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Varicella Outbreak Among Recent Arrivals to New York City, 2022–2024

Krishika A. Graham, MD[1]; Robert J. Arciuolo, MPH[1]; Olivia Matalka, MPH[1]; Beth M. Isaac, MPH[1]; Antonine Jean, MPH[1]; Noora Majid, MPH[1]; Leah Seifu, MD[1,2]; John Croft, MPH[1]; Bindy Crouch, MD[1]; Michelle Macaraig, DrPH[1]; Allison Lemkin, MD[1]; Guajira Thomas Caceres, MD[1]; Ramona Lall, PhD[1]; Cheryl Lawrence, MD[1]; Erica Silverman, MPA[3]; Fabienne Laraque, MD[4]; Alyssa Bouscaren[4]; Jennifer B. Rosen, MD[1]

Abstract

Varicella is an illness characterized by a generalized, pruritic rash and transmitted through airborne, droplet, and contact transmission. Although varicella causes mild-to-moderate symptoms in most persons, serious complications, including pneumonia and death, can occur. In October 2022, the New York City (NYC) Department of Health and Mental Hygiene (DOHMH) identified a varicella outbreak primarily involving persons who recently migrated from or through Central and South America and lived in an NYC shelter or residential facility; the outbreak is ongoing. Persons with suspected varicella were reported to DOHMH by city-run shelters and residential facilities, schools, and health care facilities. DOHMH investigations included patient interview and review of medical and immunization records. As of March 8, 2024, a total of 873 outbreak-associated varicella cases were reported. An outbreak-associated case was defined as a clinically compatible rash and either provider diagnosis of or known exposure to varicella in a person who recently had migrated from or through Central or South America or had an epidemiologic link to someone who did. The majority of cases (53.0%) were among children and adolescents aged 4–18 years, and most patients (91.9%) had no documentation of varicella vaccination at the time of symptom onset. In total, 28 varicella-associated hospitalizations and no deaths to date were reported. Among 780 (89.3%) cases with a known source of transmission, the most common sources included shelters and residential facilities (41.3%) and importation or possible importation (39.4%). School transmission accounted for only 1.2% of cases. Ongoing control measures include isolation of infectious persons, quarantine of nonimmune contacts, recommended temporary closure of shelters and residential facilities with evidence of residence-based transmission, and providing or supporting varicella vaccination operations. Approximately 27,000 varicella-containing vaccine doses have been administered to recently arrived migrant children, adolescents, and adults by vaccination vendors deployed by DOHMH and NYC's public hospital system. This outbreak highlights the importance of limiting transmission by achieving and maintaining high varicella vaccination coverage and the need for rapid, large-scale vaccination efforts given ongoing importations and exposures in shelters and residential facilities.

Investigation and Findings

Identification of Varicella Outbreak

Varicella is an illness characterized by a generalized, pruritic rash and transmitted through airborne, droplet, and contact transmission. Although varicella causes mild-to-moderate symptoms in most people, serious complications, including pneumonia and death, can occur. Varicella vaccine is highly

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effective at preventing infection. Since Spring 2022, New York City (NYC) has welcomed and provided assistance, including health services, legal services, education, and housing to approximately 180,000 migrants, many of whom are seeking asylum in the United States. Approximately 65,000 asylum seekers are currently living in city-run shelters and residential facilities. Many migrants are from countries that do not include varicella vaccine in their routine immunization programs or those where routine immunization programs have been disrupted (*1*). In October 2022, NYC's Department of Health and Mental Hygiene (DOHMH) identified three cases of varicella among persons living in a residential facility who had recently migrated from or through Central or South America, prompting further investigation. Since identification of those initial cases, an outbreak of varicella has been ongoing among this population.

Identification and Classification of Outbreak-Associated Varicella Cases

Before 2024, individual cases of varicella in NYC were not reportable by providers; however, reporting of outbreaks (defined as three or more cases) is mandated by NYC Health Code Section 11.03(c) (*2*). Since identification of this varicella outbreak, DOHMH issued provider alerts to emergency departments, hospitals, and federally qualified health centers describing the outbreak and requesting reporting of outbreak-associated cases (*3*). An outbreak-associated case was defined as a clinically compatible varicella rash (i.e., generalized maculopapular and vesicular rash) and either provider diagnosis of or known exposure to varicella or herpes zoster in a person who recently migrated from or through Central or South America since June 2022 or had an epidemiologic link to someone who did (e.g., by school, residence, or migration from other countries to the United States through the southern border). Cases were reported to DOHMH by medical providers, shelters and residential facilities, and schools, with additional case finding through patient interviews, electronic laboratory reports, and syndromic surveillance of emergency department chief complaints and discharge diagnoses (*International Statistical Classification of Diseases, Tenth Revision* codes) indicating varicella. Case investigations included patient interviews, review of medical and immunization records, and identification of venues attended during the incubation period (10–21 days before rash onset) or infectious period (from 2 days before rash onset until all lesions have crusted and no new lesions have appeared for 24 hours). This activity was reviewed by CDC, deemed not research, and was conducted consistent with applicable federal law and CDC policy.*

Characteristics of Outbreak-Associated Varicella Cases

As of March 8, 2024, a total of 873 outbreak-associated varicella cases was identified, with onset dates during September 12, 2022–March 6, 2024 (Figure). The median patient age was

*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.

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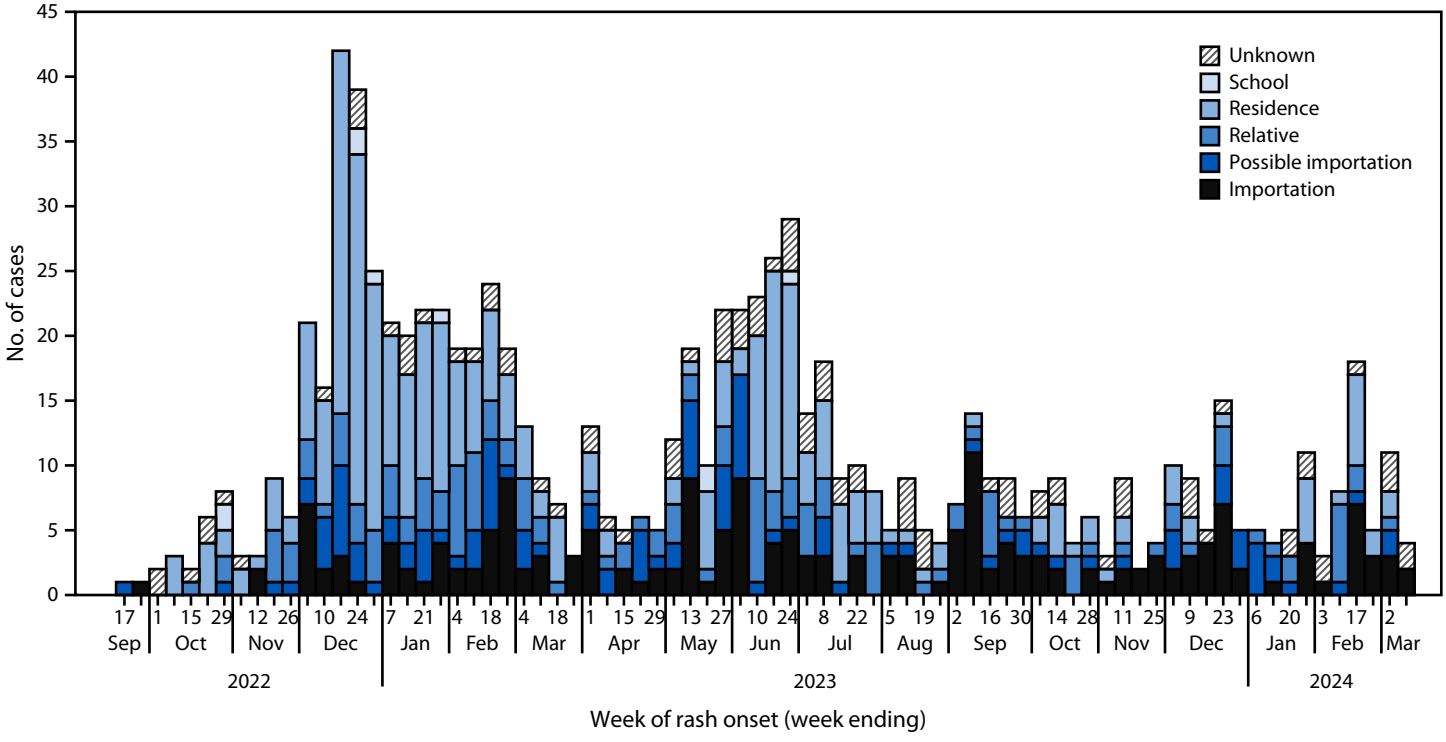
11 years (range = 2 weeks–70 years); 17.5% of cases occurred among children aged <4 years, 53.0% among children and adolescents aged 4–18 years, and 29.4% among adults aged >18 years (Table). Most (802; 91.9%) patients had no documentation of receipt of varicella vaccine at the time of symptom onset. Overall, 28 varicella-associated hospitalizations have been reported. The median age of hospitalized patients was 22 years (range = 2 weeks–43 years); 15 patients were admitted for complications, including encephalitis, pneumonia, bacteremia, and secondary bacterial skin superinfection, three for a diagnostic evaluation, and 10 for isolation or observation. Nine patients were pregnant at time of infection, five of whom delivered a newborn in NYC with a normal birth exam; four of these pregnant patients were treated with acyclovir. Two patients delivered outside NYC, and two others have not yet delivered. No varicella-associated deaths have been reported.

Sources of Transmission

Among 780 (89.3%) cases with a known source of transmission, 41.3% of persons were exposed in a shelter or residential facility, 39.4% of cases were importations or possible importations (i.e., all or part of the patient's incubation period occurred before arrival in NYC), and 18.2% were infected by a household or family member. School transmission accounted for 1.2% of cases.

Patients lived in 105 shelters and residential facilities; a median of three cases occurred in each facility (range = 1–197 cases). Notably, one large residential facility, with approximately 950 rooms used for families, has reported nearly one quarter (197, 22.6%) of all cases. This high percentage was attributed to extensive transmission at that site accounting for most of the cases during the first peak of the outbreak (December 2022–February 2023). The outbreak within this residential facility ended after an extended varicella vaccination campaign, after which the percentage of children with documentation of varicella-containing vaccine or other evidence of immunity increased from 28% in December 2022 to >80% in February 2023. A residential facility outbreak was considered to have ended when no additional cases were reported for two incubation periods (a total of 42 days) after the last case. Importation of cases into NYC is ongoing, with subsequent household spread and transmission across multiple residential facilities coinciding with the opening of new residential facilities.

FIGURE. Varicella cases, by week of rash onset and transmission source* — New York City, September 12, 2022–March 6, 2024



Abbreviation: NYC = New York City.

* Transmission sources are defined as follows: school = patient attended the same school as another patient whose infectious period overlapped with their incubation period, lived in NYC for their full incubation period, and had no known household exposure during their incubation period; residence = patient lived at the same residential facility as another patient whose infectious period overlapped with their incubation period, lived in NYC for their full incubation period, and had no known household exposure; relative = infection likely acquired from a household member whose infectious period overlapped with patient's incubation period; possible importation = patient arrived in NYC during their incubation period (10–21 days before rash onset); and importation = patient's entire incubation period (10–21 days before rash onset) occurred while living outside of NYC.

Public Health Response

Isolation, Quarantine, and Post-Exposure Prophylaxis

DOHMH worked closely with NYC agencies that oversee shelters and residential facilities to implement rapid case reporting and isolation and quarantine of susceptible contacts (children and adolescents without documentation of varicella vaccination and adults who report not having had varicella disease) as indicated. Pregnant persons exposed to varicella were screened for evidence of immunity through ascertainment of varicella vaccination records, varicella immunoglobulin G (IgG) results from previous prenatal care records, or through referral for serologic IgG testing. Pregnant contacts without evidence of varicella immunity were referred for postexposure prophylaxis with varicella zoster immune globulin (VariZIG). Beginning in February 2023, DOHMH also recommended temporary closures of sites with evidence of residence-based transmission to new residents.

TABLE. Characteristics of outbreak-associated varicella cases (N = 873) — New York City, September 12, 2022–March 6, 2024

Characteristic	No. (%)
Patient age group, yrs (n = 873)	
<4	153 (17.5)
4–18	463 (53.0)
>18	257 (29.4)
No. of documented varicella vaccine doses received at the time of symptom onset (n = 873)	
0	802 (91.9)
1	59 (6.8)
2	12 (1.4)
Place of residence (n = 873)	
Shelter or residential facility	820 (93.9)
Private residence	53 (6.1)
Hospitalizations (n = 28)	
Complications	15 (53.6)
Isolation or observation	10 (35.7)
Diagnostic evaluation	3 (10.7)
Pregnant at time of infection (n = 9)	
Delivery in NYC of newborn with normal exam at birth	5 (55.6)
Delivery outside NYC	2 (22.2)
Not yet delivered	2 (22.2)
Known source of transmission* (n = 780)	
Residence	322 (41.3)
Importation or possible importation	307 (39.4)
Relative	142 (18.2)
School	9 (1.2)

Abbreviation: NYC = New York City.

* Transmission sources are defined as follows: residence = patient lived at the same residential facility as another patient whose infectious period overlapped with their incubation period, lived in NYC for their full incubation period, and had no known household exposure; importation or possible importation = all or part of the patient's incubation period occurred before arrival in NYC (10–21 days before rash onset); relative = infection likely acquired from a household member whose infectious period overlapped with patient's incubation period; school = patient attended the same school as another patient whose infectious period overlapped with their incubation period, lived in NYC for their full incubation period, and had no known household exposure during their incubation period.

Vaccination in Shelters and Residential Facilities and Linkage to Primary Care

During the outbreak, DOHMH and other NYC agencies provided or supported vaccination operations across multiple residential facilities, prioritizing children and adolescents without documentation of varicella vaccination, by deploying vaccination vendors for onsite administration of all routine childhood vaccines. To rapidly facilitate varicella vaccination at residential facilities with multiple varicella cases, varicella vaccination was offered along with measles, mumps, and rubella (MMR) vaccine, to avoid the need to delay MMR for 28 days, because of the 28-day minimum interval recommended between administration of live viral vaccines. Influenza and COVID-19 vaccination and all routine pediatric immunizations required to attend school in NYC were also provided. Adults without documentation of varicella vaccine who reported not having had varicella disease were also offered varicella and MMR vaccination. Approximately 27,000 varicella-containing vaccine doses have been administered to recently arrived migrant children, adolescents, and adults, by vaccination vendors deployed by DOHMH (>2,900 doses) and NYC's public hospital system, NYC Health + Hospitals (>24,000 doses). Other efforts to increase vaccination included implementing door-to-door education and outreach at shelters and residential facilities to review vaccination services and school immunization requirements and creating linkages to community health centers for primary care and immunization services to ensure that remaining routine immunizations and doses needed to complete vaccination series were given. These efforts include scheduling primary care appointments for children and adolescents and providing technical support for vaccine management (assisting with vaccine ordering and reviewing vaccine storage and handling), depending on availability of clinical services onsite. DOHMH also worked closely with approximately 130 schools to notify families of children and adolescents exposed in school about reported school exposures and to recommend exclusion of susceptible children and adolescents from school until they received varicella vaccination.

Discussion

This outbreak is ongoing as of March 8, 2024. Most cases (70.6%) have occurred among children and adolescents; however, a substantial number of cases occurred among adults aged >18 years. Many recent migrants in NYC arrived from countries that do not have a routine varicella vaccination program and have a high incidence of varicella (*1*,*4*). In countries that do include varicella vaccination in routine immunization schedules, vaccination programs might have been limited or disrupted because of multiple factors, including

the COVID-19 pandemic and political instability (*5*,*6*). In addition, countries of origin were primarily tropical countries where varicella susceptibility among adults is higher; limited published data indicate a lower varicella seroprevalence among young adults than that reported in the United States (*4*,*7*,*8*). Moreover, many persons who recently migrated to NYC currently live in residential facilities. Although many of these facilities have private rooms, some are actual congregate settings, and substantial varicella transmission has been reported in one residential facility with private rooms.

This outbreak highlights the importance of high varicella vaccination coverage and the need for infrastructure to support rapid, large-scale vaccination efforts for persons who recently arrived in the United States from countries not routinely providing this vaccine. At the large NYC residential facility that experienced substantial transmission, further transmission subsided after the percentage of children with varicella immunity (i.e., vaccination or other evidence of immunity) exceeded 80%. Despite multiple exposures in schools, and approximately two thirds of cases occurring in school-aged children, minimal transmission (1.2%) was reported in this setting. This finding is likely attributable to high varicella vaccination coverage among school-aged children because of New York State law requiring documentation of 2 doses of varicella vaccine to attend school grades K–12 (*9*). In NYC, varicella vaccine coverage among kindergarten children during the 2021–22 school year was 96.7% (*10*).

Implications for Public Health Practice

Ongoing importation of varicella into NYC highlights the importance of migrants having access to varicella vaccine and other vaccines throughout their journey. Efforts to provide varicella and other routine immunizations are continuing in NYC, including through provision of onsite vaccination at residential facilities and navigation of families to primary health care services. City agencies have also set up an arrival center that offers varicella vaccinations to persons who have recently migrated at the time of their arrival in NYC. Exploring strategies to improve migrants' access to varicella and other vaccines early in their migration pathway could help increase varicella immunity in this population and limit introduction of varicella and subsequent transmission in NYC and other U.S. jurisdictions.

Syndromic surveillance and electronic laboratory reporting continue to supplement outbreak case ascertainment. In jurisdictions where individual cases of varicella are not reportable, syndromic surveillance and electronically reported laboratory results might be helpful case finding tools that could aid in identifying and responding to varicella outbreaks.

Summary

What is already known about this topic?

In October 2022, the New York City Department of Health and Mental Hygiene (DOHMH) identified a varicella outbreak among persons who recently migrated from or through Central and South America and lived in New York City (NYC) shelters or residential facilities; the outbreak is ongoing.

What is added by this report?

The majority of varicella cases (53%) occurred in persons aged 4–18 years, and most (92%) occurred in persons with no documentation of varicella vaccination. The most common sources of transmission included NYC shelters or residential facilities (41.3%) and importation or possible importation (39.4%). School transmission accounted for only 1.2% of cases. Approximately 27,000 varicella-containing vaccine doses have been administered to recently arrived migrant children, adolescents, and adults by vaccination vendors deployed by DOHMH and NYC's public hospital system.

What are the implications for public health practice?

This outbreak highlights the importance of limiting transmission by achieving and sustaining high varicella vaccination coverage and the need for rapid, large-scale vaccination efforts in light of ongoing importations and exposures in U.S. shelters and residential facilities.

Corresponding author: Krishika A. Graham, kgraham1@health.nyc.gov.

[1]New York City Department of Health and Mental Hygiene, New York, New York; [2]Epidemic Intelligence Service, CDC; [3]New York City Health and Hospitals, New York, New York; [4]New York City Department of Homeless Services, New York, New York.

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West Nile Virus and Other Nationally Notifiable Arboviral Diseases — United States, 2022

Rebekah A. Sutter, MPH[1,2]; Shelby Lyons, MPH[1]; Carolyn V. Gould, MD[1]; J. Erin Staples, MD, PhD[1]; Nicole P. Lindsey, MS[1]

Abstract

Arthropodborne viruses (arboviruses) primarily infect humans through the bite of an infected mosquito or tick. Infections are commonly asymptomatic; however, the clinical signs and symptoms can range from a mild febrile illness to severe neuroinvasive disease. This report summarizes data for six nationally notifiable arboviral diseases for 2022 reported to ArboNET, the national surveillance system for arboviral diseases, including eastern equine encephalitis, Jamestown Canyon, La Crosse, Powassan, St. Louis encephalitis, and West Nile viruses. In 2022, these viruses caused 1,247 human disease cases, 968 (78%) hospitalizations, and 103 (8%) deaths. Reported case counts decreased from 2021 for all viruses except Powassan and St. Louis encephalitis viruses. Despite a substantial decrease in reported cases from 2021, West Nile virus remained the leading cause of arboviral disease in the continental United States. Variations in annual arboviral disease incidence and distribution highlight the importance of high-quality surveillance. Health care providers should suspect arboviral infection in patients with a clinically compatible illness, consider testing, and report positive findings to their state or local health department. In areas with arboviral activity, community and household efforts to reduce vector populations (e.g., applying insecticides and reducing breeding sites) and personal protective measures to decrease mosquito and tick exposures (e.g., wearing repellents and protective clothing) can reduce arboviral disease morbidity and mortality.

Introduction

Arthropodborne viruses (arboviruses) are transmitted to humans primarily through the bite of an infected mosquito or tick. Rarely, transmission occurs through blood transfusion and organ transplantation. West Nile virus (WNV) is the leading cause of arboviral disease in the continental United States (*1*). Other domestic arboviruses cause sporadic cases and occasional outbreaks. Most arboviral infections are asymptomatic, with clinical signs and symptoms ranging from a mild febrile illness to severe neuroinvasive disease (*2*). This report summarizes nationally notifiable arboviral diseases reported to CDC for 2022.

Methods

Data for six nationally notifiable, domestic arboviruses (eastern equine encephalitis, Jamestown Canyon, La Crosse, Powassan, St. Louis encephalitis, and West Nile viruses) were analyzed and are included in this report. Chikungunya, dengue, yellow fever, and Zika virus disease cases are excluded because these infections are primarily travel-associated when they occur in U.S. states (*3*,*4*). Surveillance data are obtained from ArboNET, the national surveillance system for arboviral diseases. Disease cases are reported by state health departments to ArboNET using a standard case definition that includes clinical and laboratory criteria.* Cases reported as probable† and confirmed§ are included in this report and are reported on the basis of state and county of residence. Cases are described by demographic characteristics including age and sex, quarter year of illness onset (January–March, April–June, July–September, and October–December), clinical syndrome (neuroinvasive [acute flaccid paralysis, encephalitis, meningitis, or other neurologic signs and symptoms] versus nonneuroinvasive [all other cases]), and outcome (hospitalization and death). Incidence was calculated using 2022 midpoint population estimates from the U.S. Census Bureau.¶ All statistical analyses were conducted using SAS software (version 9.4; SAS Institute). This activity was reviewed by CDC, deemed not research, and was conducted consistent with applicable federal law and CDC policy.**

* https://ndc.services.cdc.gov/case-definitions/arboviral-diseases-neuroinvasive-and-non-neuroinvasive-2015/

† A probable case meets clinical criteria for arboviral infection and virus-specific immunoglobulin M (IgM) antibodies in cerebrospinal fluid (CSF) or serum but without other testing.

§ A confirmed case meets clinical criteria for arboviral disease and at least one of the following laboratory criteria: 1) isolation of virus from, or demonstration of specific viral antigen or nucleic acid in, tissue, blood, CSF, or other body fluid; 2) fourfold or greater change in virus-specific quantitative antibody titers in paired sera; 3) virus-specific IgM antibodies in serum with confirmatory virus-specific neutralizing antibodies in the same or a later specimen; or 4) virus-specific IgM antibodies in CSF and a negative result for other IgM antibodies in CSF for arboviruses endemic in the region where exposure occurred.

¶ https://www.census.gov/data/tables/time-series/demo/popest/2020s-state-total.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.

Results

A total of 1,247 domestic arboviral disease cases with illness onset in 2022 were reported to CDC (Table 1). Overall, 1,132 (91%) cases were caused by WNV, followed by Powassan (47; 4%), St. Louis encephalitis (33; 3%), La Crosse (22; 2%), Jamestown Canyon (12; 1%), and eastern equine encephalitis (one; <1%) viruses. Cases were reported from 414 (13%) of the 3,143 U.S. counties in 45 states and the District of Columbia (DC).

West Nile Virus Disease

The 1,132 WNV disease cases were reported from 358 counties in 42 states and DC; 966 (85%) patients had illness onset during July–September. Median patient age was 63 years, and 61% were male. A total of 862 (76%) patients were hospitalized, and 93 (8%) died. Three patients with nonfatal neuroinvasive disease were infected through solid organ transplants from a common donor.

Among all patients with WNV disease, 827 (73%) had neuroinvasive disease, 772 (93%) of whom were hospitalized, including 91 (11%) who died. The national incidence of neuroinvasive WNV disease was 0.25 per 100,000 population (Table 2). The highest WNV neuroinvasive disease incidences occurred in South Dakota (3.96 per 100,000), Colorado (2.24), and Nebraska (1.88). The largest numbers of neuroinvasive disease cases were reported from California (162), Colorado (131), and New York (75), accounting for 44% of neuroinvasive disease cases nationally. WNV neuroinvasive disease incidence increased with age from 0.01 per 100,000 among persons aged <10 years to 0.78 per 100,000 among those aged ≥70 years. Incidence of WNV neuroinvasive disease was 68% higher among males (0.32 per 100,000) than among females (0.19).

Powassan Virus Disease

Forty-seven cases of Powassan virus disease were reported from 39 counties in nine states. In 2022, Powassan virus disease was reported from Vermont for the first time. Illness onset occurred most frequently during April–June (45%) (Table 1). Median patient age was 64 years, and 55% of patients were male. Forty-three (91%) patients experienced neuroinvasive disease, 45 (96%) patients were hospitalized, and seven (15%) died. States with the highest incidence of neuroinvasive disease included Maine (0.29 per 100,000), Connecticut (0.17), and

TABLE 1. Number and percentage of reported cases of nationally notifiable nonneuroinvasive and neuroinvasive arboviral diseases, by virus type and selected patient characteristics (N = 1,247)* — United States, 2022

Characteristic	Virus type, no. (%) of cases				
	West Nile n = 1,132	Powassan n = 47	St. Louis encephalitis n = 33	La Crosse n = 22	Jamestown Canyon n = 12
Age group, yrs					
<18	25 (2)	7 (15)	0 (—)	21 (95)	0 (—)
18–59	429 (38)	14 (30)	14 (42)	0 (—)	6 (50)
≥60	678 (60)	26 (55)	19 (58)	1 (5)	6 (50)
Median age (IQR)	63 (50–73)	64 (43–72)	65 (50–74)	9 (5–11)	60 (40–74)
Sex					
Female	439 (39)	21 (45)	13 (39)	10 (45)	3 (25)
Male	693 (61)	26 (55)	20 (61)	12 (55)	9 (75)
Period of illness onset†					
Jan–Mar	9 (1)	4 (9)	0 (—)	0 (—)	1 (8)
Apr–Jun	36 (3)	21 (45)	5 (15)	0 (—)	5 (42)
Jul–Sep	966 (85)	11 (23)	15 (45)	20 (91)	2 (17)
Oct–Dec	120 (11)	11 (23)	13 (39)	2 (9)	4 (33)
Clinical syndrome					
Nonneuroinvasive	305 (27)	4 (9)	6 (18)	3 (14)	1 (8)
Neuroinvasive	827 (73)	43 (91)	27 (82)	19 (86)	11 (92)
Encephalitis§	501 (61)	29 (67)	14 (52)	16 (84)	6 (55)
Meningitis§	210 (25)	4 (9)	10 (37)	3 (16)	3 (27)
AFP§,¶,**	41 (5)	4 (9)	1 (4)	0 (—)	0 (—)
Unspecified§	75 (9)	6 (14)	2 (7)	0 (—)	2 (18)
Outcome					
Hospitalization	862 (76)	45 (96)	29 (88)	21 (95)	10 (83)
Death	93 (8)	7 (15)	3 (9)	0 (—)	0 (—)

Abbreviation: AFP = acute flaccid paralysis.

* One eastern equine encephalitis virus disease case was also reported.

† Date of illness onset is unknown for one case of West Nile virus disease.

§ Percentages of cases of encephalitis, meningitis, AFP, and unspecified neurologic signs or symptoms are percentages of neuroinvasive cases.

¶ Among the 41 West Nile virus disease cases with AFP, 10 (24%) also had encephalitis or meningitis.

** Among the four Powassan virus disease cases with AFP, three also had encephalitis or meningitis.

TABLE 2. Number and incidence* of reported cases of nationally notifiable arboviral neuroinvasive disease, by virus type and U.S. Census Bureau division and jurisdiction — United States, 2022

U.S. Census Bureau division/jurisdiction	Neuroinvasive disease cases, by virus type, no. (incidence)*				
	West Nile	Powassan	St. Louis encephalitis	La Crosse	Jamestown Canyon
United States	**827 (0.25)**	**43 (0.01)**	**27 (<0.01)**	**19 (<0.01)**	**11 (<0.01)**
New England	15 (0.10)	15 (0.10)	—†	—	3 (0.02)
Connecticut	7 (0.19)	6 (0.17)	—	—	—
Maine	—	4 (0.29)	—	—	—
Massachusetts	7 (0.10)	4 (0.06)	—	—	1 (0.01)
New Hampshire	—	—	—	—	—
Rhode Island	1 (0.09)	—	—	—	2 (0.18)
Vermont	—	1 (0.15)	—	—	—
Middle Atlantic	114 (0.27)	13 (0.03)	—	—	—
New Jersey	13 (0.14)	2 (0.02)	—	—	—
New York	75 (0.38)	7 (0.04)	—	—	—
Pennsylvania	26 (0.20)	4 (0.03)	—	—	—
East North Central	57 (0.12)	8 (0.02)	—	12 (0.03)	7 (0.01)
Illinois	27 (0.21)	—	—	—	—
Indiana	6 (0.09)	—	—	—	—
Michigan	13 (0.13)	—	—	—	3 (0.03)
Ohio	5 (0.04)	—	—	12 (0.10)	—
Wisconsin	6 (0.10)	8 (0.14)	—	—	4 (0.07)
West North Central	123 (0.57)	7 (0.03)	—	3 (0.10)	1 (<0.01)
Iowa	8 (0.25)	—	—	—	—
Kansas	6 (0.20)	—	—	—	—
Minnesota	17 (0.30)	7 (0.12)	—	3 (0.05)	1 (0.02)
Missouri	11 (0.18)	—	—	—	—
Nebraska	37 (1.88)	—	—	—	—
North Dakota	8 (1.03)	—	—	—	—
South Dakota	36 (3.96)	—	—	—	—
South Atlantic	59 (0.09)	—	—	3 (<0.01)	—
Delaware	1 (0.10)	—	—	—	—
District of Columbia	1 (0.15)	—	—	—	—
Florida	7 (0.03)	—	—	—	—
Georgia	16 (0.15)	—	—	—	—
Maryland	6 (0.10)	—	—	—	—
North Carolina	12 (0.11)	—	—	2 (0.02)	—
South Carolina	10 (0.19)	—	—	—	—
Virginia	6 (0.07)	—	—	—	—
West Virginia	—	—	—	1 (0.06)	—

See table footnotes on the next page.

Vermont (0.15) (Table 2). All patients who died were aged >60 years (median age = 67 years; range = 61–91 years).

St. Louis Encephalitis Virus Disease

Thirty-three cases of St. Louis encephalitis virus disease were reported from 12 counties in three states. Illness onset occurred most frequently during July–September (45%), although 39% of cases occurred during October–December (Table 1). All late-season cases were reported in the southwestern United States (Arizona, California, and Texas). Median patient age was 65 years, and 61% of patients were male. Twenty-seven (82%) patients had neuroinvasive disease, 29 (88%) were hospitalized, and three (9%) died. The highest incidences of neuroinvasive disease were reported from Arizona (0.16 per 100,000) and California (0.04) (Table 2). All patients who died were aged >65 years (median age = 83 years; range = 68–85 years).

La Crosse Virus Disease

Twenty-two cases of La Crosse virus disease were reported from 19 counties in five states. Twenty (91%) patients experienced illness onset during July–September (Table 1); the median patient age was 9 years, and 55% of patients were male. Nineteen (86%) patients had neuroinvasive disease. Twenty-one (95%) patients were hospitalized; none died. Ohio reported the highest number of neuroinvasive disease cases (12; 63%) (Table 2), and the highest incidences of neuroinvasive disease occurred in Ohio (0.10 per 100,000), West Virginia (0.06), and Minnesota (0.05).

Jamestown Canyon Virus Disease

Among 12 cases of Jamestown Canyon virus disease reported from 12 counties in five states, illness onset occurred most frequently during April–June (five cases) (Table 1). The median patient age was 60 years, and nine of the 12 patients were male.

TABLE 2. (*Continued*) Number and incidence* of reported cases of nationally notifiable arboviral neuroinvasive disease, by virus type and U.S. Census Bureau division and jurisdiction — United States, 2022

U.S. Census Bureau division/jurisdiction	Neuroinvasive disease cases, by virus type, no. (incidence)*				
	West Nile	Powassan	St. Louis encephalitis	La Crosse	Jamestown Canyon
East South Central	17 (0.09)	—	—	1 (<0.01)	—
Alabama	6 (0.12)	—	—	—	—
Kentucky	3 (0.07)	—	—	—	—
Mississippi	5 (0.17)	—	—	—	—
Tennessee	3 (0.04)	—	—	1 (0.01)	—
West South Central	87 (0.21)	—	1 (<0.01)	—	—
Arkansas	3 (0.10)	—	—	—	—
Louisiana	41 (0.89)	—	—	—	—
Oklahoma	4 (0.10)	—	—	—	—
Texas	39 (0.13)	—	1 (<0.01)	—	—
Mountain	187 (0.73)	—	12 (0.05)	—	—
Arizona	40 (0.54)	—	12 (0.16)	—	—
Colorado	131 (2.24)	—	—	—	—
Idaho	1 (0.05)	—	—	—	—
Montana	—	—	—	—	—
Nevada	—	—	—	—	—
New Mexico	8 (0.38)	—	—	—	—
Utah	5 (0.15)	—	—	—	—
Wyoming	2 (0.34)	—	—	—	—
Pacific	168 (0.32)	—	14 (0.03)	—	—
Alaska	—	—	—	—	—
California	162 (0.42)	—	14 (0.04)	—	—
Hawaii	—	—	—	—	—
Oregon	3 (0.07)	—	—	—	—
Washington	3 (0.04)	—	—	—	—

* Cases per 100,000 population, based on July 1, 2022, U.S. Census Bureau population estimates.
† Dashes indicate no reported cases.

All but one patient had neuroinvasive disease and 10 patients were hospitalized; no deaths were reported. Wisconsin reported the highest number of neuroinvasive disease cases (four) and the highest incidence (0.18 per 100,000) of neuroinvasive disease occurred in Rhode Island (Table 2).

Eastern Equine Encephalitis Virus Disease

One case of eastern equine encephalitis virus disease was reported. The patient was a woman aged >60 years with illness onset in August. The patient experienced neuroinvasive disease and was hospitalized.

Discussion

Overall, the number of arboviral disease cases reported in 2022 (1,247) decreased 59% compared with the 3,035 cases reported in 2021. This decrease was largely driven by a 61% decrease in reported WNV disease cases in 2022 (1,132) compared with the 2,911 cases reported in 2021, when a large WNV disease outbreak occurred in Arizona (*1*). WNV disease remained the most commonly reported domestic arboviral disease. La Crosse virus remained the most common cause of neuroinvasive arboviral disease in children.

In contrast to other arboviruses, historically high numbers of St. Louis encephalitis virus and Powassan virus disease cases were reported in 2022. The 33 St. Louis encephalitis virus disease cases represent the highest number of cases since 2003, when 49 cases were reported (*5*). The 47 Powassan virus disease cases represent the highest number ever reported in a single year; the previous high was 43 cases reported in 2019 (*6*).

Arboviral diseases remain an important cause of morbidity in the United States. Although most human infections occur through the bite of infected mosquitoes or ticks, organ transplant transmission continues to occur. Currently, no national policy exists requiring arboviral screening of deceased donors (*7*). The complex interaction among humans, animals, and environment that contributes to vectorborne transmission poses challenges to predicting and controlling disease. Timely and high-quality surveillance (e.g., accurate and complete case identification, investigation, and reporting) is important to detecting arboviral disease risk and implementing interventions to lower disease incidence such as distributing prevention messaging and performing vector control activities.

Limitations

The findings in this report are subject to at least two limitations. First, ArboNET is a passive surveillance system and, as such, likely underestimates disease prevalence. Identifying

Summary

What is already known about this topic?

Humans become infected by arboviruses primarily through the bite of an infected mosquito or tick. West Nile virus is the leading cause of arboviral disease in the continental United States.

What is added by this report?

Despite fewer total arboviral disease cases in 2022 compared with 2021, historically high numbers of St. Louis encephalitis and Powassan virus disease cases were reported.

What are the implications for public health practice?

The variable occurrence of arboviral diseases highlights the importance of surveillance efforts in targeting prevention messaging and control. Health care providers should consider arboviral testing for patients with clinically compatible illnesses. Prevention depends on reducing vector populations, implementing personal protective measures to decrease exposure, and screening blood and tissue donors.

cases via ArboNET relies on patients seeking health care, providers ordering testing and establishing a diagnosis, and laboratories and clinicians reporting cases to local and state health departments. Nonneuroinvasive disease reporting is more susceptible to underreporting because patients might not seek care or undergo arboviral testing. Previous studies have estimated that 30–70 nonneuroinvasive disease cases occur for every reported case of West Nile neuroinvasive disease (*8*). Based on the 827 neuroinvasive disease cases reported in 2022, an estimated 24,810–57,890 nonneuroinvasive disease cases occurred; however, only 305 (0.5%–1.2% of the estimated total) were reported. Second, because ArboNET does not require information about clinical signs and symptoms or laboratory findings, cases might be misclassified, potentially affecting case classification.

Implications for Public Health Practice

Understanding the epidemiology, seasonality, and geographic distribution of arboviruses is important for clinical recognition. Health care providers should consider arboviral disease testing in patients with a clinically compatible illness (e.g., febrile illness, meningitis, or encephalitis) during transmission seasons when ticks and mosquitos are active or after receipt of transplanted organs or blood transfusion. Positive test results should be reported to a state or local health department. Infections temporally associated with blood transfusion or organ transplantation should also be reported promptly to allow potentially infected products to be identified and removed from circulation. No treatments or vaccines are currently available for domestic arboviral infections. Therefore, prevention and control efforts rely on personal protective measures to decrease exposure to mosquitos[††] and ticks[§§] (e.g., wearing repellents and protective clothing), community and household effort to decrease vector populations,[¶¶] (e.g., applying insecticides and reducing breeding sites), and blood donor screening to minimize transfusion transmission.[***]

[††] https://www.cdc.gov/mosquitoes/prevention/index.html
[§§] https://www.cdc.gov/ticks/prevention/index.html
[¶¶] https://www.cdc.gov/mosquitoes/mosquito-control/index.html
[***] https://www.cdc.gov/blood-safety/about/index.html

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National Arboviral Surveillance System surveillance coordinators in state and local health departments; Surveillance and Epidemiology Team, Arboviral Diseases Branch, CDC.

Corresponding author: J. Erin Staples, auv1@cdc.gov.

[1]Division of Vector-Borne Diseases, National Center for Emerging and Zoonotic Infectious Diseases, CDC; [2]Epidemic Intelligence Service, CDC.

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Morbidity and Mortality Weekly Report

Early Safety Findings Among Persons Aged ≥60 Years Who Received a Respiratory Syncytial Virus Vaccine — United States, May 3, 2023–April 14, 2024

Anne M. Hause, PhD[1]; Pedro L. Moro, MD[1]; James Baggs, PhD[1]; Bicheng Zhang, MS[1]; Paige Marquez, MSPH[1]; Michael Melgar, MD[2]; Amadea Britton, MD[2]; Erin Stroud, MD[1]; Tanya R. Myers, PhD[1]; Jeffrey Rakickas, MD[1]; Phillip G. Blanc, MD[3]; Kerry Welsh, MD[3]; Karen R. Broder, MD[1]; John R. Su, MD[1]; David K. Shay, MD[1]

Abstract

In May 2023, the Food and Drug Administration (FDA) licensed Arexvy and Abrysvo vaccines for prevention of respiratory syncytial virus (RSV) lower respiratory tract disease in adults aged ≥60 years. In prelicensure trials, Guillain-Barré syndrome (GBS) was identified as a potential safety concern. During August 4, 2023–March 30, 2024, at least 10.6 million adults aged ≥60 years received a recommended RSV vaccine. During May 3, 2023–April 14, 2024, CDC reviewed data reported after RSV vaccination to V-safe, an active U.S. surveillance system that invites enrolled participants to complete web-based surveys, and reports to the Vaccine Adverse Event Reporting System (VAERS), a passive, voluntary surveillance system that accepts adverse event reports from the public, providers, and manufacturers. Findings from V-safe and VAERS were generally consistent with those from trials. Reporting rates of GBS after RSV vaccination in VAERS (4.4 and 1.8 reports per million doses of Abrysvo and Arexvy vaccine administered, respectively) were higher than estimated expected background rates in a vaccinated population. CDC and FDA are conducting population-based surveillance to assess risks for GBS and other adverse events. Findings from these studies will help guide development of Advisory Committee on Immunization Practices recommendations.

Introduction

Respiratory syncytial virus (RSV) infection can cause lower respiratory tract disease, hospitalization, and death in older adults and is responsible for substantial morbidity and mortality among this age group (*1*). The Food and Drug Administration (FDA) licensed Arexvy (GlaxoSmithKline Biologicals [GSK]) and Abrysvo (Pfizer Inc.) vaccines on May 3 and May 31, 2023, respectively, for prevention of lower respiratory tract disease caused by RSV in adults aged ≥60 years (*2,3*). On June 21, 2023, the Advisory Committee on Immunization Practices (ACIP) recommended that adults aged ≥60 years may receive a single dose of RSV vaccine, using shared clinical decision-making (*4*). Guillain-Barré syndrome (GBS) was identified as a potential vaccine safety concern in clinical trials of both RSV vaccines (*4*). To characterize early post-marketing vaccine safety findings in adults aged ≥60 years after RSV vaccination, CDC reviewed health surveys and adverse events reported to V-safe, an active U.S. surveillance system that sends web surveys to enrolled participants during the 6 weeks after vaccination, and the Vaccine Adverse Event Reporting System (VAERS), a passive, voluntary surveillance system that monitors adverse events after vaccination, during May 3, 2023–April 14, 2024* (*5*). During August 4, 2023–March 30, 2024, approximately 7.2 million adults aged ≥60 years received GSK RSV vaccine, and 3.4 million received Pfizer RSV vaccine.† Among the 16,220 V-safe participants aged ≥60 years who reported receiving an RSV vaccine and completed one or more daily surveys, 39.0% reported at least one symptom after vaccination; 0.4% of participants reported receiving medical care. VAERS received 3,200 reports of adverse events after RSV vaccination among persons aged ≥60 years (including 28 verified reports of GBS); 91.2% of reports were classified as nonserious. Estimated VAERS GBS reporting rates after RSV vaccination were 4.4 and 1.8 reports per million administered doses of Pfizer and GSK vaccines, respectively. CDC and the partnership between FDA and the Centers for Medicare & Medicaid Services are conducting population-based surveillance assessments of RSV vaccine safety.

Methods

V-safe (https://vsafe.cdc.gov) is a voluntary, active U.S. surveillance system that sends web surveys to enrolled participants on days 0–7 after vaccination, based on the reported vaccination date.§ V-safe surveys for adults aged ≥60 years who

* This review includes V-safe data collected during October 20, 2023–April 14, 2024, for persons vaccinated during May 3, 2023–April 1, 2024. This review includes VAERS reports collected during May 3, 2023–April 14, 2024, for persons vaccinated during May 3, 2023–April 2, 2024, and reports that are missing a date of vaccination.

† Projected doses administered during August 4, 2023–March 30, 2024, at physician medical offices (data source: IQVIA Custom Medical Claims [Dx]; data current through April 6, 2024) and during August 12, 2023–March 29, 2024, at retail pharmacies (data source: IQVIA Custom Longitudinal Prescription Claims [LRx]); data are current through April 5, 2024). IQVIA data do not include vaccinations administered at other medical settings such as public health clinics, including workplaces and community locations. IQVIA uses a proprietary methodology to project doses administered in all retail pharmacies and all office-based physicians based on a sample of retail pharmacies and a sample of office-based physicians. The projection to office-based physicians uses a list of U.S.-licensed office-based physicians maintained by the American Medical Association.

§ Registered account holders can add dependents to their accounts and complete surveys on their behalf.

received an RSV vaccine were available starting October 20, 2023. Daily surveys include questions about local injection site and systemic reactions and health impacts experienced.[¶] Participants reporting medical care for symptoms are also prompted to complete a VAERS report.

VAERS (https://vaers.hhs.gov) accepts reports of adverse events from health care providers, vaccine manufacturers, and members of the public (*5*). Reports to VAERS generally cannot be used to determine causal associations between adverse events and vaccination. Medical Dictionary for Regulatory Activities Preferred Terms (MedDRA PTs) are assigned by VAERS staff members to signs, symptoms, and diagnostic findings in VAERS reports.[**] Reports of serious events (including death) to VAERS during May 3, 2023–April 14, 2024, and relevant available medical records were reviewed by CDC experts to form a clinical impression of each reported outcome[††] (*6*). Using selected MedDRA PTs, a search was performed to identify outcomes of interest, including GBS and immune thrombocytopenia (ITP), multiple cases of which were identified in clinical reviews of serious reports.[§§]

Symptoms and health impacts reported during the week after RSV vaccination were described for V-safe participants aged ≥60 years who were vaccinated during May 3, 2023–April 14, 2024, and completed one or more daily surveys. Primary VAERS adverse event reports after RSV vaccination for persons aged ≥60 years were described by serious and nonserious classification and MedDRA PTs.[¶¶] All analyses were conducted using SAS software (version 9.4; SAS Institute). Reporting rates for GBS reports that met the Brighton Collaboration case definition (*6*) were estimated using available doses administered as the denominator. This activity was reviewed by CDC, deemed not research, and was conducted consistent with applicable federal law and CDC policy.[***]

Review of V-safe Data

During May 3, 2023–April 14, 2024, a total of 16,220 V-safe participants aged ≥60 years reported receiving an RSV vaccine and completed at least one daily survey (Table 1). The median age of these participants was 70 years (range = 60–94 years), 9,684 (59.7%) were women, 6,402 (39.5%) received GSK vaccine, 3,882 (23.9%) received Pfizer vaccine, and 5,936 (36.6%) did not know the manufacturer of the vaccine they received. Approximately one third (5,043; 31.1%) of participants reported receiving one or more other vaccines during the same visit; those most commonly reported were COVID-19 (3,370; 20.8%) and influenza (2,630; 16.2%) vaccines. During the week after vaccination, 6,328 (39.0%) participants reported symptoms they considered possibly related to RSV vaccination. Injection site symptoms were reported by 2,808 (43.9%) participants who received GSK vaccine and 787 (20.3%) who received Pfizer vaccine. Most injection site symptoms were mild (3,351; 20.7%) or moderate (1,889; 11.6%) (Table 2). Systemic symptoms were reported by 2,344 (36.6%) who received GSK and 839 (21.6%) who received Pfizer. Most systemic symptoms were mild (1,997; 12.3%) or moderate (2,184; 13.5%). The most frequently reported symptoms after RSV vaccination were pain at or near the injection site (5,026; 31.0%), fatigue or tiredness (3,327; 20.5%), and muscle or body aches (2,843; 17.5%). Among those who reported other symptoms, those most commonly reported were sore throat (54; 0.3%), dizziness (38; 0.2%), and runny nose (38; 0.2%).

During the week after vaccination, 1,264 (7.8%) participants reported that they were unable to complete their normal daily activities because of the reported symptoms; 68 (0.4%) reported receiving medical care for the reported symptoms. Among those who reported receiving medical care, five completed a report to VAERS; events reported were chalazion, lower than normal blood pressure, exacerbation of chronic obstructive pulmonary disease, injection site pain, and suspected lichen planus.

Review of VAERS Data

During May 3, 2023–April 14, 2024, VAERS received and processed 3,200 reports of adverse events among persons aged

[¶] Symptom severity is self-reported as mild (symptoms noticeable, but not problematic), moderate (symptoms limit normal daily activities), or severe (symptoms make daily activities difficult or impossible); some symptoms have additional, specific severity definitions. Participants who report "other" systemic reactions can select signs, symptoms, and health conditions from a dropdown menu. The dropdown menu of 814 common signs, symptoms, and health conditions consists of the most common self-reported MedDRA PTs among VAERS reports.

[**] Each VAERS report might be assigned more than one MedDRA PT. A MedDRA-coded event does not indicate a medically confirmed diagnosis. https://www.meddra.org/how-to-use/basics/hierarchy

[††] VAERS reports are classified as serious (http://www.accessdata.fda.gov/scripts/cdrh/cfdocs/cfcfr/CFRSearch.cfm?fr5600.80) if any of the following events are reported: hospitalization, prolongation of hospitalization, life-threatening illness, permanent disability, congenital anomaly or birth defect, or death. Medical records are requested for reports of serious adverse events, including autopsy findings and death certificates for reported deaths.

[§§] CDC experts reviewed primary reports of GBS to VAERS. Reports of GBS within 42 days of RSV vaccination that met the Brighton Collaboration case definition for GBS levels 1–3 were included. Clinical reviews of serious reports identified multiple cases of ITP. To identify other potential ITP cases, a group of MedDRA PTs for thrombocytopenia were used; two additional reports of ITP were detected with this search.

[¶¶] A primary VAERS report is the first report of an event after vaccination for a particular patient; subsequent reports pertaining to the same patient and event (from the same reporter or other reporters) are termed secondary reports. Excluded from analysis were reports with missing age (1,064) or age <60 years (388), including reports indicating pregnancy at time of vaccination (401).

[***] 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.

≥60 years who reported receiving an RSV vaccine (Table 3),[†††] including 2,193 (68.5%) for GSK vaccine, 919 (28.7%) for Pfizer, and 88 (2.8%) for which the vaccine manufacturer was unknown. The median age of persons for whom a VAERS report was received was 72 years (range = 60–112 years), and 2,237 (69.9%) reports were for women. At least one other vaccine was received at the same visit for approximately one third (1,050; 32.8%) of reports, with influenza vaccine administered most commonly (625; 19.5%). Among the 3,200 VAERS reports, 346 (10.8%) specified a vaccination error (e.g., product administered at an inappropriate site, extra dose administered, or incorrect route of product administration); 64 (2.0%) reports also indicated that an adverse health event had occurred. Overall, 2,919 (91.2%) reports were classified as nonserious, including 2,026 (92.5%) after receipt of GSK vaccine and 821 (89.1%) after receipt of Pfizer vaccine. Commonly reported events included pain in an extremity (384; 13.2%), headache (376; 12.9%), pain (373; 12.8%), injection site pain (370; 12.7%), and fatigue (355; 12.2%).

Among all VAERS reports, 281 (8.8%) were classified as serious, including 216 (6.8%) for hospitalization, 81 (2.5%) for a life-threatening illness, 66 (2.1%) for a permanent disability, and 34 (1.1%) for death. Clinical impressions of serious reports included stroke or transient ischemic attack (24), GBS (37; 28 met case definition),[§§§] atrial fibrillation (14), other thromboembolic event (13), encephalitis or aseptic meningitis (11), immune thrombocytopenia (11), sepsis, bacteremia, or

[†††] Processed VAERS reports are those that have been coded using MedDRA, deduplicated, and undergone standard quality assurance and quality control review.

[§§§] This review of reports to VAERS includes 21 of the 23 verified GBS reports after RSV vaccination presented at the February 29, 2024, ACIP meeting. Excluded from this review were one report for a person aged 50 years and one report that did not include RSV vaccine in the primary report.

TABLE 1. Symptoms and health impacts reported to V-safe for persons aged ≥60 years who received a respiratory syncytial virus vaccine, by manufacturer — United States, May 3, 2023–April 14, 2024

	% Reporting symptoms or health impact after vaccination* (no.)			
Event	**GSK**	**Pfizer**	**Do not know/Cannot recall**	**Total**
No. of participants	6,402	3,882	5,936	**16,220**
Symptoms reported as related to vaccination	48.6 (3,113)	27.3 (1,058)	36.3 (2,157)	**39.0 (6,328)**
Injection site symptoms	43.9 (2,808)	20.3 (787)	31.1 (1,846)	**33.5 (5,441)**
Pain	41.3 (2,641)	17.7 (688)	28.6 (1,697)	**31.0 (5,026)**
Swelling	11.5 (737)	5.6 (217)	8.4 (497)	**8.9 (1,451)**
Redness	10.5 (671)	5.0 (195)	8.1 (478)	**8.3 (1,344)**
Itching	6.4 (412)	4.2 (162)	5.6 (330)	**5.6 (904)**
Underarm swelling or tenderness	2.6 (165)	1.8 (69)	1.4 (84)	**2.0 (318)**
Rash	1.6 (101)	1.0 (38)	1.4 (86)	**1.4 (225)**
Systemic symptoms	36.6 (2,344)	21.6 (839)	27.9 (1,656)	**29.8 (4,839)**
Fatigue or tiredness	25.6 (1,640)	13.3 (515)	19.7 (1,172)	**20.5 (3,327)**
Muscle or body aches	22.0 (1,407)	12.5 (484)	16.0 (952)	**17.5 (2,843)**
Headache	19.2 (1,227)	10.6 (413)	13.8 (820)	**15.2 (2,460)**
Fever[†]	13.1 (836)	7.5 (293)	10.7 (636)	**10.9 (1,765)**
Chills	12.1 (772)	5.8 (226)	8.3 (493)	**9.2 (1,491)**
Joint pain	11.8 (756)	6.6 (255)	8.0 (477)	**9.2 (1,488)**
Nausea	5.0 (317)	3.2 (123)	4.2 (249)	**4.2 (689)**
Diarrhea	3.1 (201)	2.1 (80)	2.9 (172)	**2.8 (453)**
Rash	0.5 (32)	0.5 (20)	0.5 (30)	**0.5 (82)**
Vomiting	0.4 (25)	0.3 (13)	0.6 (36)	**0.5 (74)**
Other[§]	3.9 (248)	2.5 (98)	2.8 (168)	**3.2 (514)**
Health impact	10.2 (654)	6.2 (239)	8.8 (524)	**8.7 (1,417)**
Unable to complete normal daily activities	9.1 (580)	5.3 (205)	8.1 (479)	**7.8 (1,264)**
Unable to work or attend school	1.9 (119)	1.3 (51)	1.7 (99)	**1.7 (269)**
Care from health care professional[¶]	0.5 (29)	0.5 (19)	0.3 (20)	**0.4 (68)**
Office visit or urgent care	0.2 (14)	0.3 (12)	0.2 (11)	**0.2 (37)**
Telehealth	0.2 (10)	0.1 (2)	0.1 (3)	**0.1 (15)**
Emergency department	0.03 (2)	0.1 (3)	0.1 (7)	**0.1 (12)**
Hospitalization	0.02 (1)	0.03 (1)	0.03 (2)	**0.02 (4)**
Other	0.1 (8)	0.1 (2)	0 (—)	**0.1 (10)**

* Percentage of participants who reported a symptom or health impact at least once during days 0–7 postvaccination.
† Fever is a self-reported symptom and might not reflect the clinical definition of fever.
§ Among those who reported "Other" symptoms, 409 selected additional symptoms from a dropdown menu; most commonly selected were sore throat (54), dizziness (38), runny nose (38), cough (27), dizziness upon standing (17), and congestion (16).
¶ Participants can select from more than one type of care received from a health professional, including doctor appointment or urgent care clinic visit, telehealth, virtual health, or email health consultation, emergency department or emergency department visit, hospitalization, and other.

TABLE 2. Self-reported symptom severity reported to V-safe for persons aged ≥60 years who received a respiratory syncytial virus vaccine — United States, May 3, 2023–April 14, 2024

	% Reporting symptoms or health impact after vaccination† (no.)			
Symptom severity*	**GSK**	**Pfizer**	**Do not know/Cannot recall**	**Total**
No. of participants	6,402	3,882	5,936	**16,220**
Any injection site symptoms	43.9 (2,808)	20.3 (787)	31.1 (1,846)	**33.5 (5,441)**
Mild	27.2 (1,739)	12.4 (482)	19.0 (1,1130)	**20.7 (3,351)**
Moderate	15.3 (982)	7.0 (271)	10.7 (636)	**11.6 (1,889)**
Severe	1.4 (87)	0.9 (34)	1.3 (80)	**1.2 (201)**
Any systemic symptoms§	36.6 (2,344)	21.6 (839)	27.9 (1,656)	**29.8 (4,839)**
Mild	15.6 (1,001)	9.0 (350)	10.9 (646)	**12.3 (1,997)**
Moderate	16.4 (1,048)	9.6 (372)	12.9 (764)	**13.5 (2,184)**
Severe	3.8 (242)	2.2 (86)	3.5 (209)	**3.3 (537)**
Fever or feverish¶	13.1 (836)	7.5 (293)	10.7 (636)	**10.9 (1,765)**
No recorded temperature	8.2 (525)	4.5 (174)	7.1 (423)	**7.1 (1,122)**
Normal or subfebrile	3.3 (209)	2.0 (78)	2.2 (129)	**2.6 (416)**
Mild	1.5 (96)	1.0 (38)	1.3 (80)	**1.3 (214)**
Moderate	0.1 (6)	0.1 (3)	0.1 (4)	**0.1 (13)**
Severe	0 (—)	0 (—)	0 (—)	**0 (—)**

* Symptom severity was self-reported. The following definitions describe the severity of symptoms: mild = symptoms noticeable, but not problematic; moderate = symptoms limit normal daily activities; or severe = symptoms make daily activities difficult or impossible. Some symptoms have specific severity definitions.
† Percentage of participants who reported a symptom or health impact at least once during days 0–7 postvaccination.
§ The symptom severity total differs from the total systemic symptoms reported because severity is not collected for other symptoms.
¶ "Fever or feverish" is a self-reported symptom and might not correspond to a clinical definition of fever. The number of registrants (1,765) who reported having a fever or feeling feverish differs from the total who entered information about temperature (643). Severity of fever was defined as follows: normal or subfebrile = 96.0°–100.3°F (35.6°–37.9°C); mild = 100.4°–102.2°F (38.0°–39.0°C); moderate = 102.3°–103.9°F (39.1°–39.9°C); and severe = 104.0°–107.0°F (40.0°–41.7°C).

both (11), and shoulder pain (11). Among the 28 reports of GBS after vaccination that met case definition, 13 (46.4%) were after GSK vaccine (1.8 reports per 1 million doses administered), and 15 (53.6%) were after Pfizer vaccine (4.4 reports per 1 million doses administered). For the 18 reports of death with sufficient information for review, reported causes of death were acute respiratory distress syndrome, bronchopneumonia, cardiac event, cardiopulmonary arrest, ehrlichiosis, GBS (two), hepatic encephalopathy, hypoxic respiratory failure, multifocal leukoencephalopathy, respiratory failure, rhabdomyolysis, RSV infection, sepsis, sepsis secondary to pneumonia, *Pseudomonas* bacteremia, varicella-zoster virus meningoencephalitis, and vascular dementia.

Discussion

This review provides early findings from V-safe and VAERS surveillance systems during the first months of GSK and Pfizer RSV vaccine administration among U.S. adults aged ≥60 years. The findings in this report are generally consistent with those from safety data collected in prelicensure clinical trials, including the observance of GBS cases¶¶¶ (*2*,*3*).

In V-safe, injection site and systemic reactions were more frequently reported among those who received GSK than among those who received Pfizer vaccine; few participants reported receiving medical care (*2*,*3*). Expected vaccination reactions (e.g., pain in extremity, headache, and fatigue) were among the most frequently reported events among nonserious VAERS reports. Using VAERS data, estimated GBS reporting rates after RSV vaccination among persons aged ≥60 years were 4.4 and 1.8 reports per million doses of Pfizer and GSK vaccine administered, respectively.

VAERS reporting rates of GBS after mRNA COVID-19 vaccination were used to estimate expected background rates of GBS in this study population; no excess risk for GBS was observed after mRNA COVID-19 vaccinations in active Vaccine Safety Datalink surveillance (*7*). VAERS reporting rates for GBS among adults aged ≥65 years were 0.43 and 0.54 per million doses of Pfizer-BioNTech and Moderna COVID-19 vaccines, respectively**** (*8*). Thus, using the reporting rate for mRNA COVID-19 vaccines as an estimate of background rate, reports of GBS after RSV vaccination were more common than expected. Two deaths among vaccine recipients who had been diagnosed with GBS were reported.

¶¶¶ All but one verified VAERS report of GBS indicated that symptoms occurred within 21 days of RSV vaccination. The other report indicated onset of GBS symptoms 22 days after RSV vaccination. In GSK RSV vaccine clinical trials in older adults (18,304 vaccine recipients aged ≥60 years), one case of GBS was reported within 42 days after receipt of the GSK vaccine. In Pfizer RSV vaccine clinical trials in older adults (20,255 vaccine recipients aged ≥60 years), two cases of GBS were reported within 42 days after vaccination.

**** VAERS reports of GBS within 21 days of Pfizer-BioNTech and Moderna COVID-19 vaccination that met the Brighton Collaboration case definition for GBS levels 1–3 were included in reporting rate estimations.

TABLE 3. Events reported to the Vaccine Adverse Event Reporting System for persons aged ≥60 years after receipt of a respiratory syncytial virus vaccine — United States, May 3, 2023–April 14, 2024

Event	Vaccine, no. reporting (%)			
	GSK	Pfizer	Do not know/Cannot recall	Total
Total participants	**2,193**	**919**	**88**	**3,200**
Events among nonserious reports[*,†]	2,026 (92.5)	821 (89.1)	72 (81.8)	**2,919 (91.2)**
Arthralgia	183 (9.0)	85 (10.4)	7 (9.7)	**240 (8.2)**
Erythema	186 (9.2)	57 (6.9)	4 (5.6)	**384 (13.2)**
Fatigue	235 (11.6)	102 (12.4)	18 (25.0)	**355 (12.2)**
Fever	215 (10.6)	83 (10.1)	9 (12.5)	**247 (8.5)**
Headache	261 (12.9)	105 (12.8)	10 (13.9)	**376 (12.9)**
Injection site erythema	261 (12.9)	66 (8.0)	2 (2.8)	**275 (9.4)**
Injection site pain	291 (14.4)	72 (8.8)	7 (9.7)	**370 (12.7)**
Injection site swelling	187 (9.2)	51 (6.2)	2 (2.8)	**376 (12.9)**
Pain	276 (13.6)	85 (10.4)	12 (16.7)	**373 (12.8)**
Pain in extremity	282 (13.9)	94 (11.4)	8 (11.1)	**384 (13.2)**
Events among serious reports[§,¶]	167 (7.6)	98 (10.7)	16 (18.2)	**281 (8.8)**
Allergic reaction[**]	3	4	0	**7**
Anaphylaxis	1	1	0	**2**
Arrhythmia, other	4	1	1	**6**
Atrial fibrillation[††]	8	3	3	**14**
Congestive heart failure	2	2	0	**4**
Dyspnea or cough	3	2	0	**5**
Encephalitis or aseptic meningitis	5	5	1	**11**
Guillain-Barré syndrome[§§]	18	19	0	**37**
Injection site pain or reaction[¶¶]	4	0	0	**4**
Immune thrombocytopenia[***]	5	6	0	**11**
Myocardial infarction	3	1	0	**4**
Pneumonia	5	3	1	**9**
Rash	1	2	1	**4**
RSV infection	3	2	0	**5**
Sepsis, bacteremia, or both	6	5	0	**11**
Shoulder pain	7	1	3	**11**
Stroke or transient ischemic attack	13	10	1	**24**
Syncope	6	1	0	**7**
Thromboembolic event, other[†††]	7	4	2	**13**
Transverse myelitis	2	1	0	**3**
Unevaluable	2	2	0	**4**
Death[§§§]	22	11	2	**35**

Abbreviations: GBS = Guillain Barré syndrome; MedDRA PT = Medical Dictionary for Regulatory Activities Preferred Term; RSV = respiratory syncytial virus; VAERS = Vaccine Adverse Event Reporting System.

[*] Each event is a sign or symptom in a VAERS report, coded by a MedDRA PT. MedDRA PTs are assigned by VAERS staff members after review of available data. Each VAERS report might be assigned more than one MedDRA PT, which can include normal diagnostic findings. A MedDRA PT does not necessarily indicate a medically confirmed diagnosis.

[†] Includes the top 10 most frequently coded MedDRA PTs among nonserious reports.

[§] VAERS reports are classified as serious if any of the following are reported: hospitalization (216), prolongation of hospitalization (three), life-threatening illness (81), permanent disability (66), congenital anomaly or birth defect (zero), or death (34).

[¶] Serious reports to VAERS were reviewed by CDC physicians and experts to form preliminary clinical impressions. Includes 20 most common events from preliminary clinical impressions; a report might include more than one event. Because of the small number of serious reports, percentages are not provided for serious report events. Other clinical impressions included acute appendicitis, acute hepatitis, acute on chronic renal failure, acute on chronic respiratory failure, acute renal failure, altered mental status (three), anti-neutrophil cytoplasmic antibody vasculitis, angina, autoimmune hemolytic anemia, body temperature fluctuation, cellulitis in leg, chest pain (three), choked, chronic pulmonary fibrosis, chronic obstructive pulmonary disease (two), COVID-19 infection, duodenal ulcer, epidural abscess, episodic memory loss, fall, fever (two), generalized weakness (three), headache (two), hypertension (two), hypoglycemia, laryngospasm, lower extremity ischemia, myalgia (two), myocarditis, nausea and vomiting, osteoarthritis (three), pancreatitis, pancytopenia, polymyalgia rheumatica, posterior reversible encephalopathy syndrome, reactive arthritis, receptive aphasia, respiratory distress, rhabdomyolysis, subdural hematoma after fall, seizure, spinal stenosis post laminectomy, stress cardiomyopathy, systemic inflammatory response syndrome, third cranial nerve palsy, tinnitus and hearing loss (three), unevaluable (four), urinary tract infection, vaccination related anxiety, viral illness with delirium, and visual impairment.

[**] Includes two reports of angioedema.

[††] Includes eight reports of new-onset atrial fibrillation.

[§§] This review of reports to VAERS includes 21 of the 23 verified GBS reports after RSV vaccination (including one report for a person who died) presented at the February 29, 2024, Advisory Committee on Immunization Practices meeting. Excluded from this report were one report for a person aged 50 years and one report that did not include RSV vaccine in the primary report. In addition, seven reports did not meet the case definition or were unverified because of a lack of records, and two reports remain under review. Three additional unverified reports were identified using the selected MedDRA PTs search and are not included in the table.

[¶¶] Includes one report of pyoderma.

[***] Two additional nonserious reports were identified using the selected MedDRA PTs search, which are not included in the table.

[†††] Includes reports of pulmonary embolism (10), deep vein thrombosis (two), and retinal artery occlusion (one).

[§§§] For reports of death, the following reported causes of death was available for 18 reports: acute respiratory distress syndrome, bronchopneumonia, cardiac event, cardiopulmonary arrest, ehrlichiosis, GBS (two), hepatic encephalopathy, hypoxic respiratory failure, multifocal leukoencephalopathy, respiratory failure, rhabdomyolysis, RSV infection, sepsis, sepsis secondary to pneumonia, septic shock (*Pseudomonas* bacteremia), varicella-zoster virus meningoencephalitis, and vascular dementia.

Summary

What is already known about this topic?

The Food and Drug Administration licensed Arexvy and Abrysvo vaccines in May 2023 for prevention of respiratory syncytial virus (RSV) lower respiratory tract disease in adults aged ≥60 years. In trials, Guillain-Barré syndrome (GBS) was identified as a potential safety concern.

What is added by this report?

Findings are consistent with those from trials; reports of GBS (4.4 and 1.8 reports per million doses of Abrysvo and Arexvy vaccine administered, respectively) were more common than expected background rates.

What are the implications for public health practice?

The Advisory Committee on Immunization Practices (ACIP) recommends adults aged ≥60 years may receive 1 dose of RSV vaccine. Population-based surveillance will evaluate the potential risk for GBS to guide ACIP recommendations.

Limitations

The findings in this report are subject to at least four limitations. First, V-safe is a voluntary program, and data might not be representative of the vaccinated population. Second, VAERS is a passive surveillance system and is subject to reporting biases, underreporting (especially of nonserious events), and incomplete data reporting. Third, VAERS generally cannot determine causal associations between adverse events and vaccination (*5*). Finally, because these data do not include a comparison group of unvaccinated persons with a similar likelihood of receiving an RSV vaccine, estimating the magnitude of risk for serious but rare outcomes (e.g., GBS) after vaccination is not possible.

Implications for Public Health Practice

On February 29, 2024, ACIP announced that, based on a thorough review of currently available data, the estimated benefits of RSV vaccination continued to outweigh potential risks. RSV vaccination continues to be recommended for adults aged ≥60 years using shared clinical decision-making (*9*). CDC and FDA are conducting active safety evaluations to assess risks for GBS and other adverse events of special interest after RSV vaccination. Results of these studies will help guide future CDC RSV vaccine recommendations.

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Corresponding author: Anne M. Hause, voe5@cdc.gov.

[1]Division of Healthcare Quality Promotion, National Center for Emerging and Zoonotic Infectious Diseases, CDC; [2]Coronavirus and Other Respiratory Diseases Division, National Center for Immunization and Respiratory Diseases, CDC; [3]Food and Drug Administration, Silver Spring, Maryland.

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State-Specific Hepatitis C Virus Clearance Cascades — United States, 2013–2022

Clarisse A. Tsang, MPH[1]; Julius Tonzel, MPH[1,2]; Hasan Symum, PhD[1]; Harvey W. Kaufman, MD[3]; William A. Meyer III, PhD[3]; Ademola Osinubi, MS[1]; William W. Thompson, PhD[1]; Carolyn Wester, MD[1]

Abstract

Hepatitis C is a deadly, yet curable, disease. National hepatitis C elimination goals for 2030 call for at least 80% of persons with hepatitis C to achieve viral clearance. A well-tolerated treatment results in sustained viral clearance in ≥95% of cases. Hepatitis C virus (HCV) clearance cascades characterize a sequence of steps that follow the progression from testing to sustained viral clearance. Monitoring HCV clearance cascades is important for tracking progress toward elimination goals and identifying gaps in diagnosis, treatment, and prevention. State-specific HCV clearance cascades based on laboratory results were developed using longitudinal data from a large national, commercial laboratory during January 1, 2013–December 31, 2022. State-level estimates of viral testing among persons with evidence of past or current HCV infection ranged from 51% (Hawaii) to 99% (South Dakota), and hepatitis C viral clearance among persons with diagnosed HCV infection ranged from 10% (West Virginia) to 51% (Connecticut). These are the first state-level estimates using CDC guidance and data from a large commercial laboratory with national coverage to generate HCV clearance cascades. These estimates reveal substantial gaps in hepatitis C diagnosis, treatment, and prevention and can help guide prioritization of activities and resources to achieve hepatitis C elimination goals.

Introduction

During January 2017–March 2020, approximately 2 million adults in the United States were estimated to be infected with hepatitis C virus (HCV) (*1*), and new infections approximately doubled from 2013–2022, primarily in association with injection drug use (*2*). Untreated, HCV infection can lead to advanced liver disease, liver cancer, and death; hepatitis C screening is recommended for all adults (*3*). An 8–12-week course of well-tolerated, oral treatment with direct-acting antiviral (DAA) agents is recommended for nearly all persons with HCV infection (*4*); treatment results in sustained viral clearance in ≥95% of cases (*5*), making elimination of hepatitis C as a public health threat feasible. The U.S. Department of Health and Human Services (HHS) 2021–2025 Viral Hepatitis National Strategic Plan (*6*) provides a framework for hepatitis C elimination in the United States and calls for increasing the percentage of persons who have cleared HCV infection to at least 58% by 2025 and 80% by 2030.

Substantial variation exists among states with respect to hepatitis C disease incidence and public policies affecting access to hepatitis C treatment and prevention services for persons with or at risk for acquiring hepatitis C. The HCV clearance cascade process quantifies the proportions of persons with HCV at the following five steps: 1) those who were ever infected with HCV, 2) those who received complete (e.g., HCV RNA) testing, 3) those who were identified as having an initial infection, 4) those who subsequently demonstrated viral clearance either spontaneously or in response to treatment, and 5) among those who initially cleared the virus, subsequently had evidence of recurrent viremia because of either persistent infection (e.g., unsustained viral clearance because of treatment failure) or reinfection because of ongoing risk for acquiring hepatitis C. Each state should characterize its own HCV clearance cascade to monitor progress toward state-specific hepatitis C elimination goals and prioritize allocation of public health resources.

In 2021, CDC published guidance for developing a simplified HCV clearance cascade based on HCV laboratory test results, such as those contained in public health surveillance systems (*7*). However, many state public health surveillance systems do not include comprehensive HCV test results or lack the ability to receive, deduplicate, and track person-level longitudinal laboratory test results, precluding the development of state-level HCV clearance cascades. Longitudinal commercial laboratory results have been used to develop a national HCV clearance cascade (*8*). The primary goal of this study was to develop state-specific HCV clearance cascade estimates to assist states in identifying opportunities to diagnose, treat, and prevent HCV infections in their jurisdiction.

Methods

Data Source and Definitions

Ten years of data (January 1, 2013–December 31, 2022) were analyzed for patients in all 50 states and the District of Columbia (DC) who received HCV testing by Quest Diagnostics (https://www.questdiagnostics.com). Quest Diagnostics programming was applied to deidentify and deduplicate data. Using client or provider zip code data from the laboratory requisition and a hierarchical algorithm, researchers assigned persons to a state in the following order: 1) client data from the first HCV test result of the cascade (92%),

2) ordering provider's data from the first HCV test result of the cascade (8%), and 3) client data from any subsequent HCV test result in the cascade (<1%). Test results included HCV antibody (anti-HCV), HCV RNA (quantitative or qualitative), and HCV genotype. Using previously published CDC guidance (*7*), state-specific HCV clearance cascades characterized persons according to five criteria: 1) ever infected (having received any positive HCV test result [reactive anti-HCV, detectable HCV RNA or HCV genotype] during January 1, 2013–December 31, 2021 [index period]); 2) received viral testing (having had an HCV RNA test performed during January 1, 2013–December 31, 2022, among persons categorized as ever infected [follow-up period]); 3) diagnosis of initial infection (having a detectable HCV RNA test result during the follow-up period for any person with viral testing); 4) cured or cleared (having received a subsequent undetectable HCV RNA test result during the follow-up period among any person with an initial infection); and 5) persistent infection or reinfection (having received a subsequent detectable HCV RNA test result during the follow-up period in any person categorized as cured or cleared).

Data Analysis

Frequencies at each step of the clearance cascade were calculated and stratified by state. Conditional proportions for each step of the clearance cascade were calculated using methods similar to those in the CDC Laboratory-based Hepatitis C Virus Clearance Cascade: Program Guidance for Local and State Health Departments document (*7*). Jurisdictional proportions were suppressed using National Center for Health Statistics reporting guidelines, and Clopper Pearson 95% CI estimates were also calculated. For the estimated state-level proportions, data were assumed to be missing at random.* Analyses were performed using RStudio (version 4.2.2; RStudio). This activity was reviewed by CDC, deemed research not involving human subjects, and was conducted consistent with applicable federal law and CDC policy.†

Results

State-Specific Clearance Cascade Proportions

Among the sample of 1,631,609 unique patients identified as having ever been infected, 1,627,170 (99.7%) had available state information from the laboratory requisition forms (Table). Across all states, the median proportions of viral testing, initial infection, cured or cleared, and persistent infection or reinfection were 91%, 73%, 29% and 5%, respectively (Figure 1).

By state, among those ever infected, the percentages of those who received viral testing ranged from 51% (Hawaii) to 99% (South Dakota). Among persons who received viral testing, the percentage of those who had a diagnosis of initial infection ranged from 59% (New York) to 96% (South Dakota). Among those with initial infection, the percentage of those cured or cleared ranged from 10% (West Virginia) to 51% (Connecticut). The percentage cured or cleared in 37 states was less than the estimated national average of 35%; five of the seven states with the lowest cured or cleared proportions were in southern Appalachia (West Virginia) or the north or central United States (Michigan, Minnesota, Nebraska, and Ohio). Across all jurisdictions, the percentages of HCV infections cured or cleared were below the HHS 2025 goal of 58% and well below the HHS 2030 goal of 80% (Figure 2). Finally, among those who were cured or cleared, the percentage with persistent infection or reinfection ranged from 2% (Oklahoma and Maine) to 11% (California).

Discussion

This is the first state-specific HCV clearance cascade report, comprising data from all 50 U.S. states and DC, including approximately 1.7 million persons with evidence of a positive hepatitis C test result from a large commercial laboratory during 2013–2021, and followed through the 10-year period 2013–2022. This analysis provides insight into state-specific successes and gaps along each step of the HCV clearance cascade during the DAA treatment era.

The number of persons identified as ever having been infected with HCV varied widely by state, from 125 in North Dakota, to 338,715 in California. Multiple factors can affect these numbers, including differences in the state's population size, the scope of laboratory coverage within the state, and hepatitis C prevalence by state.

HCV testing is necessary to distinguish past from current infection. Among persons in this cohort identified as ever having been infected (i.e., received any positive HCV test result), the median viral testing rate (having an HCV RNA test performed) was 91% across jurisdictions, reflective of recommended best practices promoting automatic HCV RNA testing for all specimens with reactive HCV antibody results.

Among states, the median percentages of persons cured or cleared (i.e., having an undetectable HCV RNA test result) was 29% (range = 10%–51%), well below both the HHS hepatitis C viral clearance goals for 2025 (at least 58%) and 2030 (at least 80%). These findings are consistent with recent studies highlighting low DAA treatment and viral clearance rates among persons with diagnosed hepatitis C infection (*9*,*10*). The proportion of cured or cleared persons also varied substantially by state (from 10% to 51%). Southern

* https://www.cdc.gov/nchs/data/series/sr_02/sr02-200.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.

TABLE. Hepatitis C virus clearance cascade, by jurisdiction*,†,§,¶ — United States, 2013–2022

Jurisdiction	No. ever infected†	Viral testing§		Initial infection§		Cured or cleared§		Persistent infection or reinfection§	
		No.	% (95% CI)**	No.	% (95% CI)**	No.	% (95% CI)**	No.	% (95% CI)**
Total	**1,627,170**	**1,455,895**	**89.5 (89.4–89.5)**	**1,015,147**	**69.7 (69.6–69.8)**	**350,296**	**34.5 (34.4–34.6)**	**23,685**	**6.8 (6.7–6.8)**
Alabama	19,538	18,023	92.2 (91.9–92.6)	13,176	73.1 (72.5–73.8)	3,072	23.3 (22.6–24.0)	127	4.1 (3.5–4.9)
Alaska	6,752	5,760	85.3 (84.4–86.1)	4,560	79.2 (78.1–80.2)	1,534	33.6 (32.3–35.0)	98	6.4 (5.2–7.7)
Arizona	67,995	59,416	87.4 (87.1–87.6)	42,584	71.7 (71.3–72.0)	13,966	32.8 (32.4–33.2)	939	6.7 (6.3–7.2)
Arkansas	14,586	13,610	93.3 (92.9–93.7)	10,864	79.8 (79.1–80.5)	2,641	24.3 (23.5–25.1)	85	3.2 (2.6–4.0)
California	338,715	303,634	89.6 (89.5–89.7)	214,377	70.6 (70.4–70.8)	83,337	38.9 (38.7–39.1)	8,724	10.5 (10.3–10.7)
Colorado	18,635	17,425	93.5 (93.1–93.9)	11,675	67.0 (66.3–67.7)	2,984	25.6 (24.8–26.4)	76	2.5 (2,3–2.0)
Connecticut	36,389	34,485	94.8 (94.5–95.0)	20,774	60.2 (59.7–60.8)	10,660	51.3 (50.6–52.0)	619	5.8 (5.4–6.3)
DC	4,351	2,960	68.0 (66.6–69.4)	2,056	69.5 (67.8–71.1)	257	12.5 (11.1–14.0)	15	5.8 (3.3–9.4)
Delaware	4,052	3,820	94.3 (93.5–95.0)	3,050	79.8 (78.5–81.1)	708	23.2 (21.7–24.8)	28	4.0 (2.6–5.7)
Florida	191,214	175,887	92.0 (91.9–92.1)	114,913	65.3 (65.1–65.6)	49,057	42.7 (42.4–43.0)	3,353	6.8 (6.6–7.1)
Georgia	41,073	38,128	92.8 (92.6–93.1)	25,882	67.9 (67.4–68.4)	7,886	30.5 (29.9–31.0)	470	6.0 (5.4–6.5)
Hawaii	222	114	51.4 (44.6–58.1)	107	93.9 (87.8–97.5)	—††	—	—	—
Idaho	2,684	2,566	95.6 (94.8–96.3)	2,069	80.6 (79.0–82.1)	784	37.9 (35.8–40.0)	24	3.1 (2.0–4.5)
Illinois	33,881	30,389	89.7 (89.4–90.0)	20,677	68.0 (67.5–68.6)	6,253	30.2 (29.6–30.9)	315	5.0 (4.5–5.6)
Indiana	16,696	15,469	92.7 (92.2–93)	12,614	81.5 (80.9–82.2)	3,142	24.9 (24.2–25.7)	122	3.9 (3.2–4.6)
Iowa	3,483	3,138	90.1 (89.1–91.1)	2,456	78.3 (76.8–79.7)	870	35.4 (33.5–37.4)	37	4.3 (3.0–5.8)
Kansas	9,276	8,793	94.8 (94.3–95.2)	6,449	73.3 (72.4–74.3)	2,981	46.2 (45.0–47.5)	146	4.9 (4.2–5.7)
Kentucky	42,249	38,106	90.2 (89.9–90.5)	28,359	74.4 (74.0–74.9)	6,492	22.9 (22.4–23.4)	469	7.2 (6.6–7.9)
Louisiana	22,773	20,667	90.8 (90.4–91.1)	14,815	71.7 (71.1–72.3)	4,385	29.6 (28.9–30.3)	172	3.9 (3.4–4.5)
Maine	2,660	2,433	91.5 (90.3–92.5)	1,916	78.8 (77.1–80.4)	624	32.6 (30.5–34.7)	15	2.4 (1.4–3.9)
Maryland	33,507	28,261	84.3 (84.0–84.7)	18,810	66.6 (66.0–67.1)	5,415	28.8 (28.1–29.4)	287	5.3 (4.7–5.9)
Massachusetts	70,380	62,536	88.9 (88.6–89.1)	45,231	72.3 (72.0–72.7)	16,924	37.4 (37.0–37.9)	1,161	6.9 (6.5–7.3)
Michigan	27,506	24,549	89.2 (88.9–89.6)	16,987	69.2 (68.6–69.8)	3,652	21.5 (20.9–22.1)	197	5.4 (4.7–6.2)
Minnesota	4,609	4,084	88.6 (87.7–89.5)	2,435	59.6 (58.1–61.1)	511	21.0 (19.4–22.7)	19	3.7 (2.3–5.7)
Mississippi	6,135	5,525	90.1 (89.3–90.8)	4,615	83.5 (82.5–84.5)	1,276	27.6 (26.4–29.0)	45	3.5 (2.6–4.7)
Missouri	37,813	34,764	91.9 (91.7–92.2)	26,122	75.1 (74.7–75.6)	9,897	37.9 (37.3–38.5)	460	4.6 (4.2–5.1)
Montana	2,456	2,196	89.4 (88.1–90.6)	1,599	72.8 (70.9–74.7)	359	22.5 (20.4–24.6)	9	2.5 (1.2–4.7)
Nebraska	2,474	2,025	81.9 (80.3–83.4)	1,235	61.0 (58.8–63.1)	242	19.6 (17.4–21.9)	8	3.3 (1.4–6.4)
Nevada	24,065	21,947	91.2 (90.8–91.6)	13,255	60.4 (59.7–61.0)	6,155	46.4 (45.6–47.3)	319	5.2 (4.6–5.8)
New Hampshire	6,514	6,200	95.2 (94.6–95.7)	4,535	73.1 (72.0–74.2)	1,186	26.2 (24.9–27.5)	58	4.9 (3.7–6.3)
New Jersey	32,381	29,000	89.6 (89.2–89.9)	18,839	65.0 (64.4–65.5)	6,155	32.7 (32.0–33.3)	345	5.6 (5.0–6.2)
New Mexico	12,148	10,048	82.7 (82.0–83.4)	7,333	73.0 (72.1–73.8)	2,266	30.9 (29.8–32.0)	88	3.9 (3.1–4.8)
New York	98,746	77,673	78.7 (78.4–78.9)	45,935	59.1 (58.8–59.5)	17,587	38.3 (37.8–38.7)	975	5.5 (5.2–5.9)
North Carolina	19,970	16,307	81.7 (81.1–82.2)	11,615	71.2 (70.5–71.9)	3,923	33.8 (32.9–34.6)	249	6.3 (5.6–7.2)
North Dakota	125	109	87.2 (80.0–92.5)	79	72.5 (63.1–80.6)	—	—	—	—
Ohio	40,627	34,270	84.4 (84.0–84.7)	26,805	78.2 (77.8–78.7)	2,898	10.8 (10.4–11.2)	146	5.0 (4.3–5.9)
Oklahoma	2,240	2,057	91.8 (90.6–92.9)	1,693	82.3 (80.6–83.9)	410	24.2 (22.2–26.3)	9	2.2 (1.0–4.1)
Oregon	16,539	15,382	93.0 (92.6–93.4)	11,191	72.8 (72.0–73.5)	3,026	27.0 (26.2–27.9)	107	3.5 (2.9–4.3)
Pennsylvania	74,438	68,352	91.8 (91.6–92.0)	50,838	74.4 (74.0–74.7)	17,314	34.1 (33.6–34.5)	967	5.6 (5.2–5.9)
Rhode Island	1,849	1,593	86.2 (84.5–87.7)	1,274	80.0 (77.9–81.9)	287	22.5 (20.3–24.9)	11	3.8 (1.9–6.8)
South Carolina	13,131	12,130	92.4 (91.9–92.8)	10,176	83.9 (83.2–84.5)	2,880	28.3 (27.4–29.2)	106	3.7 (3.0–4.4)
South Dakota	882	872	98.9 (97.9–99.5)	838	96.1 (94.6–97.3)	240	28.6 (25.6–31.8)	13	5.4 (2.9–9.1)
Tennessee	36,558	32,308	88.4 (88.0–88.7)	22,882	70.8 (70.3–71.3)	5,771	25.2 (24.7–25.8)	346	6.0 (5.4–6.6)
Texas	124,728	114,732	92.0 (91.8–92.1)	77,124	67.2 (66.9–67.5)	27,982	36.3 (35.9–36.6)	1,486	5.3 (5.1–5.6)
Utah	3,853	3,126	81.1 (79.9–82.4)	2,197	70.3 (68.6–71.9)	490	22.3 (20.6–24.1)	13	2.7 (1.4–4.5)
Vermont	848	788	92.9 (91.0–94.6)	533	67.6 (64.2–70.9)	130	24.4 (20.8–28.3)	—	—
Virginia	13,852	11,639	84.0 (83.4–84.6)	8,022	68.9 (68.1–69.8)	2,706	33.7 (32.7–34.8)	125	4.6 (3.9–5.5)
Washington	24,289	22,710	93.5 (93.2–93.8)	16,823	74.1 (73.5–74.6)	7,015	41.7 (41.0–42.4)	228	3.3 (2.8–3.7)
West Virginia	11,394	10,375	91.1 (90.5–91.6)	8,241	79.4 (78.6–80.2)	797	9.7 (9.0–10.3)	43	5.4 (3.9–7.2)
Wisconsin	5,591	5,233	93.6 (92.9–94.2)	4,314	82.4 (81.4–83.5)	1,130	26.2 (24.9–27.5)	31	2.7 (1.9–3.9)
Wyoming	298	281	94.3 (91.0–96.6)	198	70.5 (64.8–75.7)	39	19.7 (14.4–25.9)	—	—

Abbreviations: DC = District of Columbia; HCV = hepatitis C virus.

* All 50 states and DC.

† The ever-infected category was assessed during the baseline period January 1, 2013–December 31, 2021.

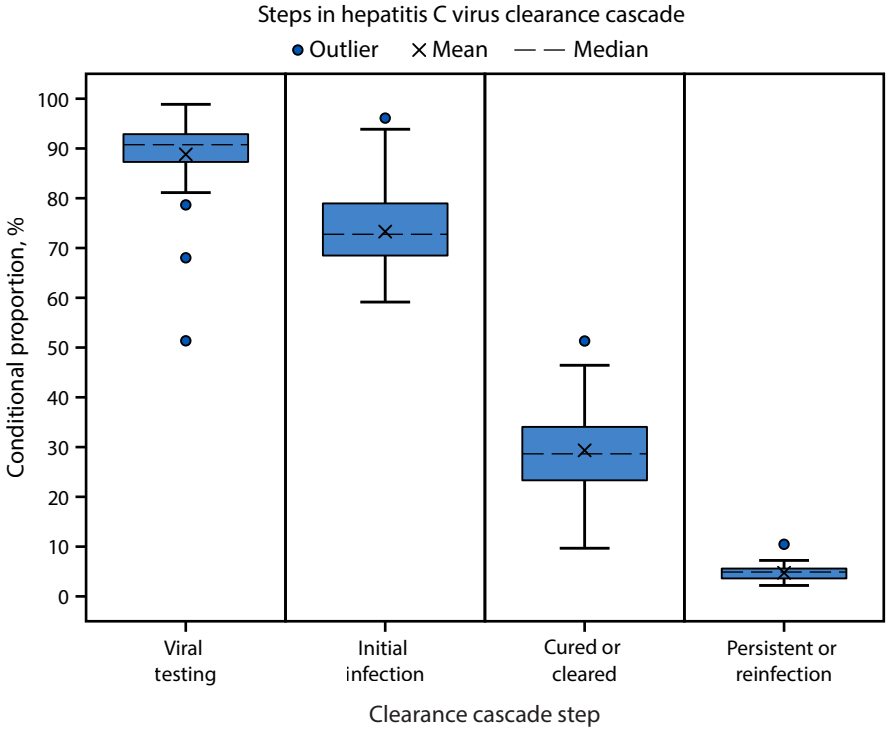
§ The viral testing, initial infection, cured or cleared, and persistent infection or reinfection categories were assessed during the follow-up period January 1, 2013–December 31, 2022.

¶ Using CDC guidance (https://pubmed.ncbi.nlm.nih.gov/32119076/), state-specific HCV clearance cascades were generated using the following definitions: 1) ever infected, defined as having received any positive HCV test result (reactive anti-HCV, detectable HCV RNA, or HCV genotype) during January 1, 2013–December 31, 2021 (index period); 2) viral testing, defined as having HCV RNA testing performed during January 1, 2013–December 31, 2022 (the follow-up period) for a person categorized as ever infected; 3) initial infection, defined as having received a detectable HCV RNA result during the follow-up period for any person who received viral testing; 4) cured or cleared, defined as having received a subsequent undetectable HCV RNA result during the follow-up period for any person with initial infection; and 5) persistent infection or reinfection, defined as receiving a subsequent detectable HCV RNA result during the follow-up period by person categorized as cured or cleared.

** Conditional proportion based on immediately preceding cascade step.

†† Dashes indicate that estimates were suppressed per National Center for Health Statistics sample guidelines. https://www.cdc.gov/nchs/data/series/sr_02/sr02-200.pdf

FIGURE 1. State-level hepatitis C virus clearance cascade estimates* — United States, 2013–2022†,§,¶



Abbreviation: HCV = hepatitis C virus.

* Conditional proportion based on immediately preceding cascade step. Quartiles are calculated using the inclusive median.

† Includes all persons ever infected during the baseline period of January 1, 2013–December 31, 2021.

§ The viral testing, initial infection, cured or cleared, and persistent infection or reinfection categories were assessed during the follow-up period of January 1, 2013–December 31, 2022.

¶ Using CDC guidance (https://pubmed.ncbi.nlm.nih.gov/32119076/), state-specific HCV clearance cascades were generated using the following definitions: 1) ever infected, defined as a person receiving any positive HCV test result (reactive anti-HCV, detectable HCV RNA, or HCV genotype) during January 1, 2013–December 31, 2021 (index period); 2) viral testing, defined as a person receiving HCV RNA testing during January 1, 2023–December 31, 2022 (the follow-up period) for a person categorized as ever infected; 3) initial infection, defined as having received a detectable HCV RNA result during the follow-up period for any person who received viral testing; 4) cured or cleared, defined as having received a subsequent undetectable HCV RNA result during the follow-up period for any person with initial infection; and 5) persistent infection or reinfection, defined as receiving a subsequent detectable HCV RNA result during the follow-up period by person categorized as cured or cleared.

Appalachian states and most north central states had HCV cure or clearance rates below the national average, highlighting the importance of improving linkage to care and treatment coverage in these regions, which are experiencing high rates of acute hepatitis C cases in association with injection drug use (*2*).

The median state-level estimate for persistent infection or reinfection (e.g., a detectable HCV RNA test result after a previously undetectable HCV RNA test result) was 5%, ranging from 2% to 11%. Because this clearance cascade does not distinguish between persistent infection and reinfection, factors contributing to these ranges might include those affecting viral clearance (e.g., duration of infection and treatment adherence) or risk for reinfection (e.g., access to syringe services programs for persons who inject drugs), highlighting the need to investigate reasons for persistent infection and reinfection.

Development of hepatitis C viral clearance cascades is important for monitoring and identifying gaps in hepatitis C elimination efforts. Ideally, each state would have comprehensive public health hepatitis C surveillance registries, including detectable and undetectable HCV RNA results, and generate their own HCV clearance cascades. Such cascades would include results from all laboratories in a state, account for persons who moved out of state or died, and use person-level data to link individual persons to treatment and prevention services.

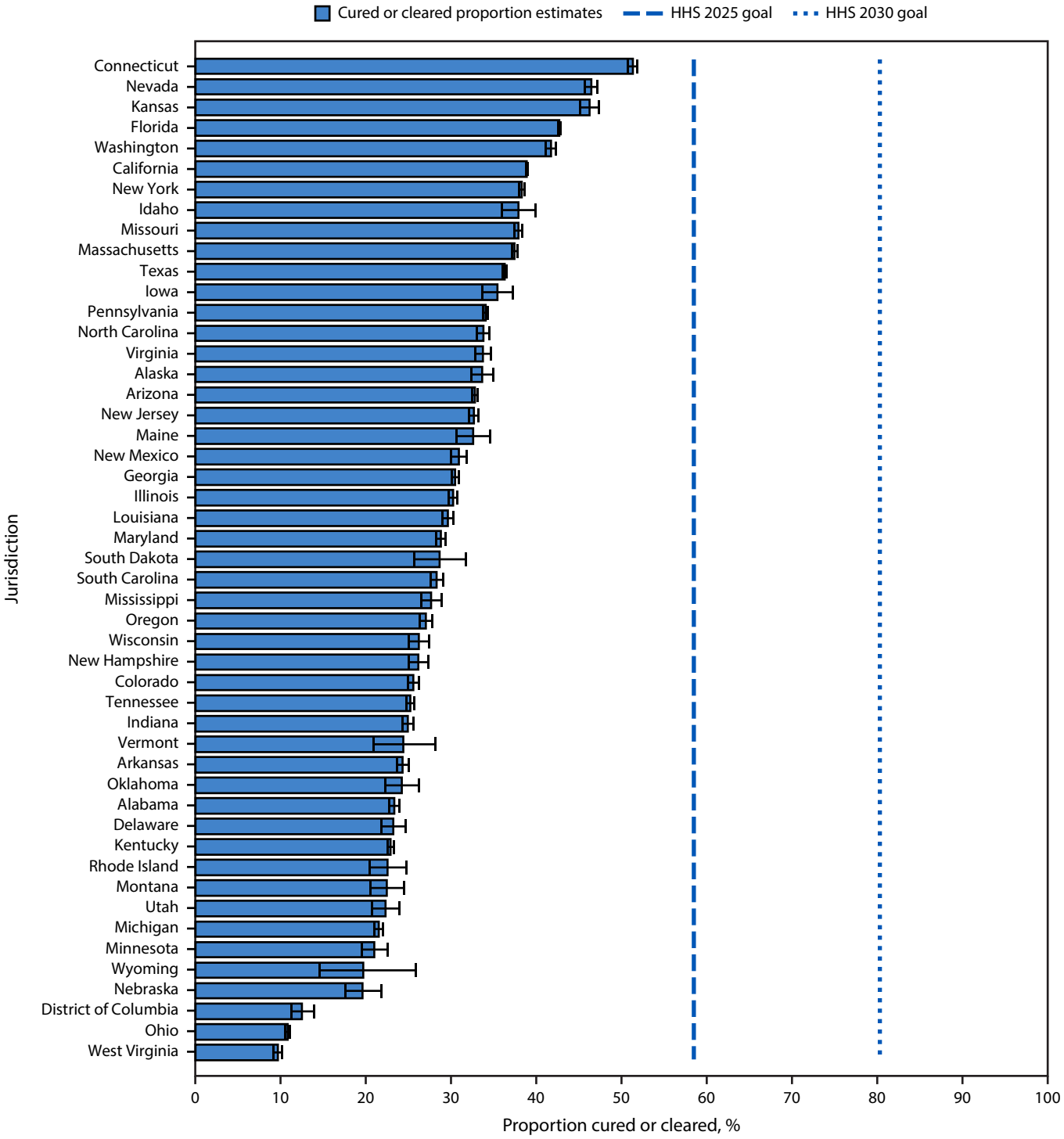
Limitations

The findings in this report are subject to at least four limitations. First, the results were based on a population of persons who received a positive test result for HCV and do not represent all persons with HCV infection. Second, data from a single laboratory are not necessarily representative of a jurisdiction and characteristics of persons tested might differ by jurisdiction. Third, results for persons who received HCV laboratory testing from laboratories other than Quest Diagnostics are not represented in these estimates; inclusion of these data could lead to different estimates reported for each step. Finally, the cascade does not capture data from persons who did not receive an HCV RNA test after initial infection or after cure or clearance, which might result in underestimation of the number and proportion of persons with viral clearance or persistent viremia, respectively.

Implications for Public Health Practice

The state-specific clearance cascades presented here facilitate the availability of data for all states, irrespective of current hepatitis C surveillance capacity to enable jurisdictional-level monitoring of hepatitis C elimination. These data demonstrate that all states have HCV clearance rates well below established national elimination goals, a finding that could serve to stimulate state-level public health action to implement best practices for diagnosing, treating, and preventing HCV infection. These practices include focusing efforts on increasing hepatitis C testing in all settings in which persons with hepatitis C receive care, ensuring unrestricted access to treatment irrespective of insurance coverage, and providing comprehensive harm reduction services for persons who use and inject drugs.

FIGURE 2. Percentage* of hepatitis C virus–infected persons with evidence of viral clearance,† by jurisdiction§ — United States, 2013–2022¶



Abbreviations: HCV = hepatitis C virus; HHS = U.S. Department of Health and Human Services.

* With 95% CIs indicated by error bars.

† Based on initial infection, which was defined as having received a detectable HCV RNA result during the follow-up period for any person who received viral testing, including all persons with initial infection during January 1, 2013–December 31, 2022.

§ All 50 states and District of Columbia, with the exception of Hawaii and North Dakota, which are not included because the cured or cleared percentages were suppressed per National Center for Health Statistics sample guidelines. https://www.cdc.gov/nchs/data/series/sr_02/sr02-200.pdf

¶ The HHS 2021–2025 national strategic plan's hepatitis C viral clearance goal is 58% by 2025 and 80% by 2030. https://www.hhs.gov/sites/default/files/Viral-Hepatitis-National-Strategic-Plan-2021-2025.pdf

Summary

What is already known about this topic?

Hepatitis C is a deadly, yet curable, disease. National goals for 2030 call for at least 80% of persons with hepatitis C to achieve viral clearance through well-tolerated, highly effective treatment.

What is added by this report?

Analysis of 2013–2022 data from a large national, commercial laboratory found that hepatitis C viral clearance proportions among persons with hepatitis C varied by state from 10% to 51% and fell below established hepatitis C viral clearance goals in all jurisdictions.

What are the implications for public health practice?

The assessment of variations in hepatitis C testing and treatment can help identify gaps, prioritize activities to improve linkage to treatment and prevention services, and allocate resources for state hepatitis C elimination programs.

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Neil Gupta, CDC.

Corresponding author: Clarisse A. Tsang, CTsang@cdc.gov.

[1]Division of Viral Hepatitis, National Center for HIV, Viral Hepatitis, STD, and TB Prevention, CDC; [2]Department of Epidemiology, School of Public Health, Louisiana State University Health Sciences Center, New Orleans, Louisiana; [3]Quest Diagnostics, Secaucus, New Jersey.

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Outbreak of Highly Pathogenic Avian Influenza A(H5N1) Viruses in U.S. Dairy Cattle and Detection of Two Human Cases — United States, 2024

Shikha Garg, MD[1]; Carrie Reed, DSc[1]; C. Todd Davis, PhD [1]; Timothy M. Uyeki, MD[1]; Casey Barton Behravesh, DVM, DrPH[2]; Krista Kniss, MPH[1]; Alicia Budd, MPH[1]; Matthew Biggerstaff, ScD[1]; Jennifer Adjemian, PhD[3]; John R. Barnes, PhD[1]; Marie K. Kirby, PhD[1]; Colin Basler, DVM[2]; Christine M. Szablewski, DVM[1]; Malia Richmond-Crum, MPH[1]; Erin Burns, MA[1]; Brandi Limbago, PhD[4]; Demetre C. Daskalakis, MD[4]; Kimberly Armstrong, PhD[5]; David Boucher, PhD[5]; Tom T. Shimabukuro, MD[1]; Michael A. Jhung, MD[1]; Sonja J. Olsen, PhD[1]; Vivien Dugan, PhD[1]

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Abstract

On April 1, 2024, the Texas Department of State Health Services reported that a dairy farm worker had tested positive for highly pathogenic avian influenza A(H5N1) virus after exposure to presumably infected dairy cattle; CDC confirmed these laboratory findings. A(H5N1) viruses were found in high concentrations in unpasteurized (raw) milk from infected cows. CDC is collaborating with the U.S. Department of Agriculture, the Food and Drug Administration, the Administration for Strategic Preparedness and Response, the Health Resources and Services Administration, the National Institute of Allergy and Infectious Diseases, and state and local public health and animal health officials using a coordinated One Health approach to identify and prepare for developments that could increase the risk to human health. Activities include monitoring of exposed persons, conducting syndromic and laboratory surveillance, planning epidemiologic investigations, and evaluating medical countermeasures. As of May 22, 2024, approximately 350 farm workers with exposure to dairy cattle or infected raw cow's milk had been monitored. These monitoring efforts identified a second human A(H5) case with conjunctivitis in Michigan, which was reported on May 22, 2024. CDC considers the current risk to the U.S. public from A(H5N1) viruses to be low; however, persons with exposure to infected animals or contaminated materials, including raw cow's milk, are at higher risk for A(H5N1) virus infection and should take recommended precautions, including using recommended personal protective equipment, self-monitoring for illness symptoms, and, if they are symptomatic, seeking prompt medical evaluation for influenza testing and antiviral treatment if indicated. Pasteurization inactivates A(H5N1) viruses, and the commercial milk supply is safe for consumption; however, all persons should avoid consuming raw milk or products produced from raw milk. Importantly, the risk to the public might change based on whether A(H5N1) viruses acquire genetic changes that increase their transmissibility to and among humans, which could increase the risk of an influenza pandemic.

Investigation and Findings

Identification of Two Human Cases of Influenza A(H5) Virus Infection

On April 1, 2024, the Texas Department of State Health Services reported, after confirmation by CDC, that a commercial dairy farm worker tested positive by real-time reverse transcription–polymerase chain reaction (RT-PCR) for highly pathogenic avian influenza (HPAI) A(H5N1) virus infection after exposure to dairy cattle presumed to be infected with A(H5N1) viruses*,†; CDC confirmed laboratory findings through RT-PCR and sequencing (*1*). The patient only experienced conjunctivitis without other signs or symptoms, was instructed to isolate, was treated with oseltamivir, and recovered. No illness was identified among the patient's household members, all of whom received oseltamivir postexposure prophylaxis. One week earlier, the U.S. Department of Agriculture had reported a multistate outbreak of A(H5N1) viruses in dairy cows.§ A(H5N1) viruses were also detected in barn cats, birds, and other animals (e.g., one raccoon and two opossums) that lived in and around human habitations and that died on affected farms.¶ Genetic sequencing of the A(H5N1) virus from infected cattle and the farm worker** identified clade 2.3.4.4b; this clade has been detected in U.S. wild birds, commercial poultry, backyard flocks, and other animals since January 2022 (*2*). On May 22, 2024, the Michigan Department of Health and Human Services reported an A(H5) case in a dairy farm worker on a farm confirmed to have A(H5N1) virus in cattle; this person was enrolled in an active text-based monitoring program and reported only eye symptoms.†† The investigation into this second case is ongoing. These two cases are the first known instances of presumed cow-to-human spread of an avian influenza A virus.

* https://www.dshs.texas.gov/news-alerts/health-alert-first-case-novel-influenza-h5n1-texas-march-2024#:~:text=Summary,patient%27s%20primary%20symptom%20was%20conjunctivitis

† https://emergency.cdc.gov/han/2024/han00506.asp

§ https://www.aphis.usda.gov/news/agency-announcements/federal-state-veterinary-public-health-agencies-share-update-hpai

¶ https://wahis.woah.org/#/in-review/4451?fromPage=event-dashboard-url

** https://www.cdc.gov/flu/avianflu/spotlights/2023-2024/h5n1-analysis-texas.htm

†† https://www.michigan.gov/mdhhs/inside-mdhhs/newsroom/2024/05/22/influenza-a-detection

Influenza A(H5N1) Viruses in U.S. Dairy Cattle

Although first reported in March 2024, A(H5N1) virus infection of U.S. dairy cows might have been occurring since December 2023, according to preliminary data (*3*). As of May 22, 2024, infected dairy cows had been identified in 52 dairy cattle herds in nine states[§§] (Colorado, Idaho, Kansas, Michigan, New Mexico, North Carolina, Ohio, South Dakota, and Texas). Signs in cattle were nonspecific and included decreased milk production, reduced rumination, and thickened (colostrum-like) milk consistency; some cows also had clear nasal discharge. High A(H5N1) virus levels have also been found in unpasteurized (raw) milk from infected cows(*4*).

Human Cases of Influenza A(H5N1) Worldwide

From 1997 through late April 2024, a total of 909 sporadic human A(H5N1) cases were reported worldwide from 23 countries; 52% of human cases have been fatal (*2*); of the 909 cases, 26 human A(H5N1) cases have been reported from eight countries, including seven deaths, since 2022. Since these numbers were last updated, two additional human A(H5) cases have been detected including the case from Michigan and one case in Australia. Nearly all reported human A(H5N1) cases had reported recent exposure to poultry. In the United States, three human A(H5) cases have been identified to date; all patients had mild illness, were not hospitalized, and fully recovered. The first occurred in April 2022 in a person from Colorado with direct exposure to infected poultry, who only reported fatigue,[¶¶] and the second and third occurred in dairy farm workers with conjunctivitis referenced in this report.

U.S. Outbreak Response Activities

Activities implemented using a One Health[***] approach to respond to this outbreak[†††] include monitoring for infections in exposed persons, conducting syndromic and laboratory surveillance, planning for epidemiologic investigations, and assessing performance of existing medical countermeasures including diagnostic tests, vaccines, and therapeutics. To assess A(H5N1) virus pathogenesis, severity, and transmissibility in an animal model of infection, CDC is also conducting laboratory experiments in ferrets.

This activity was reviewed by CDC, deemed not research, and was conducted consistent with applicable federal law and CDC policy.[§§§] Ferret studies were approved by the CDC Institutional Animal Care and Use Committee.

Monitoring of Persons Exposed to Influenza A(H5) Viruses

In 2014, CDC began monitoring persons exposed to infected poultry when HPAI A(H5) viruses were first detected in poultry and wild birds in North America (*5*). Recommendations are to monitor persons exposed to infected birds, poultry, or other animals for 10 days after their last exposure and to test symptomatic persons for influenza A viruses by RT-PCR assay using H5-specific primers and probes, in coordination with state or local health departments (*6*).

During February 2022–May 2024, approximately 9,400 persons in 52 jurisdictions have been monitored. As of May 22, 2024, approximately 350 farm workers had been or were currently being monitored for illness after exposure to infected cows or infected raw cow's milk; the number of persons monitored continues to increase; data are updated weekly.[¶¶¶] Monitoring is performed either through direct daily contact by state or local health departments or by providing persons with information on how to self-monitor and where to seek testing and possible treatment should they experience symptoms. The most recent human A(H5) case was identified through active, daily monitoring of exposed farm workers using a text-based illness monitoring program in Michigan (*7*).

National Surveillance Activities

CDC's influenza surveillance systems[****] collect information to track trends in influenza activity and detect changes in circulating influenza viruses, including detection of novel influenza A viruses year-round. Human cases of novel influenza A virus infection have been nationally notifiable since 2007; every identified case is investigated and reported to CDC.

Through approximately 300 clinical laboratories, CDC monitors changes in the percentage of influenza tests with positive results in clinical settings. The National Syndromic Surveillance Program collects data from emergency departments and other health care settings, facilitating the detection of unusual trends in influenza diagnoses, including in jurisdictions where A(H5N1) viruses have been identified in animals.

CDC's National Wastewater Surveillance System[††††] complements other existing human influenza surveillance systems in monitoring influenza trends. These monitoring methods detect influenza A viruses but do not distinguish subtypes of influenza A, meaning that current wastewater testing can detect A(H5N1) viruses but cannot distinguish them from other influenza A viruses or determine the source of the influenza A viruses (e.g., humans versus animals or animal products). Together, these systems provide visibility into U.S. influenza

[§§] https://www.aphis.usda.gov/livestock-poultry-disease/avian/avian-influenza/hpai-detections/livestock
[¶¶] https://www.cdc.gov/media/releases/2022/s0428-avian-flu.html
[***] https://www.cdc.gov/one-health/about/index.html
[†††] https://www.cdc.gov/flu/avianflu/what-cdc-doing-h5n1.htm
[§§§] 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.

[¶¶¶] https://www.cdc.gov/flu/avianflu/h5-monitoring.html
[****] https://www.cdc.gov/flu/weekly/index.htm
[††††] https://www.cdc.gov/nwss/wastewater-surveillance/Flu-A-data.html

activity. As of May 18, 2024, no indicators of unusual human influenza activity, including A(H5N1 virus), had been detected in humans through these systems.

CDC's molecular diagnostic assays are used at more than 100 public health laboratories in all 50 states and other U.S. jurisdictions to detect seasonal and novel influenza A viruses; nine centers also perform genetic sequencing for virus characterization. Statistical methods are used to determine the number of specimens needed to have 95% confidence that at least one novel influenza A virus among all influenza positive specimens per week would be detected given varying influenza prevalence; the number varies by timing during the season. Each state's contribution is proportional to its population and has been set as a national weekly goal for public health laboratory testing.[§§§§]

Spring and Summer Activities

Multiple efforts are underway to enhance influenza surveillance activities through the spring and summer as part of this response. CDC is working with commercial laboratories to increase submission of influenza-positive test specimens to public health laboratories to increase the number of specimens available for virus subtyping. Approximately 140,000 of these H5-specific tests are already prepositioned at the state and local level, and another 750,000 tests are available for distribution if needed. CDC also continues to collaborate with manufacturers of commercial diagnostic tests with the goal of having an A(H5N1) test that is widely available if needed. Surveillance for laboratory-confirmed, influenza-associated hospitalizations will also continue during the spring and summer through the Influenza Hospitalization Surveillance Network (FluSurv-NET), which typically conducts surveillance during October 1–April 30 of each influenza season. As well, CDC is working with state and local public health partners, with outreach to providers and clinics, to increase awareness about A(H5N1) so that influenza is considered in patients with conjunctivitis or respiratory illness after exposures, including agricultural fair attendance, that might increase the risk of novel influenza A virus infection.

Medical Countermeasures

As a World Health Organization Collaborating Center, and in partnership with the Administration for Strategic Preparedness and Response (ASPR), CDC regularly develops novel influenza A candidate vaccine viruses (CVVs) for pandemic preparedness. Antigenic characterization of the A(H5N1) virus isolated from the Texas farm worker (A/Texas/37/2024) with ferret antisera produced against existing CVVs confirmed two clade 2.3.4.4b A(H5) CVVs have good cross-reactivity to this virus. Under the National Pre-Pandemic Influenza Vaccine Stockpile (NPIVS) program, ASPR has shared these CVVs with Food and Drug Administration (FDA)–licensed pandemic influenza vaccine manufacturers and has completed initial production of bulk antigen. ASPR is also supporting clinical evaluation of safety and immunogenicity of vaccines using antigen manufactured from one of these CVVs, influenza A/Astrakhan/3212/2020–like virus vaccine, in combination with different adjuvants that are stockpiled under the NPIVS. The clinical study (NCT05874713)[¶¶¶¶] testing cell-based antigen combined with MF59 adjuvant, according to the AUDENZ-licensed manufacturing process, has completed enrollment. The egg-based antigen, produced according to the Q-PAN-licensed process, combined with AS03 adjuvant clinical study (NCT05975840)[*****] is also fully enrolled. ASPR is planning additional clinical studies for combining egg-based antigen with both AS03 and MF59 adjuvants with enrollment expected to start in late summer 2024. If needed, and dependent upon FDA review and regulatory action allowing use, these vaccines could be the first allotment of vaccines used while additional manufacturing, starting with the stockpiled antigens and adjuvants, ramps up for full-scale production.

Four FDA-approved antiviral drugs (baloxavir marboxil, oseltamivir, peramivir, and zanamivir) are recommended for influenza treatment in the United States.[†††††] CDC has conducted phenotypic testing of antiviral susceptibility and found that the A(H5N1) virus isolated from the Texas farm worker is susceptible to baloxavir marboxil (Xofluza, Genentech) and to neuraminidase inhibitors, including oseltamivir (generic or Tamiflu, Genentech). Oral oseltamivir treatment is recommended for persons with confirmed or suspected A(H5N1) virus infection.[§§§§§] Oral oseltamivir is also recommended for postexposure prophylaxis (using twice daily treatment dosing) of close contacts (e.g., household members) of a confirmed A(H5N1) case. Observational studies of patients infected with older and different clades of A(H5N1) viruses, (i.e., not the current clade 2.3.4.4b viruses identified in the United States) have found that starting oseltamivir treatment within 2 days of symptom onset was significantly associated with survival benefit compared with no treatment or later initiation of oseltamivir treatment after symptom onset (*8,9*). All four antivirals are available in the Strategic National Stockpile and in many

[§§§§] https://www.aphl.org/aboutAPHL/publications/Documents/ID-Influenza-Right-Size-Roadmap-Edition2.pdf

[¶¶¶¶] https://www.clinicaltrials.gov/study/NCT05874713?term=NCT05874713&rank=1

[*****] https://www.clinicaltrials.gov/study/NCT05975840?term=NCT05975840&rank=1

[†††††] https://www.cdc.gov/flu/professionals/antivirals/index.htm

[§§§§§] https://www.cdc.gov/flu/avianflu/novel-av-treatment-guidance.htm

BOX. Key epidemiologic questions to define the risk of highly pathogenic avian influenza A(H5N1) viruses to humans and to guide evidence-based recommendations — United States, 2024

1. Is there evidence of influenza A(H5N1) virus infections in human populations?
2. If human illness is identified, what is the clinical spectrum of illness?
3. What are the rates of asymptomatic human infection with influenza A(H5N1) virus?
4. What are the routes of exposure to influenza A(H5N1) virus on farms and dairies, and what is the risk for zoonotic transmission?
5. What behaviors, including use of personal protective equipment, are associated with human infection or protection from infection with influenza A(H5N1) virus?

state-managed stockpiles, both of which can be deployed to assist with supply chain constraints should they arise.

The National Institute of Allergy and Infectious Diseases (NIAID) continues to investigate the efficacy of novel direct-acting antiviral medications and host-targeted molecules as well as broadly neutralizing antibodies and more targeted monoclonal antibodies aimed at A(H5N1) viral-specific surface antigens that could protect from death or severe respiratory disease.

Epidemiologic Investigations

To better ascertain and define the risk to humans, CDC is working with states to plan epidemiologic investigations in collaboration with affected farms and health and agricultural partners at local, state, and federal levels. Important public health questions might be addressed through in-depth studies with specimen collection and surveys (Box). CDC conducted a similar study in response to poultry outbreaks of A(H5N1) in 2022 (*10*).

Discussion

CDC is collaborating with the U.S. Department of Agriculture, FDA, ASPR, the Health Resources and Services Administration, NIAID, and state and local public health and animal health officials using a coordinated One Health approach to identify and prepare for developments that could increase the risk to human health. Substantial challenges to identifying and interviewing persons exposed to cattle infected with A(H5N1) viruses for illness monitoring or epidemiologic studies exist. Workers exposed to A(H5N1) viruses might represent socioeconomically vulnerable, or otherwise hard-to-reach populations, including those who live in rural or remote areas; or they might be migrant, transient, or undocumented workers. Further, persons might not be aware of the risks or potential signs and symptoms associated with exposure; dairy farmers and the dairy industry have not previously been major partners in outreach about avian influenza. Recommendations for worker protection have been recently updated[¶¶¶¶¶] and disseminated.

Once exposed persons are identified, defining exposure periods is also difficult. A(H5N1) disease is widespread in poultry, and mortality is high. Rapid depopulation of affected flocks facilitates monitoring of exposed workers because it creates a finite 10-day monitoring window after exposure. In contrast, illness in cows can last for 2–4 weeks, and the duration of infectious virus shedding in cows is unknown. In addition, A(H5N1) virus infection has been identified in some cows without signs of illness; thus, some workers might be unaware of their exposure. Recent testing did not detect live, infectious A(H5N1) viruses in retail dairy samples; however, identification of A(H5N1) viral fragments in approximately one in five retail milk samples from across the country (*4*) suggests that A(H5N1) virus infections of cattle might be widespread. Therefore, monitoring of exposed or potentially exposed persons and animals might be protracted and resource-intensive.

Interpretation of surveillance data can be challenging given that A(H5N1) virus infections might manifest signs and symptoms similar to those associated with infections caused by other pathogens. During periods of low U.S. influenza virus circulation (e.g., spring and summer), syndromic and wastewater surveillance might more readily identify unusual

Summary

What is already known about this topic?

Influenza A(H5) virus infection was detected in two U.S. farm workers during a multistate outbreak of A(H5N1) viruses in dairy cows; these are the first known instances of presumed cow-to-human transmission of avian influenza A viruses.

What is added by this report?

Approximately 350 exposed farm workers are being monitored; one of the two cases was identified via daily, active monitoring. Surveillance has identified no unusual influenza activity trends in the United States. A(H5) candidate vaccine viruses are available, and laboratory analyses indicate that A(H5N1) viruses circulating in cows and other animals are susceptible to FDA-approved antivirals.

What are the implications for public health practice?

Current risk to the U.S. public from A(H5N1) viruses is low; however, persons exposed to infected animals or contaminated materials, including raw cow's milk, are at higher risk and should take precautions and self-monitor for illness. A One Health (human, animal, and environmental) approach is critical to preparing for circumstances that could increase risk to human health.

[¶¶¶¶¶] https://www.cdc.gov/flu/avianflu/h5/worker-protection-ppe.htm

signals in influenza-related symptoms or activity. However, using these systems to detect novel influenza A virus infection trends in the fall and winter, once seasonal influenza A virus circulation increases, will likely be complicated. Interpretation of wastewater data are further limited by the inability to distinguish between human and animal source material.

Currently circulating A(H5N1) viruses do not have the ability to easily bind to receptors that are most prevalent in the human upper respiratory tract and therefore are not easily transmissible to and between humans (*2*). However, because of the widespread global prevalence of A(H5N1) viruses in birds and other animals, continued sporadic human infections are anticipated. Further, if a novel influenza A virus acquires the ability to infect and be transmitted easily between persons in a sustained manner, an influenza pandemic could occur. Thus, investigation of every novel influenza A virus case in humans and comprehensive worldwide surveillance is critical to public health preparedness efforts.

Implications for Public Health Practice

CDC considers the current health risk to the U.S. public from A(H5N1) viruses to be low. However, persons who have job-related or recreational exposure to infected birds, poultry, dairy cattle, or other infected animals or contaminated materials, including raw cow's milk, are at increased risk for infection; these persons should take appropriate precautions, including using recommended personal protective equipment, self-monitoring for illness symptoms (*6*), and seeking prompt medical evaluation if they are symptomatic, including influenza testing and antiviral treatment if indicated. FDA has confirmed that pasteurization inactivates A(H5N1) viruses, and that the commercial milk supply is safe for consumption (*4*); however, all persons should avoid consuming raw milk or products produced from raw milk. A coordinated and comprehensive One Health response to this ongoing outbreak of A(H5N1) virus infections in dairy cows, poultry, and other animals is needed to identify and prepare for any developments that indicate an increase in the risk to public health.

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Corresponding author: Shikha Garg, sgarg1@cdc.gov.

[1]Influenza Division, National Center for Immunization and Respiratory Diseases, CDC; [2]One Health Office, National Center for Emerging and Zoonotic Infectious Diseases, CDC; [3]Office of Public Health Data, Surveillance, and Technology, CDC; [4]National Center for Immunization and Respiratory Diseases, CDC; [5]Administration for Strategic Preparedness and Response, Washington, DC.

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