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Genomic Surveillance for SARS-CoV-2 Variants: Circulation of Omicron XBB and JN.1 Lineages — United States, May 2023–September 2024

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Abstract

CDC continues to track the evolution of SARS-CoV-2, including the Omicron variant and its descendants, using national genomic surveillance. This report summarizes U.S. trends in variant proportion estimates during May 2023–September 2024, a period when SARS-CoV-2 lineages primarily comprised descendants of Omicron variants XBB and JN.1. During summer and fall 2023, multiple descendants of XBB with immune escape substitutions emerged and reached >10% prevalence, including EG.5-like lineages by June 24, FL.1.5.1-like lineages by August 5, HV.1 lineage by September 30, and HK.3-like lineages by November 11. In winter 2023, the JN.1 variant emerged in the United States and rapidly attained predominance nationwide, representing a substantial genetic shift (>30 spike protein amino acid differences) from XBB lineages. Descendants of JN.1 subsequently circulated and reached >10% prevalence, including KQ.1-like and KP.2-like lineages by April 13, KP.3 and LB.1-like lineages by May 25, and KP.3.1.1 by July 20. Surges in COVID-19 cases occurred in winter 2024 during the shift to JN.1 predominance, as well as in summer 2023 and 2024 during circulation of multiple XBB and JN.1 descendants, respectively. The ongoing evolution of the Omicron variant highlights the importance of continued genomic surveillance to guide medical countermeasure development, including the selection of antigens for updated COVID-19 vaccines.

Introduction

Approximately 5 years since SARS-CoV-2 emerged, resulting in the global COVID-19 pandemic, Omicron lineages with increased transmissibility and immune escape continue to evolve. CDC has monitored SARS-CoV-2 evolution using national genomic surveillance since December 2020, and variant proportion estimates are updated every 2 weeks on CDC's COVID Data Tracker.[†] Data from national surveillance helped guide the selection of XBB.1.5 and JN.1 lineages as the target antigens for 2023–2024 and 2024–2025 COVID-19 vaccines,[§] respectively, and also supported assessments of potential changes in vaccine and antiviral effectiveness and COVID-19 clinical severity (*1*,*2*). This report summarizes

[*] These authors contributed equally to this report.

[†] https://covid.cdc.gov/covid-data-tracker/#variant-proportions. Estimates from earlier weeks are available at https://data.cdc.gov/Laboratory-Surveillance/SARS-CoV-2-Variant-Proportions/jr58-6ysp.

[§] World Health Organization Technical Advisory Group on COVID-19 Vaccine Composition statement (https://www.who.int/news/item/26-04-2024-statement-on-the-antigen-composition-of-covid-19-vaccines); Food and Drug Administration statement (https://www.fda.gov/vaccines-blood-biologics/updated-covid-19-vaccines-use-united-states-beginning-fall-2024).

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the landscape of Omicron XBB and JN.1 lineage circulation and convergent evolution in the United States during May 14, 2023–September 14, 2024.

Methods

Data Sources and Sequence Processing

CDC's national genomic surveillance program has been previously described (*3*,*4*). CDC integrates SARS-CoV-2 sequence data from 1) the National SARS-CoV-2 Strain Surveillance (NS3) program,¶ 2) CDC-contracted commercial laboratories, and 3) public sequence data repositories.** Sequences are then quality-filtered, deduplicated, and assigned Pango lineages.†† The median interval from SARS-CoV-2 specimen collection to sequence deposition was 25 days during May 2023–September 2024 (IQR = 22–28 days).

¶ https://www.cdc.gov/coronavirus/2019-ncov/variants/cdc-role-surveillance.html; https://www.aphl.org/programs/infectious_disease/SARS-CoV-2/Pages/Sequence-Based-Surveillance-Submission.aspx

** Public sequence data repositories included the Global Initiative on Sharing All Influenza Data and National Center for Biotechnology Information GenBank databases. Sequences from public repositories are limited to those meeting baseline surveillance criteria, which ensures that they correctly record geographic, demographic, and clinical diversity. https://www.aphl.org/programs/infectious_disease/Documents/Technical%20Assistance%20for%20Categorizing%20Baseline%20Surveillance%20Update%2008112021_final.pdf

†† Quality filters included limiting sequences to human-derived sources and United States–specific sequences and excluding those with invalid state names and laboratory sources. Pango lineage definitions and methods are available online. https://github.com/cov-lineages/pango-designation; https://cov-lineages.org/

Estimation of Variant Proportions

Variant proportions for 2-week periods presented on CDC's COVID Data Tracker were estimated at national and U.S. Department of Health and Human Services (HHS)§§ regional levels by specimen collection date; Nowcast estimates for the most recent 4 weeks were not included.¶¶ Lineages were included if they constituted ≥1% (unweighted) of sequences nationally and contained spike protein substitutions of potential relevance for vaccines, therapeutics, transmissibility, or severity. Estimates included weighting to account for the complex survey design and potential sampling biases.*** The National Respiratory and Enteric Virus Surveillance System

§§ Because of limited precision, variant proportions from HHS regions with fewer than 300 sequences in a 2-week period are not reported on CDC's COVID Data Tracker. https://www.hhs.gov/about/agencies/iea/regional-offices/index.html

¶¶ For estimates on CDC's COVID Data Tracker within the most recent 4 weeks when numbers of available sequences are still accumulating, Nowcast estimates were conducted using multinomial regression fit on the previous 21 weeks of data for any lineages with ≥0.5% prevalence. In this analysis, data were limited to sequences collected beyond the most recent 4 weeks.

*** Variant proportion estimation methods account for the complex survey design of sampling, with weights based on the weekly estimated number of infections represented by each SARS-CoV-2 sequence; weights are trimmed to the 99th percentile. Each submitting laboratory source was considered a primary sampling unit, and the state and week of sequence specimen collection were considered strata. Code and model equations for variant proportion estimation methods are available online. https://github.com/CDCgov/SARS-CoV-2_Genomic_Surveillance

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(NREVSS)[†††] was the primary data source for survey weights beginning November 17, 2023.[§§§]

Characterization of Lineages

In this analysis, lineages with identical spike residue 31 and receptor binding domain substitutions (residues 332–527) were grouped and denoted as "representative lineage-like"; lineage groups are phylogenetically distinct but have similar spike protein sequences. Normalized frequencies of COVID-19 cases attributable to variants were estimated by multiplying counts of positive test results from NREVSS with variant proportions and scaling by the maximum case count. Sequenced cases were subsampled to assess counts of spike protein amino acid differences (including substitutions, insertions, and deletions).[¶¶¶] Data were current as of October 11, 2024. This activity was reviewed by CDC, deemed not research, and was conducted consistent with applicable federal law and CDC policy.[****]

Results

Sources of Analyzed SARS-CoV-2 Sequences

A total of 208,357 SARS-CoV-2 sequences from 56 U.S. jurisdictions[††††] were analyzed from NS3 (1%), commercial laboratories (34%), and public repositories (65%) during May 14, 2023–September 14, 2024. The percentage of sequences from repositories increased from 39% in 2022. The median weekly number of sequences decreased from 21,905 in 2022 to 4,752 in 2023 and 1,989 in 2024 (Supplementary Figure 1, https://stacks.cdc.gov/view/cdc/165772). Previous and updated analytic methods produced similar estimates for XBB.1.5 and HV.1 nationally and regionally (Supplementary Figure 2, https://stacks.cdc.gov/view/cdc/165773).

XBB Descendants

During May 14, 2023–September 14, 2024, all SARS-CoV-2 lineages circulating at ≥1% prevalence remained Omicron descendant lineages. The variant landscape during summer and fall 2023 was characterized by cocirculation of XBB descendants (Figure 1), many of which independently acquired identical substitutions in the spike protein receptor binding domain. Relative to XBB.1.5, EG.5-like lineages acquired the F456L substitution; FL.1.5.1-like lineages, HV.1 lineage, and HK.3-like lineages also contained the F456L substitution and also acquired K478R, L452R, and L455F substitutions, respectively (Table).

None of these XBB lineage groups attained predominance (>50% prevalence), but five groups reached a prevalence of ≥10%. Prevalence of XBB.1.16-like lineages exceeded 10% by the 2-week period ending May 27, 2023, followed by EG.5-like lineages by June 24, FL.1.5.1-like lineages by August 5, HV.1 by September 30, and HK.3-like lineages by November 11 (Figure 1). The prevalence of these lineage groups peaked at 21.2% for XBB.1.16-like lineages by July 8, 2023; 26.2% for EG.5-like lineages by September 16; 20.1% for FL.1.5.1-like lineages by September 30; 12.5% for HK.3-like lineages and 31.1% for HV.1 lineage by November 25. A relative increase in COVID-19 cases occurred in late summer and early fall 2023 as these lineages cocirculated (Figure 1).

JN.1 Predominance

BA.2.86 was reported in the United States in August 2023 through CDC's national genomic surveillance program and other complementary surveillance systems.[§§§§] BA.2.86 is a highly divergent descendant of BA.2 with >30 spike protein amino acid differences when compared with XBB.1.5, which is similar to the genetic distance from Delta (B.1.617.2) to Omicron BA.1.1 (Figure 2). BA.2.86 prevalence has remained <3% prevalence; JN.1, a descendant of BA.2.86 containing the L455S substitution, increased rapidly during late 2023 and was predominant nationally during January 6–April 27, 2024 (Figure 1). Increases in prevalence were similar across HHS regions, although predominance was attained slightly earlier on December 23, 2023, in Region 2 (New Jersey, New York, Puerto Rico, and the U.S. Virgin Islands). National predominance of JN.1 coincided with the highest frequency of positive SARS-CoV-2 test results reported to NREVSS during May 2023–September 2024, although other lineages were

[†††] NREVSS is a network of approximately 540 laboratories that passively report weekly aggregated numbers of tests performed and results that were positive, including for SARS-CoV-2. https://www.cdc.gov/nrevss/php/dashboard/index.html

[§§§] During May 11, 2023–November 17, 2023, a combination of data sources was used to estimate survey design weights. The percentage of positive SARS-CoV-2 nucleic acid amplification test results by HHS region was obtained from NREVSS, and the number of positive specimens by HHS region was obtained from COVID-19 electronic laboratory reporting (CELR). Percentages of positive test results from NREVSS and CELR correlated well. https://doi.org/10.15585/mmwr.mm7219e2

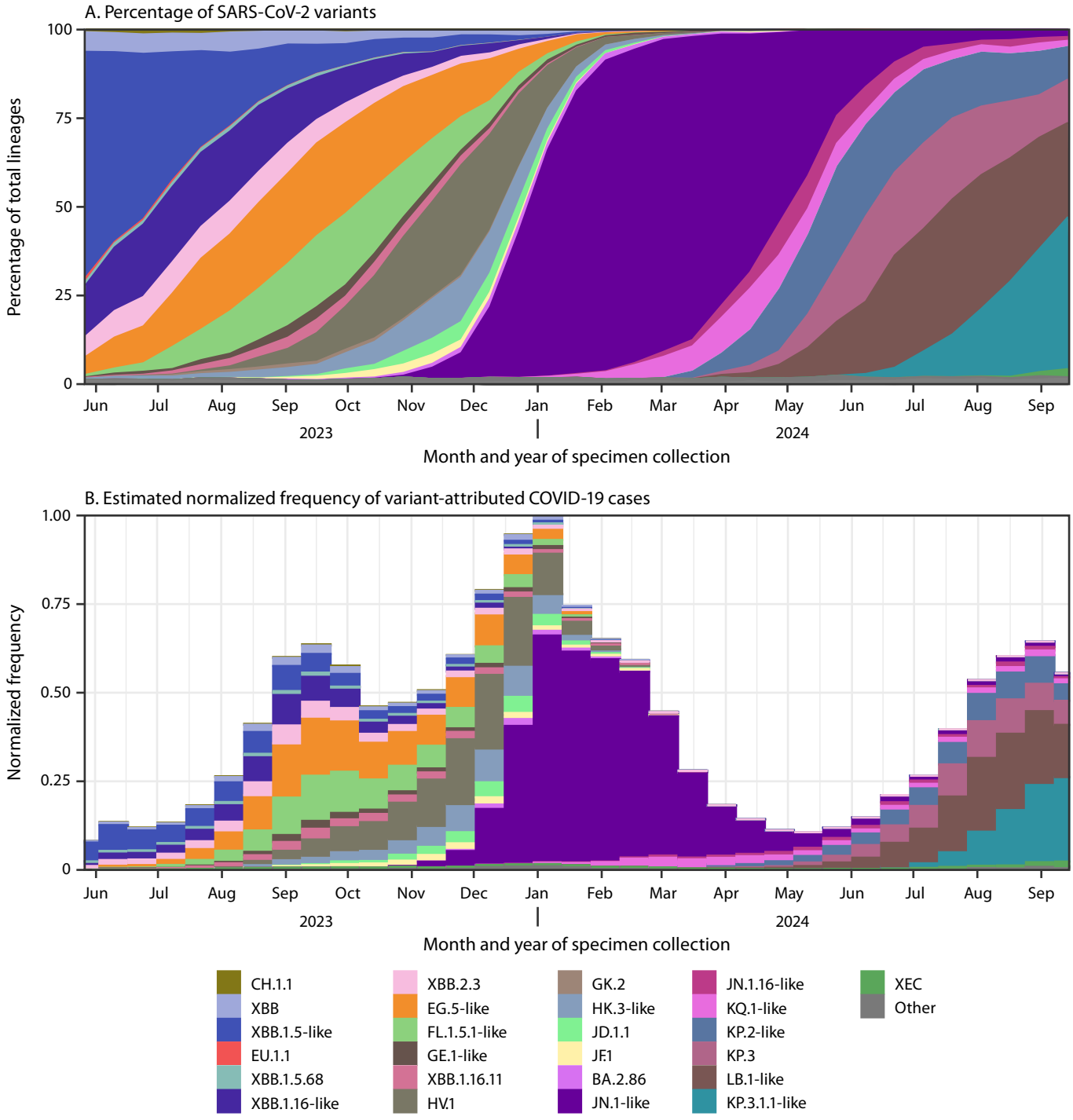
[¶¶¶] Sequences were subsampled (5,000) for analysis from an initial dataset of 1 million sequences during January 1, 2021–September 14, 2024. Each year within the study period was proportionately represented and subsampling accounted for geographic representation by ensuring that sequences from each state were included.

[****] 45 C.F.R. part 46.102(l)(2), 21 C.F.R. part 56; 42 U.S.C. Sect.241(d); 5 U.S.C. Sect.552a; 44 U.S.C. Sect. 3501 et seq.

[††††] SARS-CoV-2 sequences originated from the 50 U.S. states, District of Columbia, American Samoa, Guam, Northern Mariana Islands, Puerto Rico, and U.S. Virgin Islands.

[§§§§] CDC uses a diverse, multicomponent surveillance approach to track the emergence of new and potentially significant SARS-CoV-2 variants across the United States and globally. These surveillance systems include 1) national SARS-CoV-2 genomic surveillance, 2) traveler-based genomic surveillance, 3) the National Wastewater Surveillance System, and 4) digital public health surveillance (e.g., global data repositories, news, and social media). https://covid.cdc.gov/covid-data-tracker/#variant-summary

FIGURE 1. National estimates of biweekly proportions* of SARS-CoV-2 variants† (A) and estimated normalized frequency of variant-attributed COVID-19 cases§ (B) — United States, May 14, 2023–September 14, 2024



Abbreviations: NREVSS = National Respiratory and Enteric Virus Surveillance System; NS3 = National SARS-CoV-2 Strain Surveillance.

* Sequences are reported to CDC through NS3, contract laboratories, public health laboratories, and other U.S. institutions. Variant proportion estimation methods use a complex survey design and statistical weights to account for the probability that a specimen is sequenced. https://covid.cdc.gov/covid-data-tracker/#variant-proportions

† Lineages reaching a prevalence of ≥1% with spike protein substitutions of potential therapeutic relevance and separated out on the COVID Data Tracker website (https://covid.cdc.gov/covid-data-tracker/#variant-proportions). Lineages were ordered by date of first appearance on the COVID Data Tracker. Lineages with identical spike residue 31 and receptor binding domain amino acid sequences (residues 332–527) were grouped with a representative lineage and denoted as "representative lineage-like." "Other" represents aggregated lineages circulating at <1% prevalence nationally during all 2-week periods displayed.

§ Normalized frequency of COVID-19 cases attributable to variants was estimated by multiplying biweekly counts of positive test results from NREVSS with variant proportions and scaling by the maximum NREVSS case count, which occurred in the 2-week period ending January 6, 2024.

TABLE. Predominant amino acid deletions and substitutions in the receptor binding domain (residues 332–527) and residue 31 of the spike protein relative to XBB.1.5* among Omicron lineage groups with ≥5% prevalence† — United States, May 14, 2023–September 14, 2024

	Spike protein amino acid substitutions																			
Lineage	**31§,¶**	**332**	**346§,****	**356**	**368**	**403**	**445****	**450****	**452§,****	**455§,****	**456§,****	**475****	**478**	**481**	**483**	**484****	**486§,****	**490****	**493****	**521**
Reference sequence: XBB.1.5*	S	I	T	K	I	R	P	N	L	L	F	A	K	N	V	A	P	S	Q	P
XBB	—††	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	S	—	—	—
XBB.1.16-like (HF.1, XBB.1.16, XBB.1.16.1, and XBB.1.16.17)	—	—	—	—	—	—	—	—	—	—	—	—	R	—	—	—	—	—	—	—
XBB.2.3	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	S
EG.5-like (EG.5, EG.6.1, FD.1.1, FE.1.1, XBB.1.5.10, XBB.1.5.59, and XBB.1.5.72)	—	—	—	—	—	—	—	—	—	—	L	—	—	—	—	—	—	—	—	—
FL.1.5.1-like (FL.1.5.1 and XBB.1.16.6)	—	—	—	—	—	—	—	—	—	—	L	—	R	—	—	—	—	—	—	—
HV.1	—	—	—	—	—	—	—	—	R	—	L	—	—	—	—	—	—	—	—	—
HK.3-like (EG.5.1.8, GK.1.1, HK.3, JG.3, and XBB.1.5.70)	—	—	—	—	—	—	—	—	—	F	L	—	—	—	—	—	—	—	—	—
JD.1.1	—	—	—	—	—	—	—	—	—	F	L	V	—	—	—	—	—	—	—	—
JN.1-like (JN.1, JN.1.13, JN.1.32, JN.1.7, JN.1.8.1, JN.1.4.3, KV.2, and XDP)	—	V	R	T	L	K	H	D	W	S	—	—	—	K	—	K	—	F	—	—
JN.1.16-like (JN.1.11.1, JN.1.16, KW.1.1, KP.1.2, and XDV.1)	—	V	R	T	L	K	H	D	W	S	L	—	—	K	—	K	—	F	—	—
KQ.1-like (JN.1.13.1, JN.1.18, and KQ.1)	—	V	—	T	L	K	H	D	W	S	—	—	—	K	—	K	—	F	—	—
KP.2-like (JN.1.16.1, KP.1.1, KP.2, KS.1, KP.4.1, and LF.3.1)	—	V	—	T	L	K	H	D	W	S	L	—	—	K	—	K	—	F	—	—
KP.3 (XEC§§)	—	V	R	T	L	K	H	D	W	S	L	—	—	K	—	K	—	F	E	—
LB.1-like (KP.1.1.3, KP.2.3, LB.1, and LP.1)	Δ	V	—	T	L	K	H	D	W	S	L	—	—	K	—	K	—	F	—	—
KP.3.1.1-like (MC.1)	Δ	V	R	T	L	K	H	D	W	S	L	—	—	K	—	K	—	F	E	—

Abbreviations: A = alanine; C = cysteine; D = aspartic acid; Δ = deletion; E = glutamic acid; F = phenylalanine; G = glycine; H = histidine; I = isoleucine; K = lysine; L = leucine; M = methionine; N = asparagine; P = proline; Q = glutamine; R = arginine; RBD = receptor binding domain; S = serine; T = threonine; V = valine; W = tryptophan; Y = tyrosine.

* The XBB.1.5 spike protein sequence was used as a reference because of its inclusion in 2023–2024 COVID-19 vaccines. Substitutions present relative to Wuhan-Hu-1 are underlined. XBB.1.5-like lineages also include FD.2, XBB.1.42.2, XBB.1.5, XBB.1.5.1, XBB.1.9.1, and XBB.1.9.2.

† Lineages with identical spike residue 31 and RBD (residues 332–527) amino acid sequences were grouped with a representative lineage and denoted as "representative lineage-like." Lineage groups with ≥5% prevalence in at least one 2-week period and substitutions present in ≥50% of sequences belonging to a lineage were included. Lineages were ordered by date of first appearance on CDC's COVID Data Tracker.

§ Indicates sites of independent substitutions in at least two different evolutionary lineages.

¶ Residue 31 in the N-terminal domain of the spike protein is included because of multiple independent acquisition of deletions in different descendant lineages of JN.1.

** Indicates sites identified in a previous study (https://www.nature.com/articles/s41586-021-04385-3) associated with in vitro reductions in binding by monoclonal antibodies that were previously Food and Drug Administration–authorized.

†† Dashes indicate the same amino acid as the reference sequence.

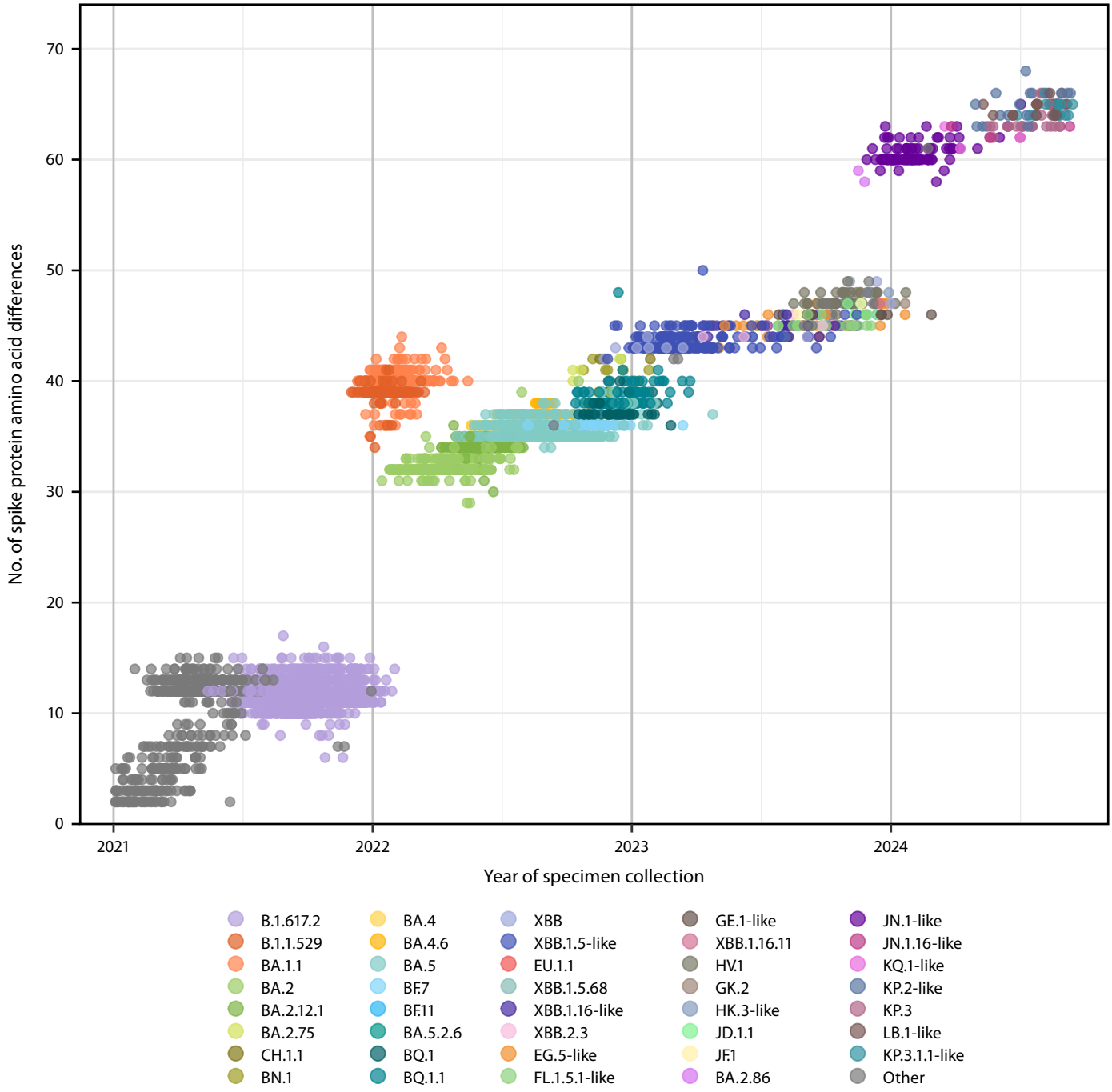
§§ XEC is a recombinant of JN.1 lineages KS.1.1 and KP.3.3 and contains the same RBD sequence as KP.3. XEC also has substitutions T22N and F59S.

predominant during the first half of the winter surge (Figure 1). The rate of increase in prevalence of JN.1was similar to that of XBB.1.5 after reaching 1% prevalence, but was slower compared with Omicron BA.1.1 and BA.5 (Supplementary Figure 3, https://stacks.cdc.gov/view/cdc/165774).

JN.1 Descendants

In spring and summer 2024, multiple descendants of JN.1 acquired spike protein substitutions convergently and began increasing in prevalence (Figure 1). Relative to JN.1, JN.1.16-like lineages contain the F456L substitution, KQ.1-like lineages contain R346T, KP.2-like lineages contain both substitutions, and KP.3 contains F456L and Q493E (Table). LB.1-like lineages and KP.3.1.1 acquired a deletion outside the spike receptor binding domain at residue 31 and increased in prevalence during May–September 2024 (Figure 1). KQ.1-like and KP.2-like lineages each reached >10% prevalence by April 13, 2024, KP.3 and LB.1-like lineages by May 25, and

FIGURE 2. Subsampled* SARS-CoV-2 sequences,† by lineage group,§ date of specimen collection, and number of spike protein amino acid differences (including substitutions, insertions, and deletions) relative to Wuhan-Hu-1 reference — United States, January 1, 2021–September 14, 2024



* Sequences were subsampled (5,000) for analysis from an initial dataset of 1 million sequences spanning January 1, 2021–September 14, 2024. Each year within the study period was proportionately represented, and subsampling accounted for geographic representation by ensuring that sequences from each state were included.

† Sequences are reported to CDC through the National SARS-CoV-2 Strain Surveillance program, contract laboratories, public health laboratories, and other U.S. institutions.

§ Lineages reaching a prevalence of ≥1% with spike protein substitutions of potential therapeutic relevance and separated out on the COVID Data Tracker website (https://covid.cdc.gov/covid-data-tracker/#variant-proportions). Lineages were ordered by date of first appearance on the COVID Data Tracker. Lineages with identical spike residue 31 and receptor binding domain amino acid sequences (residues 332–527) were grouped with a representative lineage and denoted as "representative lineage-like." "Other" represents aggregated lineages circulating at <1% prevalence nationally during all 2-week periods displayed.

Summary

What is already known about this topic?

CDC's national SARS-CoV-2 genomic surveillance program previously detected the emergence and circulation of major variants, including Delta and Omicron.

What is added by this report?

During May 2023–September 2024, SARS-CoV-2 lineages primarily comprised descendants of Omicron XBB and JN.1. Multiple XBB descendants circulated in summer and fall 2023 with immune escape characteristics. JN.1, which was not an XBB descendant, contained substantial genetic differences and became predominant by January 2024. Descendants of JN.1 subsequently emerged. Increases in COVID-19 cases occurred during both variant predominance and cocirculation periods.

What are the implications for public health practice?

Given the unpredictable nature of SARS-CoV-2 evolution, continued monitoring for genetic changes and their impact on disease severity and medical countermeasure effectiveness remains essential.

KP.3.1.1 by July 20. The prevalence of XEC, a recombinant of JN.1 lineages KS.1.1 and KP.3.3 (Table), increased from 0.4% on August 17 to 2.3% on September 14. Normalized frequencies of positive SARS-CoV-2 test results increased during late summer 2024 as these descendants of JN.1 circulated (Figure 1).

Discussion

During May 2023–September 2024, SARS-CoV-2 lineages reported by CDC's genomic surveillance program primarily comprised descendants of XBB and JN.1. Parallels in the evolutionary trajectories of these two lineages and their descendants were observed. The detections of XBB and BA.2.86 in fall 2022 and late summer 2023 (*5*), respectively, represented a substantial genetic shift, but XBB and BA.2.86 had relatively limited spread. These lineages subsequently acquired key spike substitutions (S486P in XBB leading to XBB.1.5 and similar lineages and L455S in BA.2.86 leading to JN.1) (*6*); by January of the following years, XBB.1.5 and JN.1 became predominant nationwide until late spring. The shift to JN.1 was followed by increased COVID-19 activity in summer 2024 and cocirculation of descendant lineages with identical substitutions, including the S31 deletion, R346T, and F456L (*7*,*8*), similar to trends after XBB.1.5 predominance. Continued monitoring to determine whether this pattern of divergent variant emergence followed by subsequent stepwise evolutionary changes continues will be important for updating COVID-19 vaccines and anticipating surges in COVID-19 activity.

Limitations

The findings in this report are subject to at least four limitations. First, the precision of recent SARS-CoV-2 variant proportion estimates might be low because of limited data and potential biases in specimen collection or sequencing. Second, current analyses might differ from previous analyses because of changes in data sources and methods. Third, difficulties exist in ascertaining whether shifts in predominant SARS-CoV-2 variants drive COVID-19 epidemic surges, or whether increases in infection allow new variants to emerge and become predominant. Finally, decreases in sample sizes have reduced estimate precision and frequency, underscoring the need for sustainable surveillance data sources. Sensitivity analyses indicate current estimates are qualitatively similar to previous periods with larger sample sizes (*3*). The power of this platform to detect emerging variants can be maintained with continued submission of sequences from representatively sampled specimens, including during periods of low overall COVID-19 activity.

Implications for Public Health Practice

National genomic surveillance was essential for detecting the emergence of JN.1 and other variants in the United States and demonstrating that SARS-CoV-2 continues to undergo large genetic shifts. However, surveillance data indicate that the consequences of these changes on rates of COVID-19 hospitalization and death have been reduced (*9*), likely because of widespread immunity to SARS-CoV-2.¶¶¶¶ Nonetheless, careful genomic monitoring remains important, as highlighted by evidence suggesting diminished 2023–2024 COVID-19 vaccine protection against JN.1 hospitalization (*2*). Data on variant proportions were used by the Food and Drug Administration to recommend inclusion of JN.1 lineages (preferentially KP.2) in updated 2024–2025 COVID-19 vaccines and are expected to guide composition of future vaccines (*10*). Given the unpredictability of SARS-CoV-2 evolution, continued monitoring for genetic changes and the impact of those changes on COVID-19 disease severity and medical countermeasure effectiveness remains essential to maintain preparedness.

¶¶¶¶ Data on COVID-19 hospitalizations, deaths, and seroprevalence, an indicator of previous SARS-CoV-2 infection or vaccination, are available on CDC's COVID Data Tracker at https://covid.cdc.gov/covid-data-tracker/#covidnet-hospitalization-network, https://covid.cdc.gov/covid-data-tracker/#trends_weeklydeaths_select_00, and https://covid.cdc.gov/covid-data-tracker/#nationwide-blood-donor-seroprevalence-2022.

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Locally Acquired (Autochthonous) Mosquito-Transmitted *Plasmodium vivax* Malaria — Saline County, Arkansas, September 2023

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Abstract

A case of locally acquired (autochthonous) mosquito-transmitted *Plasmodium vivax* malaria was diagnosed in Arkansas in September 2023. This represents the 10th autochthonous case identified nationally in 2023, after 20 years without recorded local mosquitoborne malaria transmission in the United States. The public health response included case investigation, active case surveillance, mosquito surveillance and control, assessment of medical countermeasures, and clinical and public outreach. Prompt diagnosis and appropriate treatment of malaria can improve clinical outcomes and, in addition to vector control, minimize risk for local transmission. Clinicians should consider malaria among patients who have traveled to countries where malaria is endemic, or with unexplained fever regardless of travel history. Although the risk for autochthonous malaria in the United States remains very low, its reemergence highlights the importance of vectorborne disease preparedness and response. Examples of such efforts include improving awareness among clinicians, access to diagnostics and antimalarial medications, and capacity for mosquito surveillance and control. Collaboration and communication among CDC, health departments, local jurisdictions, clinicians, hospitals, laboratories, and the public can support rapid malaria diagnosis, prevention, and control. Before traveling internationally to areas where malaria is endemic, travelers should consult with their health care provider regarding recommended malaria prevention measures, including chemoprophylaxis and precautions to avoid mosquito bites, to reduce both personal and community risk.

Investigation and Results

On September 28, 2023, a previously healthy person living in Saline County, Arkansas was evaluated at a local hospital for a 10-day history of headache, fever, chills, night sweats, fatigue, and a 1-day history of nausea and vomiting. The patient had no reported history of international travel, blood transfusion, organ transplant, or other bloodborne pathogen exposure. Initial laboratory evaluation revealed anemia, thrombocytopenia, and hyperbilirubinemia. The patient was admitted for possible hematologic malignancy; anemia and thrombocytopenia worsened (hemoglobin 7.3 g/dL [reference range 12.0–16.0 g/dL]; platelets 14 K/μL [reference range 150–400 K/μL]), and the patient was transfused one unit of packed red blood cells and one unit of platelets.

On repeat complete blood count analysis (September 30, 2023), the patient's thin peripheral blood smear was noted to have ring forms concerning for malaria and verified 7 hours later as *Plasmodium* (non-*falciparum*) by positive result from a BinaxNOW malaria rapid diagnostic test (RDT; Abbott). *Plasmodium* species and parasitemia percentage were initially unavailable; the patient was treated with intravenous (IV) artesunate pending results.[†] A pathologist's review of thick and thin blood smears verified presence of *Plasmodium vivax/Plasmodium ovale* gametocytes and ring forms with parasitemia of 0.26%. The patient was transitioned to artemether-lumefantrine and primaquine for relapse prevention. Thin smear images were referred to CDC for telediagnosis, which confirmed the presence of *P. vivax/P. ovale*. CDC performed direct morphologic examination of thin smears (Figure) followed by 18S rRNA real-time polymerase chain reaction testing of ethylenediaminetetraacetic acid whole blood, which confirmed the species-level identity of *P. vivax*. To exclude transfusion-associated malaria, a pretransfusion peripheral blood smear was re-reviewed by both pathologist-in-chief at the local hospital and CDC and confirmed to have ring forms and gametocytes consistent with *P. vivax/P. ovale*. The patient completed treatment and fully recovered.

Public Health Response

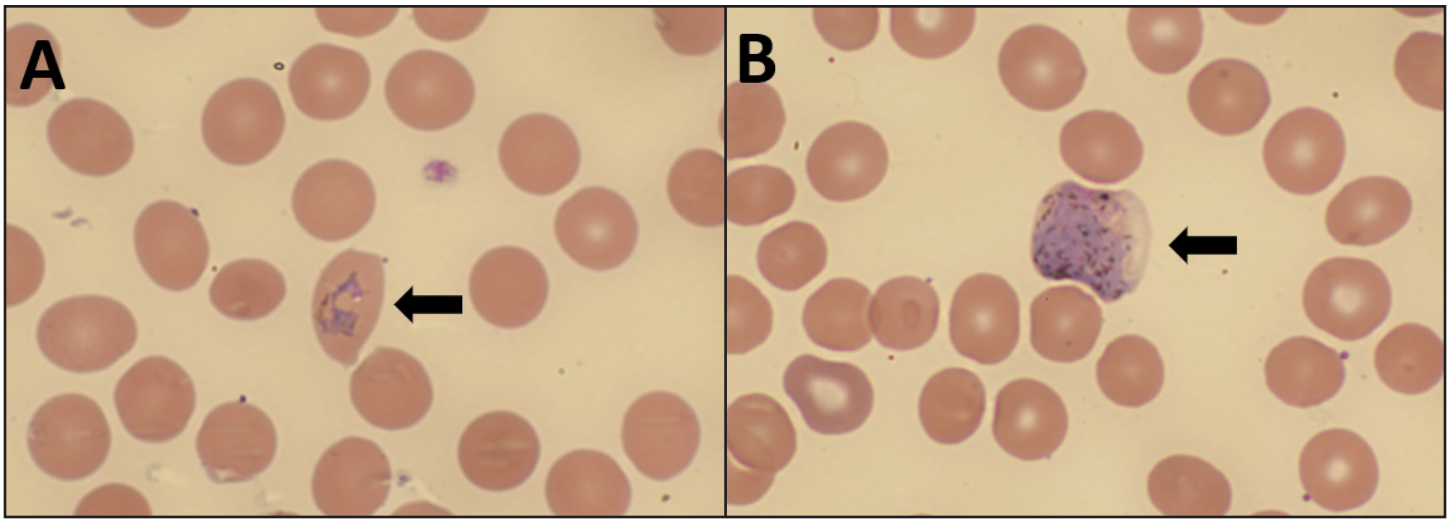
CDC supported the Arkansas Department of Health (ADH) in the investigation and response to this case. This activity was reviewed by CDC, deemed not research, and was conducted consistent with applicable federal law and CDC policy.[§]

[*] These senior authors contributed equally to this report.

[†] IV artesunate is the first-line drug for treatment of severe malaria in the United States. Clinical manifestations of severe malaria include impaired consciousness, seizures, circulatory collapse/shock, pulmonary edema or acute respiratory distress syndrome, acidosis, acute kidney injury, abnormal bleeding or disseminated intravascular coagulation, severe anemia (hemoglobin <7 g/dL), and high percent parasitemia (≥5%). https://www.cdc.gov/malaria/hcp/clinical-guidance/treatment-of-severe-malaria.html

[§] 45 C.F.R. part 46, 21 C.F.R. part 56; 42 U.S.C. Sect. 241(d); 5 U.S.C. Sect. 552a; 44 U.S.C. Sect. 3501 et seq.

FIGURE. Thin blood smear* from the patient, demonstrating *Plasmodium vivax/ovale* ring-form trophozoite (A) and gametocyte (B) — Arkansas, September 2023



Photos/Arkansas Children's Hospital, Clinical Microbiology Laboratory
* Wright-Giemsa stain (x1000 magnification).

Additional Case Investigation

ADH confirmed the patient had never traveled internationally and did not have other risk factors for acquiring malaria in the United States. Outdoor activities and possible mosquito exposure locations during the 4 weeks before symptom onset were assessed; these did not overlap geographically or temporally with any 2023 imported malaria cases in Arkansas, which were all caused by *P. falciparum.*

Active Case Surveillance

ADH confirmed that all household members living with the patient were asymptomatic. On October 9, 2023, prospective enhanced case finding was implemented using the Electronic Surveillance System for the Early Notification of Community-Based Epidemics (ESSENCE) syndromic surveillance system. Of eight local hospitals in Saline County and Little Rock, three were operational within ESSENCE, two were onboarded but not yet fully operational, and three were not participating. The ADH syndromic surveillance team adapted a query originally developed by the Florida Department of Health to identify potential malaria cases¶ (*1*). Syndromic surveillance continued for 9 weeks after the patient's symptom onset. Eight potential malaria cases were identified; all patients received alternative diagnoses.

Mosquito Surveillance and Control

On October 5, 2023, ADH began enhanced mosquito surveillance at two sites in Saline County near the patient's residence and a location where the patient spent time outdoors during the preceding 4 weeks. Five CDC miniature light traps with and without carbon dioxide, which is a mosquito attractant, were set up at each site during the early evening and collected approximately 14 hours later the next day, October 6, 2023. This process was repeated six additional times, with the final mosquito collection occurring on October 24, 2023. Of the 244 total mosquitos collected, 25 female *Anopheles* mosquitoes were identified and sent to CDC for *Plasmodium* testing**; all specimens tested negative.

ADH provided guidance on mosquito control efforts based on local capabilities in consultation with CDC.†† The affected municipality lacked routine mosquito control capabilities and partnered with another municipality that donated adulticide, an ultra-low volume (ULV) sprayer, and a dedicated spray truck. On October 5, 2023, the affected municipality started control efforts for adult mosquitoes near the patient's residence. The ULV truck-mounted sprayer treated for 5 nonconsecutive nights over a 7-day period using 30% permethrin (active

¶ The query used *International Classification of Diseases, Tenth Revision* codes and free text to identify references to 1) malaria or *Plasmodium* spp., 2) fever or chills, abdominal pain, and anemia or thrombocytopenia (with terms to exclude records without fever), or 3) splenomegaly. The ESSENCE system algorithm identified records matching query parameters and alerted epidemiologists by email. Raw data in the Rhapsody Integrated Development Environment were monitored twice daily through a parallel Structured Query Language data query used to search Health Level 7 messages from the facilities in staging.

** Mosquitos were tested by both 1) bead assay for circumsporozoite protein in head-thorax for *P. falciparum, P. vivax* vk210 and *P. vivax* vk247, and 2) *Plasmodium* cytochrome c oxidase subunit I polymerase chain reaction using DNA extracted from abdomens.

†† CDC provides clinical assistance through the Malaria Hotline at 770-488-7788 or 855-856-4713 (toll-free) Monday–Friday, 9:00 a.m.–5:00 p.m. ET. After hours, on weekends, and on federal holidays, health care providers can call 770-488-7100 and ask to speak with the malaria clinician on call and diagnostic laboratory support. https://www.cdc.gov/parasites/contact/?CDC_AAref_Val=https://www.cdc.gov/parasites/contact.html

ingredient)/30% piperonyl butoxide (synergist). Control efforts started within 1 mile (1.6 km) of the patient's residence, expanding for two additional nights in 1-mile (1.6-km) concentric rings, where roads permitted travel. The final two nights focused on potential mosquito breeding areas near the patient's residence and another location where the patient spent time outdoors. Control efforts were discontinued after treatment on October 11, 2023, because of resource limitations and falling temperatures in the area, which can reduce mosquito activity.

Assessment of Medical Countermeasures

Starting October 6, 2023, local hospitals in Saline County and Little Rock were contacted to assess malaria diagnostic and treatment capabilities. Seven of eight local hospitals reported ability to examine and interpret thick and thin blood smears, and two reported use of malaria RDTs. The Arkansas State Public Health Laboratory can consult on blood smears upon request and refer slides and whole blood as needed to CDC.[§§] Three hospitals reported availability of artemether-lumefantrine, the first-line drug in the United States for uncomplicated *P. falciparum* or unknown malaria species. No hospitals stocked IV artesunate, the first-line drug for treatment of severe malaria in the United States.[¶¶]

Clinical and Public Outreach

On October 4, 2023, ADH issued a press release notifying the public of a case of locally acquired mosquito-transmitted malaria. The press release included information about malaria symptoms, importance of seeking medical care if symptomatic, and mosquito control and bite prevention.[***]

On October 5, 2023, ADH distributed a Health Advisory (Identification of Locally Acquired Mosquito-Transmitted Malaria in Arkansas) via email through the Arkansas statewide Health Alert Network. This advisory provided guidance to clinicians, hospitals and laboratories and included recommendations and resources related to malaria clinical presentation, diagnosis, treatment, prevention, and case reporting. On October 11, 2023, ADH hosted a 1-hour informational webinar for clinicians to discuss the health advisory and highlight available resources.

Discussion

The total number of malaria cases reported in the United States trended upward during 1972–2019, with 2,048 cases reported to CDC in 2019 (*2*). Most of these cases were associated with travel to 85 countries where malaria remains endemic and could represent a potential source of *Plasmodium* infection for locally acquired mosquito-transmitted cases (*3*). *Anopheles* mosquito species are present across the United States and can acquire *Plasmodium* infection from patients with travel-associated malaria; these competent vectors can then transmit the parasite to persons who haven't traveled (*4*). Although the source of this autochthonous malaria case in Arkansas remains unknown, local *Anopheles* mosquitoes might have become infective after obtaining a blood meal from a person with undiagnosed travel-associated malaria in a nearby geographic area (*4*). This represents the 10th autochthonous malaria case reported to CDC in 2023 after 20 years without recorded local transmission, thus highlighting the ongoing need for coordinated public health response and prevention efforts (*4*,*5*).

Prompt diagnosis and appropriate treatment[†††] of malaria can improve clinical outcomes and lower risk for ongoing local transmission (*5*). Although the risk for locally acquired mosquito-transmitted malaria in the United States remains very low, clinicians should consider malaria for all patients who have traveled to countries where malaria is endemic, or who have unexplained fever, regardless of travel history (*5*). The Clinical and Laboratory Standards Institute (CLSI) developed guidelines to support accurate and timely malaria diagnosis, including recommendations for specimen collection, blood film preparation, staining procedures, and identification of *Plasmodium* spp.[§§§] Many U.S. laboratories report the capability to perform the gold-standard malaria diagnostic test: microscopic examination of thick and thin blood smears; however, few adhere to all CLSI guidelines, which could contribute to diagnostic delays (*6*). Resources such as proficiency testing programs, guidelines, bench aids, continuing education workshops, and telediagnosis are available for maintenance and improvement of laboratory capacity (*6*–*8*). RDTs can be used to aid diagnosis but should be used alongside microscopy because they are less sensitive and cannot reliably confirm species-level identification or determine parasitemia density (*5*). Stocking IV artesunate, the first-line drug for treatment of severe malaria in the United States, might improve timeliness of patient treatment and minimize risk for death; emergency procurement is also available (*9*). Treatment of uncomplicated malaria varies by *Plasmodium* species, expected drug susceptibility, and previous use of antimalarials (*9*). If primaquine or tafenoquine are indicated, quantitative glucose-6-phosphate dehydrogenase (G6PD) testing should be conducted before administration because of risk of hemolytic anemia and need

[§§] ADH ordered 15 boxes of malaria RDT kits to help support local malaria diagnostics.

[¶¶] https://www.cdc.gov/malaria/hcp/clinical-guidance/iv-artesunate-us.html?CDC_AAref_Val=https://www.cdc.gov/malaria/diagnosis_treatment/artesunate.html

[***] https://healthy.arkansas.gov/article/locally-acquired-malaria-identified-in-arkansas/

[†††] https://www.cdc.gov/malaria/hcp/clinical-guidance/index.html

[§§§] https://clsi.org/standards/products/microbiology/documents/m15/

Summary

What is already known about this topic?

After 20 years without locally acquired mosquito-transmitted malaria in the United States, nine cases were reported to CDC during May–August 2023.

What is added by this report?

In September 2023, a 10th U.S. case of locally acquired malaria was diagnosed, in Arkansas. The public health response included case investigation and surveillance, mosquito surveillance and control, assessment of hospital preparedness, and clinical and public outreach.

What are the implications for public health practice?

Prompt diagnosis and appropriate treatment of malaria can improve clinical outcomes and lower risk for ongoing transmission. Although the risk for locally acquired malaria in the United States remains very low, its reemergence highlights the importance of vectorborne disease preparedness and response efforts.

for a modified regimen or alternative medication if G6PD deficiency is detected (*9*).

Malaria is a nationally notifiable condition, and case reporting guides local and national prevention and response activities (*10*). Enhanced case finding might also occur through syndromic surveillance, highlighting the importance of participation of local health care facilities in state syndromic surveillance systems. Vectorborne disease outbreak preparedness varies by jurisdiction; local partnerships and resource sharing can improve vector control capacity (*4*). Collaboration and communication with clinicians, hospitals, laboratories, and the public can support rapid malaria identification, prevention, and control. As of September 2024, no additional autochthonous malaria cases had been identified in Arkansas. Before traveling internationally to areas where malaria is endemic, travelers should consult with their health care provider regarding recommended malaria prevention measures, including chemoprophylaxis and precautions to avoid mosquito bites, to reduce both personal and community risk.

Arkansas Locally Acquired Mosquito-Transmitted Malaria Response Team

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Two Outbreaks of Legionnaires Disease Associated with Outdoor Hot Tubs for Private Use — Two Cruise Ships, November 2022–July 2024

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Abstract

Legionnaires disease is a serious pneumonia caused by *Legionella* bacteria. During November 2022–June 2024, CDC was notified of 12 cases of Legionnaires disease among travelers on two cruise ships; eight on cruise ship A and four on cruise ship B. CDC, in collaboration with the cruise lines, initiated investigations to ascertain the potential sources of on-board exposure after notification of the second potentially associated case for each ship. Epidemiologic data collected from patient interviews and environmental assessment and sampling results identified private hot tubs on selected cabin balconies as the most likely exposure source. To minimize *Legionella* growth, both cruise lines modified the operation and maintenance of these devices by removing the heating elements, draining water between uses, and increasing the frequency of hyperchlorination and cleaning. Hot tubs offer favorable conditions for *Legionella* growth and transmission when maintained and operated inadequately, regardless of location. Private hot tubs on cruise ships are not subject to the same maintenance requirements as are public hot tubs in common areas. Given the range of hot tub–type devices offered as amenities across the cruise industry, to reduce risk for *Legionella* growth and transmission, it is important for cruise ship water management program staff members to inventory and assess private balcony hot tubs and adapt public hot tub maintenance and operations protocols for use on private outdoor hot tubs.

Investigation and Results

Cruise Ship A Outbreak (November 2022–April 2024)

During December 2022–May 2023, CDC was notified of five Legionnaires disease (LD) cases among patients (patients 1–5) who had traveled on cruise ship A during the 14-day exposure period* (Table) (Figure 1). All five cases (four laboratory-confirmed and one probable) were among passengers traveling on the same voyage in November 2022 (Supplementary Table; https://stacks.cdc.gov/view/cdc/165771) (*1*). During August–September 2023, two additional laboratory-confirmed cases with travel on different cruise ship A voyages were reported to CDC (patients 6 and 7). In April 2024, an additional laboratory-confirmed case was identified in a guest who traveled on cruise ship A the previous month (patient 8). No lower respiratory specimens were available; six patients were hospitalized, and no patients died. Local health departments interviewed patients to identify potential exposures on and off the ship, including hotel stays, health care visits, or other activities (Table). Patients 6 and 7 reported staying in cabins with a hot tub located on the private balcony (Figure 2).

In response to notification of the second case in February 2023, CDC reviewed the vessel's *Legionella* environmental sampling results from the preceding 6 months and water management program records. A total of 150 water samples were tested for

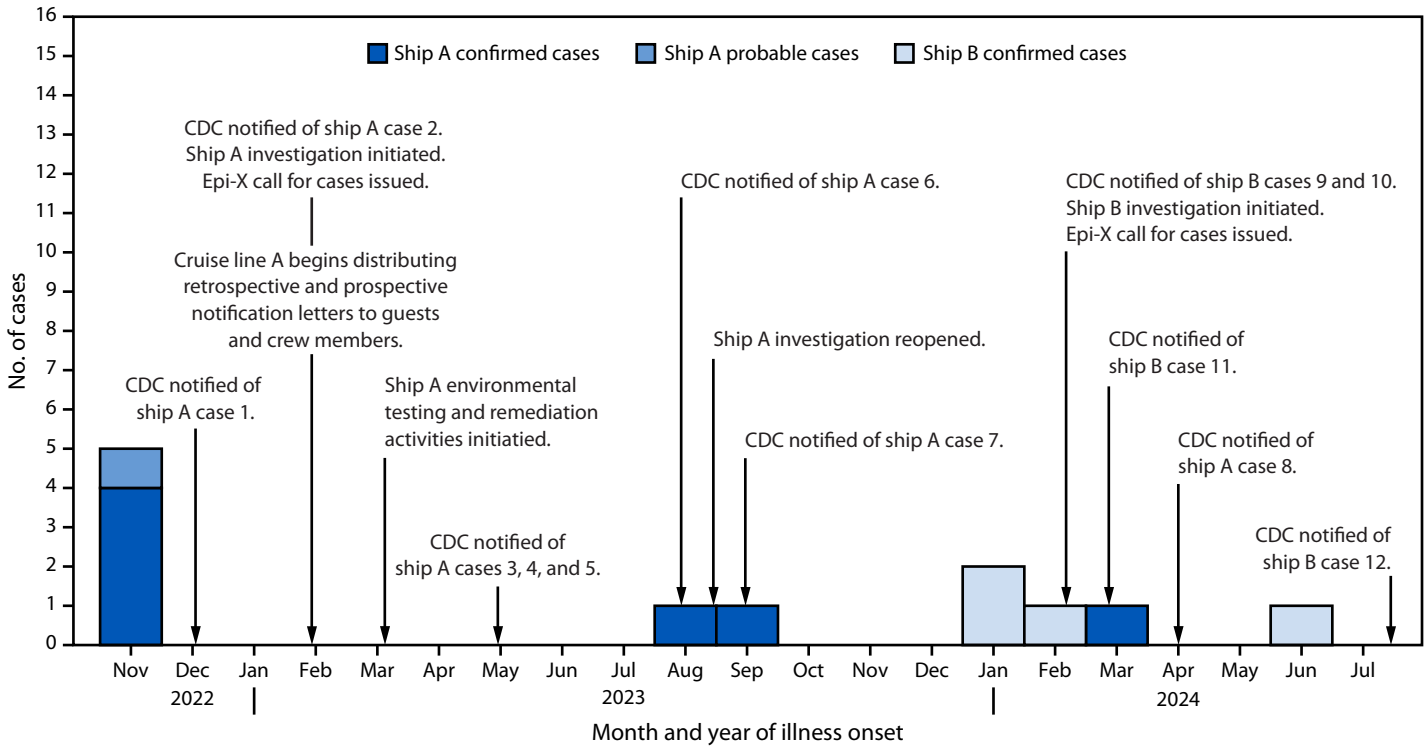
TABLE. Selected characteristics of patients with confirmed and probable* Legionnaires disease — two cruise ships, November 2022–July 2024

Characteristic	No. (%) of Legionnaires disease cases	
	Cruise ship A n = 8	Cruise ship B n = 4
Age, yrs		
Age, mean (range)	70 (39–78)	63 (60–66)
Age, median	73	63
Male sex	6 (75)	3 (75)
U.S. resident	8 (100)	2 (50)
Outcome		
Hospitalized	6 (75)	4 (100)
Survived	8 (100)	4 (100)
Disease status		
Confirmed	7 (88)	4 (100)
Probable	1 (12)	0 (—)
Potential exposures on board cruise ship		
Nights spent on board		
No. of nights, mean (range)	8 (7–10)	9 (7–14)
No. of nights, median	7	8
Potential exposure location		
Spent time in or near public hot tubs	5 (63)	2 (50)
Stayed in cabin with private balcony hot tub	2 (25)	0 (—)
Visited the spa	5 (63)	0 (—)
Shoreside excursions during cruise voyage	4 (50)	2 (50)
Other potential travel exposures	3 (38)	2 (50)

* A confirmed Legionnaires disease case is defined as a clinically compatible case with confirmatory laboratory evidence for *Legionella*. A probable case is a clinically compatible case with an epidemiologic link during the exposure period without laboratory evidence for *Legionella*. https://www.cdc.gov/investigate-legionella/php/data-research/case-definitions.html

* A confirmed LD case is defined as a clinically compatible case with confirmatory laboratory evidence for *Legionella*. A probable case is a clinically compatible case with an epidemiologic link during the exposure period without laboratory evidence for *Legionella*. The likely exposure period is defined as the 14 days preceding symptom onset. https://www.cdc.gov/investigate-legionella/php/data-research/case-definitions.html

FIGURE 1. Investigation of two Legionnaires disease outbreaks* associated with private balcony hot tubs — two cruise ships, November 2022–July 2024



Abbreviation: Epi-X = Epidemic Information Exchange.

* A confirmed Legionnaires disease case is defined as a clinically compatible case with confirmatory laboratory evidence for *Legionella*. A probable case is a clinically compatible case with an epidemiologic link during the exposure period without laboratory evidence for *Legionella*. https://www.cdc.gov/investigate-legionella/php/data-research/case-definitions.html

FIGURE 2. Images of hot tubs associated with cases of Legionnaires disease located on balconies only accessible via private cruise ship cabins* — two cruise ships, November 2022–July 2024

Photos/CDC Vessel Sanitation Program

* Images are of devices before modification. Each device had components that can increase the risk for *Legionella* growth and transmission, including aerosol-generating jets, retention of water between uses, and presence of a heating element and recirculation and filtration systems.

Legionella during August 2022–February 2023 as part of the cruise line's routine water management program validation. A single non-*pneumophila Legionella* detection was identified in the potable water system during that time (August 2022); after localized hyperchlorination of the water system, *Legionella* was not detected. All potable water parameters were within control limits and monitored according to CDC requirements[†] (*2*). Review of operation and maintenance records for public hot tubs in common areas indicated that CDC requirements had been met (*2*). In March 2023, in response to the outbreak, the cruise line collected 260 1-L water samples from representative points of use, cabins of infected patients, heat exchangers, potable water tanks, decorative fountains, and public hot tubs in common areas. No *Legionella* was detected. The cruise line also conducted ship-wide hyperchlorination after sampling. An additional 76 potable and recreational water samples were collected during spring and summer 2023; no *Legionella* was detected.

In August 2023, upon identification of the case in patient 6, in which private balcony hot tub use was first reported, CDC requested all 10 private balcony hot tubs on the ship be closed and sampled because they had not been tested previously. *L. pneumophila* serogroup 2–14 (Lp2–14) and non-*pneumophila Legionella* species were detected in six of 10 hot tubs. Of the six private balcony hot tubs with *Legionella* detections, four had concentrations of *Legionella* >100 colony-forming units (CFU)/mL, and two had concentrations >1,000 CFU/mL. The hot tubs remained closed until their operation and maintenance protocols were modified and non-detectable *Legionella* sampling results were obtained. *Legionella* was not detected in environmental sampling of the potable water system or any recreational water features, including the balcony hot tubs, after the change in operation and maintenance protocols. During March 2024, when patient 8 traveled on ship A, to August 2024, approximately 300 samples were collected, and no *Legionella* was detected.

Cruise Ship B Outbreak (January–June 2024)

During February–July 2024, CDC was notified of four confirmed LD cases in patients who traveled on cruise ship B during their exposure period (patients 9–12) (Table) (Figure 1). Two of the cases occurred in passengers traveling on the same voyage in January 2024 (patients 9 and 10); one of the passengers traveled on two consecutive voyages. The voyages of patients 11 and 12 were in February and May, respectively. Three patients received a positive *Legionella* urinary antigen test result, and one received a positive culture test result in which *L. pneumophila* was detected; four patients were hospitalized, and no patients died.

In response to the outbreak, CDC requested immediate closure of all hot tubs on the ship, including those in common areas and private balconies, and sampling of all hot tubs and representative potable water locations. *L. pneumophila* serogroup 1 (Lp1) and Lp2–14 species were detected in all eight private balcony hot tubs on the ship, and Lp2–14 was detected in a single location in the potable water system. Of the testing performed on the eight private balcony hot tubs, two samples had Lp1 concentrations >10 CFU/mL. All balcony hot tubs remained closed until each had nondetectable *Legionella* postremediation sampling results. As the cruise line implemented changes to the operation and maintenance of the balcony hot tubs, Lp1 and Lp2–14 continued to be detected in two of the eight hot tubs, prompting additional remediation efforts and further refinement of operational and maintenance protocols. This activity was reviewed by CDC, deemed not research, and was conducted consistent with applicable federal law and CDC policy.[§]

Public Health Response

CDC published two Epidemic Information Exchange (Epi-X) calls for cases and notified the European Centre for Disease Prevention and Control to identify other cruise-associated patients with LD because both ships included itineraries in Europe. Cruise operators of both ships notified guests and crew of the potential for *Legionella* exposure while the investigations were ongoing. CDC reviewed illness logs from both ship clinics. CDC also notified cruise operators of the risk for *Legionella* growth associated with private balcony hot tubs during regularly scheduled calls with industry partners in December 2023 and June 2024.

Both cruise lines ultimately modified the operation and maintenance of the private hot tubs so that heating elements were removed; tubs were only filled upon guest request, drained between uses, and cleaned and disinfected more frequently. Ship A devices were additionally modified to remove filtration elements. Sampling is ongoing for both vessels.

[†] The CDC Vessel Sanitation Program 2018 Operations Manual addresses current public health issues related to cruise ship sanitation. Requirements concerning the potable water disinfectant level and monitoring point are in Sections 5.4.1.2.1 and 5.5.1.1.1. Requirements related to public and private whirlpool spa operations are in Sections 6.3, 6.4, and 6.6. Public whirlpool spa requirements include continuous and automatic disinfectant dosing and monitoring, frequent shock halogenation, and filter cleaning and replacement procedures. "Whirlpool spa" is a synonymous term for "hot tub." https://www.cdc.gov/vessel-sanitation/media/files/vsp_operations_manual_2018-508.pdf

[§] 45 C.F.R. part 46, 21 C.F.R. part 56; 42 U.S.C. Sect. 241(d); 5 U.S.C. Sect. 552a; 44 U.S.C. Sect. 3501 et seq.

Discussion

Travel on cruise ships is a recognized risk factor for LD (*3*). CDC defines a cruise-associated outbreak as the occurrence of two cases in patients who had traveled on the same ship with voyages within 1 year of each other (*4*). In these investigations, both outbreaks involved patients with overlapping voyages, most notably ship A with five patients who traveled on the November 2022 voyage. The outbreak on cruise ship A is the largest cruise-associated LD outbreak investigated by CDC since 2008.

On ship A, the private balcony hot tubs were identified as a potential source of exposure after interviews with patients 6 and 7. These devices were found to be operating for months in a manner conducive to *Legionella* growth, which included maintaining a water temperature in the *Legionella* growth range (77°F–113°F [25°C–45°C]) for multiple days without draining and operating with no residual disinfectant. In addition, some of these devices were located on decks only one floor above or below common outdoor amenities; previous investigations have shown that hot tubs located in private areas can disseminate aerosols to common areas and result in exposures, even in persons who do not use the hot tubs themselves (*5*,*6*). Environmental testing revealed extensive *Legionella* colonization. Subsequent identification of *Legionella* in private balcony hot tubs operating on ship B strengthened the case that these devices were the likely exposure source.

According to current CDC requirements, private hot tubs are not required to have automated continuous disinfectant dosing and monitoring or pH monitoring, as is standard for public hot tubs. To meet CDC requirements, private hot tubs must only be shock-chlorinated, drained, and refilled weekly or between occupancies, whichever is sooner (*3*). Although the cruise lines adhered to current CDC requirements for operating and maintaining private hot tubs on ships A and B, these measures were insufficient to prevent *Legionella* growth.

Limitations

The findings in this report are subject to at least three limitations. First, clinical isolates were not available for comparisons to determine genetic relatedness. Second, although clinical tests indicated patients were infected with Lp1, environmental testing detected other *Legionella* species and serogroups in the balcony hot tubs of ship A. However, the presence of any *Legionella* species indicates that conditions supporting growth existed in these devices. Finally, multiple patients reported other possible exposure locations during their travel, such as hotels and shoreside excursions at ports of call, although the cruise ships were the only common exposure among the infected patients.

Summary

What is already known about this topic?

Legionnaires disease is a serious pneumonia caused by *Legionella* bacteria. Hot tubs can be a source of *Legionella* growth and transmission when they are inadequately maintained and operated.

What is added by this report?

Epidemiologic, environmental, and laboratory evidence suggests that private balcony hot tubs were the likely source of exposure in two outbreaks of Legionnaires disease among cruise ship passengers. These devices are subject to less stringent operating requirements than are public hot tubs, and operating protocols were insufficient to prevent *Legionella* growth.

What are the implications for public health practice?

It is important for cruise ship operators to inventory hot tub–style devices across their fleets, evaluate the design features that increase the risk for *Legionella* growth and transmission, and test for *Legionella*.

Implications for Public Health Practice

This report describes a previously unidentified source of *Legionella* exposure on cruise ships: hot tubs located on private cabin balconies, which have become more common as new ships enter service and older ones are renovated. A wide range of hot tub–style devices are used by cruise, hotel, and recreational water industries, including public hot tubs, jetted bathtubs, and hydrotherapy pools. Cruise lines and the hospitality industry should be aware of hot tub features that increase the risk for *Legionella* growth and transmission, including outdoor use, retention of water between uses, and the presence of recirculation, filtration, or heating systems.

Private outdoor hot tubs, as described in this report, are not unique to cruise ships A and B. Inventory of hot tub–style devices by cruise ship operators to ensure that they are included in the vessel's water management program and are routinely tested for the presence of *Legionella* could help prevent cruise ship outbreaks of LD. Adapting public hot tub maintenance and operations protocols for use on private outdoor hot tubs can reduce the risk for *Legionella* growth and transmission.

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Notes from the Field

First Locally Acquired Dengue Virus Infections — Pasadena, California, October–December 2023

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Global incidence of dengue is increasing (*1*). Dengue, a mosquitoborne arboviral disease caused by four dengue viruses (DENV 1–4), is transmitted to humans by *Aedes* species mosquitoes; invasive *Aedes* species are found in California (*2*,*3*). During 2013–2022, six cases of travel-acquired dengue were reported in Pasadena, California. On October 2, 2023, the Pasadena Public Health Department (PPHD) received a laboratory report of elevated dengue antibodies in a symptomatic patient with no recent travel history. The most common symptom of dengue is fever and can include headache; pain behind the eyes; muscle, joint, or bone pain; nausea; vomiting; and rash (*2*). The patient (person A) first experienced symptoms of arboviral illness in mid-September 2023, and required hospitalization. PPHD activated community risk mitigation measures and conducted an epidemiologic investigation in coordination with the San Gabriel Valley Mosquito and Vector Control District (SGVMVCD).

Investigations and Outcomes

Vector Risk Mitigation

On October 2, PPHD alerted SGVMVCD that person A had a suspected case of arboviral disease. During October 2–9, SGVMVCD trapped, counted, and tested mosquitoes within 0.16 miles (250 m) of person A's home, per guidance from the California Department of Public Health* (*4*). *Aedes* mosquito counts were eight times as high as in other routine surveillance areas in the San Gabriel Valley for the same period (80 versus an average of 10.5 adult *Aedes* mosquitoes per trap) (*5*). During the same period, SGVMVCD conducted a door-to-door mosquito prevention educational campaign and two rounds of truck-mounted adulticide and larvicide treatments in the San Gabriel Valley. Mosquito trap counts 1 week after baseline confirmed a 62% reduction in the mean number of trapped adult mosquitoes (80 per trap pretreatment versus 30 posttreatment). Reverse transcription–polymerase chain reaction (RT-PCR) testing on mosquito pools were negative for arboviruses.

Public Health Investigations

PPHD activated community risk mitigation measures and conducted an epidemiologic investigation. This activity was reviewed by CDC, deemed not research, and was conducted consistent with applicable federal law and CDC policy.†

Interviews with person A confirmed no recent travel history. The objectives of the investigation were to identify a potential index case preceding person A with relevant travel, identify potential additional secondary infections, and conduct enhanced case investigation in the surrounding neighborhood. During October 10–November 14, PPHD attempted to contact 175 households; 14 (8.0%) declined, and 31 (17.7%) could not be reached. Among the 130 (74.3%) households with a completed interview, 15 (12%) had a member with recent travel to regions where dengue is endemic, eight (6%) had a member with recent symptoms consistent with arboviral illness, and one (1%) had a member with both. Testing by RT-PCR confirmed person A to have DENV-1 infection on October 18. On December 5, follow-up interviews of the 24 households with at least one person with travel or symptoms were conducted, and six consenting adults provided serum samples. From these samples, one additional person (person B) was confirmed as having DENV-1 infection by RT-PCR. Person B had no recent travel history, no symptoms consistent with dengue, and no reported contact with recent travelers or symptomatic persons.

Preliminary Conclusions and Actions

This first confirmed symptomatic case of locally acquired dengue in California was identified in October 2023, with subsequent evidence of a second asymptomatic person with infection. Rapid deployment of vector control resources and epidemiologic investigations before laboratory confirmation were vital to timely mitigation of arboviral risk. Established, active partnership among public health and vector control agencies is important for rapid reduction of mosquito populations when local transmission of arboviral disease is suspected.

*This information was current when accessed October 2, 2023. In 2023, the recommended radius was 0.16 miles (250 meters); however, in 2024, the recommended radius is 0.09 miles (150 meters).

†45 C.F.R. part 46.102(l)(2), 21 C.F.R. part 56; 42 U.S.C. Sect. 241(d); 5 U.S.C. Sect. 552a; 44 U.S.C. Sect. 3501 et seq.

Summary

What is already known about this topic?

During 2013–2022, six cases of travel-acquired dengue were reported in Pasadena, California.

What is added by this report?

On October 2, 2023, the Pasadena Public Health Department received a laboratory report of elevated dengue antibodies from a symptomatic patient with no recent travel history. Dengue virus 1 infection was confirmed on October 18 by reverse transcription–polymerase chain reaction. Subsequent epidemiologic investigation of the surrounding neighborhood identified an asymptomatic second person with infection. Vector mitigation, conducted during October 2–9, resulted in a 62% reduction of trapped adult mosquitoes.

What are the implications for public health practice?

Swift vector mitigation response reduced adult mosquito population levels to lower community risk. Partnerships among local health departments and vector control agencies are important to ensure rapid response to locally acquired dengue cases.

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