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EDITED BY

David Weetman,
Liverpool School of Tropical Medicine,
United Kingdom

REVIEWED BY

Luca Facchinelli,
Liverpool School of Tropical Medicine,
United Kingdom
Athanas Badolo,
University of Ouagadougou, Burkina Faso

*CORRESPONDENCE

David P. Tchouassi

✉ dtchouassi@icipe.org

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Patterns of *Aedes aegypti* abundance, survival, human- blood feeding and relationship with dengue risk, Kenya

Winnie W. Kamau^{1,2}, Rosemary Sang¹, Gilbert Rotich¹,
Sheila B. Agha¹, Nelson Menza², Baldwin Torto^{1,3}
and David P. Tchouassi^{1*}

¹International Centre of Insect Physiology and Ecology, Nairobi, Kenya, ²Kenyatta University, Nairobi, Kenya, ³Department of Zoology and Entomology, University of Pretoria, Pretoria, South Africa

Dengue virus (DENV) transmission risk is influenced by the bionomic traits of the key vector, *Aedes aegypti*. We investigated patterns of abundance, survival, and human blood-feeding of *Ae. aegypti* populations in two environments in Kenya: peri-urban Rabai (coastal Region, dengue-endemic) and rural Kerio Valley (Rift Valley Region, no reported dengue outbreak). In both environments, *Ae. aegypti* survival (estimated by parity), was inversely correlated with vector abundance, and this was influenced by weather conditions, notably temperature and relative humidity. In Rabai, *Ae. aegypti* mostly fed on humans (human blood index=51%), a pattern that corroborates with dengue cases in the coastal region. *Aedes aegypti* additionally, exhibited opportunistic feeding (livestock, rodents, reptiles, birds), suggesting the risk of human exposure to zoonotic pathogens *via* spillover transmission events aided by the vector. Abundance and human blood-feeding rates were consistently lower in Kerio Valley likely related to the degree of urbanization. Remarkably, the periods of high human feeding in Rabai coincided with high vector survival rates, a trend that could potentially drive intense DENV transmission at certain times of the year. We found a genetic influence of *Ae. aegypti* on the degree of anthropophagy but this could be influenced by potential seasonal shifts in human feeding. The findings of this study have implications both for DENV transmission risk and vector control strategies, but also in modeling which should integrate vector bionomic factors beyond vector abundance.

KEYWORDS

Aedes aegypti, genetic forms, vector survival, human feeding, vectorial capacity, dengue risk, urbanisation, sub-Saharan Africa

Introduction

Dengue has re-emerged as one of the most important infectious arboviral diseases across the globe and it is exerting a toll not only on human health but also on the economic development of affected countries (1). The disease is caused by four distinct dengue virus (DENV) serotypes namely Dengue 1, 2, 3 and 4, which are transmitted to humans primarily through the bite of an infected *Aedes aegypti* mosquito (2, 3). According to the WHO, about half of the world's population is currently at risk of dengue infection, especially in tropical and subtropical areas. Globally, dengue cases have increased >10-fold between 2000 and 2019 (500,000 to 5.2 million), indicating expanding epidemiology of the disease. Reported deaths increased four-fold during the same period (~1000 in 2000 to ~4000 in 2015) (1). The global trend is unparalleled in the eastern African region where frequent dengue outbreaks continue to occur in Kenya and in neighboring countries like Tanzania, Somalia, Djibouti, Eritrea, Sudan and Ethiopia (1, 4–8). For instance, in Kenya the public health impact of dengue has continued to rise sharply, with successive recent outbreaks (between 2011–2022) resulting in hundreds of thousands of human cases and multiple fatalities (9). These frequent outbreaks and the co-circulation of all four DENV serotypes (10) are an indication of the significant burden posed by dengue.

The geographic spread of dengue occurs in part against a backdrop of limited understanding of the transmission dynamics, and ecology, including the bionomic role of geographic populations of the known vectors. Convergence in the basic components of the disease cycle: the virus, vector, and susceptible human hosts; in a permissive environment, provides the necessary ingredients that facilitate local arboviral pathogen emergence (11, 12). Yet, amidst the geographic spread, dengue risk patterns at local scales can be substantially heterogeneous (1, 13, 14). A better understanding of the complex interactions among these factors is required to predict the risk of dengue spread (15), but knowledge on vector populations and adaptation under changing habitat conditions are critical to achieving this.

Epidemic dengue cycles occurring in urban/peri-urban environments are increasing in eastern Africa and are driven primarily by the adaptation and expansion of vector range (e.g., *Ae. aegypti*) (16). Tracking changes in relevant biological parameters that define vectorial capacity can improve the prediction and response to infections or outbreaks in a timely manner (17, 18). Key among these is human blood-feeding preference (including multiple feeding) and survival (longevity) of the vector which controls opportunities for infection and transmission intensity (19–21). Besides density, measuring these vector traits in natural mosquito populations could be useful in risk assessment and to guide the implementation of vector control strategies. Mosquito longevity is a limiting factor for the transmission of arboviral pathogens, as pathogens must undergo a period of development (extrinsic incubation period - EIP) within the vector before it becomes transmissible *via* the salivary glands. EIP is temperature-sensitive with mean values of 15 and 6.6 days estimated for DENV at 25°C and 30°C, respectively (22). Few studies especially in Africa have described components of vectorial capacity (VC) for *Ae. aegypti* mostly relating to human blood meal patterns (13, 21, 23). Also, survivorship of natural populations of *Ae. aegypti* is seldom estimated (20, 24). Additionally, little information currently exists

regarding possible differences in vector survival, as well as human blood-feeding among the two known ecotypes: the sylvan *Ae. aegypti formosus* and the domestic *Ae. aegypti aegypti*. Variations in virus vectoring abilities and geographic distribution between the forms have been described (21, 25).

Weather parameters (e.g., temperature, rainfall, humidity) modulate various biological and behavioural processes of mosquito vectors. These and other non-climatic variables such as human mobility and urbanization have been implicated as important drivers of dengue spread and outbreak occurrence (15). How these factors interact to influence bionomic traits and local transmission has received little attention.

To improve our understanding of local-scale variation in dengue occurrence, this study investigated the survival and blood-feeding patterns of wild *Ae. aegypti* in two ecosystems that vary in dengue outbreak occurrences: peri-urban (coastal Rabai) and rural (Rift Valley Kerio Valley) in Kenya. Also, we examined the relationship between *Ae. aegypti* age structure and abundance and assessed whether the genetic variability in the vector correlates with the extent of human blood-feeding.

Materials and methods

Ethical approval

The study received approval from the Scientific Ethics Review Unit (SERU) of the Kenya Medical Research Institute (Protocol NO. SSC 2787). Additionally, consent was sought from household heads to set up traps around their homesteads.

Study sites

Host seeking female *Ae. aegypti* collected outdoors around residential areas in two environments- peri-urban environment (human density ~600/km²) in Rabai and rural environment (human density ~45/km²) in Kerio Valley (KV) were used in this study. Rabai (Kilifi County) is located northeast and ~25 km from Mombasa City in the dengue-endemic coastal Kenya (26) while KV with a history of YF outbreak (27) (no reported dengue outbreak) is in the Rift Valley Region (Figure 1). The larval habitats of *Ae. aegypti* differ in both areas, with KV providing a rural woodland setting with numerous tree holes for mosquito breeding as opposed to Rabai, a peri-urban setting providing common water storage containers for mosquitoes to breed in addition to outdoor breeding in plant axils and water receptacles.

Mosquito surveys and weather parameters

Aedes aegypti mosquitoes were trapped using CO₂-baited BG-Sentinel traps supplemented with chemical attractants (28) at three-time points: KV (November 2019) and Rabai (August–September 2019; February 2020). Each trapping covered a period of 2–3 weeks. Being a day-active mosquito, traps were set outdoors around homesteads at 06:30 h and retrieved at 18:00 h on the same day. Sampling was intended to

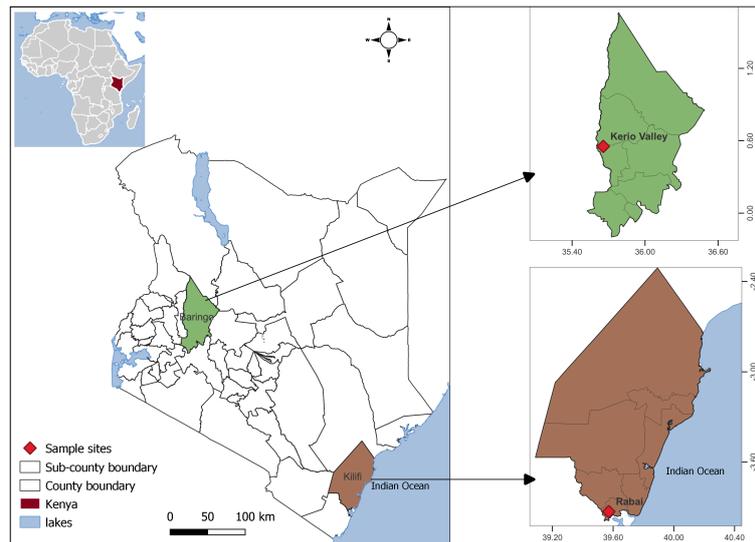


FIGURE 1

Map of Kenya showing location of the study sites. The map was designed using ArcMap 10.2.2. with the ocean and lakes base layer derived from Natural Earth (<http://www.naturalearthdata.com/>), a free GIS data source). The locations were collected using a GPS gadget (garmin etrex 20, <https://buy.garmin.com/en-US/US/p/518046>), and the county boundaries for Kenya derived from AfricaOpendata (<https://africaopendata.org/dataset/kenya-counties-shapefile>, license Creative Commons).

encompass a large spatial area per site. Collected samples were immobilised using triethylamine, preserved in liquid nitrogen in the field and transported to the laboratory at *icipe*. *Ae. aegypti* among the specimens were identified morphologically using taxonomic keys and then stored at -80°C .

The weather-related parameters during the trapping periods were as follows: August–September 2019 (mean daily temperature= 25.4°C ; mean daily rainfall= 0.58mm ; relative humidity= 75.9%) and February 2020 (mean daily temperature= 27.4°C ; mean daily rainfall= 0.30mm ; relative humidity= 80.3%) in Rabai and November 2019 (mean daily temperature= 19.9°C ; mean daily rainfall= 3.76mm ; relative humidity= 72.4%) in KV. These were derived from sourced weather data for each study site using the GPS location data. Daily weather data including relative humidity, precipitation, and temperature during the trapping period was extracted from NASA (National Aeronautics and Space Administration) POWER (Prediction of Worldwide Energy Resource) at the NASA Langley Research Center - <https://power.larc.nasa.gov/>. This is a satellite sensed weather dataset derived from satellite imagery, ground observations and assimilation models. The platform provides global gridded daily meteorological data from 1981 to near real time at a spatial resolution of 0.5° . Satellite-sensed weather data was used in place of the ground observed weather data due to large spatial gaps in weather station coverage in the study areas. Studies have proven that there is a strong correlation between the NASA data and ground station data (29, 30).

Parity rate, daily survival, and longevity estimation

Adult female mosquitoes were dissected for parity (31), which estimates vector survival in natural populations. Daily survival rates were estimated from parity data for each sampling period as described

previously (32) using the formula: $P^n = M$, where P is the daily survival rate, M the parity rate and n representing the gonotrophic cycle i.e., the number of days between adult female blood meal and first oviposition. Published data on parity for *Ae. aegypti* range from 3–4 days for populations outside of Africa (33–36) and this reduces with dry conditions. For tropical Africa with much higher temperatures, we assumed a value of $n=3$. Mosquito longevity (life expectancy in days) was derived using the formula: $1/(-\ln P)$ where P is the estimated daily survival rate (37).

Analysis of blood meals

Blood-fed specimens were individually dissected by separating the abdomen containing engorged blood from the head/thorax. The head/thorax was preserved for each mosquito and subjected to DNA extraction and molecular speciation (described below). Genomic DNA was extracted from the abdomen using the ISOLATE II Genomic DNA Kit (Bioline, Meridian Bioscience, Germany) as per the manufacturer's instructions. DNA was amplified by targeting a 500 bp fragment of the 12S mitochondrial rRNA gene using the primers 12S3F [5'-GGGATTAG ATACCCCACTATGC-3'] and 12S5R [5'-TGCTTACCAT GTTACGACTT-3'] (38) as described previously (18, 26). PCRs in a 10 μl reaction volume comprised 2 μl 2x MyTaq Mix (Bioline, Germany), 10 μM of each primer, 0.2 U of Mytaq DNA polymerase and 1 μl of the template DNA ($\sim 20\text{ ng}$). Thermal cycling conditions were 95°C for 3 min followed by 40 cycles at 95°C for 20 s, 59°C for 30 s and 72°C for 30 s and 72°C for 7 min. Amplicons were resolved on 1.2% agarose gel electrophoresis against a 100bp DNA HyperLadder (Bioline, Meridian Bioscience, Tennessee, USA). The PCR products were purified using the SureClean Plus kit (Bioline, Meridian Bioscience) and outsourced to MacroGen Europe BV (Amsterdam, The Netherlands) for Sanger sequencing using the forward primer. DNA sequences were compared

using the BLAST algorithm and the GenBank database (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>). Species level identification was determined when sequences exhibited $\geq 98\%$ identity spanning at least 300 bp as described previously (18, 26).

Discrimination of *Ae. aegypti* genetic forms among blood-fed specimens

The *Ae. aegypti* genetic forms, domestic *Ae. aegypti aegypti* (Aaa) and forest *Ae. aegypti formosus* (Aaf) cannot be reliably identified morphologically, requiring genetic approaches. To achieve this, genomic DNA was extracted from the head/thorax of each blood fed specimen as described above. PCR was then performed targeting an 860 bp barcode region of mitochondrial Cytochrome C Oxidase subunit 1 (COI) gene. DNA was amplified using the primers COI-22-F 5'-TGTAATTGTAACAGCTCATGCA-3' and COI-22-R 5'-AATGATCATAGAAGGGCTGGAC-3' (39). This marker has shown utility in resolving differences between Aaa and Aaf (13). The PCR was performed using MyTaq HS Mix kit (Bioline, Germany), the reaction volume comprised of 5 μ l of 2xMyTaq HS mix polymerase, 10 M of each primer and a template DNA of 2 μ l using the thermal cycling conditions of 95°C for 2 min followed by 40 cycles at 95°C for 30 s, 60°C for 30 s and 72°C for 45 s and 72°C for 7 min. Amplicons were confirmed by gel electrophoresis and the PCR products similarly purified and sequenced as explained earlier; however, in both the forward and reverse direction.

Cleaned sequences were aligned and maximum likelihood (ML) trees constructed with nodal support for the different groupings evaluated through 1000 bootstrap replications utilizing the Tamura 3-parameter with gamma distribution and proportion of invariant sites as best-fit model of sequence evolution. The haplotypes generated in this study were deposited in GenBank under accession numbers OP920609 - OP920647.

Statistical analyses

The parity rate calculated as the percentage of parous mosquitoes to the total number dissected was established for each trapping period and comparisons were made by Pearson chi-squared tests. The 95% confidence intervals (CIs) for the parity rates were estimated using *binom.confint*

function. The human blood index (HBI) expressed as the proportion of blood-feeding on humans of the total number of

engorged mosquitoes with successful host identification, was compared by trapping periods or mitochondrial COI lineages using Pearson chi-squared tests. All analyses were performed at $\alpha=0.05$ level of significance using R v. 4.21.

Results

Ae. aegypti survival rate varies by site and study periods

A total of 981 *Ae. aegypti* (non-blood fed) were successfully scored for parity from KV and Rabai across the three sampling periods recording an overall parous rate of 74.9% (735/981; 95%CI 72.1-77.5%). Parous rates in Rabai were 67.7% (212/313; 95%CI 62.4-72.7%) in August-September 2019 and 77.8% (277/356; 95%CI 73.2-81.8%) in February 2020, and 78.8% (246/312; 95%CI 74.0-83.0%) in KV in November 2019. Parous rates differed significantly only between the collection periods in Rabai ($\chi^2 = 8.10$, $df = 1$, $p=0.004$) (Table 1). In Rabai, estimated daily survival rates ranged from 0.87 in August-September 2019 to 0.91 in February 2020. A value of 0.92 was estimated for KV in November 2019. Overall, estimated longevity ranged from 7.7 to 12.7 days across the periods (Table 1).

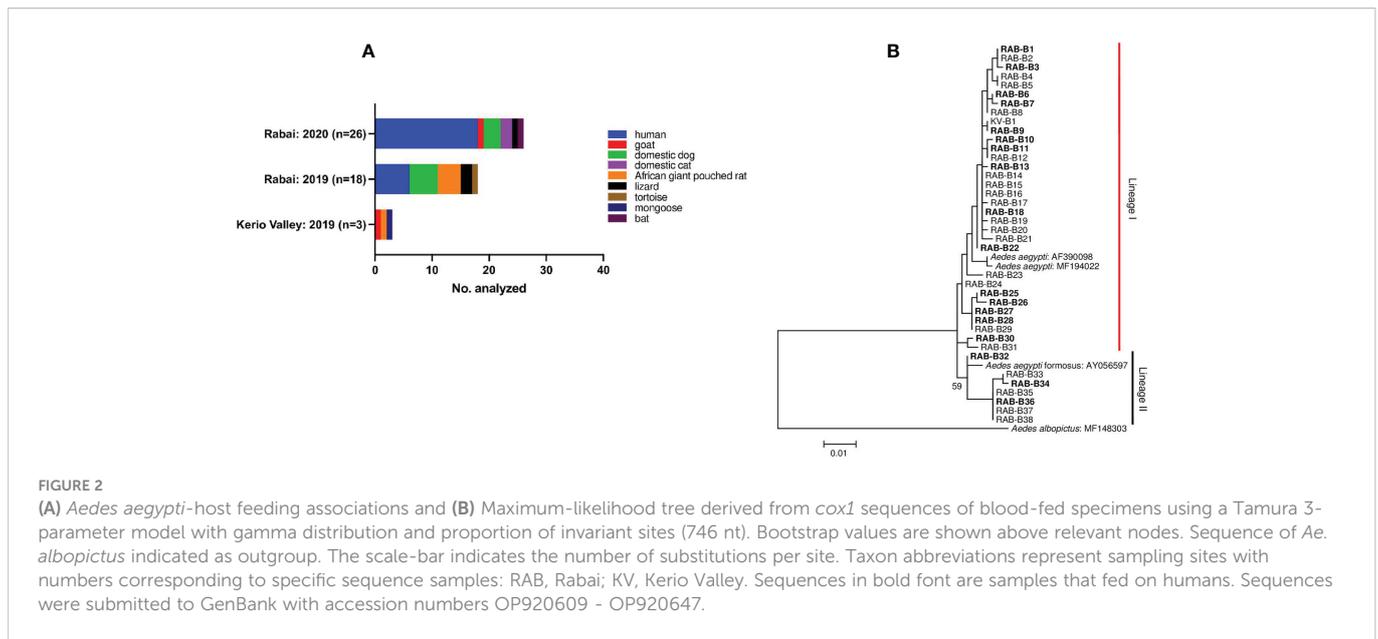
Ae. aegypti human feeding rates vary by area and survey period

Of the 53-blood fed *Ae. aegypti* analysed from both areas, blood meal sources were successfully profiled in 47 (88.7%) of which 44 (94%) were from Rabai and 3 (6%) from KV. Nine hosts were represented in individual blood meals with the highest proportion from humans (24/47; Figure 2A). This was followed by blood meals from domestic dog (8/47), African giant pouched rat (4/47), lizard (3/47), and minor representation of domestic cat (2/47), goat (2/47), bat (1/47), tortoise (1/47) and mongoose (1/47). The hosts commonly utilised in both areas were humans, domestic dog and lizard (Figure 2A). The three engorged specimens from KV had each fed on mongoose, goat and African giant pouched rat. Collectively, the HBI was 51% (24/47), although when disaggregated by trapping period, the HBI varied from 0 (0/3) in KV, 0.33 (6/18) in Rabai August-September 2019, to 0.69 (18/26) in Rabai February-2020. The HBI was significantly different between the study periods in Rabai ($\chi^2 = 4.18$, $df = 1$, $p = 0.04$).

TABLE 1 Estimated parity, daily survival and age for *Ae. Aegypti*.

Site	Survey period	Parity (% (n))	Daily survival rate	Longevity (days)
Rabai	August-September 2019	67.7 (313) ^a	0.87	7.7
	February 2020	77.9 (356) ^b	0.91	12
Kerio Valley	November 2019	78.8 (312) ^b	0.92	12.7

Columns followed by different letters are significantly different at $p<0.05$.



Human-biting *Ae. aegypti* represented among mitochondrial *COI* lineages

Next, we addressed whether human blood feeding rates varied between the *Ae. aegypti* genetic forms. Phylogenetic analysis was performed on sequences of 37 blood-fed *Ae. aegypti* (successful of the 47 processed) from both study areas (KV=1, Rabai=36). Two mitochondrial lineages were recovered in the maximum likelihood phylogenetic tree. Most of the specimens (n=30) clustered in lineage I containing the domestic form (*Ae. aegypti aegypti* — GenBank Accession no: AF390098 and MF194022) (Figure 2B). Lineage II grouped with the feral form (*Ae. aegypti formosus*—GenBank Accession no. AY056597) and had few samples (n=7). Estimated HBI for lineage I was 0.53 (16/30) and 0.43 (3/7) for lineage II and the rates did not differ significantly (p=0.94). The one engorged specimen from KV represented in lineage I, had fed on rodent.

Mosquito survival is inversely related to trap densities

A summary of the parity rates, mean *Ae. aegypti* densities and prevailing weather conditions (mean temperature, relative humidity and rainfall) for each of the trapping periods are presented in Table 2. Mean daily *Ae. aegypti* catches/trap were 2.9, 18.7 and 8.8 in KV (November 2019), Rabai in August-September 2019 and February 2020, respectively, and correlate inversely with respective parity rates

during these periods. When data were stratified by trapping periods in coastal Rabai, we found increased mosquito survival with an increase in mean temperature (25.4°C to 27.4°C) and relative humidity (75.9 to 80.3) from August-September 2019 to February 2020 (Table 2). Notably, both *Ae. aegypti* HBI and survival were higher in February 2020 than in August-September 2019 in coastal Rabai. Also, HBI values increased as rainfall decreased between the two trapping periods in Rabai with a similar inverse relationship observed between survival and rainfall.

Discussion

Like other mosquito-borne pathogens, the transmission efficiency of DENV is dependent on critical components of vectorial capacity such as mosquito density, survival and human feeding preference. Here, we document how these factors could interact with each other to influence dengue dynamics influenced by weather factors. We found variation in vector parameters as a function of trapping period, a pattern that appears to mirror the observed seasonal variation in transmission risk in the Kenyan coast (40, 41).

Mosquito abundance increases the likelihood of vector-human contact and is an important parameter in climate-based models to predict dengue dynamics (42). While vector presence is a prerequisite for DENV transmission, increasingly, vector density could be a poor predictor of DENV infection risk in humans. For instance, an area with the lowest *Ae. aegypti* density in Vietnam displayed the highest

TABLE 2 Summary of *Ae. aegypti* bionomic estimates in relation to weather variables during the trapping periods.

Site	Period	Survival	HBI	Density (n)	Rainfall (mm)	RH	Temperature (°C)
Rabai	August-September 2019	67.7	0.29	18.7 (n=67)	0.6	75.9	25.4
	February 2020	77.8	0.69	8.8 (n=68)	0.3	80.3	27.4
Kerio Valley	November 2019	78.8	0	2.9 (n=70)	3.8	72.4	19.9

n=number of trap replicates; HBI, human blood index; RH, relative humidity; Density, *Ae. aegypti* catches/trap.

incidence of dengue while the converse effect was true in another province (43). A similar inverse relationship between *Ae. aegypti* abundance and dengue endemicity was observed in Mexico (44). Also, higher abundance of *Ae. aegypti* in the Kenyan city of Kisumu than Mombasa, could not explain the lack of outbreaks in the former, yet recurrent in the latter (14). In our study, high vector survival rate was associated with reduced trap catches, a proxy for mosquito abundance. The strong association between mosquito age and dengue endemicity (44) or onset and offset of DENV transmission season (24), could indicate that vector demographic structure is a better predictor of dengue risk than density.

The estimated survival rates for *Ae. aegypti* from this study are consistent with the range of data for this species reported in the literature (parous rates: 27-92%) (24, 35, 45). Parity assumes age-independent survival (46), although Hugo et al. (24), found no difference employing age dependent and independent models in the estimation of mosquito age. The samples analyzed in our study were representative of captures over several days within a spatial scale for each trapping period potentially increasing the reliability of the estimates as previously suggested (46). Of note, parity estimates could be affected by the mosquito population recruitment whether growing, stable, or declining (47) which we did not assess at the different study sites.

The blood meal profiles for *Ae. aegypti* included humans but also a diverse range of animals. We observed a moderate HBI (0.51) in Rabai, a value which is comparable or even higher than the previously reported estimate (of 0.4) in coastal Kenya (13). In this study, *Ae. aegypti* is observed to exhibit zoophilic characteristics, an observation that contradicts the primarily anthropophilic behavior (HBI > 0.87-1) of this species in other dengue endemic areas out of Africa (21, 48, 49). The difference in *Ae. aegypti* HBI could be related to the origin of the samples (indoor vs outdoor) and habitat (urban vs rural/sylvatic). Lower blood fed specimens were encountered in KV (n=3), none of which had fed on humans. Thus, the difference in *Ae. aegypti* blood feeding between Rabai and KV could relate to the degree of urbanization i.e., human population density, which is an important risk parameter of dengue risk (2, 14). The observation of a more anthropophilic population in Rabai compared to KV may also point to fundamental differences in the behavior of *Ae. aegypti* populations in areas/regions of differing dengue endemicity in Kenya which, requires further elucidation. While the blood meal data provides insights into the trophic habit of this species, this inference could be affected by the relatively low number of engorged specimens analyzed (n=53). Our trapping methodology mainly targeted host-seeking females generally biased against blood-feeding cohorts whose catches can be improved by incorporating resting collections (50).

Genetic differences underlie the preference for human over other vertebrate hosts between Aaa and Aaf (51). We asked whether this can be verified through correlational studies of the genetics and host meal sources of individually analysed wild blood-fed specimens. Our data show that the mtCOI lineage that grouped with the domestic form Aaa was more associated with a higher human feeding rate (0.53 (16/30)) compared to the lineage having the feral form (0.43 (3/7)) (Figure 2B). We suspect that the lack of a significant difference in the human feeding rates between the lineages may have been masked by tropic shifts between the trapping periods observed at the coast. Our findings point to sympatric occurrence of *Ae. aegypti* ecotypes, however, with possible higher

abundance of the domestic than feral form in coastal Kenya as previously suggested (13, 52). The potential consequence of seasonality in their occurrence, biting patterns and effect on transmission risk merit additional studies. Feeding on diverse hosts including humans by both lineages representing the forms increases the risk of transmission to humans of diverse vector-borne pathogens (e.g., dengue, chikungunya, and Zika viruses) that are known to have animal reservoirs (53). The contribution of multiple human feeding, a common trait in *Ae. aegypti* (19, 54) could not be determined based on the single marker used in our present study. PCR followed by amplicon sequencing analysis underestimates the resolution of multiple host meals from individually engorged mosquitoes compared to next-generation sequencing approaches (55, 56).

Coastal Kenya has been particularly prone to multiple dengue outbreaks in the last decade (3, 57) with annual upsurges experienced after the short and long rains typically between February and June (40, 41). While rainfall may increase mosquito abundance and perhaps biting rates, the reasons for this outbreak occurrence patterns are not fully understood. Focusing on our coastal data, we analyzed trends in vector indices and weather-related variables during the two sampling periods of August-September 2019 and February 2020. The data showed that higher vector survival coincided with higher human feeding rates (i.e., HBI) in February 2020. Both values were consistently lower in August-September 2019 (Parity=77% vs 67% and HBI=69% vs 29% for February 2020 and September 2019, respectively). High human feeding rates have been shown to correlate with heightened period of dengue risk (33,54). February 2020 are generally dry/cool periods which have been found to correlate positively with enhanced vector survival rates and dengue transmission as observed in Vietnam (24). Higher vector survival was associated with both increases in mean temperature and relative humidity, during this period compared to August-September 2019, suggesting them as influential factors affecting mosquito age (or longevity) consistent with previous findings (58). It is noteworthy that temperature increases including a 1°C rise can accelerate a reduction in the extrinsic incubation period (EIP) and thereby, increase pathogen transmission potential (59). Our results suggest that intense DENV transmission and perhaps onset of outbreaks at specific times of the year may be punctuated by enhanced *Ae. aegypti* vectorial capacity linked to increased vector survival and human feeding in concert with suitable weather conditions. A convergence of these biotic and abiotic attributes could be critical in reinitiating the seasonal pattern of dengue virus transmission in coastal Kenya. The low temperature conditions, low human biting may have dampened the estimated dengue risk in KV despite evidence of high survival rates. It is also noteworthy that we assumed a uniform gonotrophic cycle (3 days) in our estimates of daily survival and longevity and this value has been observed to vary as a function of temperature and seasons (35, 60). Thus, further studies should consider this likely discrepancy which could influence interpretation of the findings.

Conclusion

We conclude that, *Ae. aegypti* exhibits local variation in important components of vectorial capacity (VC)- abundance, survival, and human blood feeding. In coastal Rabai, vector density was inversely related to mosquito age which together with human feeding are the most sensitive

VC parameters (20, 26). Convergence of high survival and propensity to feed on humans as noted in coastal Rabai, could drive intense DENV transmission or onset of outbreaks at certain times of the year; however, in concert with suitable weather conditions. Genetic factors likely underpin the degree of anthropophagy in *Ae. aegypti* but may be influenced by potential seasonal shift in human feeding rates. Despite high representation of humans in the trophic habit, *Ae. aegypti* exhibited opportunistic feeding, a trend which increases human exposure to risk of zoonotic pathogens. Modeling transmission is increasingly seen as an important component of disease risk prediction. For dengue, quantifying transmission risk needs to integrate vector bionomic factors beyond abundance together with climatic parameters in simulation studies for reliability of any developed models (15, 61).

Data availability statement

The original contributions presented in the study are included in the article/supplementary material. Further inquiries can be directed to the corresponding author.

Ethics statement

The study received approval from the Scientific Ethics Review Unit (SERU) of the Kenya 116 Medical Research Institute (Protocol NO. SSC 2787). Additionally, consent was sought from household heads to set up traps around their homesteads.

Author contributions

Conceptualization, RS and DT. Investigation and Methodology, WK, RS, GR, DT. Data analyses, WK, DT. Validation, RS, DT. Supervision, RS, NM, DT. Funding acquisition, RS, BT, DT. Writing—original draft, DT. Writing—review and editing, WK, RS, GR, SA, NM, BT, DT. All authors contributed to the article and approved the submitted version.

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Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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