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Genotype-Specific Detection of Measles Virus Using Wastewater Surveillance — Wisconsin, February 2026

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Abstract

In February 2026, two travel-associated cases of measles were reported to the Wisconsin Department of Health Services (WDHS). Public health investigations for each case included wastewater (sewage) surveillance for wild-type measles, which was first implemented by the WDHS Wastewater Monitoring Program in June 2025. The virus from one case, caused by measles genotype D8, was detected by a wastewater surveillance assay before the case was identified by local health authorities, leading to public health notifications and action. Measles virus from the second case, caused by measles genotype B3, was not detected by the assay. Additional analysis of the measles wastewater assay, which is among the most widely used assays in the United States, revealed that the assay was not able to detect an internationally circulating variant of the measles B3 genotype. Two alternative assays confirmed that measles virus was present and detectable in the wastewater. The assay developers designed and released a modified assay that incorporated an additional probe that could detect the B3 variant. These cases demonstrate the potential benefit of wastewater surveillance in detecting wild-type measles virus from a single case, while also highlighting the importance of regularly monitoring wastewater assays with respect to available genomic data. These activities should be supported by up-to-date libraries of publicly available whole-genome sequencing data.

Introduction

Wastewater surveillance has become a valuable tool for improving community-level surveillance for many pathogens, including influenza, COVID-19, respiratory syncytial virus, and monkeypox and is now increasingly used for tracking measles in U.S. communities. Recent findings demonstrate that measles virus nucleic acid can be detected in wastewater before outbreaks are recognized, thereby helping public health officials respond quickly to local cases (*1*). Several commercial and published assays, adapted for the two primary digital polymerase chain reaction (dPCR) platforms (*2,3*), have become available since mid-2025 to monitor wild-type measles in wastewater. However, interlaboratory proficiency testing conducted by the Wisconsin State Laboratory of Hygiene in February 2026, found that performance across four of the most commonly used measles assays varied widely, highlighting the importance of regular monitoring for assay performance (Wisconsin State Laboratory of Hygiene, unpublished data, 2026).

The Wisconsin Department of Health Services (WDHS) Wastewater Monitoring Program routinely tests influent wastewater from 44 municipal wastewater treatment plants across Wisconsin, covering approximately 50% of the state's total population served by a participating sewershed. Surveillance for wild-type measles began in June 2025, using an established measles assay (*2*). This assay was already in use by a large commercial wastewater laboratory and numerous state public health laboratories, making it one of the most widely used measles wastewater assays in the United States during 2025–2026.

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U.S. DEPARTMENT OF HEALTH AND HUMAN SERVICES
CENTERS FOR DISEASE CONTROL AND PREVENTION

Investigation and Findings

In February 2026, two measles cases (in patients A and B, who lived in areas served by different sewersheds) were reported to WDHS (Figure). Contact investigations found that each case was travel associated, and the cases were not epidemiologically linked. WDHS used wastewater surveillance for wild-type measles to support each investigation. This investigation was reviewed by CDC, deemed not research, and conducted consistent with applicable federal law and CDC policy.*

Patient A

Detection of measles virus in a wastewater sample. On February 5, 2026, the WDHS Wastewater Monitoring Program detected wild-type measles virus in a sample collected on February 2, by a wastewater treatment plant serving approximately 30,000 residents in Wisconsin.

Notification to WDHS of confirmed measles case. Later the same day, WDHS was notified of a confirmed case of measles in an adult (patient A) who had returned to Wisconsin on January 29, after traveling domestically; during this period (4 days before through 4 days after rash onset), the patient was infectious. Rash onset occurred during travel (January 29), and the patient isolated at home in Wisconsin on arrival. When the positive wastewater sample was collected (February 2), patient A was still isolated at the Wisconsin residence, which was located within the sewershed where the wastewater detection occurred. Patient A's measles case was clinically diagnosed without laboratory genotyping but was epidemiologically linked to an out-of-state measles outbreak of genotype D8, the predominant circulating measles genotype in the United States (*4*).

Patient B

Notification to WDHS of confirmed measles case. On February 1, 2026, WDHS received laboratory confirmation of a measles case in a Wisconsin resident (patient B). Investigation indicated that patient B had become infected with measles while abroad, patient B's measles case was not epidemiologically linked to patient A's case, and patient B lived in a different Wisconsin county from patient A, which was served by a different sewershed. Sequencing of the specimen identified the virus as measles virus B3 genotype,† an internationally circulating measles genotype that accounted for approximately 5%–10% of U.S. cases in 2025 (*4*). The onset of patient B's rash occurred on January 29, and the patient remained isolated at home during the infectious period (January 25–February 2).

Additional testing after no measles virus detected in wastewater samples. Despite confirmation that the patient was at home during the infectious period, the standard measles wastewater assay did not detect measles virus in any of the eight wastewater samples collected during

* 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.

† Specimen genotyping of the sample from patient B was performed by the Wisconsin State Laboratory of Hygiene, Communicable Disease Division, using Sanger sequencing of the measles *N450* gene region.

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January 25–February 2, 2026, from the wastewater treatment facility serving the patient's residence (*2*). Additional laboratory testing indicated that the measles wastewater assay was unable to detect measles virus either in the clinical isolate or in an available B3 reference strain.[§] Follow-up testing of wastewater samples involved two independent methods. One method involved using an alternative dPCR assay for measles used by the program's laboratory (*5*) to analyze a subsewershed sample collected on February 1, from the area where patient B lived. The second method involved using an untargeted approach known as shotgun metagenomic viral sequencing to analyze citywide wastewater samples; this approach attempts to sequence all viral genetic material in a sample and can identify novel or unexpected pathogens (*6*). Both methods confirmed the presence of measles virus at detectable levels in the wastewater samples. The metagenomic sequencing results of the wastewater sample from February 2, were identical to the whole-genome sequencing results for patient B's clinical measles isolate,[¶] providing strong evidence that patient B was the source of the measles virus detected in the wastewater.

Public Health Response

Patient A

State and local authorities were informed about the measles virus detection in wastewater, and information regarding the wastewater detection was included in a public media release. All wastewater monitoring results for measles in Wisconsin are shared with local health departments and published on CDC's national measles wastewater dashboard. Case and contact investigations for patient A were conducted by the local health department. Known contacts were notified of potential exposure, and notices of public exposure locations were issued. No further cases were identified in connection with patient A. In addition, no measles virus was detected in wastewater samples collected before or after the initial detection, suggesting that public health measures might have effectively contained the travel-related introduction.

Patient B

WDHS notified CDC and the assay developers that the wastewater assay was unable to detect the measles virus B3 genotype (*2*). Using publicly available whole-genome sequencing data, the assay developers identified an *N* gene mutation in recent measles virus genotype B3 samples; this mutation caused the assay failure. On March 2, the developers released a modified assay that incorporated an additional probe[**] to bind to the mutation and improve coverage of the assay. Case and contact investigations for patient B were conducted by the local health department. Known contacts were notified of potential exposure, and notices of public exposure locations were issued. No further cases were identified in connection with patient B.

Discussion

These two measles cases demonstrate the benefits of and potential challenges associated with wastewater surveillance as a public health tool. The detections of measles virus in wastewater associated with patient A's measles case adds to a growing body of evidence that wastewater surveillance can detect measles virus from a single case (in this instance, one known case in a sewershed serving approximately 30,000 persons). This high level of sensitivity underscores the potential for wastewater surveillance to detect cases or outbreaks and prompt public health action that can prevent additional cases.

The experience with the second measles case (in patient B) highlights several other considerations that are important for ensuring that wastewater surveillance continues to provide accurate and actionable data. In this case, a widely used wastewater assay for measles surveillance was unable to detect an internationally circulating variant of measles genotype (B3). The developers of the original wastewater assay (*2*) used 97 measles sequences (43 B3 sequences and 54 D8 sequences) and the measles vaccine strain (i.e., Edmonston strain), all obtained from the National Center for Biotechnology Information in March 2025, to design the assay. They performed computer (i.e., in-silico) modeling to confirm specificity to circulating measles genotypes B3 and D8. The assay design was made publicly available and has been used in many U.S. states since May 2025.

A mutation in a section of the *N* gene of the measles B3 virus, which the original assay targeted, was rarely detected before the assay was developed; <2% of available measles B3 sequences contained the mutation.[††] However, during the period after the assay was released (May 2025–February 2026), 75% (169 of 226) of available measles B3 sequences contained the mutation. Sample collection dates for these sequences suggest that this

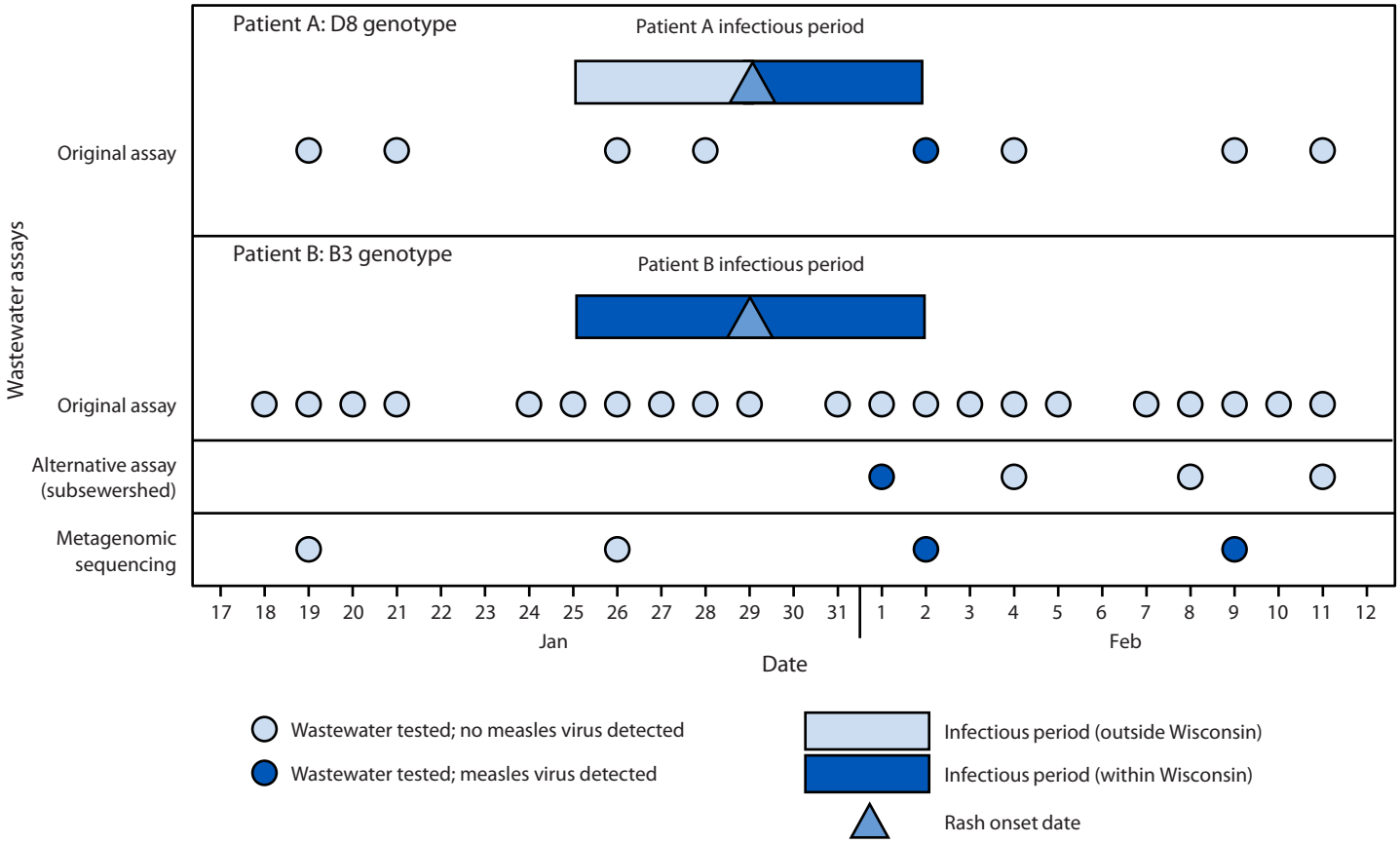
[§] Measles genotype B3 reference strain was cultured by CDC from a 2024 case sample and distributed by BEI (MVs/Tennessee. USA/40.24).

[¶] Metagenomic sequencing of the wastewater sample from February 2, 2026, had five reads ranging from 92 to 148 base pairs that perfectly matched the consensus genomes from patient B in the *H* and *L* gene regions. CDC performed whole-genome sequencing of the patient sample to establish a match with the wastewater in May 2026 after conclusion of the investigation. Specimen identifiers for whole-genome sequencing, patient B: MVs/Wisconsin.USA/Jan.26/2166 and MVs/Wisconsin.USA/Jan.26/2801.

[**] The original assay probe was CATGATGATCC**A**AGTAGTAGTGA. For genotype B3, an adenine-to-guanine (A-to-G) mutation in the probe-binding region (nucleoprotein gene) caused the mismatch. A modified probe was added in March 2026: CATGATGATCC**G**AGTAGTAGTGA.

[††] Data on measles B3 sequences were obtained from Measles Virus | Pathoplexus and the National Center for Biotechnology Information. Two samples (collected in 2020 and 2024) were identified with sequences containing the *N*-gene mutation before the original wastewater assay for measles was developed.

FIGURE. Timeline of wastewater testing results* for measles virus genotypes D8 (patient A) and B3 (patient B) using multiple assays† — Wisconsin, 2026



* Dates for wastewater surveillance indicate the beginning of the 24-hour composite sample collection.

† The original (standard) assay used to detect the measles virus in wastewater has been described previously (https://doi.org/10.1039/D6EW00020G). The alternative assay (https://doi.org/10.1039/d6ew00020g) is a quantitative, gene-specific, real-time reverse transcription–polymerase chain reaction assay used to detect measles virus in clinical specimens. This alternative assay, which was only used after the original assay did not detect measles virus in the wastewater samples from the wastewater treatment facility serving patient B's residence, is not used routinely because it is not specific for wild-type measles. Alternative assay results are only shown for samples from subsewershed interceptors that collected wastewater from the area within the sewershed where patient B lived.

variant has been the predominant B3 variant in international circulation since July 2024.

The CDC-validated wastewater assay for measles, adapted from a multiplexed reverse transcription-droplet dPCR assay (*3*), targets the *M* gene of the measles virus (and therefore was not affected by the *N*-gene mutation). However, jurisdictions relying on the original assay for measles surveillance might have experienced reduced sensitivity for detecting B3-associated cases or outbreaks before the assay was modified through the addition of a second probe.

This gap in surveillance for the measles B3 genotype highlights the need for improved monitoring and follow-up of wastewater assays with respect to available genomic data. Regular computer modeling and wet laboratory evaluations of assay primers and probes for circulating virus strains are critical for identifying and correcting assay probe mismatches with circulating lineages before they affect overall surveillance. These findings also highlight the importance of performance testing of wastewater assays.

With various laboratory assays available for measles wastewater surveillance, and a lack of standardized performance testing across assays, future genetic evolution of the measles virus might limit detection by current wastewater assays, affecting surveillance and requiring frequent revalidation. Ongoing assay development and updates should be supported by the availability of a robust and up-to-date library of publicly available whole-genome sequencing data. Development of sequencing-based approaches for detection of measles and other emerging public health threats could address this problem by monitoring mutating viruses without requiring updates to targeted approaches.

Summary

What is already known about this topic?

Wastewater (sewage) surveillance has been increasingly used to support public health surveillance for infectious diseases, including measles, in the United States.

What is added by this report?

In February 2026, two unrelated measles cases were reported to the Wisconsin Department of Health Services. Wastewater surveillance detected measles virus associated with one case of measles caused by the D8 genotype, before the case was reported. However, the same widely used wastewater surveillance assay for measles failed to detect the virus from the second case, which was caused by a different genotype (B3). After the assay limitation was identified by public health officials, the developers released a modified assay that improved detection of the measles B3 genotype.

What are the implications for public health practice?

To ensure that wastewater data are as accurate and useful as possible, wastewater assays should be standardized and revalidated against circulating viruses and supported by publicly available whole-genome sequencing data.

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Increase in Disseminated Gonococcal Infections — Alaska, 2023–2024

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Abstract

Disseminated gonococcal infection (DGI) is a rare but serious complication of *Neisseria gonorrhoeae* infection that can result in severe illness or death. In April 2024, the Alaska Section of Epidemiology (SOE) identified an increase in suspected DGI cases in Anchorage, Alaska, prompting enhanced surveillance. The state's gonorrhea surveillance system and electronic health records were used to review all likely and verified DGI cases reported to SOE during January 2023–December 2024. Thirty-five DGI cases were identified, accounting for 0.35% (eight of 2,289) of all gonorrhea cases in 2023 and 1.3% (27 of 2,079) in 2024. The median patient age was 36 years, 51% of patients were male, and 37% had a documented substance use disorder. Overall, 21 (60%) patients experienced septic arthritis, and three (9%) patients developed endocarditis; 28 (80%) patients lacked mucosal symptoms. No deaths were reported. Eighteen available isolates collected during 2020–2024, including 14 from cases reported during 2023 and 2024, underwent antimicrobial susceptibility testing and whole-genome sequencing. Laboratory analyses identified a cluster of highly related isolates with a novel multilocus sequence type (MLST-18036) and markers of increased virulence; however, no resistance to first-line therapy (ceftriaxone) was detected. Clinicians should maintain a high index of suspicion for DGI in patients at risk for gonococcal infection, even in the absence of mucosal symptoms. Prompt diagnosis and treatment, prompt case reporting, and robust partner services are critical to preventing transmission and reducing DGI morbidity.

Introduction

Disseminated gonococcal infection (DGI) is a rare but serious complication of gonorrhea, occurring in <1% of reported cases (*1*). DGI develops when *Neisseria gonorrhoeae* invades the bloodstream, causing bacteremia, and spreads from an initial localized mucosal site (e.g., the genital tract, oropharynx, or rectum) to distant sites. Clinical signs and symptoms can include septic arthritis, skin lesions, asymmetric polyarthralgia, and tenosynovitis. Rare but severe complications include endocarditis, meningitis, and death (*1*); a study of 274 DGI cases in 13 U.S. states during 2020–2022 reported a case-fatality rate of 2.2% (*2*). In April 2024, the Alaska Section of Epidemiology (SOE) was notified by an infectious disease physician of an increase in suspected DGI among patients seeking care for joint pain at Anchorage emergency departments. A review of statewide surveillance data revealed a sustained rise in DGI cases beginning in July 2023. This report describes the epidemiologic investigation of DGI cases reported in Alaska during January 2023–December 2024 and accompanying laboratory analyses of available DGI isolates collected during 2020–2024 to contextualize changes in circulating strains, virulence, and public health risk.

Methods

Data Sources and Case Ascertainment

Two data sources were used to identify and review DGI cases: CDC's National Electronic Disease Surveillance System Base System (NBS) and patient electronic health records (EHRs). Consistent with the Council of State and Territorial Epidemiologists case definition, a verified DGI case was defined as isolation or detection of *N. gonorrhoeae* from a disseminated site of infection (e.g., skin, synovial fluid, blood, or cerebrospinal fluid) by culture or a nucleic acid amplification test (NAAT). A likely DGI case was defined by clinical signs and symptoms compatible with disseminated infection without other known causes and with *N. gonorrhoeae* detected only from a mucosal site by culture or NAAT (*3*).

Beginning in September 2024, all verified or likely DGI cases were assigned to SOE disease investigation staff members for chart review, clinician follow-up, isolate submission to public health laboratories, and patient interviews using CDC case reporting standards. Age, sex, race and ethnicity, and county of residence were identified by report in NBS and revised as needed based on available information from medical records or patient interviews. EHR data describe additional behavioral and clinical information not routinely collected for patients with gonorrhea. All likely and verified DGI cases reported to SOE during January 1, 2023–December 31, 2024, were included in the epidemiologic case analysis. Data were analyzed using R statistical software (version 4.4.3; R Foundation). This activity was reviewed by CDC, deemed not research, and conducted consistent with applicable federal law and CDC policy.*

* 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.

Laboratory Testing

Available gonococcal isolates from disseminated sites of infection (DGI isolates) collected during 2020–2024 were submitted to CDC for antimicrobial susceptibility testing (AST) and whole-genome sequencing (WGS). AST was conducted by agar dilution; minimum inhibitory concentrations (MICs) were interpreted according to Clinical and Laboratory Standards Institute guidelines. MIC interpretive criteria used to classify antimicrobial susceptibility were as follows: isolates with MICs ≤1.0 μg/mL for azithromycin, ≤0.25 μg/mL for cefixime, and ≤0.25 μg/mL for ceftriaxone were classified as susceptible, whereas isolates with MICs ≥1.0 μg/mL for ciprofloxacin, ≥2.0 μg/mL for penicillin, and ≥2.0 μg/mL for tetracycline were classified as resistant. Isolate relatedness was determined by single nucleotide polymorphism (SNP) analysis. Phylogenetic comparisons were conducted using DGI isolates and all urogenital isolates (101) collected in Anchorage County, Alaska, and nearby counties during 2019–2024 through the Gonococcal Isolate Surveillance Project and other available urogenital isolates (nine) from patients with uncomplicated gonorrhea. No urogenital isolates available from the DGI cases were available for inclusion in the analysis.

Results

Patient Characteristics

In 2024, a total of 27 DGI cases were reported to SOE, accounting for 1.3% of 2,079 reported gonorrhea cases that year (Figure). This percentage of DGI cases is 3.7 times the 0.35% reported in 2023 (eight of 2,289 cases) and 10 times the 0.13% reported in 2022 (three of 2,304 cases).

Demographic characteristics. Among the 35 patients with diagnosed DGI during 2023–2024, the median age was 36 years (IQR = 15 years); 51% were male (Table 1). A majority of patients (71%) lived in Anchorage County. Overall, 74% of cases were verified by culture or NAAT of a specimen from a disseminated site of infection (synovial fluid, 58%; blood, 42%).

Clinical signs and symptoms. The most common clinical signs and symptoms were septic arthritis (60%), fever (37%), and polyarthralgia (34%); three patients (9%) developed endocarditis. Eighty percent of patients did not report mucosal symptoms. Thirteen patients (37%) had a documented substance use disorder, including methamphetamine use (29%) or injection drug use (17%). Other comorbidities included diabetes (9%) and hepatitis C (14%). One patient had a history of a prior episode of DGI.

Patient outcomes. Overall, 83% of patients completed recommended DGI treatment with intravenous ceftriaxone; outcomes were unknown for six patients who either left the hospital against medical advice or were lost to follow-up after diagnosis. Nearly all patients (89%) required hospitalization, and 20 (57%) required surgical intervention (18 joint aspirations, washouts, or debridements and two heart valve replacements); no deaths were reported. Among the 25 (71%) patients with urogenital site specimens collected, 15 (60%) received a positive *N. gonorrhoeae* test result.

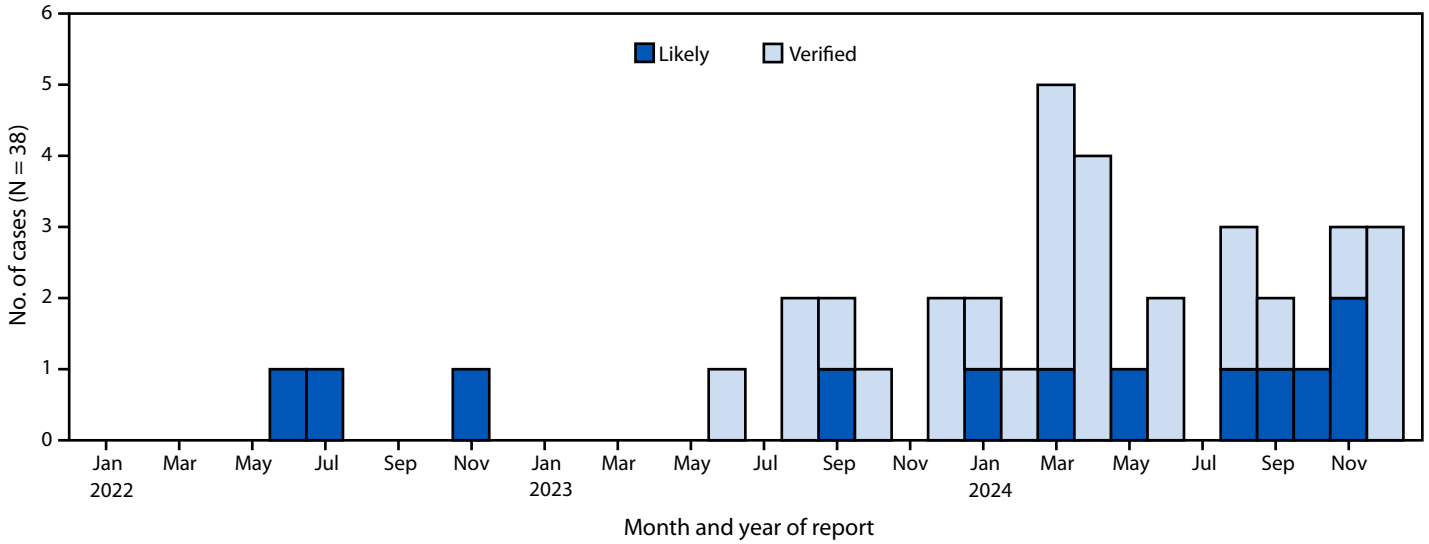
Isolate Characteristics

Eighteen DGI isolates from 18 patients collected during 2020–2024, including 14 from cases reported during 2023–2024, were available for AST and WGS. All isolates were susceptible to ceftriaxone and cefixime; multiple isolates demonstrated high-level resistance to penicillin and tetracycline, based on Clinical and Laboratory Standards Institute–defined breakpoints and confirmed by presence of beta-lactam resistance gene (*blaTEM)* and *tet*(*M)* plasmids, and 13 carried ciprofloxacin resistance markers (gyrase subunit A mutations) (Table 2). Thirteen (72%) isolates had the *porB1A* allele, which is associated with gonococcal dissemination. Eight (44%) isolates (collected during December 2023–April 2024) shared a novel gonococcal multilocus sequence type (MLST-18036) that has not been previously reported in the United States. All MLST-18036 isolates carried the *porB1A* allele, showed high-level tetracycline resistance, and formed a tight phylogenetic cluster (with an average distance of fewer than seven SNPs). Thirteen of the 18 DGI isolates carried the *porB1A* allele, compared with <1% (one of 110) of urogenital isolates included in the analysis. SNP analysis of DGI and urogenital isolates collected during 2023–2024 found that none of the DGI isolates was closely genetically related to the urogenital isolates (Supplementary Figure).

Discussion

The sustained increase in DGI case counts and the high genetic relatedness of DGI cases described in this report raise concerns about the circulation of gonococcal strains with increased virulence in Alaska. Consistent with findings from recent DGI investigations in California and Michigan (*4*,*5*), many patients lacked mucosal symptoms and did not belong to populations for whom routine gonorrhea screening is recommended (e.g., sexually active females aged <25 years) (*6*,*7*); these factors increase the risk for delayed or missed diagnoses. A recent investigation described DGI cases with isolated pharyngeal gonorrhea, which is often asymptomatic and a possible disposing factor for DGI, highlighting the importance of collecting specimens from anatomic sites of sexual exposure from patients with suspected DGI (*6*,*8*). Detecting and treating DGI is critical because untreated DGI can result in severe complications, including septic shock, endocarditis,

FIGURE. Number of likely and verified disseminated gonococcal infection cases, by month and year of case reported — Alaska, June 2022–December 2024*



* Epidemiologic case analyses were restricted to cases reported during 2023–2024; 2022 cases are included to provide historical and laboratory context.

Summary

What is already known about this topic?

Disseminated gonococcal infection (DGI) is a rare but serious complication of gonorrhea that can result in severe illness or death.

What is added by this report?

Alaska reported 35 DGI cases during 2023–2024, representing a substantial increase compared with the three cases reported in 2022. Cases occurred across a range of demographic groups, and patients often lacked mucosal symptoms. Whole-genome sequencing identified one cluster with a novel sequence type demonstrating increased virulence and antimicrobial resistance.

What are the implications for public health practice?

Clinicians should maintain a high index of suspicion for DGI in patients with DGI-compatible signs and symptoms to facilitate prompt diagnosis and treatment and to prevent severe complications. Prompt reporting of cases can expedite public health investigations and contain spread.

and death. Alaska's first known DGI-associated death was reported in July 2025 (*8*).

SOE expanded partner services in October 2024 to strengthen detection, treatment, and epidemiologic case investigations, which can guide the prioritization of preventive services in the community and prevent onward transmission of circulating strains that might be predisposed to dissemination. Patient sexual networks were difficult to define, likely because of undiagnosed asymptomatic infections and challenges with timely testing. Per CDC's *Sexually Transmitted Infections Treatment Guidelines*, if DGI is suspected based on clinical signs or symptoms, NAAT and culture specimens from exposed mucosal sites should be collected and processed, in addition to NAAT and culture specimens from disseminated sites of infection (*6*). Missed opportunities for mucosal testing and limited culture collection before empiric treatment might contribute to missed cases (*6*). These findings underscore the importance of gonorrhea screening among persons who might be at increased risk for infection. Comprehensive risk assessments during clinical evaluations, including thorough social and sexual histories, are also important to improving the detection of infections that might progress to DGI. In response to this investigation, SOE broadened Alaska's gonorrhea screening recommendations to include all sexually active patients with risk factors including substance use, multiple sexual partners, or a history of sexually transmitted infections (*8*,*9*).

Limitations

The findings in this report are subject to at least five limitations. First, the number of DGI cases is likely underestimated because 1) diagnosis is often based on clinical signs and symptoms, 2) sterile-site cultures are not always obtained or might be negative, 3) underlying mucosal infections might be asymptomatic, and 4) certain clinical signs and symptoms can be more indolent (*1*). Second, incomplete specimen collection and testing might limit diagnosis and accurate case reporting. Third, epidemiologic investigations rely on patient interviews. The responses might be subject to recall bias, and some patients might not disclose their sexual and substance use histories, limiting the identification of potential transmission links and case attributes that help guide local prevention strategies. Fourth, AST and WGS were only performed on available isolates, and

TABLE 1. Sociodemographic and clinical characteristics of patients with disseminated gonococcal infection — Alaska, 2023–2024

Characteristic	No. of cases (column %)		
	2023	2024	2023–2024
Total	**8**	**27**	**35**
Age group, yrs			
Median age (IQR)	35.0 (14.8)	36.0 (18.0)	36.0 (15.0)
<20	0 (—)	1 (3.7)	1 (2.9)
20–29	3 (37.5)	5 (18.5)	8 (22.9)
30–39	2 (25.0)	11 (40.7)	13 (37.1)
40–49	3 (37.5)	3 (11.1)	6 (17.1)
50–59	0 (—)	4 (14.8)	4 (11.4)
≥60	0 (—)	3 (11.1)	3 (8.6)
Sex			
Female	5 (62.5)	12 (44.4)	17 (48.6)
Male	3 (37.5)	15 (55.6)	18 (51.4)
Sexual identity			
Heterosexual (not bisexual, lesbian, or gay)	8 (100.0)	11 (40.7)	19 (54.3)
Bisexual	0 (—)	1 (3.7)	1 (2.9)
Lesbian or gay	0 (—)	1 (3.7)	1 (2.9)
Unknown	0 (—)	14 (51.9)	14 (40.0)
Case status			
Likely	1 (12.5)	8 (29.6)	9 (25.7)
Verified	7 (87.5)	19 (70.4)	26 (74.3)
Race and ethnicity*			
American Indian or Alaska Native	4 (50.0)	7 (25.9)	11 (31.4)
Asian	1 (12.5)	0 (—)	1 (2.9)
Black or African American	0 (—)	2 (7.4)	2 (5.7)
Hispanic or Latino	0 (—)	2 (7.4)	2 (5.7)
Native Hawaiian or Pacific Islander	1 (12.5)	4 (14.8)	5 (14.3)
White	1 (12.5)	6 (22.2)	7 (20.0)
Multiracial	1 (12.5)	6 (22.2)	7 (20.0)
Other	0 (—)	1 (3.7)	1 (2.9)
Unknown	0 (—)	1 (3.7)	1 (2.9)
Alaska county of residence			
Anchorage County	6 (75.0)	19 (70.4)	25 (71.4)
Other counties†	2 (25.0)	8 (29.6)	10 (28.6)
Substance use during past 12 months			
Methamphetamines	3 (37.5)	7 (25.9)	10 (28.6)
Injection drugs	2 (25.0)	4 (14.8)	6 (17.1)
Preexisting medical condition§			
Diabetes	1 (12.5)	2 (7.4)	3 (8.6)
HIV infection	0 (—)	1 (3.7)	1 (2.9)
Hepatitis C	1 (12.5)	4 (14.8)	5 (14.3)
Receiving immunosuppressive therapy (i.e., steroids)	0 (—)	1 (3.7)	1 (2.9)
Pregnancy	1 (12.5)	0 (—)	1 (2.9)
Cirrhosis	1 (12.5)	0 (—)	1 (2.9)
Previous DGI	1 (12.5)	0 (—)	1 (2.9)
Systemic lupus erythematous	0 (—)	1 (3.7)	1 (2.9)
Substance use disorder	5 (62.5)	8 (29.6)	13 (37.1)
Urogenital, pharyngeal, or rectal signs or symptoms present¶	2 (25.0)	5 (18.5)	7 (20.0)
DGI clinical signs and symptoms§			
Septic arthritis	8 (100.0)	13 (48.1)	21 (60.0)
Fever	4 (50.0)	9 (33.3)	13 (37.1)
Polyarthralgia	3 (37.5)	9 (33.3)	12 (34.3)
Bacteremia	1 (12.5)	4 (14.8)	5 (14.3)
Tenosynovitis	4 (50.0)	5 (18.5)	9 (25.7)
Skin lesions	2 (25.0)	2 (7.4)	4 (11.4)
Myositis	1 (12.5)	0 (—)	1 (2.9)
Endocarditis	0 (—)	3 (11.1)	3 (8.6)
Sterile site specimen collected (n = 26)**			
Blood	1 (14.3)	10 (52.6)	11 (42.3)
Joint or synovial fluid	6 (85.7)	9 (47.4)	15 (57.7)
Urogenital site specimen collected (n = 25)			
Positive	6 (100.0)	9 (47.4)	15 (60.0)
Negative	0 (—)	10 (52.6)	10 (40.0)
Completed DGI treatment††			
Yes	8 (100.0)	21 (77.8)	29 (82.9)
Unknown	0 (—)	6 (22.2)	6 (17.1)
Hospitalization required	4 (50)	27 (100.0)	31 (88.6)
Surgical intervention required§§	7 (87.5)	13 (48.1)	20 (57.1)

Abbreviation: DGI = disseminated gonococcal infection.

* Categories are not mutually exclusive; persons who identified as multiple races identified as multiracial. Persons of Hispanic or Latino (Hispanic) origin might be of any race but are categorized as Hispanic; all racial groups are non-Hispanic.

† Includes one or more cases from Matanuska Susitna, Bethel, Kenai Peninsula, North Slope, and Northwest Arctic counties.

§ Categories are not mutually exclusive; individual patients could have more than one of the conditions listed.

¶ At the time of diagnosis or <1 month before diagnosis.

** Specimen collection site for all laboratory-confirmed DGI cases.

†† Intravenous or intramuscular ceftriaxone treatment received; unknown indicates confirmation of treatment completion status was unavailable.

§§ Includes joint aspiration; joint washout, debridement, or operative incision and drainage; or heart valve replacement surgery.

the small number of cases limits generalizability and might not represent all strains circulating in Alaska or elsewhere. Finally, interviews and chart reviews began later in the outbreak and might have missed early links.

Implications for Public Health Practice

The Alaska Division of Public Health recommends that clinicians maintain a high index of suspicion for patients with clinical signs and symptoms of DGI, even in the absence of mucosal symptoms, and obtain a detailed sexual history (*8*,*9*). When DGI is suspected, clinicians should obtain specimens from suspected disseminated sites of infection, in addition to urogenital, rectal, and pharyngeal specimens based on reported sexual exposures; all gonococcal isolates should undergo AST (*6*). DGI treatment recommendations in CDC's current *Sexually Transmitted Infection Treatment Guidelines* should be followed; hospitalization that includes an infectious disease consultation is advised for initial therapy recommendations, particularly for severe cases (*6*). Prompt reporting of confirmed or suspected DGI cases and collaboration with public health partners can facilitate public health investigation to ensure appropriate diagnosis and treatment, interrupt transmission, and prevent severe complications, including death (*4*).

TABLE 2. Antimicrobial susceptibility testing* and molecular markers of resistance results of *Neisseria gonorrhoeae* isolated from patients with disseminated gonococcal infection — Alaska, 2020–2024

DGI case no.	Specimen collection year	Specimen source (type)	PEN MIC, μg/ml	AMR for PEN; *blaTEM* plasmid present	TET MIC, μg/ml	AMR for TET; tetM plasmid present	CIP MIC, μg/ml	AMR for CIP; *gyrA* aa91	AZM MIC, μg/ml	AMR for AZM; mtrR mosaic	CFX MIC, μg/ml	CRO MIC, μg/ml
1	2020	Synovial fluid	0.5	Yes	1	No	0.004	Wild type	0.5	No	0.03	0.015
2	2021	Blood	0.5	Yes	0.5	No	0.008	Wild type	0.25	No	0.03	0.015
3	2021	Synovial fluid	1	Yes	4	No	16	Mutant	2	Yes	0.03	0.03
4	2022	Abscess tissue	0.25	Yes	1	No	0.03	Wild type	≤0.008	No	0.015	0.008
5	2023	Blood	0.5	Yes	1	No	0.004	Wild type	0.25	No	0.06	0.03
6	2023	Synovial fluid	2	Yes	1	No	4	Mutant	0.03	No	0.03	0.015
7	2023	Synovial fluid	8	Yes	32	Yes	4	Mutant	0.03	No	0.015	0.015
8	2024	Blood	8	Yes	32	Yes	4	Mutant	0.03	No	0.015	0.008
9	2024	Blood	8	Yes	32	Yes	4	Mutant	0.03	No	0.015	0.008
10	2024	Synovial fluid	4	Yes	32	Yes	4	Mutant	0.03	No	0.015	0.004
11	2024	Synovial fluid	8	Yes	32	Yes	4	Mutant	0.03	No	0.015	0.008
12	2024	Blood	8	Yes	32	Yes	4	Mutant	0.03	No	0.015	0.008
13	2024	Blood	4	Yes	16	Yes	2	Mutant	0.06	No	0.015	0.004
14	2024	Blood	0.5	No	1	No	4	Mutant	0.125	No	0.008	0.004
15	2024	Blood	1	No	1	No	4	Mutant	0.25	No	0.016	0.008
16	2024	Blood	2	Yes	32	Yes	0.5	Mutant	0.06	No	0.016	0.004
17	2024	Blood	2	Yes	32	Yes	4	Mutant	0.25	No	0.03	0.008
18	2024	Blood	2	Yes	32	Yes	4	Mutant	0.25	No	0.03	0.008

Abbreviations: AMR = antimicrobial resistance; AZM = azithromycin; *blaTEM* = beta-lactam resistance gene; CFX = cefixime; CIP = ciprofloxacin; CRO = ceftriaxone; DGI = disseminated gonococcal infection; *gyrA* aa91 = gyrase subunit A protein amino acid 91; MIC = minimum inhibitory concentration; *mtrR* = methionine synthase reductase gene; PEN = penicillin; TET = tetracycline.

* MIC interpretive criteria used to classify antimicrobial susceptibility were as follows: isolates with MICs ≤1.0 μg/mL for azithromycin, ≤0.25 μg/mL for cefixime, and ≤0.25 μg/mL for ceftriaxone were classified as susceptible, whereas isolates with MICs ≥1.0 μg/mL for ciprofloxacin, ≥2.0 μg/mL for penicillin, and ≥2.0 μg/mL for tetracycline were classified as resistant.

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All authors have completed and submitted the International Committee of Medical Journal Editors form for disclosure of potential conflicts of interest. No potential conflicts of interest were disclosed.

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Erratum

Vol. 75, No. SS-4

The report "Surveillance for *Candida auris* — United States, 2022–2024" contained an error.

On page 6, the *Candida auris* surveillance team members listed for the New York State Department of Health should have read, "**Coralie Bucher, Warangkana Sangchan, Jeffrey Wu,**".

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