



Shifting Anopheline Vector Dynamics in Djibouti: The Reappearance of Native Malaria Vectors After a Decade of Anopheles stephensi Dominance

Alia Zayed^a, John So^b, Westen Archibald^b, Rebecca Pavlicek^c

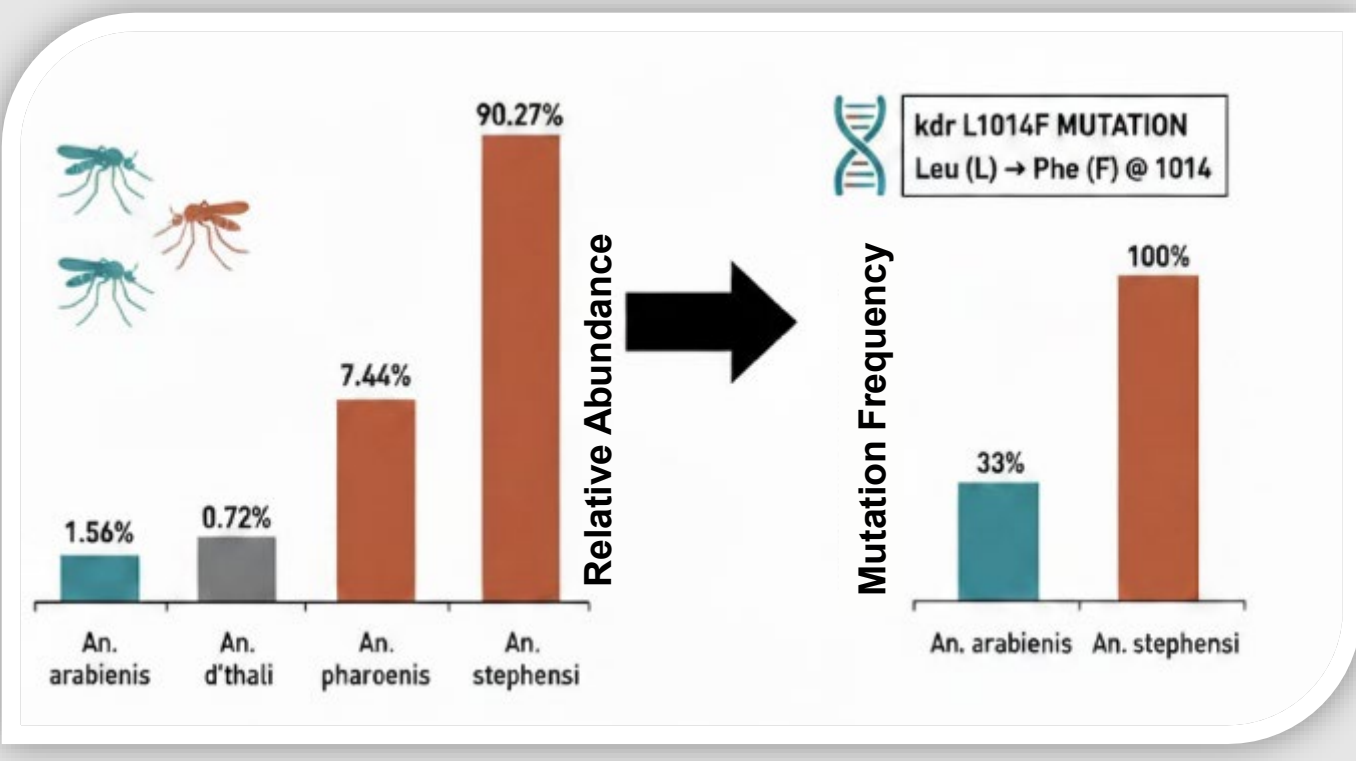
^a Goldbelt Apex, Contracted support to U.S. Naval Medical Research Unit NAMRU EURAFCENT, Cairo, Egypt

^b Expeditionary Medical Facility, Camp Lemonnier Djibouti

^c U.S. Naval Medical Research Unit NAMRU EURAFCENT, Cairo, Egypt



GRAPHICAL ABSTRACT



The Return of Native Malaria Vectors Coincides with *An. stephensi* Invasion



METHODOLOGY

- Mosquito collection:** Weekly surveillance (2024–2026) at Camp Lemonnier. 27 sites (2 km²) near dwellings, offices, and recreation areas.
- Trapping:** CDC Light Traps (dry-ice CO₂) & Mosquito Magnet® (propane CO₂).
- Identification and processing:** Mosquitoes were sorted out and identified to species level. *Anopheles* specimens were separated into head, thorax, and abdomen.
- kdr* mutation in L1014:** Abdomens were extracted individually and tested for *kdr* mutation using conventional PCR. Frequency of resistant allele (*f*(*R*)) was calculated as: 2x (No. *RR* individuals)+ (No.*RS* individuals)/2x (Number of tested individuals).
- Spatial distribution and hot-spot analysis:** Datasets were geo-referenced and projected on maps using ArcGIS10.

RESULTS

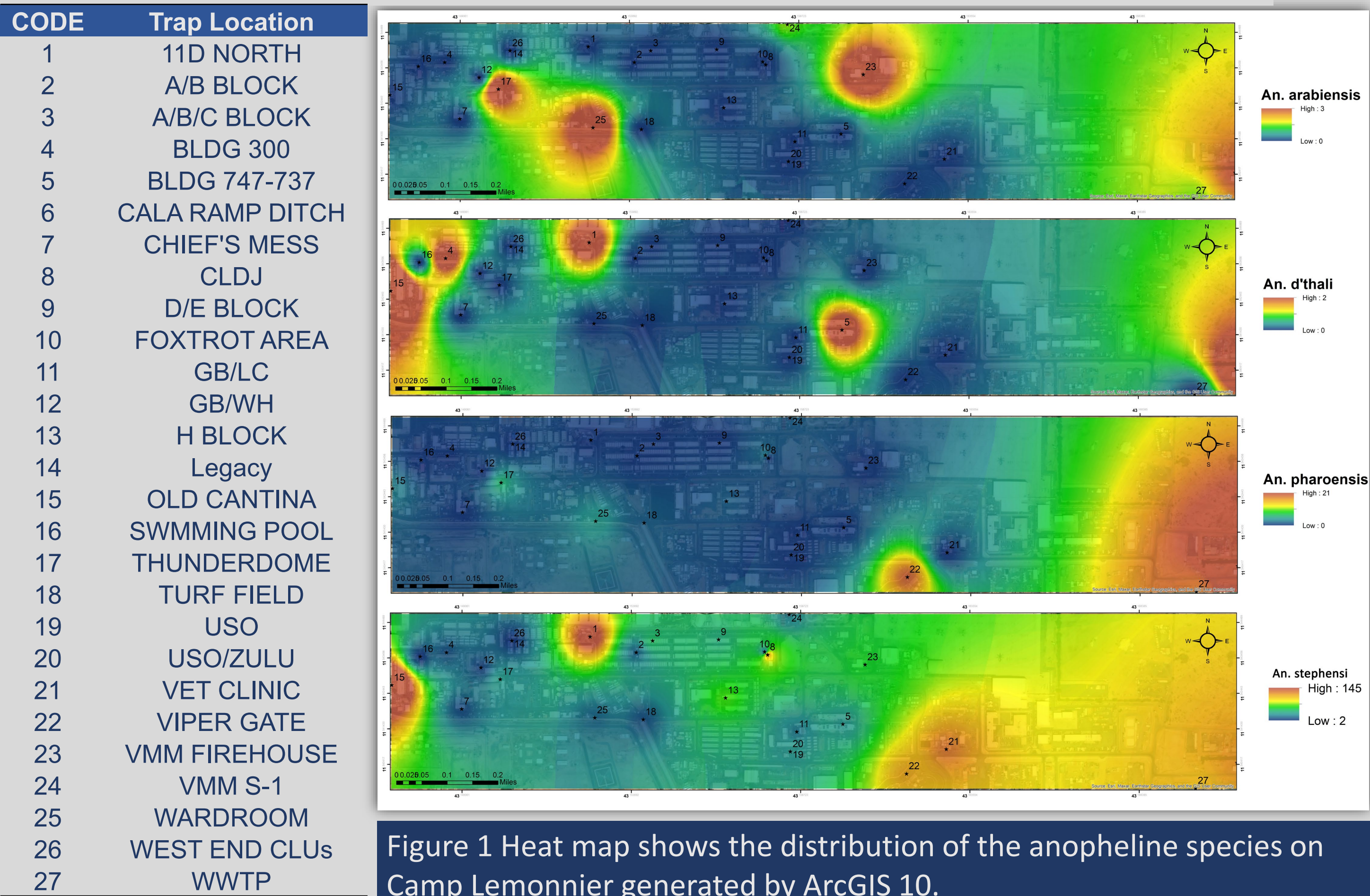


Figure 1 Heat map shows the distribution of the anopheline species on Camp Lemonnier generated by ArcGIS 10.

Ecological Categories of Sites	<i>An. arabiensis</i>	<i>An. d'thali</i>	<i>An. pharoensis</i>	<i>An. stephensi</i>
	Averages			
Outdoor Gathering Hubs	3	1.5	2.5	50
Perimeter	2.33		5	30.5
Residential		1	1.5	15.45
Water & Drainage	1.5	1	17	29.33

Table 1 Distribution of the anopheline species based on the ecological variation among sites on Camp Lemonnier

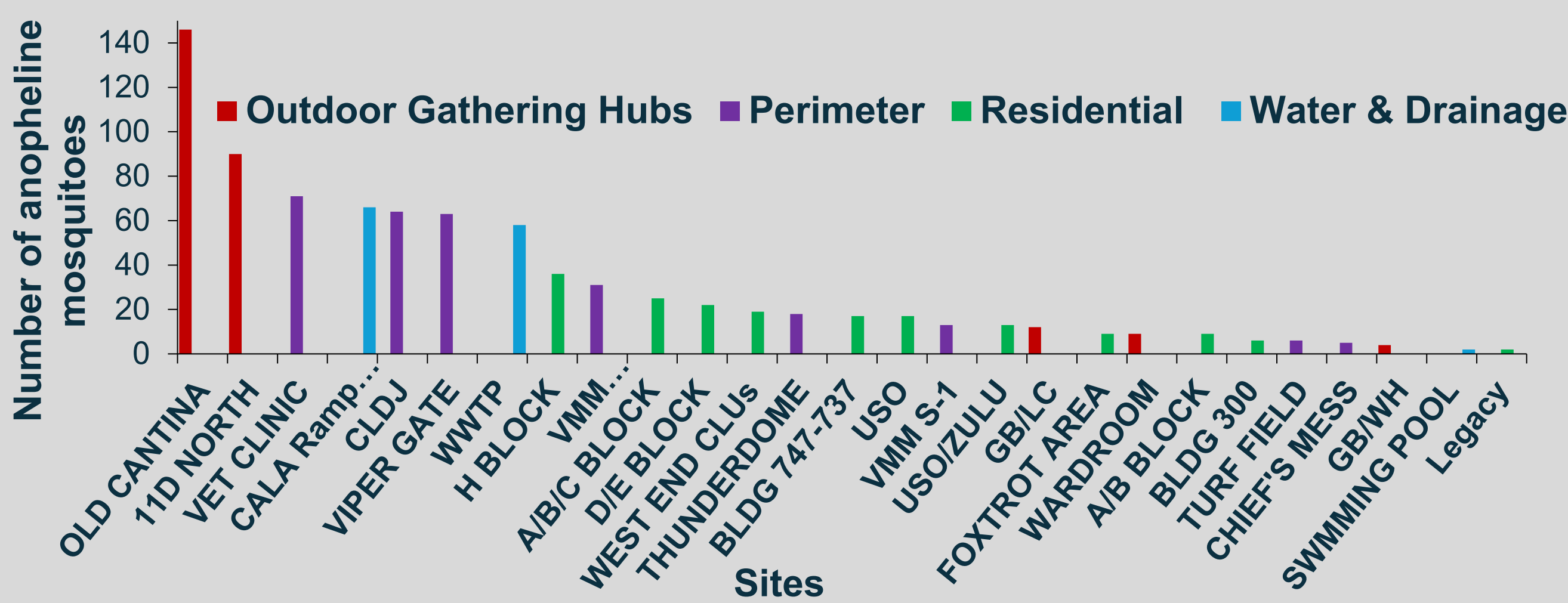


Figure 2 Spatial dynamics of the anopheline species based on environmental characteristics of the sites.

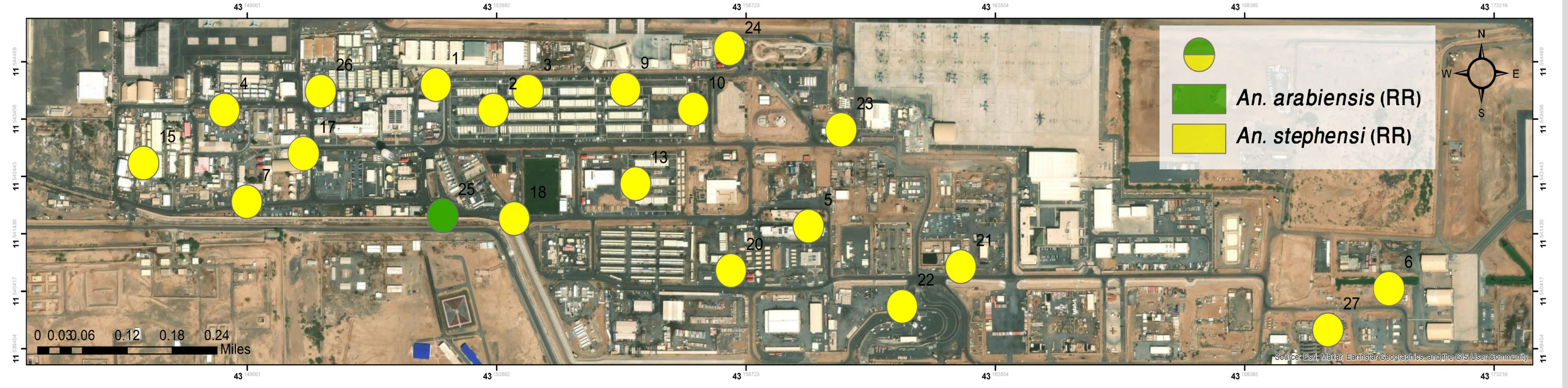


Figure 3 Spatial distribution of homozygous resistance mutation of *Anopheles arabiensis* and *An. stephensi* members.

Site Code	Sites	<i>An. arabiensis kdr L1014F</i>			<i>An. stephensi kdr L1014F</i>		
		No. tested	RR	<i>f</i> (<i>R</i>)	No. tested	RR	<i>f</i> (<i>R</i>)
1	11D NORTH				17	17	1
2	A/B BLOCK				4	4	1
3	A/B/C BLOCK				2	2	1
4	BLDG 300				3	3	1
5	BLDG 747-737				6	6	1
6	CALA RAMP DITCH	1			1	1	1
7	CHIEF'S MESS				2	2	1
9	D/E BLOCK				6	6	1
10	FOXTROT AREA				3	3	1
13	H BLOCK				11	11	1
15	OLD CANTINA				4	4	1
17	THUNDERDOME	1			2	2	1
18	TURF FIELD				2	2	1
20	USO/ZULU				6	6	1
21	VET CLINIC				19	19	1
22	VIPER GATE				11	11	1
23	VMM FIREHOUSE	1			9	9	1
24	VMM S-1	1			5	5	1
25	WARDROOM	3	1	0.33			
26	WEST END CLUs				4	4	1
27	WWTP				11	11	1
Total		7	1		173	173	

RR Homozygote resistant. *f*(*R*): Resistant allele frequency. No RS heterozygote resistant mutants were detected.

Table 2 Frequency of the *kdr* L1014F mutation in members of the *Anopheles arabiensis* and *An. stephensi* caught on Camp Lemonnier, Djibouti

Discussion

General Points:

- The invasive vector, *An. stephensi* was the predominant species and demonstrated 100% frequency (*f*(*R*) = 1.0) of the *kdr* resistance allele across all 18 collection sites.
- The *An. pharoensis* was collected around water treatment plant and perimeters.
- The native *An. arabiensis* was less prevalent around water areas, perimeters and outdoor gathering places. Its *kdr* resistance was detected in 14% of the tested individuals vs. 86% wild type susceptible.
- An. pharoensis kdr*-mutation tests were not successful and further protocols are on-going to characterize the resistance status.
- Although the *kdr* mutation is not yet fixed and densities remain low, the resurgence of *An. arabiensis* presents a critical concern for malaria within a confined military footprint.

Ecological Shift

- For nearly a decade, the invasive urban vector *An. stephensi* has dominated the landscape at CLDJ, effectively displacing native mosquito populations. However, the simultaneous presence of a dominant urban vector alongside returning native species creates a highly complex, multi-threat environment for deployed forces.

Ecological Drivers of Vector Abundance

- High-Traffic Feeding Hubs:** Outdoor gathering and dining areas (e.g., Old Cantina, 11D North) experienced the highest absolute vector abundance. The invasive *An. stephensi* heavily exploits these zones of concentrated human activity for blood-feeding.
- Refuges for Native Vectors:** Open-water infrastructure, particularly drainage ditches (CALA Ramp Ditch) and wastewater sites, served as critical habitats supporting the re-emerging native *An. pharoensis* populations.
- Residential Exposure:** Containerized Living Units (CLUs) and tent areas maintained persistent populations of highly resistant *An. stephensi*, indicating a sustained localized transmission risk directly at personnel sleeping quarters.

KEY FINDINGS

- The epidemiological landscape at CLDJ is complex, defined by the **co-occurrence** of a dominant, **invasive urban** vector and **two re-emerging native** vectors.
- Outdoor gathering areas** are critical hotspots.
- The re-appearance of native vectors after a near-decade absence, alongside the highly prevalent *An. stephensi*, significantly heightens the potential risk of local **malaria transmission**.
- A critical threat: **Pervasive Resistance** in Invasive Species. *An. stephensi* is widespread and shows establishment of the **pyrethroid-resistance *kdr* gene**. Insecticide resistance is a major concern and is almost entirely concentrated within the *An. stephensi* population, complicating control efforts.

Recommendations & Future Directions

- Enhance surveillance.
- Re-evaluate control strategies.
- Implement targeted Interventions in areas with high resistance prevalence, focusing on managing the dominant, highly resistant *An. stephensi* population.

PARTNERS/COLLABORATORS



EXPEDITIONARY MEDICAL FACILITY, CAMP LEMONNIER DJIBOUTI

Acknowledgements

The authors are acknowledging the role of Drs. Reham Tageldin, Nermeen Fahmy and Karim Omar for the confirmatory identification/processing, molecular testing and generating the ArcGIS maps, respectively.