inopinata was the mite involved in the dogs affected in Spain (*5*). In the report from Austria, *N. autumnalis* was the infesting mite. Late summer and autumn (August–October) are risk periods mirrored in all reported cases.

In the previously reported cases of dogs in Austria with neurologic signs caused by *N. autumnalis*, authors described severe infestations of mites as follows: In dogs, when infestation is severe, the mites are so densely packed […] they resemble orange-red, brick-dust-like coatings or crusts. They often form clusters between the toes (translated from German) (*4*). That description mirrors our observation of orange-red staining on or between the digits. The clinical signs (e.g., vomiting) and neurologic signs reported in previous cases also closely resembled those observed in our cases (*4*,*5*). Paresis of the lower jaw also was reported in 2 dogs (*4*), a feature not seen in our cases.

In conclusion, *N. autumnalis* infestation should be considered a differential diagnosis for acute onset of neurologic signs in dogs that occur in late summer or autumn, especially in the presence of orange-red stains (on closer examination identified to be mites) on the digits, fur, or skin. Suspected cases warrant a careful inspection for mites to rule out infestation.

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Enhanced Risk for Epidemic Cholera Transmission, Haiti

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Sporadic cholera outbreaks continue to occur in Haiti. We used a novel space-time analysis to gain insight from limited government surveillance data. We identified concerning patterns of disease spread in areas known to be at high risk for epidemic cholera in and around the capital city of Port-au-Prince.

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The potential for a major cholera outbreak in Haiti should concern countries of the Americas, particularly at a time when political turmoil has encouraged emigration from Haiti. Cholera was introduced into Haiti by United Nation peacekeepers in October 2010 (*1*). The resulting epidemic lasted until 2019, killing ≈10,000 persons and sickening >820,000 persons. In September 2022, a new cholera outbreak occurred, in which illness was caused by strains matching previously isolated environmental toxigenic *Vibrio cholerae* O1 strains

from the Jacmel region south of the capital city of Port au Prince (PaP) (*2*,*3*). By the end of 2023, the resulting epidemic had caused ≈80,000 clinically diagnosed cases (*4*–*6*). Many of the affected neighborhoods along the coast in and proximate to PaP swelled because of migration by persons displaced by the 2010 earthquake. Those areas have informal settlement characteristics, including poorly constructed and densely packed residential areas, a lack of access to safe water, inadequate drainage, and poor sanitation. Adding further complexity, most of those areas are now controlled by violent gangs, which has resulted in an estimated 130,000 additional persons being displaced since the beginning of 2025 (*7*). Taken together, those factors have created a complex infectious disease vulnerability.

For the outside world, acquiring the data needed to understand the current cholera situation in Haiti is extremely difficult. Starting in June 2024, Haiti's Ministere de La Publique et de La Population began releasing data on its website, including numbers of suspected cholera cases by commune (*4*,*5*). Those data, although likely to reflect a profound undercount

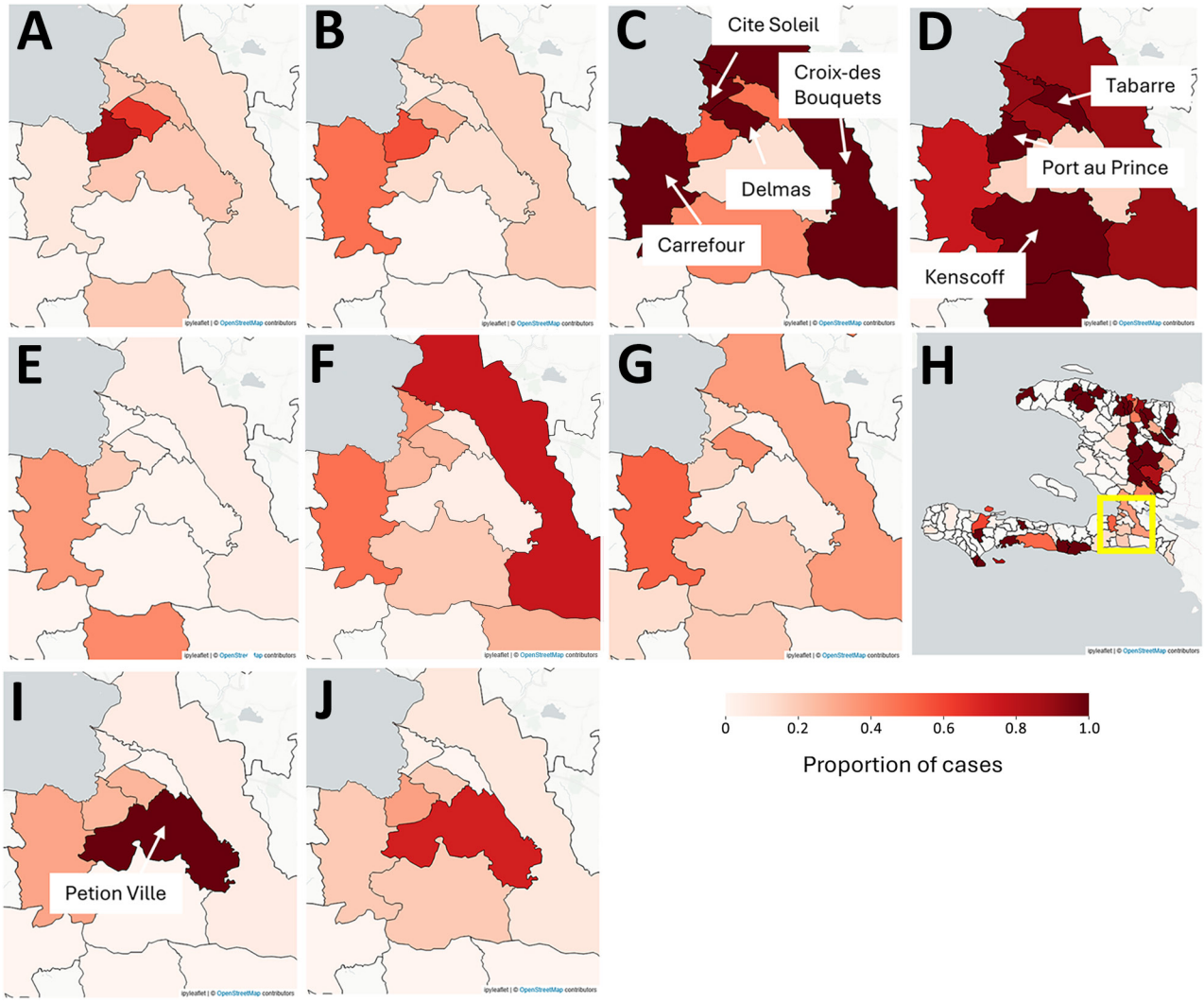

Figure. Enhanced risk for epidemic cholera transmission, Haiti. Extracted cartography are from the grid heat map disease monitoring system for Port-au-Prince during the summer surge of suspected cholera cases between the weeks ending April 20–October 13, 2025. A) April 20; B), April 27; C) May 14; D) June 1; E) June 20; F) June 29; G) August 20; H) August 20; I) October 7; J) October 13. The mapped area is identified on the August 20 map (panel H; yellow outline) for the whole country, which also shows the broader geographic spread of suspected cholera for that reporting period. The shading should be interpreted carefully because each commune is mapped according to where it falls along its own epidemiologic curve for that week. Each commune also can be compared to its neighbors in the same week by where they also fall along their curves, given that communes with the darkest shade are at their peak number of cases. The maps should not be interpreted as visualizing the actual number of cases per commune per week using the same classification scheme as one would in a typical cartographic display. Maps created by using OpenStreetMap (https://www.openstreetmap.org).

(especially in areas controlled by gangs), can be used to track the rise and spread of cholera in and around PaP. We describe a methodology that is simple to implement, can easily be updated to provide a near real-time assessment, and can be adopted to monitor disease outbreaks in other countries.

A grid heat map, an exploratory space-time epidemic surveillance tool, is an alternative to traditional geographic information systems (GIS) mapping. Our grid includes all suspect cholera cases by commune for each week of the epidemic. As further weekly data become available, the grid recalculates to update the pattern. A neighborhood version of this grid heat map had previously been developed for Haiti during the 2023 epidemic (*6*). For 2024–2025, we visualized cholera in each commune by using the darkest shading for the week with most cases, then coloring all other weeks as a proportion of that maximum disease count. If the next week had even higher cases for that commune, the previous weeks are recalculated as a proportion of the new total. The finished heat map, which conceptually displays the epidemic curve for each commune, can reveal regional patterns that might be washed out using typical GIS approaches.

We constructed a combined grid and cartographic heatmap interface programmed in Python (https://www.python.org) into which each weekly disease sheet is ingested when available (Appendix, https://wwwnc.cdc.gov/EID/article/31/12/25-1157-App1.pdf). We also extracted key maps from the grid heatmap coinciding with the rise in cases around PaP in the spring and summer of 2025 (Figure).

In early 2025, PaP and its vicinity started to see a concerning rise in cases (Figure; Appendix Figure). An earlier version of the grid heatmap in April 2025 captured the emergence of that signal. As cases rose, crucial weeks were those ending April 20, May 14, and June 1, when each of the communes in and around PaP had their highest total case counts. Although Cité Soleil, one of the most vulnerable communes within PaP, registered the highest number of cases (week ending April 20, 73 cases; May 14, 393 cases; June 1, 359 cases, and June 29, 145 cases), reflecting a similar pattern seen in the 2023 epidemic (*6*), traditional GIS mapping would have missed the situation in the less dense communes of Kenscoff (week ending June 1, 5 cases) and Tabarre (week ending June 1, 17 cases). Those maps suggest that although conditions in the coastal neighborhoods might be driving cholera amplification, epidemic spread beyond the city and into the surrounding communes is evident. That pattern carried into October, when Petion-Ville, south of PaP, saw some of its highest case numbers. We also observed a rise of intensity to the north, which matched geographic patterns previously seen in summer 2024 (Appendix Figure). The communes in the west of Haiti also saw some of their highest case numbers during the same week.

We believe those patterns reveal the widespread cholera vulnerability across Haiti. Although in summer 2025 we were concerned that the situation around PaP might have been primed for another sizeable cholera outbreak, by December 2025 that had not occurred, but the area in and around PaP continues to generate cases, especially in Petion-Ville commune. Even if the data are incomplete or suffer from inconsistent updates, they can still provide vital early warning signals. We continue to use this method to monitor changes in the cholera situation in Haiti. Available data underscore the critical need for near real-time analysis of surveillance data for countries like Haiti.

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Dr. Curtis is the co-director of the GIS Health and Hazards Laboratory in the School of Medicine at Case Western Reserve University, Cleveland, Ohio. His research interests include the development of spatial techniques to collect and analyze epidemic data at the scale of intervention, including in low resource environments with limited or sporadic data reporting.

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Metatranscriptomic Identification of Trubanaman Virus Sequences in Patient with Encephalitis, Australia

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Using metatranscriptomics, we identified Trubanaman virus in cerebrospinal fluid from a severely immunocompromised man who died of encephalitis in Queensland, Australia. Virus sequences were related to orthobunyaviruses previously detected in mosquitoes in Australia. Testing for other causes yielded negative results, suggesting that Trubanaman virus was the cause of this fatal encephalitis case.

Approximately 50% of global encephalitis cases remain undiagnosed by conventional testing (*1*). Metagenomic next-generation sequencing (mNGS), particularly metatranscriptomics (i.e., total RNA sequencing), is an emerging approach to infection diagnosis that reveals all nucleic acid in a sample, making it ideal for detecting novel and emerging pathogens (*2*).

Orthobunyavirus (order Bunyavirales) is a diverse genus of negative-sense single-stranded RNA viruses recognized to cause febrile illness and encephalitis in humans globally (*3*). The best described orthobunyaviruses are La Crosse virus and Jamestown Canyon virus, both of which rarely cause encephalitis, permanent neurologic sequalae, or death (*4*,*5*). Jamestown Canyon virus is associated with meningoencephalitis in immunocompromised persons (*5*), whereas the emerging Oropuche virus is associated with fever, headache, myalgias, and rare cases of meningoencephalitis and has recently expanded its range in Central and South America (*6*). We used metatranscriptomics to investigate a case of encephalitis in an immunocompromised person in Australia.

The study was approved by the Metro-North Health Human Research Ethics Committee and written informed consent was obtained from the patient and his next of kin. Metatranscriptomic sequencing and analysis methods are detailed (Appendix, https://wwwnc.cdc.gov/EID/article/31/12/25-1190-App1.pdf).

A man in his 50s who lived in West Moreton, Queensland, Australia, was admitted for a volunteer unrelated donor allogeneic hemopoietic stem cell transplantation with posttransplant cyclophosphamide and tacrolimus for B-cell acute lymphoblastic leukemia in complete remission one. There was no central nervous system involvement. He received 8 cycles of rituximab-hyper cyclophosphamide, vincristine, doxorubicin, and dexamethasone before transplantation. The transplant was complicated by a polymicrobial bloodstream infection that was successfully treated with intravenous daptomycin, as well as mucositis and diarrhea.

On day 18 after the hemopoietic stem cell transplantation, the patient experienced fever to 38.8°C, tachycardia to 10^9 beats/min, muscular pain, intermittent headache, and confusion manifesting as slow and tangential answers to questions, difficulty word-finding, reduced oral intake, disorientation to time and place, and delusions such as thinking that he had been in a car accident. The onset coincided with recovery of his neutrophil and lymphocyte