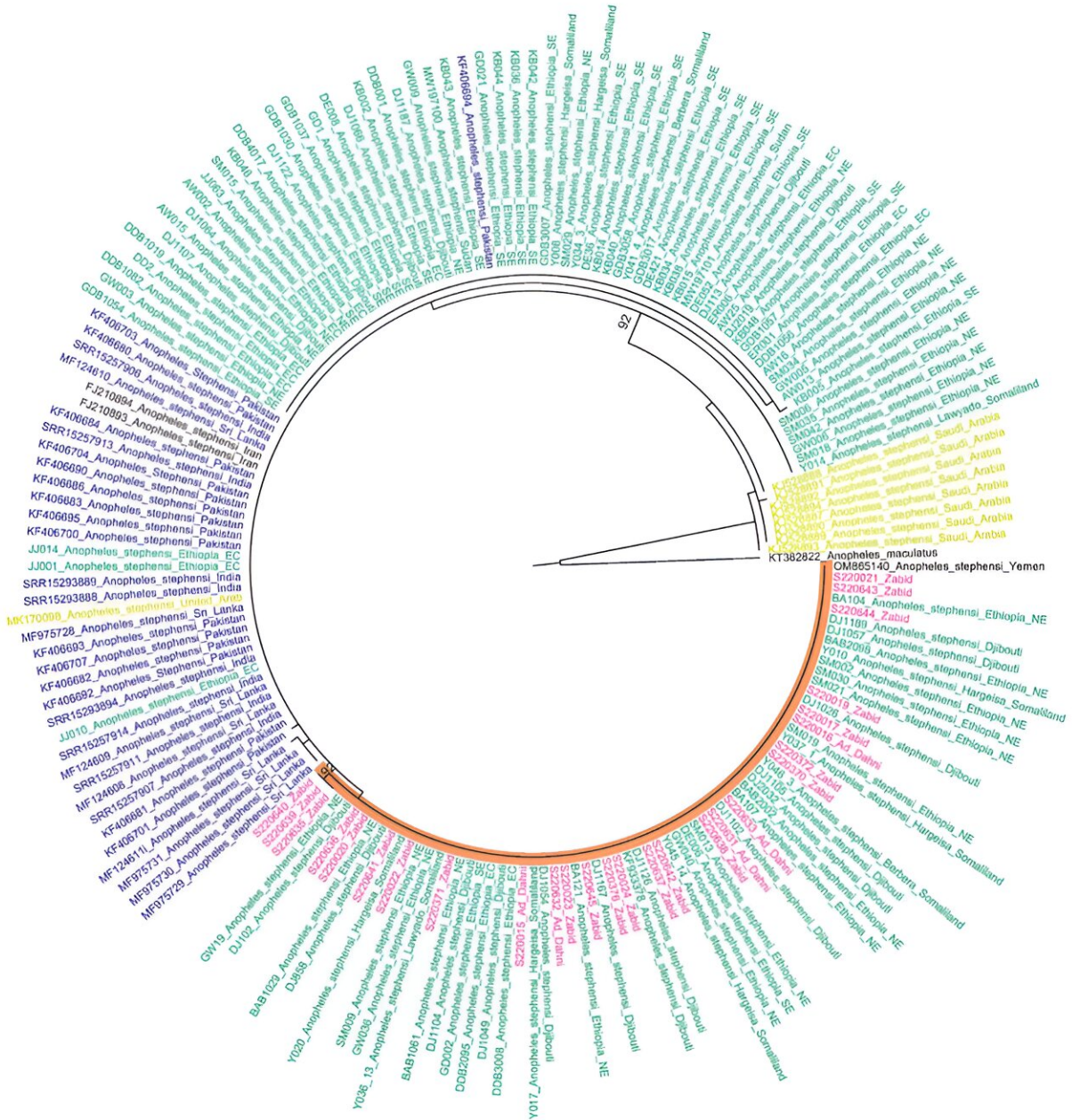


Research reveals spread of malaria-carrying *Anopheles stephensi* mosquitoes in Yemen

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Maximum-likelihood phylogenetic analysis of cytochrome c oxidase subunit 1 gene sequences for *Anopheles stephensi* mosquitoes collected in Yemen. Pink indicates sequences from Yemen, blue indicates sequences from South Asia, green indicates sequences from the Horn of Africa, and yellow-green indicates sequences from the Arabian Peninsula. Orange shading indicates branch containing Yemen and Horn of Africa specimens only. Numbers along branches

indicate bootstrap values. Only values >70 are shown. Scale bar indicates the number of nucleotide substitutions per site. Credit: *Emerging Infectious Diseases* (2024). DOI: 10.3201/eid3007.240331

Malaria remains a significant global health issue, with around 249 million cases reported in 2022 by the World Health Organization. The malaria-carrying mosquito, *Anopheles stephensi*, has recently spread to Africa and has now been detected in Yemen, according to new Baylor University research.

Baylor mosquito researcher Tamar Carter, Ph.D., assistant professor of biology and a tropical disease biologist, and the Ministry of Health in Yemen's capital of Sana'a have [published](#) a study in the journal *Emerging Infectious Diseases*, in which they detail the spread of the invasive mosquito in Yemen and their connection to East Africa.

The research highlights the ongoing threat of [malaria](#) in regions previously unaffected by the *Anopheles stephensi* mosquito species.

"Concerns are growing about the status and spread of the *Anopheles stephensi* mosquito species in the Mediterranean region," Carter said. "We are seeing growing evidence of this mosquito's resistance to multiple classes of insecticides, its association with a recent malaria outbreak and genomic evidence that outbreak sites may also be central locations for this invasive mosquito to travel to new areas."

Carter along with Dr. Methaq Assada, lead investigator and manager of the Yemen National Malaria Control Program, analyzed immature mosquitoes collected from two semiurban locations in Yemen: in the Ad Dahi district in December 2021 while conducting *Aedes aegypti* mosquito surveillance during a dengue fever outbreak, and in the Zabid

district during monthlong Anopheles surveillance in March 2022. The specimens morphologically identified as Anopheles stephensi mosquitoes were preserved and sent to Carter's lab at Baylor University for molecular analysis.

Key findings

The study, Carter said, provides critical insights into the genetic diversity of Anopheles stephensi mosquitoes in Yemen.

The researchers' key findings include:

- **Detection and confirmation:** Anopheles stephensi mosquitoes were first detected in Aden, Yemen, in 2021 and confirmed by molecular analysis in 2023. Subsequent surveillance revealed their presence in the Ad Dahi and Zabid districts of Al Hudaydah.
- **Genetic insights:** Through DNA sequencing, two haplotypes of the mosquito's cytochrome c oxidase subunit I (COI) gene were identified. One haplotype matches those found in East Africa, while the other is newly discovered, providing crucial insights into the [genetic diversity](#) and spread of these mosquitoes.
- **Implications for malaria control:** The findings emphasize the urgent need for continued vector surveillance and control measures to mitigate the spread of malaria in Yemen and potentially other regions of the Arabian Peninsula.

Recommendations and future directions

Carter had previously [discovered](#) critical insights into the spread of the

invasive *Anopheles stephensi* mosquito in the Horn of Africa, posing a significant public health threat in those new regions.

With her latest new research detecting the mosquito in Yemen, Carter advocates for extensive genomic analysis and increased surveillance efforts across Yemen and neighboring regions to better understand and control the spread of *Anopheles stephensi*. These steps, she said, are vital to addressing the public health impact of malaria, particularly in high-prevalence areas.

More information: Methaq Assada et al, Molecular Confirmation of *Anopheles stephensi* Mosquitoes in the Al Hudaydah Governorate, Yemen, 2021 and 2022, *Emerging Infectious Diseases* (2024). [DOI: 10.3201/eid3007.240331](https://doi.org/10.3201/eid3007.240331)

Provided by Baylor University

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