Eumelanomyia</i>	<i>Eumelanomyia</i>	<i>rubinotus</i>	BANV ¹ , GERV ^{1,5} , RVFV ²
		<i>annulioris</i>	MIDV ⁵ , WSLV ⁵
		<i>poecilipes</i>	RVFV ^{5,11} , WNV ^{5,12,19} , MIDV ⁵ , PGAV ⁵ , BBKV ⁵ , NRIV ⁵
		<i>chrysogaster</i>	MIDV ^{1,5} , RVFV ^{1,2} , SFV ⁵
<i>Eretmapodites</i>	<i>Mansonioides</i>	<i>africana</i>	BANV ¹ , BUNV ^{1,5,12} , CHIKV ^{1,5} , LEBV ¹ , MIDV ^{1,5} , PGAV ^{1,5} , SHOV ¹ , SPOV ^{1,4} , USUV ^{1,5} , WSLV ^{1,5} , RVFV ^{2,20} , WNV ⁵ , BBKV ⁵
		<i>uniformis</i>	BUNV ^{1,5,12} , MIDV ^{1,5} , RRV ¹ , SPOV ^{1,4} , WSLV ^{1,5} , ZIKAV ^{1,5} , WNV ^{5,11} , CHIKV ⁵ , BANV ⁵ , RVFV ⁵
<i>Mansonia</i>			
<i>Uranotaenia</i>	<i>Pseudoficalbia</i>	<i>mashonaensis</i>	WSLV ⁵

BANV = Banzi virus; BBKV = Babanki virus; BGIV = Bangui virus; BUNV = Bunyamwera virus; BWAV = Bwamba virus; CHIKV = Chikungunya virus; DENV-1 = Dengue type 1 virus; DENV-2 = Dengue type 2 virus; DEN-3 = Dengue type 3 virus; DEN4 = Dengue type 4 virus; DUGV = Dugbe virus; EEEV = Eastern Equine Encephalitis virus; GERV = Germiston virus; ILEV = Ilesha virus; JBEV = Japanese Encephalitis virus; KOUV = Koutango virus; KUNV = Kunjin virus; LACV = LaCrosse Encephalitis virus; LEBV = Lebombo virus; MIDV = Middelburg virus; MTBV = Marituba virus; MURV = Murray Valley virus; NDOV = Nyando virus; NRIV = Ngari virus; ONNV = Onyong-Nyong virus; OROV = Oropouche virus; ORUV = Orongo virus; PGAV = Pongola virus; RRV = Ross River virus; RVFV = Rift Valley Fever virus; SFV = Semliki Forest virus; SHOV = Shokwe virus; SINV = Sindbis virus; SLEV = St. Louis Encephalitis virus; SPOV = Spondweni virus; TAHV = Tahyna virus; TATV = Tataguine virus; USUV = Usutu virus; VEEV = Venezuelan Equine Encephalitis virus; WANV = Wanowrie virus; WEEV = Western Equine Encephalitis virus; WSLV = Wesselsbron virus; WNV = West Nile virus; YFV = Yellow Fever virus; ZIKAV = Zika virus.

¹The International Catalogue of Arboviruses. ²Meegan & Bailey 1988. ³McIntosh et al. 1972. ⁴ARBOCAT (<http://www.cdc.gov/arbocat/index.asp>). ⁵Institut Pasteur de Dakar. 2000. ⁶Monath 1988. ⁷McCrae & Kirby 1982. ⁸McIntosh 1986. ⁹Lutwama et al. 1999. ¹⁰Woodhall 1964. ¹¹Diallo et al. 2005. ¹²Traore-Lamizana 2001. ¹³Mahaffy et al. 1942. ¹⁴Smithburn & Haddow 1946. ¹⁵Williams et al. 1965. ¹⁶Corbet et al. 1961. ¹⁷Smithburn et al. 1948. ¹⁸McIntosh et al. 1961. ¹⁹Hubálek & Halouzka 1999. ²⁰Fontenille et al. 1998. ²¹Germain et al. 1980. ²²Diallo et al. 2003. ²³Marchette et al. 1969. ²⁴Lee & Moore 1972. ²⁵Jupp et al. 1986.

Cx. pipiens and *Cx. quinquefasciatus*, important vectors of WNV, correlates with the fact that WNV was first detected in this region of the country (Smithburn et al. 1940).

Overall, we report 72 mosquito species in northwestern Uganda; 54 species of which were detected for the first time and 18 detected in both 1951 and 2011. The majority of specimen captured in 2011, 81.6%, belonged to 2 genera *Coquillettidia* and *Mansonia*,

suggesting that the conditions in northwestern Uganda especially in drier seasons were favorable to these 2 genera. A third of the 72 species detected belonged to the genus *Culex* suggesting that species in this genus are well adapted to northwestern Uganda. Interestingly, *Culex* dominance has been observed in other parts of the country (Mutebi et al. 2012, Mayanja et al. 2014), suggesting that the dominance may not be specific to northwestern Uganda alone. The number

of *Anopheles* species detected (14) was similar to that detected in western Uganda (13) (Mutebi et al. 2012) but higher than that detected in central Uganda (3) (Mayanja et al. 2014). The number of *Aedes* species captured was comparable to the numbers reported in the other parts of the country (Mutebi et al. 2012, Mayanja et al. 2014) suggesting more or less even *Aedes* species distribution across the country. More studies are needed to shade more light on the distribution and the ecology of the various mosquito genera and species in Uganda.

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