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Outbreak of *Neisseria meningitidis* Conjunctivitis in Military Trainees — Texas, February–May 2025

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Abstract

Viral and allergic conjunctivitis are more common than bacterial conjunctivitis in healthy immunocompetent adults. *Neisseria meningitidis* is an uncommon cause of bacterial conjunctivitis. During February–May 2025, an outbreak of 41 meningococcal conjunctivitis cases occurred among healthy, communally housed, military trainees at Joint Base San Antonio-Lackland in San Antonio, Texas; all had received the quadrivalent meningococcal vaccine. One patient was hospitalized with periorbital cellulitis and received intravenous antibiotics; all other patients were treated successfully with topical antibiotics. Whole genome sequencing of isolates from the first two cases suggested that the organism was unencapsulated (nongroupable) and that the cases were related. After the identification of two cases of *N. meningitidis* conjunctivitis among military trainees within a 3-week period in February 2025, an investigation was initiated by the base health surveillance team. Investigation of basic trainee hygiene and cleaning practices found that all protocols were followed; no source for the outbreak was found. When outbreaks of mucopurulent conjunctivitis occur in congregate living settings, culturing exudate can identify outbreak etiology, and whole genome sequencing can help guide treatment and response. Previous studies indicated that systemic antimicrobial therapy might be needed to prevent invasive infections of *N. meningitidis* cases; findings from this investigation suggest that nongroupable *N. meningitidis* conjunctivitis in otherwise healthy persons might be successfully treated with topical antimicrobials.

Introduction

In February 2025, two cases of *Neisseria meningitidis* bacterial conjunctivitis were identified in otherwise healthy basic military trainees at Joint Base San Antonio-Lackland in San Antonio, Texas; an investigation was conducted to identify the source of the outbreak and to make recommendations for treatment. Ultimately, 41 cases of *N. meningitidis* conjunctivitis and 32 cases of *Haemophilus* species conjunctivitis were identified among 11,797 trainees. This report describes the investigation and outbreak response, including the characteristics of the cases and the isolates, and response to treatment with topical antibiotics.

Investigation and Results

Housing and Prophylaxis for Trainees on Arrival at Joint Base San Antonio-Lackland

U.S. Air Force basic training takes place at Joint Base San Antonio-Lackland in San Antonio, Texas. Trainees are organized into rolling military units averaging 900 entering and graduating trainees per week, with each unit further divided into groups of approximately 52 trainees. Trainees are assigned to specific dormitories, which typically house 50–60 persons, sleeping in beds that alternate head directions, creating a foot-to-head orientation in the bay. Trainees arrive weekly and undergo a standardized 7.5-week basic military training (BMT) curriculum organized by week of training, resulting in training activities and associated exposures that are typically consistent for each class.

To prevent invasive meningococcal and streptococcal disease outbreaks, all trainees receive quadrivalent meningococcal

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(Groups A, C, Y, and W) (Menveo) vaccine within 72 hours of arrival and a single dose of penicillin G benzathine injectable suspension, respectively, within 7 days of arrival (*1*). Penicillin-allergic trainees receive weekly oral azithromycin to prevent streptococcal disease during BMT.

Identification of First Two Conjunctivitis Cases

On February 5, 2025, a case of *N. meningitidis* bacterial conjunctivitis was identified in an otherwise healthy BMT trainee who had experienced 2 days of mucopurulent ocular discharge; the trainee had no known exposure to *N. meningitidis*. Although the symptoms initially suggested viral conjunctivitis (*2*), the copious unilateral discharge led the health care provider to culture the exudate, which was positive for *N. meningitidis* 6 days later. Microbial isolates were tested and identified by Vitek 2 (bioMerieux). On February 21, a second trainee (from a different training unit) was also evaluated for unilateral copious mucopurulent ocular discharge associated with periocular edema without corneal involvement. The culture of the exudate from this trainee's eye was positive for *N. meningitidis*, raising concern about potential cases of invasive meningococcal disease. An investigation was initiated to identify additional cases, determine the risk for invasive meningococcal disease, and describe the patients and evaluate their response to treatment. The local human research protection program, Defense Health Agency San Antonio Market Office of Research Protocol Support, determined these activities not to be research.*

* Reference number FWH20250060N.

Surveillance for Conjunctivitis

The first two cases, which occurred among trainees who started training 2 weeks apart, both occurred during both patients' fourth week of BMT. On February 23, the day that the second patient's culture result was received, the Trainee Health Surveillance team (a group of epidemiologists and preventive medicine physicians responsible for active and passive disease surveillance of the BMT population) established a registry and began active surveillance to identify cases of mucopurulent conjunctivitis and ensure that a sample was obtained for culture for each case. A confirmed case was defined as a positive *N. meningitidis* culture result from ocular discharge collected from a person with conjunctivitis. A probable case was defined as symptomatic conjunctivitis with exudate in a patient who had contact with a person with a confirmed case of meningococcal conjunctivitis but without laboratory confirmation. A suspected case was defined as symptomatic conjunctivitis with exudate in a person with no known contact with a confirmed case. Clinicians who worked in emergency departments or primary care on the base were requested to assist in active surveillance by submitting samples of ocular discharge from patients with conjunctivitis to the microbiology laboratory for culture and reporting suspected or probable cases to the Trainee Health Surveillance registry rather than providing standard empiric treatment without culture. Patients with confirmed meningococcal conjunctivitis received topical ocular erythromycin, ciprofloxacin, or moxifloxacin and were referred for an ophthalmologic assessment of corneal involvement.

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Identification of Additional Cases

During February 23–May 9, 2025, a total of 79 cases of mucopurulent conjunctivitis were identified among 11,797 trainees who started BMT in San Antonio (6.7 per 1,000); cultures from 41 (52%) patients were positive for *N. meningitidis*, and 32 (41%) were positive for *Haemophilus* species. Four (5%) patients received negative culture results, one patient's ocular culture was positive for *Corynebacterium macginleyi*, a known cause of conjunctivitis (*3*), and for one patient, no specimen was collected for culture. Among the 41 laboratory-confirmed cases of *N. meningitidis* conjunctivitis, 23 (56%) occurred within 1 month of onset of the second case (Figure 1). Among the 32 *Haemophilus* species conjunctivitis cases, 29 (91%) were identified during the first 3 weeks of training, whereas 36 (87.8%) of the positive *N. meningitidis* ocular cultures were identified during or after the fourth week of training (Figure 2).

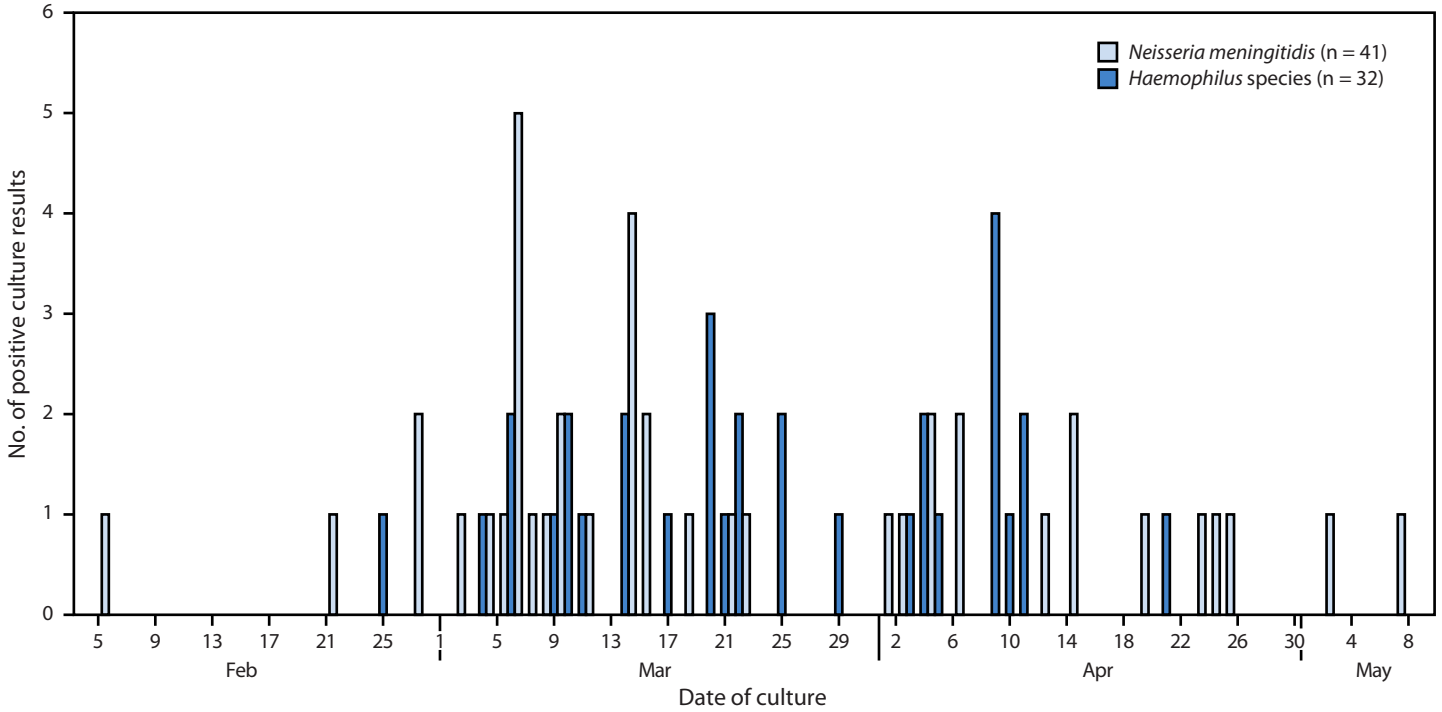
Clinical Characteristics of Patients with *N. meningitidis* Conjunctivitis

The 41 confirmed cases of *N. meningitidis* conjunctivitis occurred in trainees in 37 unique BMT groups. During this period, men constituted 78% of the BMT population but accounted for 90% of the *N. meningitidis* cases. Among trainees with confirmed *N. meningitidis* conjunctivitis, 33 (80%) reported an antecedent upper respiratory infection (Table). Overall, 35 (85%) patients had unilateral eye involvement. All patients improved within 24 hours of starting treatment with topical moxifloxacin, ciprofloxacin, or erythromycin. One patient was hospitalized after a delay in initiating topical moxifloxacin that led to progression of infection to periorbital cellulitis, requiring a short course of intravenous antibiotics. No patients developed invasive corneal ulceration or orbital cellulitis. Contact tracing, including prophylactic antibiotics for close contacts, was deferred, because prophylaxis is currently recommended only for close contacts of persons with invasive disease (bacteremia or meningitis) (*4*). Whereas cases of *Haemophilus* species conjunctivitis occurred in patients who received either penicillin or azithromycin prophylaxis, *N. meningitidis* infections only occurred in patients who received penicillin.

Whole Genome Sequencing

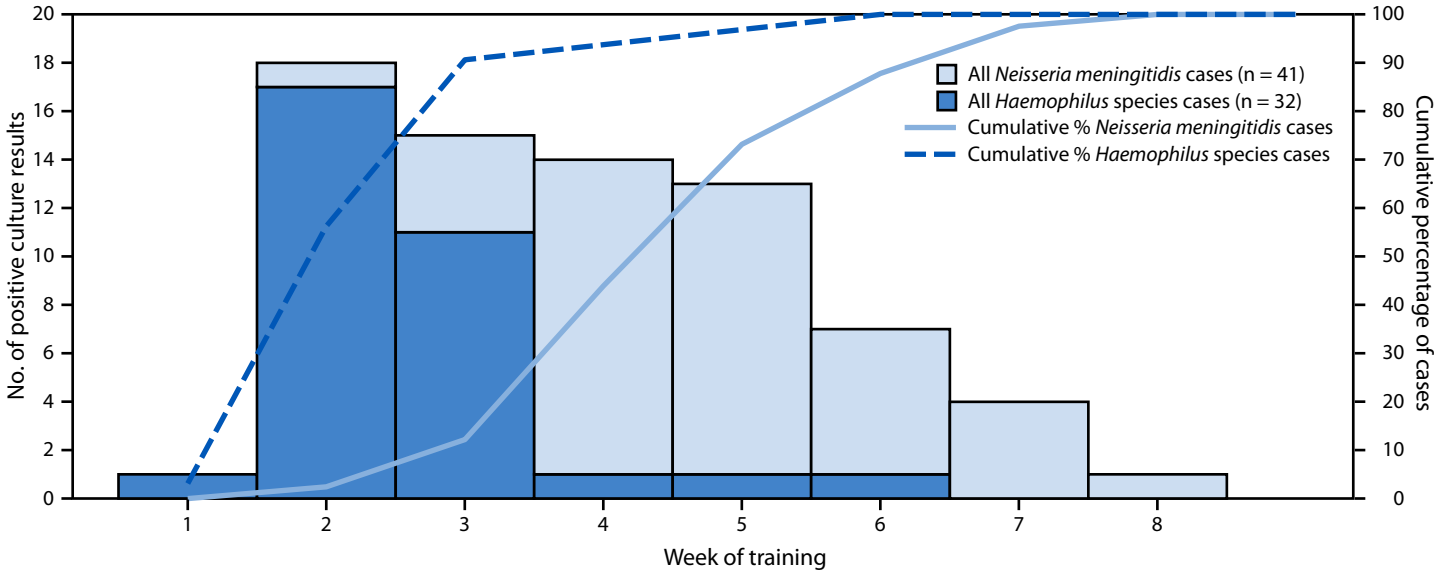
While serogrouping and sequencing are commonly performed by local, state, and federal public health laboratories for *N. meningitidis* isolates from cases of invasive meningococcal disease, neither is typically performed for isolates from noninvasive disease cases. However, after diagnosis of the second case, and to guide the public health response, whole genome sequencing of isolates from the first two ocular cultures was

FIGURE 1. Number of positive bacterial ocular discharge culture results among military trainees, by date of culture and pathogen (N = 73)* — Joint Base San Antonio-Lackland, Texas, February 5–May 9, 2025



* Includes one basic military trainee instructor with conjunctivitis who received a positive *N. meningitidis* culture result on March 15, 2025.

FIGURE 2. Number of positive bacterial ocular discharge culture results and cumulative percentage of positive results among military trainees, by week of training and pathogen (N = 73) — Joint Base San Antonio-Lackland, Texas, February–May 2025



performed to determine whether they were related, predict antimicrobial resistance, and ascertain whether virulence factors associated with invasive disease were present. As has been reported for other cases of meningococcal conjunctivitis (*5*), both isolates were nongroupable, without the presence of c*saB*, *csb*, *csc*, *csw*, and *csy* genes associated with encapsulation, suggesting low risk for development of invasive disease. Sequencing demonstrated that the two isolates were both sequence type (ST) 32 and were closely related. ST-32 has previously been associated with meningococcal disease outbreaks caused by the encapsulated serogroup B *N. meningitidis*; however, because this strain was not encapsulated, it was not expected to cause invasive disease in otherwise healthy patients. The sequenced isolates indicated decreased susceptibility to penicillin based on a mutation in the *penA* gene, otherwise no other genetic correlates of antimicrobial resistance were identified.

Environmental Investigation and Training Activity Evaluation

The Trainee Health Surveillance team evaluated dormitory cleanliness, including the showers and common areas, and reviewed established cleaning protocols. No environmental specimens were collected for testing. Various field training activities during the fourth week of training were also evaluated to ascertain their risk as a source of transmission and to confirm adherence to cleaning protocols. The health team who observed gas mask cleaning noted that staff members followed recommended cleaning and sanitizing protocols, using liquid sodium hypochlorite disinfecting solution (bleach) at recommended concentrations. As the outbreak continued, other potential common sources of transmission were investigated, including cardiopulmonary resuscitation training. However, because trainees did not practice rescue breathing on the mannequin, this activity posed a low risk for transmission. Evaluation of the military shooting range also did not identify any potential common source of transmission; safety goggles were not shared and were cleaned with hypochlorite disinfectant wipes at the end of each training session.

Public Health Response

During February 13–18 (after identification of the first two cases), the Trainee Health Surveillance team conducted training site visits and provided a CDC infographic on conjunctivitis prevention to the BMT staff members. Because the *N. meningitidis* conjunctivitis cases were noninvasive and caused by a nongroupable strain, postexposure prophylaxis was not recommended for close contacts of patients with confirmed cases and additional vaccination was not indicated (*4*).

Discussion

Invasive meningococcal disease outbreaks have been associated with congregate living settings, including military or college dormitories; however, no reported outbreaks of meningococcal conjunctivitis were identified in the literature by an English-language search of Ovid MEDLINE via PubMed using keywords "primary meningococcal conjunctivitis," "Meningococcal," and "conjunctivitis." This outbreak occurred in a group of young persons with few comorbidities, all of whom had recently received the quadrivalent meningococcal vaccine, which is not expected to protect against the unencapsulated organisms detected in this outbreak. Whole genome

TABLE. Characteristics of military trainees* with *Neisseria meningitidis* conjunctivitis cases (N = 41) — Joint Base San Antonio-Lackland, Texas, February–May 2025

Characteristic	No. (%)
Average age, yrs (range)	22 (17–39)
Sex	
Male	37 (90.2)
Female	4 (9.8)
Week of training	
1	0 (—)
2	1 (2.4)
3	4 (9.8)
4*	13 (31.7)
5	12 (29.3)
6	6 (14.6)
7	4 (9.8)
8	1 (2.4)
Antecedent upper respiratory infection	
Yes	33 (80.5)
No	8 (19.5)
Signs or symptoms	
Cough	27 (65.9)
Congestion	27 (65.9)
Sore throat	22 (53.7)
Rhinorrhea	15 (36.6)
Ocular pain	12 (29.3)
Prophylactic antibiotics received at arrival	
Azithromycin	0 (—)
Penicillin	40 (97.6)
None	1 (2.4)
Wore eyeglasses	
No	20 (48.8)
Yes	19 (46.3)
Unknown	2 (4.9)
Involved eye	
Right	19 (46.3)
Left	16 (39.0)
Both	6 (14.6)
Hospitalized	
No	40 (97.6)
Yes	1 (2.4)

* Includes one instructor with conjunctivitis and who received a positive *N. meningitidis* culture result on March 15, 2025, who was instructing a unit during the fourth week of training and did not receive penicillin or azithromycin prophylaxis.

sequencing was used to determine that the outbreak was caused by an unencapsulated strain, supporting the decision to treat with topical antibiotics only, which was associated with rapid improvement of patient symptoms. The source of this outbreak and mechanism of transmission was not identified.

Bacterial conjunctivitis in adults involves direct inoculation into conjunctival membranes without entering the bloodstream or central nervous system. The estimated *N. meningitis* nasopharyngeal carriage rate (including encapsulated and unencapsulated strains) is as high as 5%–10% in some U.S. populations, with a peak prevalence of 23.7% in adults aged 19 years (*6*). Because the average age of a military trainee includes this age, colonization with *N. meningitidis* is expected to be high. Despite this high likelihood of colonization, invasive meningococcal disease is rare, and only one case of meningococcal meningitis has been previously reported among military trainees at this base in 2021 (*7*,*8*). Characterization of the isolates early in the outbreak was critical to understanding the risk for invasive meningococcal disease.

Previous studies, primarily among children before meningococcal vaccines were widely available, led some countries to recommend systemic therapy for patients with meningococcal conjunctivitis; however, no such recommendation exists in the United States (*9*). In this immunocompetent population with recent quadrivalent meningococcal vaccination, cases of conjunctivitis were caused by an unencapsulated pathogen, and no cases of systemic invasive disease occurred. With the exception of one patient who received intravenous antibiotics for periorbital cellulitis, patients with meningococcal conjunctivitis in this setting rapidly improved with topical moxifloxacin, ciprofloxacin, or erythromycin only. If characterization of isolates is not available, systemic therapy might be warranted.

Given the timing of the *N. meningitidis* cases and the association with trainees who had received penicillin (but not azithromycin) streptococcal prophylaxis, the outbreak might be related to the *penA* gene mutation conferring decreased sensitivity to penicillin noted in isolates from the first two cases, combined with the subsequent decline in serum levels of benzathine penicillin approximately 3 weeks after administration (*10*). A definitive cause of the outbreak was not identified during this period.

Limitations

The findings in this report are subject to at least two limitations. First, only the first two isolates underwent whole genome sequencing. Because meningococcal conjunctivitis is a rare disease, cases in the outbreak were treated as if all the isolates were clonal. However, with unknown carriage of *N. meningitidis* in this cohort, other isolates were possibly introduced during the several months of the public health response. In addition, the original isolate might have mutated during the outbreak, resulting in a change in antimicrobial resistance or virulence; however, cases identified throughout the outbreak responded to topical antimicrobial treatment. Second, because this outbreak occurred in a group of healthy, young military trainees with few underlying medical comorbidities, the findings might not be generalizable to other settings or populations.

Implications for Public Health Practice

This report demonstrates the role for serogrouping noninvasive *N. meningitidis* isolates during a possible outbreak to help guide the public health response. In this outbreak in a healthy population, meningococcal conjunctivitis caused by an unencapsulated strain was adequately treated with topical

Summary

What is already known about this topic?

Bacterial conjunctivitis is uncommon in immunocompetent adults. *Neisseria meningitidis* is an unusual bacterial cause of conjunctivitis.

What is added by this report?

Forty-one cases of *N. meningitidis* conjunctivitis caused by an unencapsulated (nongroupable) strain identified by whole genome sequencing occurred in young, healthy military trainees living in a communal setting; all had received quadrivalent meningococcal vaccine. No source was identified. One patient developed periorbital cellulitis and received intravenous antibiotics; all other patients were treated successfully with topical antibiotics.

What are the implications for public health practice?

When outbreaks of mucopurulent conjunctivitis occur in congregate living settings, culturing exudate can identify etiology, and whole genome sequencing can help guide treatment and outbreak response. Nongroupable *N. meningitidis* conjunctivitis in otherwise healthy persons might be successfully treated with topical antimicrobials.

antibiotics and did not lead to severe ocular involvement or systemic infections. Conjunctivitis caused by nongroupable *N. meningitidis* might not require systemic treatment in immunocompetent persons if cases are promptly identified (by group) and appropriately treated, even among persons at high risk for person-to-person exposure living in congregate settings.

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References

1. Bernstein SH, Feldman HA, Harper OF Jr, Klingensmith WH. Massoral penicillin prophylaxis in control of streptococcal disease. AMA Arch Intern Med 1954;93:894–8. PMID:13157675 https://doi.org/10.1001/archinte.1954.00240300088008
2. Azari AA, Arabi A. Conjunctivitis: a systematic review. J Ophthalmic Vis Res 2020;15:372–95. PMID:32864068 https://doi.org/10.18502/jovr.v15i3.7456
3. Joussen AM, Funke G, Joussen F, Herbertz G. *Corynebacterium macginleyi*: a conjunctiva specific pathogen. Br J Ophthalmol 2000;84:1420–2. PMID:11090486 https://doi.org/10.1136/bjo.84.12.1420
4. Rubis A, Schillie S. Meningococcal disease. Manual for the surveillance of vaccine preventable diseases. 5th ed. https://www.cdc.gov/surv-manual/php/table-of-contents/chapter-8-meningococcal-disease.html. Accessed October 30, 2024.
5. Clark SA, Heymer E, Campbell H, et al. Clinical and microbiological characteristics of meningococcal eye infections: retrospective national surveillance in England, 2010-2022. Clin Infect Dis 2025;ciaf274; Online ahead of print. PMID:40452554 https://doi.org/10.1093/cid/ciaf274
6. Christensen H, May M, Bowen L, Hickman M, Trotter CL. Meningococcal carriage by age: a systematic review and meta-analysis. Lancet Infect Dis 2010;10:853–61. PMID:21075057 https://doi.org/10.1016/S1473-3099(10)70251-6
7. Marcus JE, Bennett WN, Frankel DN, et al. Response to a serogroup B meningococcal disease case among military trainees. Open Forum Infect Dis 2022;9(5):ofac162. PMID:35493127 https://doi.org/10.1093/ofid/ofac162
8. Broderick MP, Phillips C, Faix D. Meningococcal disease in US military personnel before and after adoption of conjugate vaccine. Emerg Infect Dis 2015;21:377–9. PMID:25625525 https://doi.org/10.3201/eid2102.141037
9. Parikh SR, Campbell H, Mandal S, Ramsay ME, Ladhani SN. Primary meningococcal conjunctivitis: summary of evidence for the clinical and public health management of cases and close contacts. J Infect 2019;79:490–4. PMID:31669376 https://doi.org/10.1016/j.jinf.2019.10.015
10. Neely M, Kaplan EL, Blumer JL, Faix DJ, Broderick MP. A population pharmacokinetic modeling approach shows that serum penicillin G concentrations are below inhibitory concentrations by two weeks after benzathine penicillin G injection in the majority of young adults. Antimicrob Agents Chemother 2014;58:6735–41. PMID:25182635 https://doi.org/10.1128/AAC.02744-14

Highly Pathogenic Avian Influenza A(H5N1) Virus Infection in a Child with No Known Exposure — San Francisco, California, December 2024–January 2025

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Abstract

In response to a highly pathogenic avian influenza (HPAI) A(H5N1) outbreak in U.S. dairy cows detected in March 2024, with subsequent identification of human cases, the San Francisco Department of Public Health instituted enhanced influenza surveillance (influenza A virus subtyping of a sample of specimens weekly) in June 2024. As of January 1, 2025, 37 human cases of influenza A(H5N1) had been detected in California, none of which occurred in San Francisco. On January 9, 2025, enhanced surveillance detected a human influenza A(H5N1) virus genotype B3.13 infection in a school-aged child in San Francisco with mild illness. Case investigation and contact tracing were conducted to ascertain exposures and detect possible human-to-human transmission. Activities comprised a household visit that included an environmental assessment, close contact interviews and surveys, and molecular and serologic testing. Sixty-seven close contacts (household, school, and health care) were identified. Upper respiratory tract specimens collected from seven asymptomatic household contacts and four symptomatic school contacts all tested negative for influenza virus by real-time reverse transcription–polymerase chain reaction (rRT-PCR). Although antibodies against influenza A(H5N1) were detected in the index patient, serologic testing of a convenience sample of nine close contacts identified no detectable A(H5)-specific antibodies. Despite an extensive investigation, the infection source remains unknown; no human-to-human transmission was identified among close contacts by rRT-PCR and serologic testing. Continued enhanced surveillance and timely subtyping of a subset of influenza A–positive specimens are essential components of a comprehensive strategy to detect human novel influenza A virus infections, including among persons without known exposures to A(H5N1) viruses.

Introduction

An outbreak of highly pathogenic avian influenza (HPAI) A(H5N1) virus in Texas dairy cows was detected in March 2024; the first associated human A(H5N1) case was identified in Texas in April 2024 (*1,2*). By January 1, 2025, a total of 66 human A(H5N1) cases had been detected nationwide, including 37 (56%) in California that were associated with the 2024–2025 dairy cow outbreak (*3*). Although historically, severity of A (H5N1) cases varied widely, recent U.S. cases have been associated with mild illnesses (*4*). No human-to-human transmission has been documented in the United States (CDC Report on Missouri H5N1 Serology Testing).

In response to the outbreak, the San Francisco Department of Public Health (SFDPH) strengthened influenza surveillance in June 2024 by performing additional influenza A virus subtyping, including A(H5) testing at the SFDPH Public Health Laboratory (PHL) (*5,6*). This additional subtyping was recommended for 1) specimens from patients with epidemiologic risk factors for HPAI and a clinically compatible illness, 2) influenza A virus specimens that were untypeable in the clinical laboratory, and 3) a sample of influenza A virus specimens submitted weekly from health care systems for enhanced surveillance. For the enhanced surveillance component, depending on local epidemiology, clinical laboratories submitted all or a random sample of influenza A–positive specimens from pediatric and adult outpatients, hospitalized patients, and emergency department patients, resulting in a total of 20–100 specimens submitted weekly.

On January 9, 2025, through the testing of an influenza A virus specimen submitted from a health care system for enhanced surveillance, SFDPH identified its first presumptive positive A(H5N1) virus infection in a young child with asthma but no other known health conditions. Case investigation and contact tracing were conducted to ascertain exposures and assess for possible human-to-human transmission.

Methods

Initial Public Health Notification and Case Investigation

After notification of the A(H5N1) virus detection, SFDPH immediately conducted a telephone interview with the patient's family and a medical chart review to assess the child's exposures, testing, and clinical course. Within 24 hours, SFDPH visited the household, collected nasal and oropharyngeal swabs from all adults and children in the household for real-time reverse transcription–polymerase chain reaction (rRT-PCR) testing, and completed an environmental assessment (e.g., evaluation of potential animal and food exposures).

Contact Investigation and Public Health Response

Close contacts were defined as persons with prolonged exposure to the patient at a distance of ≤6 feet, without use of

recommended personal protective equipment (PPE) (CDC Interim Guidance). All close contacts were investigated.

Household contacts. All household contacts (three adults and four children) were interviewed to determine whether any had signs or symptoms clinically compatible with influenza (i.e., fever, cough, sore throat, shortness of breath, or conjunctivitis) 10 days before or after the patient's illness. Nasal and oropharyngeal swabs were collected from all household contacts, and the three adult household contacts received serologic testing. Active symptom monitoring continued for 10 days after the index patient's last positive test result.

School contacts. Close contacts were identified from the index patient's school classrooms. A list of close contacts with absences during the 10 days preceding the patient's illness onset through 10 days after the exposure period ended (defined as the last day that an A(H5N1)-positive specimen was obtained from the child) was requested. School close contacts with absences were interviewed to ascertain whether they had experienced recent illnesses, sought health care, and received any diagnostic testing, or treatment.

Health care worker contacts. Health care workers who had possible contact with the patient during any visit while the patient's rRT-PCR test result was positive received an online survey. SFDPH requested information about patient contact, PPE use (i.e., eye protection, respiratory protection at least as protective as an N95 filtering facepiece respirator, gown, and gloves), signs and symptoms during the 10 days after exposure, and whether the workers had sought health care, or received diagnostic testing or treatment.

School and health care close contacts with influenza-compatible respiratory or constitutional symptoms at the time of interview were offered influenza testing. Household members, school contacts with recent respiratory illnesses, and health care workers were offered serologic testing for antibodies to A(H5N1) virus.

Laboratory Procedures

SFDPH PHL used influenza A rRT-PCR to test the patient's respiratory specimens, followed by CDC's A(H5) subtyping assay. rRT-PCR–positive patient specimens were amplified using multisegment (M)-RTPCR (*7*); libraries were then generated from these amplicons and sequenced on an Illumina MiSeq next-generation sequencing platform.* Virus genotype was determined by whole genome sequencing, and phylogenetic analysis was performed to compare specimens collected from the patient with previous human and animal specimens. Sera from the patient and the patient's close contacts were tested at CDC for evidence of recent A(H5N1) virus infection using microneutralization (MN) assays and hemagglutinin inhibition (HI) assays against wild-type clade 2.3.4.4b viruses, A/Texas/37/2024 (B3.13), A/Michigan/90/2024 (B3.13), and A/Washington/240/2024 (D1.1); MN testing against seasonal influenza A(H1N1)pdm09 virus (A/Victoria/2570/2019) was used as a control (*8*). Seropositivity to A(H5N1) was defined as a neutralizing antibody titer ≥40 and HI antibody titer ≥40 (World Health Organization H5 Case Definitions). These activities were reviewed by CDC, deemed not research, and conducted consistent with applicable federal law and CDC policy.†

Results

Identification of the Index Patient

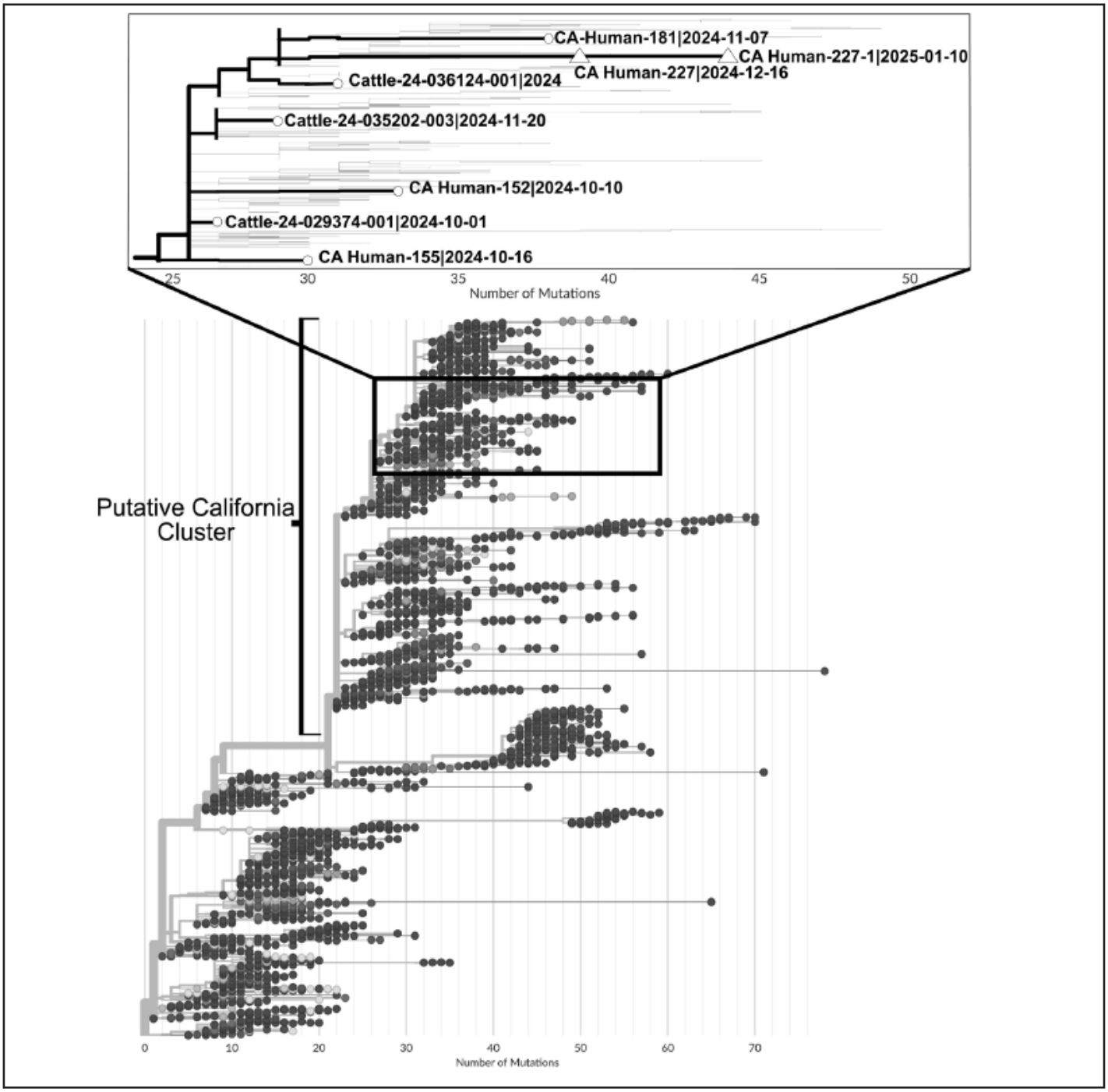
The index patient's illness began on December 13, 2024. Signs and symptoms included, fever, abdominal pain, myalgias, and conjunctivitis, which lasted approximately 1 week and resulted in two health care visits (December 16 and 17). The first visit was to a local emergency department on December 16, where testing for influenza, respiratory syncytial virus, and COVID-19 was performed on a nasopharyngeal specimen. That day, an influenza A–positive rRT-PCR result was received, and the specimen was subsequently sent to SFDPH PHL for further testing as a part of enhanced surveillance. On January 9, 2025, the original specimen tested positive for A(H5) (cycle threshold [Ct] value approximately 29, with Ct values <38 considered positive) using the CDC assay at SFDPH PHL and was confirmed by CDC using the same A(H5) primer and probe set on January 14. A second specimen (oropharyngeal) collected by SFDPH on January 10 (25 days after the first specimen, when the child had been asymptomatic for 21 days), was positive for A(H5) (Ct value approximately 37); specimens collected 4 days later were negative.

Sequencing revealed clade 2.3.4.4b, genotype B3.13 viruses, closely related to B3.13 viruses detected in humans and animals in California (Figure 1). Phylogenetic analyses revealed that the sequences clustered together on an independent branch relative to other California human and dairy cattle sequences. Nucleotide and amino acid changes in the hemagglutinin (HA) and nucleoprotein (NP) genes were observed between the two sequences, consistent with viral replication, and no critical markers of mammalian adaptation (increased virulence or transmission risk) were identified.

* Libraries were generated from M-RT-PCR amplicons and sequenced on an Illumina MiSeq using quarter reactions of Illumina DNA Prep but otherwise following manufacturer recommendations. The amplicons of the second specimen, A/California/227–1/2024, were further sequenced using enrichment capture with the Comprehensive Viral Research Panel (Twist Bioscience) following manufacturer recommendations for the Fast Hybridization methodology. The enriched and unenriched whole genome libraries were sequenced on an Illumina MiSeq (paired end 300 cycle kit).

† 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.

FIGURE 1. Phylogenetic tree* of highly pathogenic avian influenza (H5N1) genotype B3.13 whole genome sequences† — United States, March 2024–July 2025



Abbreviations: HA = hemagglutinin; NP = nucleoprotein.

* Phylogenetic tree was created with the Ultrafast Sample placement on Existing tRee (UShER) tool using the pathogen option "H5N1 B3.13 (cattle) 2024 outbreak: concatenated segments." UCSC UShER: Upload. The inset shows that the San Francisco pediatric case (CA Human-227 and CA Human 227-1) is closely related to other B3.13 cases from California. The number of mutations is relative to concatenated B3.13 cattle sequences from March 2024. Texas cattle sequences (ID: 24-008749-007, 24-009110-018) were used for gene segments PB2, PB1, PA, NP, M, NS, and a New Mexico cattle sequence (ID: 24-010193-003) was used for gene segments HA and NA.

† (A/California/227/2024 and A/California/227-1/2024; GISAID accession: EPI_ISL_20059245; EPI_ISL_20143473). Changes of HA E34G, A156V, K325R (mature H5 HA numbering) and NP R175X (R-65%|K-35%), V270X (A-56%|V-44%), V414X (V-70%|A-30%) were identified between the first positive sample (nasal swab) and the second positive sample (oropharyngeal swab) collected 25 days apart.

Index Case Investigation

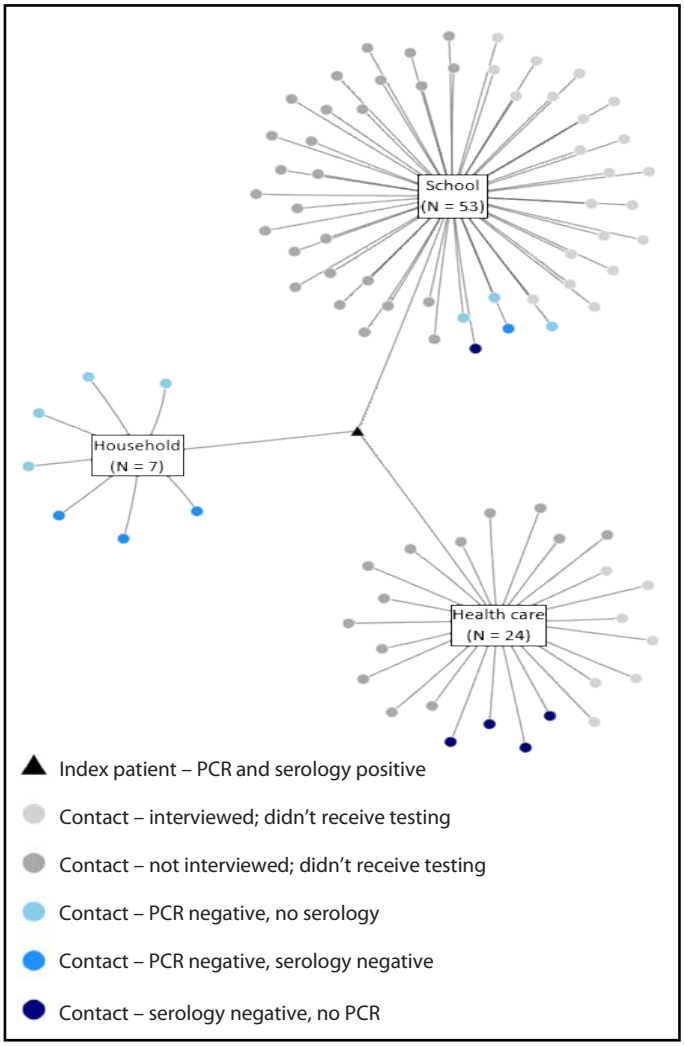
The index patient lived in an urban environment, did not travel, and had no reported exposure to dairy cows, cats, poultry, birds or other wild animals in the 10 days prior to the illness onset; the family had a pet dog. There were no animals at school, and the patient's family did not work in occupations that increase risk for A(H5N1) virus infection (handling, slaughtering, defeathering, butchering, culling, caring for, or milking infected animals). A member of the patient's family purchased raw poultry at a live bird market 2 weeks before the child's illness onset; the poultry was cooked and consumed the same day it was purchased.

Investigation of Close Contacts

Among 84 persons identified as possible contacts of the index patient (seven household, 53 school, and 24 health care), 67 (80%) met the close contact definition (Figure 2). No household contacts reported illness. School absences were reported for 34 (64.2%) school contacts, 26 (76.5%) of whom were interviewed (one teacher and parents of 25 children). All interviewed parents reported respiratory illnesses in their children, including seven who were symptomatic at the time of interview. The teacher had had influenza-compatible symptoms but was asymptomatic at the time of interview. Four persons were tested for one or more respiratory viruses (COVID-19, RSV, or influenza) previously while ill; all test results for influenza were negative. Among the 24 health care worker contacts from three facility visits (two urgent care, one emergency department), 11 (45.8%) completed a survey, including seven who had close contact with the patient; none reported influenza-compatible symptoms. All 11 available respiratory (oropharyngeal and nasal) specimens from close contacts (seven household and four school) were A(H5)-negative by rRT-PCR.

Serum specimens were collected from the index patient (32 days from onset to convalescent serum collection), three adult household contacts, two school contacts, and four health care contacts. Among these nine contacts, the median interval between their first exposure to the index patient and serum collection was 45 days (range = 9–47 days), and the median interval between their last exposure and serum collection was 26 days (range = 0–46 days). The patient had antibodies to all three wild-type A(H5N1) viruses, with elevated antibody titers in all assays, consistent with recent H5N1 infection: A/Texas/37/2024 (B3.13) (MN titer = 160, HI titer = 320); A/Michigan/90/2024 (B3.13) (MN titer = 320, HI titer = 226); and A/Washington/240/2024 (D1.1) (MN titer = 113, HI titer = 320). All nine close contacts' serology results were negative for all three wild-type A(H5N1) viruses.

FIGURE 2. Network analysis of human A(H5N1) influenza cases and possible contacts (N = 84)* — San Francisco, California, January 2025



* Each node indicates a unique contact and the contact's molecular and serologic testing status. This network diagram represents the volume of possible contacts, interview status, and their diagnostic results. The length and location of the spokes do not signify any degree of relatedness and are spaced to fit all contacts into one hub. Each hub and spoke section represents one setting for contacts, all of whom are linked to the patient. After further investigation, 67 (80%) of the 84 contacts met the close contact definition (i.e., persons with prolonged exposure to the patient at a distance of ≤6 feet, without use of recommended personal protective equipment CDC Interim Guidance).

Discussion

Although no exposure was identified, clinical presentation, molecular testing, and positive serology with elevated antibody titers confirmed HPAI A(H5N1) infection in this child. The absence of laboratory (molecular and serologic) evidence of current or recent A(H5N1) virus infection among close contacts suggests no human-to-human transmission. At least two other U.S. patients with confirmed A(H5N1) infection, including

Summary

What is already known about this topic?

As of January 1, 2025, 37 human cases of highly pathogenic avian influenza (HPAI) A(H5N1) had been detected in California, none of which occurred in San Francisco.

What is added by this report?

On January 9, 2025, a case of HPAI A(H5N1) infection was identified in a school-aged child in San Francisco through enhanced surveillance (influenza A virus subtyping of a sample of specimens weekly). No source of exposure was identified, and investigations found no laboratory evidence of human-to-human transmission among close contacts.

What are the implications for public health practice?

Enhanced surveillance and timely subtyping of a subset of influenza A–positive specimens, including specimens from persons without known A(H5N1) exposure, are important to detect avian influenza A virus infections. Public health investigations are critical to monitoring for human-to-human transmission.

another unrelated pediatric patient in the San Francisco Bay Area, had no known exposure to A(H5N1) virus–infected domestic poultry, wild birds, dairy cows, or other infected animals (*3*,*4*).

Although no dairy processing facilities are located in San Francisco, the city is situated on a migratory bird route, and in 2024, A(H5) virus was detected in a live bird market, wild birds, and San Francisco wastewater (H5N1 bird flu detected in SF, first in California city wastewater). Although the family purchased poultry at a live bird market (the child did not accompany them to the market), the parents were confident that the child was not exposed to raw poultry, recent A(H5) testing in the market was negative, the cooked poultry consumption occurred more than 2 weeks before the child's symptom onset, and neither parent had evidence of infection, arguing against infected poultry exposure as the source. Although no wild bird exposure was reported, the child did spend time outside at school; therefore, environmental exposure is theoretically possible. As there were no clear risk factors or exposure to A(H5N1) virus, the infectious source remains unknown.

The genetic differences between the patient's two positive specimens collected at separate time points likely reflect replication in the child during the intervening 25 days. Persistently positive influenza PCR test results have been previously reported, yet the duration of A(H5N1) viral nucleic acid detection and infection in humans is unknown and likely varies with virus and host factors (*9*). Although the second (oropharyngeal) swab collected from the patient was positive for A(H5N1) 4 weeks after the first, sequencing did not reveal mutations indicating mammalian adaptation.

Limitations

The findings in this report are subject to at least three limitations. First, because this case was identified through enhanced surveillance, which at the time included batch testing, there was a delay between specimen collection and the influenza A virus subtyping that led to detection of the case: as a result, the investigation occurred after the patient's illness had resolved and at the end of the 10-day monitoring period for close contacts, subjecting interviews to recall bias and limiting public health interventions such as real-time testing, isolation, antiviral treatment, and postexposure antiviral prophylaxis. Second, it was not possible to interview or collect respiratory and serum specimens from all close contacts; therefore, assessment of signs and symptoms and immunologic response was not comprehensive. Lastly, although household and health care contacts were assessed for asymptomatic infection, only symptomatic school contacts received molecular or serologic testing; thus, asymptomatic infection might have been missed.

Implications for Public Health Practice

A(H5N1) virus infections in humans without a clear animal exposure have rarely occurred in the United States (CDC Confirms H5N1 Bird Flu Infection in a Child in California) but have been documented in other countries where A(H5N1) viruses have circulated in wild birds for years. Continued enhanced surveillance and real-time subtyping of a subset of influenza A positive specimens at public health laboratories, including among persons without known risk for exposure to A(H5N1) virus, is an important part of comprehensive novel influenza surveillance strategies (Summer 2025 Influenza Surveillance).

Although the child had no known dairy cow exposure, sequencing results indicated that this case was associated with the 2024–2025 California dairy cow outbreak. The B3.13 genotype associated with this outbreak has also been detected in birds and felines (*10*), highlighting the continued transmissibility of the virus across susceptible species. Given the wild and domestic animal reservoirs for A(H5N1), a continued One Health approach supports surveillance of wild and domestic animal reservoirs for identification of additional animal cases and risk factors for cross-species and animal-to-human transmission.

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References

1. Garg S, Reed C, Davis CT, et al. Outbreak of highly pathogenic avian influenza A(H5N1) viruses in U.S. dairy cattle and detection of two human cases—United States, 2024. MMWR Morb Mortal Wkly Rep 2024;73:501–5. PMID:38814843 https://doi.org/10.15585/mmwr.mm7321e1
2. Uyeki TM, Milton S, Abdul Hamid C, et al. Highly pathogenic avian influenza A(H5N1) virus infection in a dairy farm worker. N Engl J Med 2024;390:2028–9. PMID:38700506 https://doi.org/10.1056/nejmc2405371
3. Zhu S, Harriman K, Liu C, et al.; Los Angeles County H5 Response Team; California Department of Public Health H5 Laboratory Response Team. Human cases of highly pathogenic avian influenza A(H5N1)—California, September–December 2024. MMWR Morb Mortal Wkly Rep 2025;74:127–33. PMID:40080512 https://doi.org/10.15585/mmwr.mm7408a1
4. Garg S, Reinhart K, Couture A, et al. Highly pathogenic avian influenza A (H5N1) virus infections in humans. N Engl J Med 2025;392:843–54. PMID:39740051 https://doi.org/10.1056/nejmoa2414610
5. CDC; Association of Public Health Laboratories (APHL). Influenza virologic surveillance right size roadmap, 2nd edition. Atlanta, GA: US Department of Health and Human Services, CDC; 2022. https://www.aphl.org/aboutAPHL/publications/Documents/ID-Influenza-Right-Size-Roadmap-Edition2.pdf
6. CDC. 2024–2025 influenza season: surveillance or novel influenza A and seasonal influenza viruses. Atlanta, GA: US Department of Health and Human Services, CDC; 2024. https://www.cdc.gov/bird-flu/php/monitoring-bird-flu/surveillance-novel-seasonal.html
7. Zhou B, Donnelly ME, Scholes DT, et al. Single-reaction genomic amplification accelerates sequencing and vaccine production for classical and Swine origin human influenza a viruses. J Virol 2009;83:10309–13. PMID:19605485 https://doi.org/10.1128/jvi.01109-09
8. Levine MZ, Liu F, Bagdasarian N, et al. Neutralizing antibody response to influenza A(H5N1) virus in dairy farm workers, Michigan, USA. Emerg Infect Dis 2025;31:876–8. PMID:40053378 https://doi.org/10.3201/eid3104.250007
9. Kitano T, Kitagawa D, Murata M, et al. Duration of PCR positivity by type of respiratory virus among children using a multiplex PCR test. J Med Virol 2024;96:e29890. PMID:39188069 https://doi.org/10.1002/jmv.29890
10. Caserta LC, Frye EA, Butt SL, et al. Spillover of highly pathogenic avian influenza H5N1 virus to dairy cattle. Nature 2024;634:669–76. PMID:39053575 https://doi.org/10.1038/s41586-024-07849-4

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