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Risk Factors for Household Vector Abundance Using Indoor CDC Light Traps in a High Malaria Transmission Area of Northern Zambia

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Abstract. Malaria transmission is dependent on the density and distribution of mosquito vectors, but drivers of vector abundance have not been adequately studied across a range of transmission settings. To inform intervention strategies for high-burden areas, further investigation is needed to identify predictors of vector abundance. Active household (HH) surveillance was conducted in Nchelenge district, Luapula Province, northern Zambia, a high-transmission setting with limited impact of malaria control. Between April 2012 and July 2017, mosquitoes were collected indoors during HH visits using CDC light traps. Demographic, environmental, and climatological correlates of vector abundance were identified using log-binomial regression models with robust standard errors. The primary malaria vectors in this setting were *Anopheles funestus* sensu stricto (s.s.) and *Anopheles gambiae* s.s. *Anopheles funestus* predominated in both seasons, with a peak in the dry season. *Anopheles gambiae* peaked at lower numbers in the rainy season. Environmental, climatic, and demographic factors were correlated with HH vector abundance. Higher vector counts were found in rural areas with low population density and among HHs close to roads and small streams. Vector counts were lower with increasing elevation and slope. *Anopheles funestus* was negatively associated with rainfall at lags of 2–6 weeks, and *An. gambiae* was positively associated with rainfall at lags of 3–10 weeks. Both vectors had varying relationships with temperature. These results suggest that malaria vector control in Nchelenge district should occur throughout the year, with an increased focus on dry-season transmission and rural areas.

INTRODUCTION

Malaria transmission is dependent on the density and distribution of competent anopheline mosquito vectors, and vector control has been identified as a key intervention to reduce the global malaria burden.[1,2] Current strategies for vector control include improved coverage of long-lasting insecticide-treated bed nets (LLINs), expanded indoor residual spraying (IRS), and larval source management, with the aim to manage insecticide resistance using sustainable and evidence-based policies.[2–5] In conjunction with rapid diagnostic testing, artemisinin combination therapies (ACTs), and intermittent preventive treatment of pregnant women and children, these strategies have led to substantial reductions in the malaria burden throughout sub-Saharan Africa.[1,4] However, progress has occurred disproportionately in regions with low or moderate malaria transmission, with less success in high-transmission areas despite implementation of control activities.[1,6] Increasing vector resistance to insecticides further threatens to reverse progress in vector control across epidemiologic settings.[5,7,8]

To guide successful vector control in high-burden areas, there is a need to investigate malaria vector dynamics and bionomics in these settings. The distribution and abundance of malaria vectors is known to vary by time and space; however, little research has been conducted to identify correlates of vector abundance.[9,10] Among the few existing studies, indoor vector counts have been associated with household (HH) construction, HH occupancy, environmental features, and climate, although results differ by locale and species. Higher vector counts have been found in HHs located in rural areas, in closer proximity to breeding sites, at lower elevations, and with natural roofing and open eaves.[11–15] Higher numbers of HH residents have been associated with increased vector counts.[13,14,16] Counts of *Anopheles gambiae* species tend to be positively associated with rainfall, whereas *Anopheles funestus* counts have been negatively associated with rainfall and positively associated with temperature and humidity.[11,12,16–21]

Zambia is a country of particular interest to identify optimal vector control strategies. Despite nation-wide scale-up of malaria control activities, there was a resurgence of cases in 2009 after almost a decade of steady decline.[22] Cases in Zambia have increased nearly every subsequent year, and the country reported 3.1 million cases and 7,000 deaths in 2016, an increase of nearly a million cases from 2010.[1] This resurgence was largely driven by provinces northeast of the border with the Democratic Republic of the Congo (DRC) and Copperbelt Province, whereas parasite prevalence in Lusaka, Eastern, and Southern Provinces continued to fall.[23–25] The heterogeneity of malaria transmission under this comprehensive vector control strategy and the growing burden of disease in the north indicate a need to further investigate drivers of vector abundance across transmission settings in Zambia.

The primary malaria vectors in Zambia are members of the *An. funestus* and *An. gambiae* complexes. Studies have identified that *Anopheles arabiensis* is the predominant vector in the south, with some isolated pockets of *An. funestus* sensu stricto (s.s.), whereas *An. funestus* s.s. and *An. gambiae* s.s. predominate in the north and east of the country.[22,26–30] Both *An. funestus* and *An. gambiae* are highly anthropophilic (feed on humans), endophagic (bite indoors), and endophilic (rest indoors).[31,32] Because of their indoor biting and resting

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behaviors, these species may be vulnerable to indoor vector control interventions, including LLINs and IRS. However, increasing resistance in Zambia to pyrethroids, organochlorines, and carbamate insecticides has reduced the efficacy of these interventions.[24,26]

Drivers of vector abundance in Zambia have not been comprehensively investigated. Nchelenge district, Luapula Province, in the north is a priority site to investigate barriers to malaria control due to the persistently high transmission in this setting. A vector bionomics study from 2012 to 2014 in this region identified season, HH water source, open eaves, and proximity to Lake Mweru as correlates of HH vector abundance.[28] This analysis builds on these results to further determine correlates of HH malaria vector abundance by species over a 5-year period in northern Zambia, with the aim of guiding malaria interventions.

MATERIALS AND METHODS

Study site. This study was conducted in Nchelenge district, Zambia, by the Southern and Central Africa International Centers of Excellence for Malaria Research.[23,33] Nchelenge district is located in the marshlands east of Lake Mweru and the Luapula River, one of the early tributaries of the Congo River. This river forms the border with the DRC to the west, with a land border to the north. There is a single rainy season from approximately October to April, followed by a dry season with little to no rainfall. The inland area has an extensive stream network leading to the lake, and the lakeside and riverbank regions include swamplands that remain inundated with water throughout the year.

This environment supports both *An. funestus* s.s. and *An. gambiae* s.s. with differing ecologic patterns and distributions throughout the year, resulting in year-round malaria transmission. *Anopheles funestus* is the most abundant vector, with high numbers collected from HHs throughout the year and a peak in the dry season.[27,28] *Anopheles gambiae* peaks with smaller numbers during the rainy season, particularly in the areas near the lake.[27,28] Both vectors are strongly anthropophilic and have relatively long adult life spans (mean of 23 days for *An. gambiae*, 28 days for *An. funestus* under laboratory conditions), which can facilitate rapid and widespread malaria transmission.[31,34,35] The cumulative entomologic inoculation rate is estimated to be 80–140 infective bites per year in Nchelenge.[28,36] Household construction in this region is generally rudimentary, with most people living in huts with natural flooring and walls, thatch roofs, and open eaves, and a smaller number living in finished housing with metal roofs and concrete walls.

The study site in Nchelenge district represents high malaria transmission with limited impact of control efforts. As per Zambia's National Malaria Strategic Plan, malaria control strategies in this region include free malaria rapid testing and treatment with ACTs, LLIN distribution in antenatal and vaccination clinics, and yearly IRS in selected areas using pyrethroid (2008–2010), carbamate (2011–2012), and organophosphate insecticides (Actellic® 300CS formulation of pirimiphos-methyl, 2014 to present [Syngenta, Basel, Switzerland]).[37,38] Despite these activities, this region continues to experience holoendemic transmission, with a resurgence of cases since 2009 and an average malaria prevalence of approximately 70% in children younger than 17 years.[24,39]

Data collection. Households were selected for active surveillance through a modified cluster sampling design. QuickBird™ satellite images of the study areas were purchased (DigitalGlobe Services, Denver, CO), and a 1 × 1 km grid was overlaid on the study area in ArcGIS version 10.2 (ESRI, Redlands, CA). Households were enumerated, and grid quadrants were selected using spatially balanced random sampling to ensure inclusion of the full range of ecology in the region. Each month, 25–30 HHs were randomly selected using probability proportional to population size sampling, with between one and six HHs selected per grid quadrant.[40] If all HHs in a grid quadrant had already been sampled, an adjacent grid quadrant was selected, and the same random sampling method was used. Households were recruited into either cross-sectional or longitudinal cohorts with alternating bimonthly frequency to examine different outcomes of malaria transmission among HH residents. Longitudinal HHs were visited every other month for 1 year and then replaced with a new longitudinal cohort. Cross-sectional HHs were visited once and replaced with new HHs for each cross-sectional data collection.

At each HH visit, mosquitoes were collected using CDC light traps (John W. Hock, Ltd., Gainesville, FL). Study staff placed traps indoors in a sleeping area where an LLIN was already hung. Consenting HH participants were instructed to turn the traps on at 18:00 and to tie closed the vector collection bags and turn the traps off at 6:00 the following morning to collect mosquito vectors overnight. The traps were collected the following day, and consenting HH members were administered a questionnaire. Information was collected on HH GPS coordinates, house structure, demographic characteristics, HH water source, reported LLIN use, and history of HH IRS. The traps were transported to the field station in Kashikishi, Nchelenge district, where mosquitoes were killed by freezing, identified morphologically to genus and sex, enumerated, and stored dry on silica. Samples were transported to the Tropical Diseases Research Centre (TDRC) headquarters in Ndola once per month for final laboratory identification using standard morphological keys.[41,42] Molecular identification methods were used to validate morphological identification in a subsample of collections.[43,44] More detailed methods of vector identification are described elsewhere.[28]

Climatological data were collected from a HOBO Micro Station (Onset Computer Corporation, Bourne, MA) located on the grounds of the TDRC field station in Kashikishi and from the African Flood and Drought Monitor online tool.[45,46] Climatological data were aggregated by day from January 2012 to July 2017. Meteorological and hydrological variables included minimum and maximum daily temperature in °C, rainfall in mm/day, evaporation in mm/day, wind speed in m/second, streamflow in m^3/second, and percent soil moisture. For this analysis, the start and end of the rainy season each year was defined as the first and last weeks in which the average rainfall exceed 1 mm.

Data management. Entomologic and survey data collected at participating HHs were uploaded into REDCap secure file sharing software and downloaded as comma separated values formatted files.[47] Household locations were plotted in ArcGIS (Figure 1). To investigate spatial distributions, vector counts were spatially joined to sampling grid quadrants and plotted over the study area as a function of absolute and relative abundance by species and season.

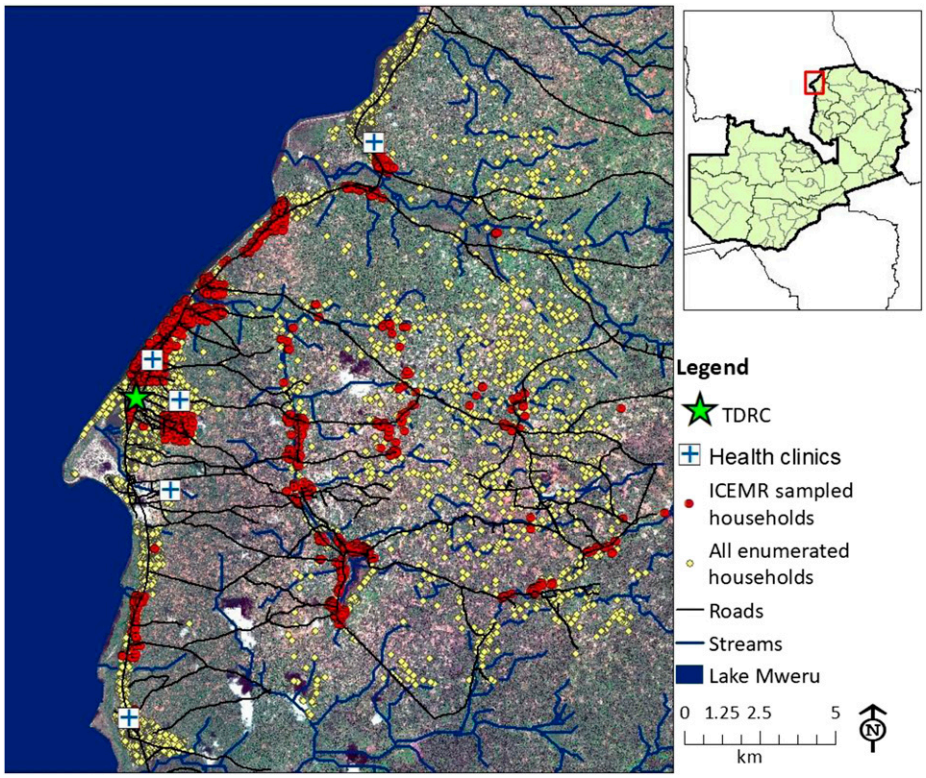

FIGURE 1. Nchelenge district sampled and enumerated households from April 2012 to July 2017. This figure appears in color at www.ajtmh.org.

Several geographic and environmental covariates were developed. Because of a natural break in HH density, HHs were classified as "lakeside" if they were within 3 km of Lake Mweru and as "inland" if they were further than 3 km from the lake. Population density for each HH was calculated as the number of other HHs within a 500-m buffer. Household elevation, slope, and normalized difference vegetation index (NDVI) were extracted from raster files downloaded from the Shuttle Radar Topography Mission (SRTM) version 3 and from Landsat 5 data, as described previously.[39] Normalized difference vegetation index values range from −1 to +1, with negative values corresponding to bodies of water and positive values increasing with increasing photosynthetic vegetation, or "greenness." Stream networks were developed using the SRTM elevation data in the ArcHydro Tools module of ArcGIS.[48] Streams were classified as categories 1–4 using the Strahler classification system, in which the smallest streams are defined as category 1, two category one streams join to form a category 2 stream, and so on.[49] The distances to roads, health clinics, Lake Mweru, and category 1–4 streams were calculated for each HH.

Statistical analysis. The primary aim of the analysis was to identify risk factors for HH vector abundance by species. Data were analyzed using STATA 13.1 (Stata Corporation, College Station, TX) and R version 3.4.2 (R Core Team, Vienna, Austria). Entomological, epidemiological, environmental, and climatological data for all HH visits between April 2012 and July 2017 were merged by HH and day. Vector counts did not differ significantly between longitudinal and cross-sectional cohorts, so data from all enrolled HHs were combined into one dataset for analysis.

Potential HH-level covariates included natural versus finished HH flooring, thatch versus metal roof, open versus closed HH eaves, open versus protected HH water source, self-reported history of HH IRS with pirimiphos-methyl in the past year, level of education completed by the head of household (HoH), and whether the HoH was in permanent employment. Because of the high degree of resistance to pyrethroid and carbamate insecticides and limited coverage of IRS with these insecticides in the past, the history of IRS with these compounds was not included in models. Geographic and environmental covariates as described above included population density within 500 m, NDVI, elevation, slope, and distances to roads, health clinics, Lake Mweru, and category 1–4 streams. Household demographics included the number of HH occupants and the proportion of occupants who were male, younger than 5 years, or slept under a bed net.

Bivariate and multivariate models were developed by species using negative binomial models with robust standard errors.[50,51] The unit of analysis was the HH, with indoor vector counts by species as the outcome. Generalized estimating equations were used to account for repeat visits to HHs.[52,53] Bivariate comparisons by species were conducted for all covariates listed above, and covariates that were significant at the $P = 0.1$ level or identified as relevant in the literature were retained for multivariate analyses. The variables for roof type and HH eaves were available in only a subsample of HHs and were therefore excluded from further analyses.

A series of climate covariates was developed to account for the effect of weather and hydrology on interannual variation in vector abundance. The impact of climate was expected to be delayed because of the duration of vector life cycles, but appropriate time lags have not been explored in this setting. A

cross-correlation approach was adapted for this analysis to investigate the most etiologically relevant time period for each climate variable to predict HH vector counts.[54,55] Using this method, the average value of each climate variable (e.g., rainfall) was calculated at time intervals of 1–12 weeks and lags of 1–12 weeks from each day of data collection, returning 144 potential covariates for each climatological factor. For each species, a preliminary list of the most predictive climatological covariates was identified using random forest algorithms, which are designed to handle a large number of collinear variables.[56,57] Final model selection was conducted from all relevant variables using stepwise regression and akaike information criterion (AIC) optimization methods.[58,59]

RESULTS

Vector species composition. From April 2012 through July 2017, a total of 13,780 female anopheline mosquitoes were collected during 1,724 visits to 1,084 unique HHs. The species composition based on morphological identification included 12,365 *An. funestus*, 1,371 *An. gambiae*, 43 *Anopheles coustani*, and 1 *Anopheles maculipalpis*. There was a mean of 7.8 female anophelines per HH visit (median 0; range: 0–230), including 7.0 *An. funestus* (median 0; range: 0–226) and 0.8 *An. gambiae* per HH (median 0; range: 0–35). The distribution of nightly HH vector counts was highly skewed, with no anopheline mosquitoes collected from 53% of HH visits and 5% of HH visits yielding between 50 and 230 anophelines (Figure 2). By species, no *An. funestus* were collected from 60.7% of HH visits and no *An. gambiae* were collected from 77.5% of HH visits.

Throughout the year, a higher number of vectors were collected in inland areas, with especially large collections occurring in the dry season along a large inland lagoon, which spans an area of approximately 0.5 km^2 in the dry season and 0.90 km^2 in the rainy season (Figure 3). As anticipated,

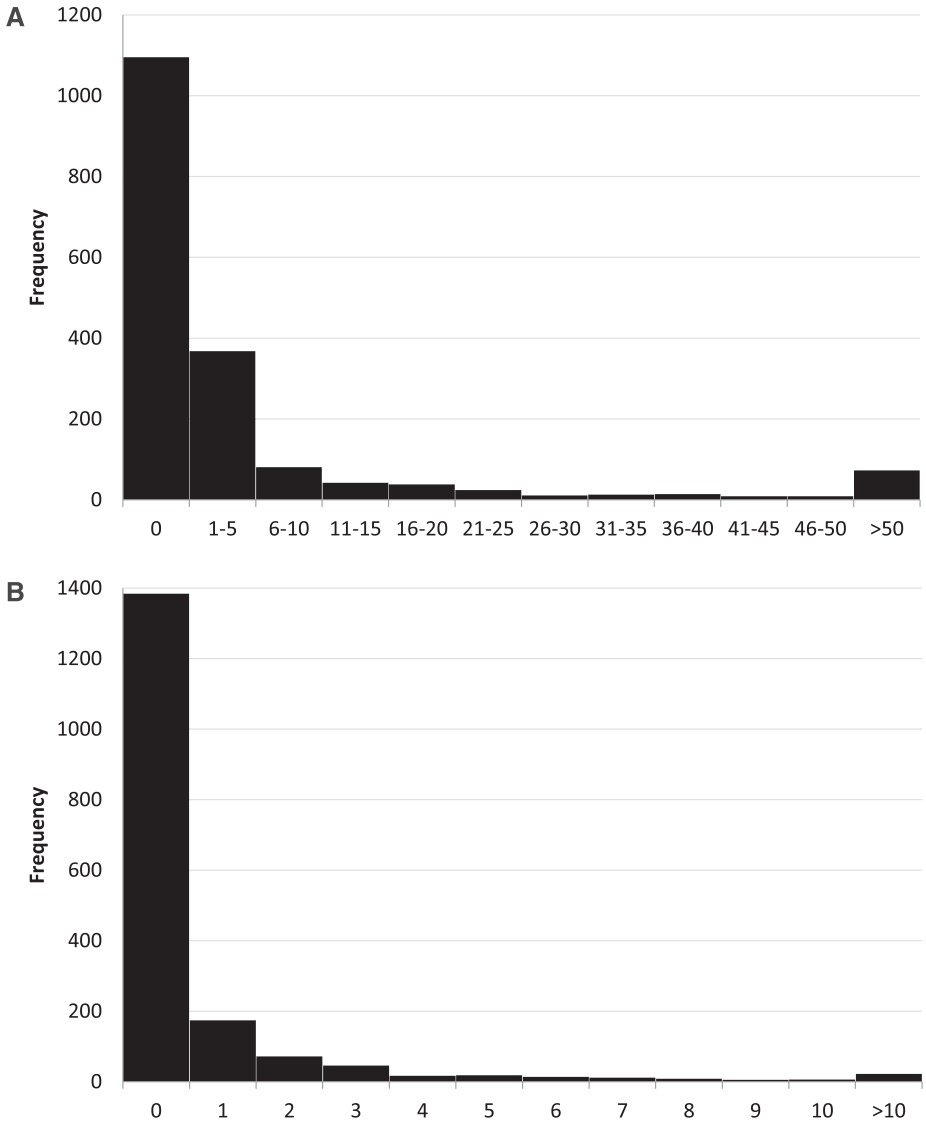

FIGURE 2. Histograms of household (HH) vector counts by species for (**A**) *Anopheles funestus* and (**B**) *Anopheles gambiae*, with N = 1,724 total HHs.

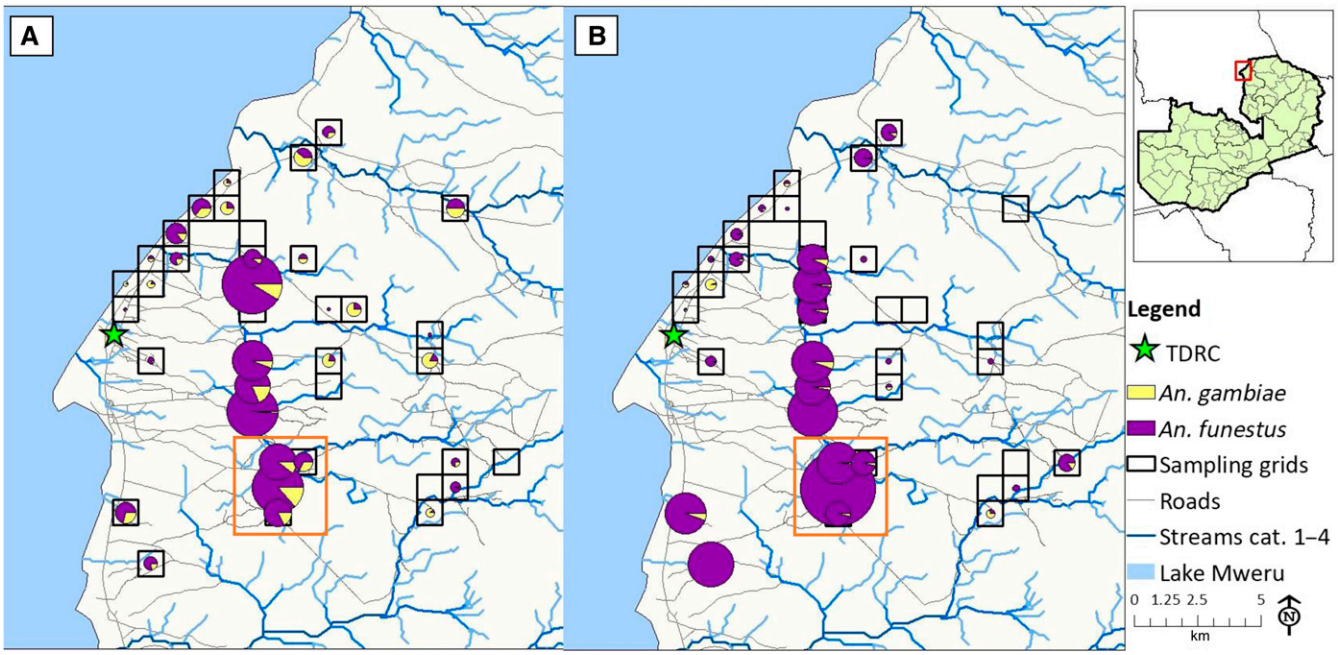

FIGURE 3. Distribution of *Anopheles funestus* and *Anopheles gambiae* in sampled grid quadrants throughout the study area in Nchelenge district, Zambia, in (**A**) rainy season (October–April) and (**B**) dry season (May–September). An inland lagoon area is identified in an orange box. This figure appears in color at www.ajtmh.org.

An. funestus was the predominant vector, with higher HH counts than *An. gambiae* in both rainy and dry seasons. *Anopheles funestus* counts peaked shortly after rains ceased and remained high throughout the dry season (Figure 4). *Anopheles gambiae* were nearly absent in the dry season collections. Counts rose at the onset of the rains and then increased throughout the rainy season (Figure 4). *Anopheles gambiae* was the predominant vector in some lakeside grid quadrants during the rainy season, although overall numbers remained low (Figure 3).

Climate, environment, and HH-level factors. In the rainy season from approximately October to April, daily minimum temperature averaged 19.7°C (range: 11.4–25.3) and daily maximum temperature averaged 29.2°C (range: 19.4–34.1). Precipitation averaged 6.8 mm/day (range: 0–64.6). There was an average of 56% soil moisture, 2.7 mm/day of evaporation, 1.5 m/second wind speed, and 2,983 m^3/second of streamflow. In the dry season from May to September, daily minimum temperature averaged 15.7°C (range: 10.2–23.7) and daily maximum temperature averaged 28.4°C (range: 23.1–33.5). Precipitation averaged 0.06 mm/day. There was an average of 26% soil moisture, 0.3 mm/day of evaporation, 2.5 m/second wind speed, and 143 m^3/second of streamflow. Household elevation ranged from 920 to 1,055 m, and HH slope ranged from 0 to 10.4°. Normalized difference vegetation index ranged from 0.29 to 0.78. For each HH, there were between 10 and 1,021 HHs within 500 m. Ninety percent of HHs had open eaves and 89% had thatch roofs, with nearly complete correlation between the two. Eighty-eight percent of HHs had a dirt floor, and 56% used an open water source, including open wells, surface water, or lakes and streams.

Correlates of HH vector counts. In bivariate analyses, vector counts were associated with geography and environment, HH occupancy, HH construction, and history of malaria control activities (Table 1). Household counts of both *An. funestus* and *An. gambiae* increased with increasing distance from Lake Mweru and decreasing population density, both potential markers of rural residence. Counts of *An. funestus* also increased with increasing distance from health clinics. Higher counts of *An. funestus* and *An. gambiae* were found in HHs that used an unprotected water source, that were closer to category 2 streams, and that were located in areas with higher NDVI, indications of potential larval sites. *Anopheles funestus* counts were also higher in HHs located at lower elevations, at steeper slopes, and farther from category 4 streams. Counts of both vectors were higher in HHs with a larger proportion of children younger than 5 years, and counts of *An. funestus* increased with higher HH occupancy. Higher counts of *An. funestus* were found in HHs with rudimentary construction, including natural floors, natural roofing, and open eaves. *Anopheles funestus* counts were significantly lower in HHs with a reported history of IRS with pirimiphos-methyl, but *An. gambiae* counts were not. Higher numbers of both species were collected in HHs with a higher rate of bed net use. Longitudinal versus cross-sectional HH selection was not significantly associated with vector counts of either species.

In multivariate models, *An. funestus* counts were positively associated with NDVI and negatively associated with population density, lakeside residence, distance from roads and category 1 streams, elevation, slope, and reported history of IRS with pirimiphos-methyl (Table 2). For each 10% increase in NDVI, counts were 30% higher (incidence rate ratio (IRR) = 1.3; 95% CI = 1.1–1.5). Counts were 35% lower with each additional 100 HHs within 500 m (IRR = 0.65; 95% CI = 0.54–0.77) and were 72% lower if the HH was within 3 km of Lake Mweru (IRR = 0.28; 95% CI = 0.16–0.47). Counts decreased 20% with each additional 100 m from a road (IRR = 0.80; 95% CI = 0.74–0.86) and decreased almost 50% with each additional 1 km from category 1 streams (IRR = 0.52;

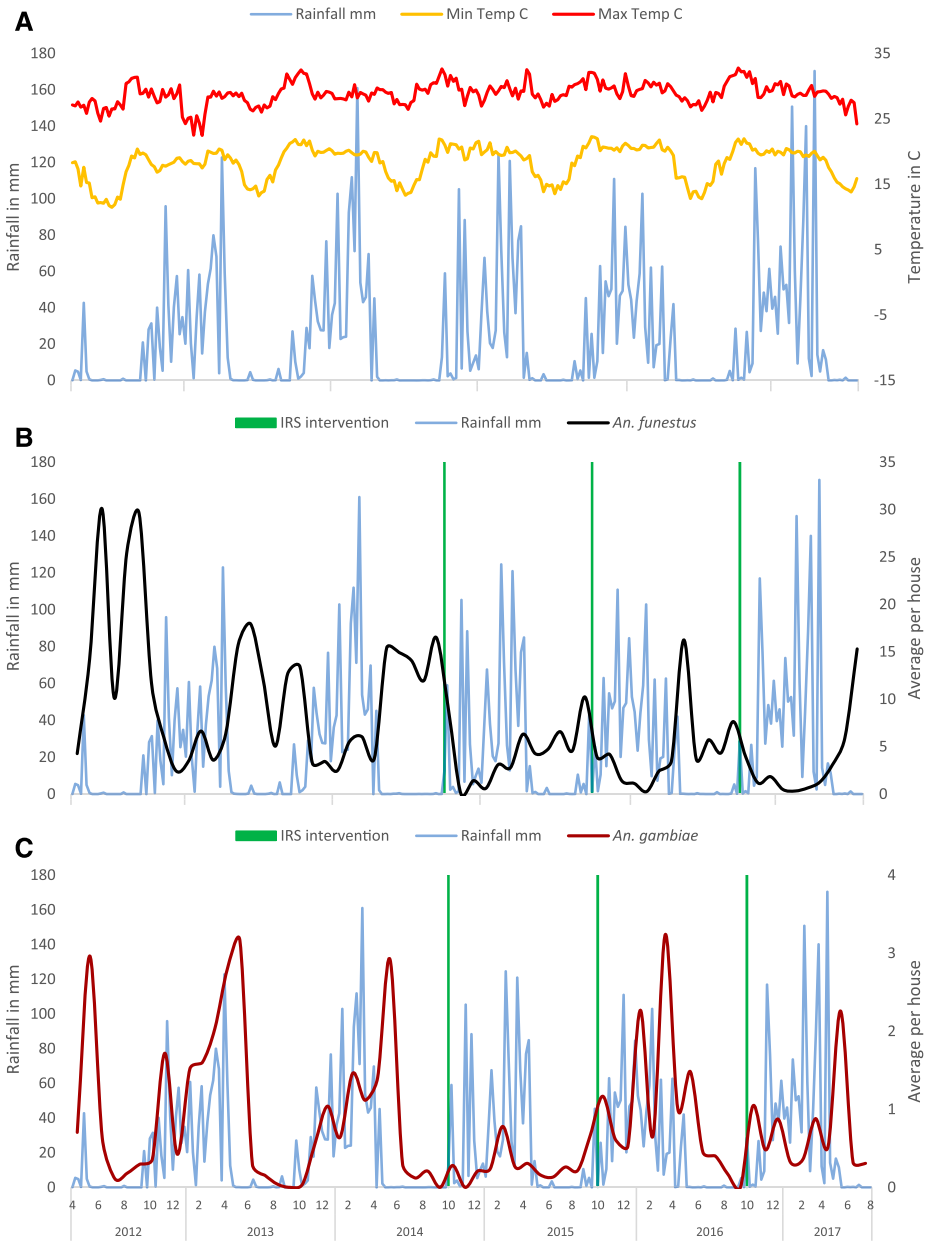

FIGURE 4. Time series of (**A**) weather patterns, (**B**) *Anopheles funestus*, and (**C**) *Anopheles gambiae* counts by month. This figure appears in color at www.ajtmh.org.

95% CI = 0.32–0.86). Counts were nearly 50% lower with each 10 m increase in elevation (IRR = 0.53; 95% CI = 0.47–0.61) and were 12% lower with each additional degree of slope (IRR = 0.88; 95% CI = 0.80–0.97). Households that reported a history of IRS with pirimiphos-methyl had 55% lower counts than unsprayed HHs or HHs sprayed with a different insecticide (IRR = 0.45; 95% CI = 0.32–0.62).

The strongest climatic predictors of *An. funestus* counts in multivariate models were rainfall and maximum temperature, with the most predictive time lags identified as between 2 and 12 weeks (Figure 5). Vector counts of this species decreased with increasing rainfall. Counts of *An. funestus* were 71% lower for each additional 10 mm of rain at a time lag of 2–4 weeks (IRR = 0.29; 95% CI = 0.17–0.47) and were 44% lower for each additional 10 mm of rain at a time lag of 4–6 weeks (IRR = 0.56; 95% CI = 0.36–0.86). Correlations with temperature were complex. Counts were 8% higher for each 1°C increase in maximum temperature at a time lag of 2–4 weeks (IRR = 1.08; 95% CI = 1.00–1.2) but were 24% lower for each 1°C increase in maximum temperature at a time lag of 4–12 weeks (IRR = 0.76; 95% CI = 0.69–0.85).

In multivariate models, *An. gambiae* counts were negatively associated with population density, lakeside residence, and distance from the lake, roads, and category 1 streams (Table 2). With each additional 100 HHs within 500 m, counts decreased 18% (IRR = 0.82; 95% CI = 0.75–0.89). Overall counts were 75% lower in lakeside areas (IRR = 0.25; 95% CI = 0.14–0.43). Within both lakeside and inland areas, counts also decreased 18% with each additional 1 km from the lake (IRR = 0.82; 95% CI = 0.75–0.89). This relationship was consistent in stratified models, indicating that counts of *An. gambiae* were lower in the lakeside area overall, but

TABLE 1

Factors associated with HH counts of *Anopheles funestus* and *Anopheles gambiae* using bivariate negative binomial models with robust standard errors and generalized estimating equation clustered by HH, $N = 1,724$

	An. funestus			*An. gambiae*		
	IRR	95% CI	*P*-value	IRR	95% CI	*P*-value
HH characteristics						
Longitudinal HH type	1.01	(0.62–1.6)	0.9	0.73	(0.52–1.03)	0.08
Use unprotected water source	2.0	(1.4–2.9)	*< 0.001*	1.9	(1.4–2.7)	*< 0.001*
History of IRS by self-report*	0.35	(0.25–0.49)	*< 0.001*	0.92	(0.63–1.3)	0.7
Dirt floor in home	4.3	(2.2–8.2)	*< 0.001*	1.3	(0.78–2.2)	0.3
Metal roof*	0.20	(0.10–0.39)	*< 0.001*	0.68	(0.40–1.2)	0.2
Closed eaves*	0.23	(0.12–0.46)	*< 0.001*	0.70	(0.40–1.3)	0.2
HH demographics						
Number of HH participants	1.1	(1.04–1.2)	*0.001*	1.03	(0.96–1.1)	0.4
Proportion who use bed net (by 10%)	1.09	(1.05–1.1)	*< 0.001*	1.06	(1.02–1.1)	*0.002*
Proportion younger than 5 years (by 10%)	1.2	(1.1–1.3)	*< 0.001*	1.1	(1.02–1.2)	*0.02*
Proportion male (by 10%)	1.00	(0.97–1.03)	0.9	0.99	(0.95–1.03)	0.6
Environmental variables						
HHs within 500 m (by 100 HH)	0.61	(0.50–0.73)	*< 0.001*	0.80	(0.74–0.87)	*< 0.001*
Elevation (by 10 m)	0.86	(0.82–0.90)	*< 0.001*	1.00	(0.93–1.07)	0.9
Slope (by 1°)	1.1	(1.07–1.2)	*< 0.001*	0.96	(0.89–1.05)	0.4
NDVI (by 10%)	2.1	(1.8–2.5)	*< 0.001*	1.5	(1.2–1.8)	*< 0.001*
Distance from Lake Mweru (in km)	1.2	(1.1–1.2)	*< 0.001*	1.06	(1.02–1.1)	*0.002*
Distance from health clinics (in km)	1.3	(1.2–1.3)	*< 0.001*	1.09	(1.05–1.1)	*< 0.001*
Distance from roads (in 100 m)	0.93	(0.82–1.05)	0.2	0.89	(0.75–1.05)	0.2
Distance from cat. 1 streams (in km)	0.63	(0.38–1.04)	0.07	0.68	(0.40–1.17)	0.2
Distance from cat. 2 streams (in km)	0.59	(0.47–0.74)	*< 0.001*	0.78	(0.67–0.91)	*0.002*
Distance from cat. 3 streams (in km)	0.82	(0.72–0.95)	*0.007*	0.95	(0.85–1.06)	0.4
Distance from cat. 4 streams (in km)	1.2	(1.06–1.3)	*0.001*	1.08	(0.99–1.2)	0.09

HH = household; IRR = incidence rate ratio; IRS = indoor residual spraying; NDVI = normalized difference vegetation index. *P*-value *if* < 0.05.
* Indoor residual spraying with pirimiphos-methyl.
† Subsample of all HHs, $N = 1,383$.

that counts decreased in an eastern direction in both lakeside and inland regions (Figure 3). Counts were 18% lower with each additional 100 m from a road (IRR = 0.82; 95% CI = 0.75–0.89) and were 36% lower with each additional 1 km from category 1 streams (IRR = 0.64; 95% CI = 0.46–0.89).

The strongest climatic predictors of *An. gambiae* counts in multivariate models were rainfall, minimum temperature, and maximum temperature, with the most predictive time lags identified as between 2 and 10 weeks (Figure 5). Counts of *An. gambiae* were 34% lower for each additional 10 mm of rain lagged 2–3 weeks (IRR = 0.66; 95% CI = 0.46–0.95), but they

TABLE 2

Negative binomial multivariate models of predicting *Anopheles funestus* ($N = 1,665$) and *Anopheles gambiae* ($N = 1,724$) counts per HH, using robust standard errors and generalized estimating equation clustered by HH

	An. funestus			*An. gambiae*		
	IRR	95% CI	*P*-value	IRR	95% CI	*P*-value
History of IRS by self-report*	0.45	(0.32–0.62)	*< 0.001*	–	–	–
HH within 500 m (by 100 HH)	0.65	(0.54–0.77)	*< 0.001*	0.82	(0.75–0.89)	*< 0.001*
Elevation (by 10 m)	0.53	(0.47–0.61)	*< 0.001*	–	–	–
Slope	0.88	(0.80–0.97)	*0.01*	–	–	–
NDVI (by 10%)	1.3	(1.08–1.5)	0.004	–	–	–
Lakeside	0.28	(0.16–0.47)	*< 0.001*	0.25	(0.14–0.43)	*< 0.001*
Distance from Lake Mweru (in km)	–	–	–	0.82	(0.75–0.89)	*< 0.001*
Distance from roads (in 100 m)	0.80	(0.74–0.86)	*< 0.001*	0.82	(0.74–0.90)	*< 0.001*
Distance from cat. 1 streams (in km)	0.52	(0.32–0.84)	*0.007*	0.64	(0.46–0.89)	*0.007*
Lagged rainfall (by 10 mm)†	0.29	(0.17–0.47)	*< 0.001*	–	–	–
Lagged rainfall (by 10 mm)‡	0.56	(0.36–0.86)	*0.008*	–	–	–
Lagged rainfall (by 10 mm)§	–	–	–	0.66	(0.46–0.95)	*0.02*
Lagged rainfall (by 10 mm)‖	–	–	–	2.3	(1.4–3.8)	*0.002*
Lagged maximum temperature (in °C)†	1.08	(1.00–1.2)	*0.05*	–	–	–
Lagged maximum temperature (in °C)¶	0.76	(0.69–0.85)	*< 0.001*	–	–	–
Lagged maximum temperature (in °C)#	–	–	–	0.75	(0.68–0.82)	*< 0.001*
Lagged minimum temperature (in °C)#	–	–	–	1.3	(1.2–1.4)	*< 0.001*

HH = household; IRR = incidence rate ratio; IRS = indoor residual spraying; NDVI = normalized difference vegetation index. *P*-value *if* < 0.05.
* Indoor residual spraying with pirimiphos-methyl.
† Lag = 2–4 weeks.
‡ Lag = 4–6 weeks.
§ Lag = 2–3 weeks.
‖ Lag = 3–10 weeks.
¶ Lag = 4–12 weeks.
# Lag = 3–7 weeks.

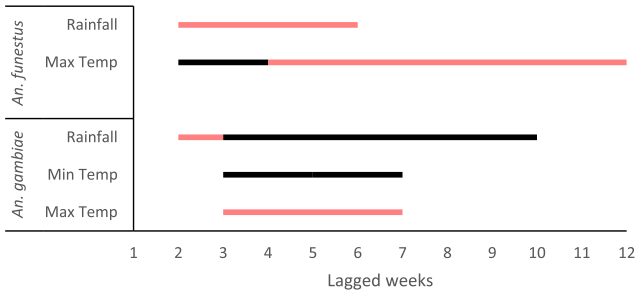

FIGURE 5. Most etiologically relevant time lags for climatic predictors of *Anopheles funestus* and *Anopheles gambiae* household (HH) counts. Red represents a negative correlation, corresponding with lower HH counts, and black represents a positive correlation, corresponding with higher HH counts. This figure appears in color at www.ajtmh.org.

were 230% higher for each additional 10 mm of rain at a time lag of 3–10 weeks (IRR = 2.3; 95% CI = 1.4–3.8), indicating that *An. gambiae* abundance is strongly correlated with increased rainfall except at short time lags. Correlations with temperature were again complex. Counts were 30% higher for each 1°C increase in minimum temperature at a time lag of 3–7 weeks (IRR = 1.3; 95% CI = 1.2–1.4), but counts were 25% lower with each 1°C increase in maximum temperature over this same time period (IRR = 0.75; 95% CI = 0.68–0.82).

DISCUSSION

This study described HH-level, environmental, and climatic drivers of indoor abundance for two key malaria vectors in a high-transmission setting in northern Zambia. Despite control activities, HH vector counts were high in this setting, with up to 230 female anophelines collected in a night from a single HH. As previously described,[27,28] *An. funestus* was the dominant vector in this region, and an average of approximately seven *An. funestus* and one *An. gambiae* were collected per HH during the duration of the study (range: 0–226 and 0–35, respectively).

Vector abundance for both species was consistently highest in remote inland regions of the study area. Counts were strongly negatively correlated with HH density and proximity to Lake Mweru, and consequently, HHs in the rural inland area were likely to have higher vector abundance than HHs in the peri-urban lakeside area. This result indicates a disparity in malaria control among rural residents in Nchelenge district, even accounting for the high overall level of transmission. Rural regions with low population density are not typically included in IRS campaigns in northern Zambia, and the high vector counts collected in these HHs suggest that vector control efforts with LLINs and sparse IRS have not significantly or sufficiently reduced vector populations in this region. Higher vector counts were also measured in HHs close to roads and small streams, which may serve as mosquito breeding sites because of the presence of puddles or ditches, and higher counts of *An. funestus* were found in areas of high NDVI, where vegetation cover may provide harborage and moisture. *Anopheles funestus* counts declined with increasing elevation and slope in multivariate models, which may correlate with less hospitable breeding habitats.

These results are generally consistent with previous studies. Indoor *An. gambiae* and *An. funestus* abundance has been positively associated with residence in rural areas and proximity to roads, rivers, and agricultural land,[11,13] and has been negatively associated with higher elevation and slope.[11,12,15] However, vegetation cover has been found to have negative associations with vector counts in some studies.[12,15] In the analysis conducted in Nchelenge district from 2012 to 2014, higher mean counts of *An. gambiae* and *An. funestus* were also found in the inland area, although this relationship was no longer significant for *An. funestus* in multivariable models controlling for season, house construction, and vector control activity.[28]

Although not significant or included in multivariate models, markers of socioeconomic status were strongly associated with HH vector abundance in bivariate analyses. These factors included HH construction, HH water source, and number of HH occupants younger than 5 years. Households with dirt floors or unimproved water sources had up to four times the number of mosquitoes in unadjusted analyses, and houses with metal roofs or closed eaves yielded 30–80% fewer mosquitoes by species. These associations with open eaves and water source were also seen for *An. gambiae* in the previous analysis in Nchelenge district.[28] These results show a direct connection between poverty and malaria risk and provide opportunities for intervention. Household construction including eaves, roofing, and wall materials have been a consistent predictor of vector abundance and malaria risk,[13–15,60–63] and interventions to reduce mosquito entry could be impactful in future malaria control efforts. For example, interventions that block eaves have been shown to successfully reduce HH entry of *An. gambiae*.[61,62]

A history of IRS with pirimiphos-methyl was found to be protective, with a 55% reduction in *An. funestus* counts compared with HHs that either did not report IRS or that were sampled before the use of this insecticide. Despite being an important vector in the rainy season, there was no significant reduction in *An. gambiae*, potentially because of consistently low trap counts of this vector coupled with several outliers with very high *An. gambiae* counts. An analysis of the impact of IRS with pirimiphos-methyl on vector abundance and parasite prevalence will be presented separately (Hast et al, unpublished data). Interestingly, higher numbers of both vector species were collected in HHs with higher rates of bed net use, which contrasts with previous results.[28] A potential explanation of this result is that larger indoor mosquito populations in the context of high pyrethroid resistance drove bed net use in this setting.

Climate was also a significant driver of HH vector abundance, but patterns differed considerably by species. *Anopheles gambiae* counts were strongly positively associated with rainfall. There was a 230% increase in captured *An. gambiae* per 10 mm of rainfall at time lags of 3 weeks or more, and this species was effectively absent during the dry season. This pattern for *An. gambiae* has been consistently described,[11,12,16–21] with few exceptions.[13] At shorter time lags, rainfall was found to be negatively associated with *An. gambiae*, potentially indicating that high amounts of recent rainfall may flush out existing eggs or larvae. Counts of *An. gambiae* were positively associated with higher minimum temperature but negatively associated with higher maximum temperature, suggesting that there is an ideal temperature range for *An. gambiae* survivorship. The relationship between *An. gambiae* and temperature has been inconsistent in the literature; however, study

methodologies differed with regard to data collection, use of time lags, and location.[11–13,16,19,64] It is plausible that *An. gambiae* is dependent on rainfall to complete its life cycle but that the species' qualitative relationship with temperature depends on the setting. Previous studies found associations between *An. gambiae* abundance and wind speed, humidity, and evaporation.[11,12,19] In Nchelenge district, evaporation and soil moisture were positively associated with *An. gambiae* counts in preliminary analyses but were not predictive in multivariate models, suggesting these factors covary with rainfall.

Conversely, *An. funestus* abundance declined steeply with increasing rainfall. There was a 70% decrease in captured *An. funestus* per 10 mm of rainfall at short time lags and a 44% decrease at longer time lags. This suggests that breeding or larval habitats of this species are likely vulnerable to being flushed out, which corresponds well with observations for this species of preferences for larger semipermanent and permanent water bodies that accumulate water from smaller tributaries over a longer temporal period. Larval sites may include the marshes or small streams widespread in the area, which are likely to be more susceptible to long-term inundation before settling and returning to viable larval mosquito habitat. The negative correlation with rainfall agrees with some studies and previous research in Nchelenge district,[11,12,28] although others have found no relationship between *An. funestus* and precipitation.[17,18,21] Interestingly, counts of *An. funestus* were positively correlated with maximum temperature at shorter lags of 2–4 weeks but negatively correlated with maximum temperature at longer time lags, suggesting that there may be a varying relationship with temperature at different mosquito life stages. Previous studies found a positive association between *An. funestus* and evaporation and wind speed.[11,12] In preliminary analyses, wind speed, soil moisture, streamflow, and evaporation were negatively associated with counts of *An. funestus*, but these were not significant in multivariate models.

Although overall vector abundance in Nchelenge district was high, these results highlight some key preliminary findings on the impact of vector control and disparities in current implementation practices and opportunities for additional interventions. In particular, HHs in more rural low-population density areas showed a clear increased risk of transmission because of their elevated vector numbers. Historically, in this area of Zambia, vector control measures have been concentrated in areas of highest human population density, and this study indicates that more effort is needed in remote areas to regionally suppress transmission. Household construction emerged as another potential avenue for intervention, particularly simple actions such as closing eaves and replacing thatch roofs with more durable materials that may reduce vector entry and provide less harborage for mosquitoes. The characterization of vector abundance by geographic and environmental factors can further help guide interventions to HHs at greatest risk in the context of limited resources. The strong relationship between vector abundance and climatic factors and the more detailed characterization of relevant time lags can be exploited to develop more specific interventions by species with the most impactful temporal and spatial deployment. For example, *An. gambiae* can be targeted just before the rainy season, whereas *An. funestus* in this region would be best targeted at the onset of the dry season just before their numbers peak.

This study had several limitations. The high number of bivariate comparisons by species could increase the chance of spurious associations. Furthermore, the use of light traps may underestimate true indoor vector counts. The traps catch only host-seeking mosquitoes in the room they are deployed, and for each individual host-seeking mosquito, there is a chance that it will not be captured and observed in the trap because of a variety of natural stochastic processes. Mathematically, this would have a larger impact for HHs with low vector densities, which may have contributed to the high number of zero counts and thereby limited power to investigate relationships. However, underestimation of HH counts can occur with any vector collection method because all methods are tailored to capture mosquitoes displaying a particular behavior. The considerable benefits of using light traps for active surveillance, including logistical ease, low cost, and high acceptability, outweigh drawbacks in comparison with other methods of vector collection that are more costly and more time- and laboratory-intensive.[65]

A major strength of this analysis is the availability of a long time series of entomologic surveillance data collected in a consistent manner from a high-transmission area. Many high-burden regions are difficult to access for long-term surveillance because of logistic difficulties or instability, and this dataset is unusual in both duration and scope. The length and frequency of data collection allowed a comprehensive investigation into interannual variation and appropriate time lags for climatological variables to determine the most etiologically relevant time period to predict HH vector abundance (Figure 5). This has direct relevance for developing and implementing future vector control interventions.

CONCLUSION

Malaria vector abundance in Nchelenge district, Zambia, was high throughout the year, indicating that vector control in this region has had a limited impact. In particular, vector counts were high among more rural populations and in HHs with lower sociodemographic indicators. To successfully reduce malaria transmission in northern Zambia, these results suggest that malaria vector control activities should be conducted throughout the year with increased focus on rural areas, dry-season transmission, and transmission by *An. funestus*. The timing and location of interventions should further take into account observed correlations with climate and geography. Improvements in HH construction including screening eaves and windows provide another option to reduce HH entry of malaria vectors.

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