

PUBLIC HEALTH ALERTS | IN PARTNERSHIP WITH CIDRAP

# Domestic Measles Importations in Washington State, January 2026

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## Abstract

Measles outbreaks are increasing in frequency and size in the United States. Within 2 weeks, there were five distinct out-of-state measles importations into Washington State epidemiologically connected to an outbreak in South Carolina, resulting in a total of 26 measles cases during January–February 2026. Genomic analyses supported epidemiologic conclusions regarding exposure sources of imported cases and independence among importations. Adherence to isolation and quarantine likely limited onward transmission in undervaccinated communities. Combining timely genomic data analysis with epidemiologic information can strengthen understanding of measles outbreaks as public health jurisdictions prepare to respond to increases in imported measles cases.

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## Introduction

Measles is a highly contagious, vaccine-preventable disease. Large measles outbreaks during 2025 and 2026 now threaten the United States' measles elimination status.<sup>1</sup> During January 2026, five out-of-state measles importations into Washington State were identified. We describe epidemiologic and genomic characteristics of resulting measles cases. This activity was reviewed by the Centers for Disease Control and Prevention and determined to be exempt from institutional review board review.

## Investigation and Outcomes

We identified 26 measles cases among Washington residents (Fig. S1 in the Supplementary Appendix).<sup>2,3</sup> When specimens were available, measles was confirmed by polymerase chain reaction testing at Washington State Public Health Laboratories (n=10) or commercial

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measles serology testing (n=1). High-quality, whole viral genomes were generated for 10 cases (Supplementary Methods). Public health jurisdictions and community leaders developed messaging for undervaccinated communities focused on nonvaccine measles control strategies, including isolation, quarantine, and calling ahead to health care facilities.

### IMPORTATION 1

On January 12, 2026, a rash developed in a Washington resident of County A, who reported exposure to ill contacts during South Carolina travel; this case was laboratory-confirmed as measles.<sup>4</sup> One secondary case in a close contact (County B resident) was confirmed by epidemiologic linkage (rash onset: January 31). This individual adhered to isolation and quarantine recommendations. No further cases were identified. The measles virus whole genome from the County A case matched sequences from South Carolina measles cases with 100% nucleotide identity across 12,089–15,677 base pairs (bp) (Fig. 1).

### IMPORTATION 2

South Carolina residents visited public locations in Washington while contagious for measles, leading to an outbreak with 14 confirmed cases among County C residents.<sup>5,6</sup> The first four cases were among individuals who reported contact with South Carolina residents or exposure locations, experienced rashes during January 13–24, and were laboratory-confirmed as measles. These residents visited schools, health care facilities, and a church. Secondary cases were among close contacts (n=9) or were present at an exposure location (n=1) and were confirmed by epidemiologic linkage or extended epidemiologic linkage<sup>7</sup> (rash onsets: January 15–February 17). Secondary cases adhered to isolation and quarantine recommendations. Measles virus whole genomes from the first four County C cases were indistinguishable from each other or separated by one nucleotide mutation and matched sequences from South Carolina cases with 100% nucleotide identity across 13,297–15,677 bp.

### IMPORTATION 3

Two measles cases among County B residents were among persons who reported exposure to ill contacts during South Carolina travel, experienced rash onsets during January 15–16, and were confirmed by epidemiologic linkage.<sup>8</sup> Both persons were in South Carolina during exposure and infectious periods. Contact tracing for Washington

residents exposed to these cases in South Carolina did not identify secondary cases among Washington residents.

### IMPORTATION 4

A Washington resident of County D reported exposure to ill contacts during out-of-state travel, experienced a rash on January 16, and was laboratory-confirmed as having measles. The individual adhered to isolation and quarantine recommendations. No public exposures or secondary cases in Washington were identified.

### IMPORTATION 5

A Washington resident reported exposure to ill contacts during out-of-state travel, resulting in a measles outbreak with seven confirmed cases among County D residents.<sup>9,10</sup> This person experienced a rash on January 19, and measles was laboratory-confirmed. While contagious, the person visited a school and health care facility. Six secondary cases were identified among close contacts (four confirmed by laboratory testing and two by epidemiologic linkage; rash onsets: January 26–29) who adhered to isolation and quarantine. No further cases or public exposures were identified. Measles virus whole genomes from five laboratory-confirmed cases were indistinguishable and matched sequences from South Carolina cases with 100% nucleotide identity across 13,787–14,824 bp.

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## Case Characteristics

Among 26 measles cases in Washington residents during January–February 2026, nine (35%) directly resulted from exposure to South Carolina's outbreak. Almost all (16 of 17) secondary cases were among close contacts; one was linked to a public exposure. Twenty-one cases (81%) were part of two distinct Washington outbreaks (importations 2 and 5). Most cases were among children (4 were <5 years of age and 16 were 5–17 years of age). All occurred among unvaccinated persons (n=24) or persons with unknown vaccine status (n=2). No hospitalizations or deaths were reported. The schools with measles exposures had two-dose measles-containing vaccine coverage between 92% and 96% (Table S1). Whole-genome sequencing showed that all measles viruses from Washington cases matched sequences from South Carolina. Sequences associated with distinct importations (1, 2, and 5) were more closely related to South Carolina sequences than Washington sequences from other importations. Turnaround time for genomic analyses was 2 to 3 weeks from sample submission.

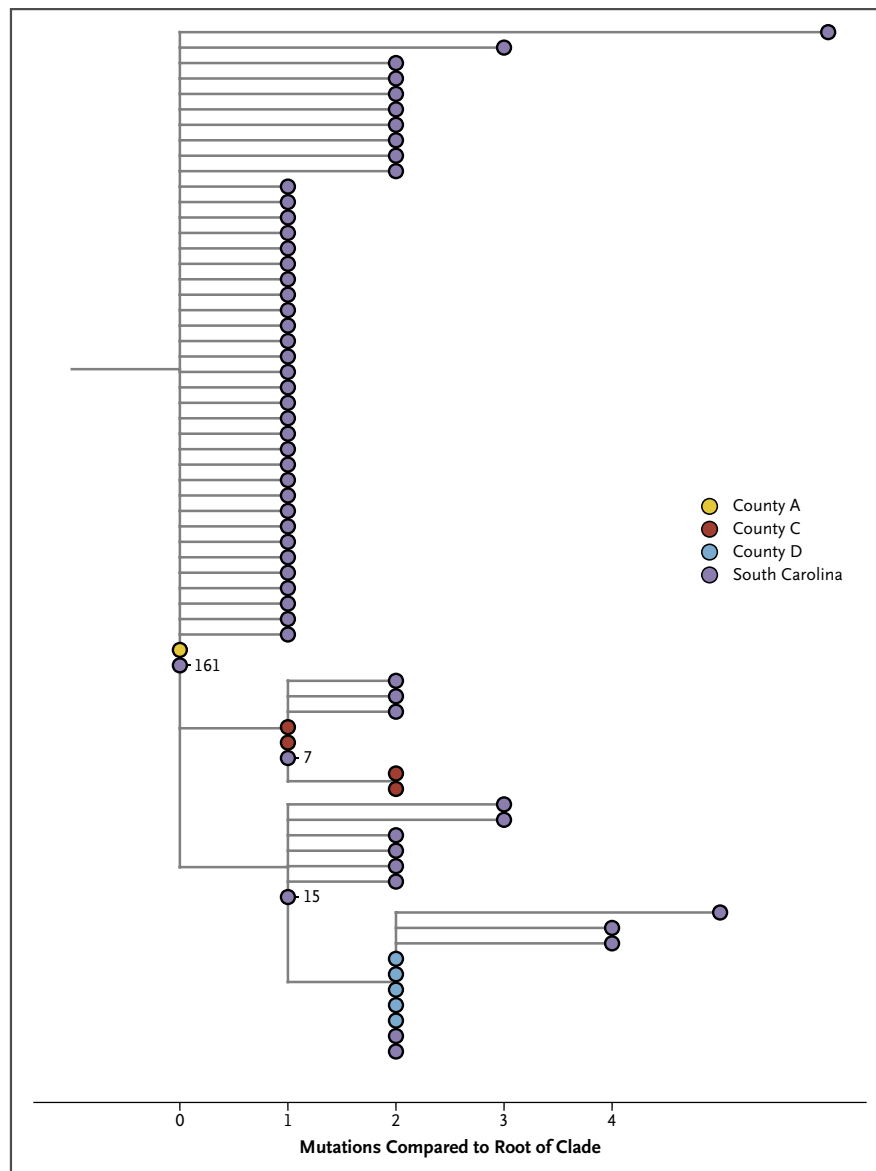


Figure 1. Maximum Likelihood Phylogenetic Tree of Measles Virus Whole-Genome Sequences.

Ten sequences are from Washington State (Counties A, C, and D), representing Importations 1, 2, and 5. Contextual sequences from other regions were also included in the analysis. The clade shown was extracted from the larger tree and represents all descendants of the most recent common ancestor of Washington State sequences. Branches were removed that were descendent of nodes containing Washington sequences, to better focus on Washington outbreak genomes and their relationships with publicly available genomes. Indistinguishable contextual sequences are represented as a single tip annotated with the number of observations. Tips are colored by geographic region of sampling. Branch lengths show genetic distance as the number of nucleotide differences, compared with the most recent common ancestor.

## Limitations and Preliminary Conclusions

Limitations of this investigation include that approximately half of cases were confirmed by epidemiologic

linkage alone, limiting specimens available for sequencing. Additional cases of measles might not have been identified by public health or health care providers.

As public health jurisdictions prepare to respond to increased measles importations linked to domestic measles outbreaks,

while remaining vigilant for international importations, timely whole-genome sequencing can supplement epidemiologic information to help differentiate distinct importations from local transmission and inform outbreak response. Most Washington residents with measles followed isolation and quarantine recommendations, which likely helped limit onward transmission. Public health messaging focused on nonvaccine measles control measures may have improved community acceptance of public health recommendations.

## Disclosures

Author disclosures and other supplementary materials are available at [evidence.nejm.org](https://evidence.nejm.org).

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The findings and conclusions in this report are those of the authors and do not necessarily represent the official position of the Centers for Disease Control and Prevention, the U.S. Department of Health and Human Services, or the Association of Public Health Laboratories.

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