

The confirmed vector competence of *Ae. albopictus* mosquitoes for YFV under experimental conditions (10), combined with our findings, highlights its potential epidemiologic role at the sylvatic-urban interface. Our findings also underscore the importance of enhancing entomological surveillance in urban green areas to detect shifts in transmission dynamics early and prevent the re-urbanization of yellow fever in Brazil.

Acknowledgments

We thank the field teams at the Pasteur Institute involved in the mosquito collections.

This study was funded, in part, by the State Research Institutes Modernization Program, supported by São Paulo Research Foundation (grant no. 2017/50345-5). K.K. is a Conselho Nacional de Desenvolvimento Científico e Tecnológico research fellow (grant no. 309396/2021-2). C.M.R. received a grant from São Paulo Research Foundation (São Paulo Research Foundation Iniciativa Amazonia +10; grant no. 2022/10408-6).

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Molecular Evidence of Dengue Virus Serotype 2 in Travelers Returning to Israel from the Sinai Peninsula

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DOI: <https://doi.org/10.3201/eid3111.250991>

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We report 4 dengue cases in travelers returning to Israel from Sharm-El-Sheikh, Egypt, all confirmed as dengue virus type 2 infections. Phylogenetic analysis showed clustering with strains from Pakistan. Our findings provide molecular evidence of dengue circulation in the Sinai desert, highlighting the need for increased awareness among travelers and health authorities.

Dengue virus (DENV) is the most widespread arbovirus globally; its incidence has increased tenfold in the past 2 decades, largely driven by climate change and globalization (1). Although transmission is well documented in Southeast Asia and the Americas, autochthonous emergence is increasingly reported in nonendemic regions, including Europe.

We report 4 confirmed dengue fever cases in travelers returning to Israel after visiting Sharm El-Sheikh, a desert resort city in South Sinai, Egypt, during April–June 2024. Sharm El-Sheikh has not previously been recognized as an area of dengue transmission, the arid environment of the Sinai Peninsula is considered unfavorable for the DENV primary vectors, *Aedes* mosquitoes.

The cases (Table) were unrelated; travel dates were nonoverlapping and accommodations varied and were located 3–25 km apart. Patients had typical dengue symptoms such as fever, headache, myalgia, and rash. All were hospitalized, received supportive care, and recovered. One patient exhibited meningeal irritation; cerebrospinal fluid testing results were unremarkable, although DENV serotype 2 (DENV-2) RNA was detected by quantitative real-time PCR (cycle threshold 32.5). All samples were collected within 1 week of symptom onset. Serum testing confirmed DENV-2 by multiplex quantitative real-time PCR (2); additional nonstructural protein 1 antigen and IgM/IgG positivity was detected in some cases.

To explore the geographic origin of the DENV-2 cases, we performed DENV whole-genome sequencing. We captured DENV-2 using specific whole-genome primers (<https://grubaughlab.com/open-science/amplicon-sequencing>); we prepared sequencing libraries using Nextera-XT and ran them on

the Illumina NovaSeq (<https://www.illumina.com>). We generated consensus sequences by mapping to the DENV-2 reference genome (GenBank accession no. NC_001474.2) and deposited resulting sequences into GenBank (Appendix Table, <https://wwwnc.cdc.gov/EID/article/31/11/25-0991-App1.xlsx>). Use of the samples in this study was approved by the Sheba Medical Center Institutional Review Board (approval no. SMC-6190-19).

Samples yielded sufficient DENV-2 genome coverage, except in the case of patient no. 4 (possibly because of high cycle threshold [34]), which was excluded. Phylogenetic analysis with global DENV-2 sequences (n = 1,492) clustered the Israel sequences within the Cosmopolitan genotype. All 3 sequences formed a distinct cluster, sharing a common ancestor and differing by 32 mutations from the nearest global strain. The closest related sequences were from Pakistan. The only publicly available sequence geographically close to Sinai, from the United Arab Emirates in 2023, clustered separately within another Cosmopolitan lineage with strains from China, India, and Bangladesh (Figure, panel A).

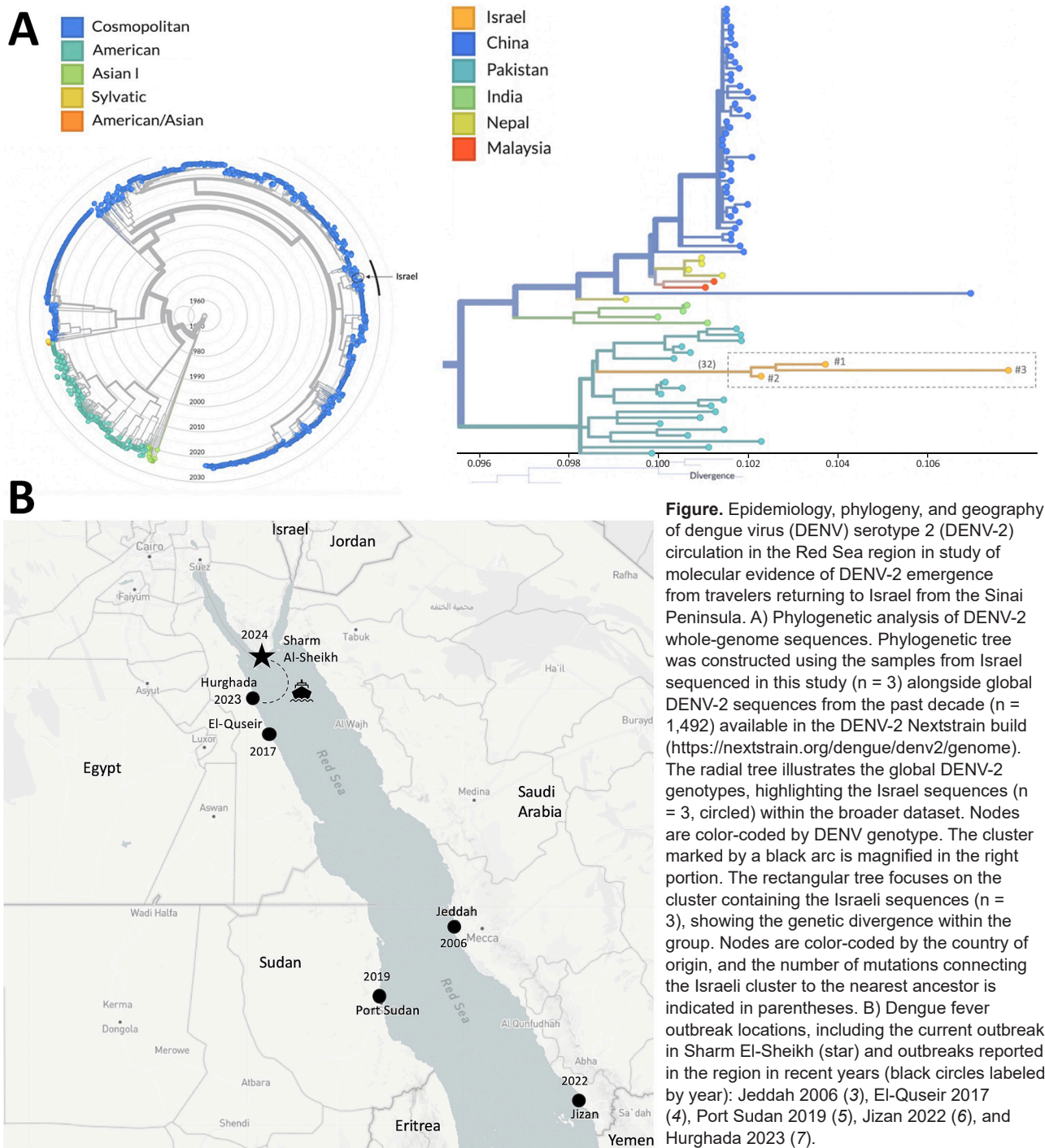
Our findings describe 4 confirmed DENV-2 infections in travelers from Sharm El-Sheikh, Egypt, a city in the arid Sinai Peninsula, previously considered unsuitable for *Aedes* mosquitoes and without previous dengue reports. Genomic analysis showed clustering of cases, likely from a single outbreak, most closely related to strains from Pakistan. Aside from 1 United Arab Emirates 2023 sequence clustering separately, no recent data from Sinai are available, underscoring a major surveillance gap. Those results align with reports of DENV-2 spread along the Red Sea and recent cases in Florence, Italy (8).

During the past 2 decades, *Ae. aegypti* mosquito populations have expanded in Egypt, especially along the Red Sea coast (Figure, panel B), correlating with dengue outbreaks. However, no entomologic data exist for Sinai. The arid climate challenges mosquito survival, but clustering of cases in 1 resort area suggests local adaptation, possibly supported by urban microhabitats (9). Maritime and air travel might drive

Table. Epidemiology and test results of patients in study of molecular evidence of DENV-2 emergence from travelers returning to Israel from the Sinai Peninsula*

Characteristic	Patient 1	Patient 2	Patient 3	Patient 4
Patient age, y/sex	33/M	40/F	45/M	19/M
DENV laboratory diagnostic analysis				
Sample collection date	2024 Apr 22	2024 May 7	2024 Jun 5	2024 Jun 10
Serum quantitative real-time PCR	DENV-2 (Ct 28)	DENV-2 (Ct 26.5)	DENV-2 (Ct 27)	DENV-2 (Ct 34)
Serum EIA IgM	Negative	Negative	Positive	Positive
Serum EIA IgG	Negative	Negative	Positive	Negative
DENV nonstructural protein 1 antigen	Positive	Positive	Negative	Positive

*Ct, cycle threshold; DENV, dengue virus; DENV-2, DENV serotype 2; EIA, enzyme immunoassay.



repeated introductions of *Ae. aegypti* mosquitos and DENV into the Red Sea region. However, the pattern of DENV-2 outbreaks in Red Sea port cities support maritime transport as a key driver of spread (6,7,10). The daily ferries from Hurghada, where dengue recently emerged, to Sharm El-Sheikh might be especially relevant (Figure, panel B). Genetic data from a 2019 Jizan outbreak and strains from Saudi Arabia (1992–

2014) further suggest multiple introductions linked to an imported DENV-2 variant genetically similar to strains from Malaysia, Singapore, Korea, and China (6). Additional analyses from the DENV-2 strains isolated in Saudi Arabia during 1992–2014 reveal strong clustering with viruses from countries that contribute the largest numbers of Hajj and Umrah pilgrims: Indonesia, Pakistan, and India (10). Indeed, phylogenetic

analysis shows that our dengue sequences are closest to recent strains from Pakistan. However, the scarcity of sequences from Egypt and neighboring regions limits inference on viral origin, circulation, and distribution, and observed variability suggests undersampling and additional undetected cases.

This report of 4 cases over 3 months in different localities of Sharm El-Sheikh suggests sustained DENV-2 transmission and emphasizes the importance of enhanced vector surveillance and control, providing an alert to public health authorities. The genetic data presented might help address gaps in regional DENV sequence reporting and contribute to understanding its molecular epidemiology and origins.

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Dr. Zuckerman leads the Bioinformatics and Genomics Center at Israel's Central Virology Laboratory, Ministry of Health, and is affiliated with Tel Aviv University's School of Public Health. Her work focuses on genomic surveillance, molecular epidemiology, and bioinformatics applications in the study of viral pathogens

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