Research Square

Preprints are preliminary reports that have not undergone peer review.
They should not be considered conclusive, used to inform clinical practice,
or referenced by the media as validated information.

Central Nervous System Infection by Vibrio cholerae Diagnosed by Metagenomic Next-Generation Sequencing: A Case Report

Xuehua Li
fuxin central hospital
Zeng Lu
fuxin central hospital
Qianqian Liu
fuxin central hospital
Shisong Yang
fuxin central hospital
Zhongyan Li
adui1234567890120163.com

fuxin central hospital

Case Report

Keywords: Vibrio cholerae, central nervous system infection, metagenomic next-generation sequencing (mNGS), case report

Posted Date: July 30th, 2026

DOI: https://doi.org/10.21203/rs.3.rs-10352170/v1

License: This work is licensed under a Creative Commons Attribution 4.0 International License.
Read Full License

Additional Declarations: No competing interests reported.

Abstract

Introduction

:*Vibrio cholerae*central nervous system (CNS) infection is extremely rare, typically reported in immunocompromised patients. Diagnosis is challenging due to non-specific presentation and low culture yield from cerebrospinal fluid (CSF).

Case presentation

: A 66-year-old male farmer presented with seizure followed by coma. Empirical meropenem was initiated. Cerebrospinal fluid (CSF) metagenomic next-generation sequencing (mNGS) identified 89 reads of V. cholerae with 99.9% homology. However, before the mNGS results were available, the patient was transferred to a tertiary hospital at the family's request and subsequently lost to follow-up; targeted anti-V. cholerae therapy was not administered at our institution.

Conclusion

mNGS of CSF enables rapid etiological diagnosis of unusual CNS infections and should be considered early, even in immunocompetent patients, when routine workup is inconclusive.

1. Introduction

Vibrio cholerae is a Gram-negative bacterium classically causing cholera. Extraintestinal infections are rare and occur predominantly in immunocompromised hosts, with CNS involvement being exceptionally uncommon, reported mainly in patients with hematological malignancies or liver cirrhosis [1]. Diagnosis is often delayed because CSF cultures are frequently negative. Metagenomic next-generation sequencing (mNGS) has emerged as a powerful tool for unbiased pathogen detection directly from clinical specimens, particularly valuable[2,3] for rare or fastidious organisms. We report a case of *V. cholerae* CNS infection diagnosed by CSF mNGS in a previously healthy adult, highlighting its diagnostic utility.

2. Case Presentation

A 66-year-old male farmer of Han ethnicity presented with a 3-hour history of generalized seizure followed by loss of consciousness. One day prior, he developed fever and localized pain over the right wrist and lateral right thigh. He had no diarrhea or gastroenteritis.His remote duodenal ulcer had been medically managed without complications, and his untreated hypertension had not required prior intervention. He had no immunodeficiency or immunosuppressive therapy.

On admission (July 11, 2022), he was comatose Glasgow Coma Scale (GCS) score of 3 (GCS 3). Vital signs: T 36.7°C, HR 114/min, BP 120/76 mmHg, SpO_2 95%. Pupils were equal and reactive sluggishly. Chest had scattered crackles. Neurological examination revealed increased muscle tone and bilateral Babinski signs negative.Positive cervical rigidity. Head CT showed lacunar infarction without hemorrhage or mass. Routine CSF culture yielded no bacterial growth after 72 hours. Laboratory tests revealed coagulopathy (APTT 49.5s, PT 16.9s, D-dimer 6.72 mg/L). Based on clinical experience, meropenem 2.0 g has been administered intravenously every 8 hours (Q8H), anti-epileptics, and intracranial pressure-lowering measures were initiated.

Insert Table 1 here

Given the light yellow and slightly turbid appearance of the cerebrospinal fluid, intracranial infection was suspected. Nocturnal CSF testing was unavailable at our institution. We prioritized CSF mNGS analysis before transfer to provide a potential etiological clue for the receiving hospital. Due to time sensitivity, the sample was directly sent for mNGS analysis. Results returned four days later: 19,894,259 total reads, Q30 94.9%, with 89 reads specifically mapping to *V. cholerae*genome. No other significant pathogens were detected.

At 00:10 on July 12, the patient was transferred to a tertiary hospital at family's request, before mNGS results were available. Targeted anti-*V. cholerae* therapy was not administered at our institution. The patient was lost to follow-up despite attempts to contact the receiving hospital

Table 1
Timeline of key clinical events

Date/Time	Event
July 10, 2022	Fever and limb pain
July 11, 2022, afternoon	Admitted to county hospital, seizure, coma
July 11, 2022, 21:00	Admitted to our ICU
July 11, 2022, 22:26	First progress note, CSF sent for mNGS
July 12, 2022, 00:10	Transferred to tertiary hospital
July 16, 2022	mNGS report: V. cholerae detected

The patient's comatose state and rapid transfer posed significant challenges to completing a comprehensive diagnostic workup.

3. Discussion

We report a rare case of confirmed *V. cholerae* CNS infection diagnosed solely by CSF mNGS in an immunocompetent patient. The absence of gastrointestinal symptoms suggests extraintestinal dissemination, possibly through hematogenous seeding from an occult focus—the localized limb pain

might represent a primary entry site or bacteremic source.However, this case did not present any significant skin defects or wounds. Furthermore, the patient was in a deep sedated state, making it impossible to determine whether there was a history of trauma or injury.Non-O1/non-O139 serogroups are more frequently associated with extraintestinal infections[4] ; serotyping was unavailable here.

The clinical presentation was non-specific, and routine diagnostics failed to identify the pathogen. mNGS provided a definitive etiological clue, demonstrating its value in cases where conventional methods are negative or unavailable. While mNGS has limitations including contamination risk and inability to distinguish colonization from infection, the high read count (89 reads), genome-wide distribution, and compatible clinical context strongly support a genuine infection.

Management of V. cholerae CNS infection lacks standardized guidelines; recommended agents with CNS penetration include doxycycline, azithromycin, or fluoroquinolones. Early targeted therapy guided by mNGS could improve outcomes, but in our case the result came too late due to transfer. This underscores the need for rapid turnaround and on-site mNGS capacity in ICU. The strength of this report lies in the use of mNGS to achieve a definitive etiological diagnosis in a case where conventional methods were unrevealing, highlighting the potential of this technology in critical care settings.

Our case has limitations: loss to follow-up, lack of culture and susceptibility data, and no serotyping. Nevertheless, it illustrates the clinical utility of mNGS for diagnosing atypical CNS infections.

Differential diagnoses considered included bacterial meningitis (ruled out by negative routine culture), viral encephalitis (CSF PCR for HSV/enterovirus was not performed but mNGS showed no viral reads), and tuberculous meningitis (CSF ADA and AFB smear not available; clinical course was too rapid). The detection of V. cholerae by mNGS, combined with the absence of other pathogens, supported the diagnosis of V. cholerae CNS infection

4. Conclusion

Clinicians should consider unusual pathogens like *V. cholerae*in CNS infections of unknown etiology, even in immunocompetent hosts. Early CSF mNGS can expedite accurate diagnosis [5]and guide targeted antimicrobial therapy, potentially improving prognosis in critically ill patients.

Authors' contributions:

Xuehua Li and Zeng Lu collected data; Shisong Yang drafted the manuscript; Qianqian Liu assisted with literature; Zhongyan Li supervised and revised. All authors approved the final version.

Declarations

Ethics approval and consent to participate

This case report was conducted in accordance with the Declaration of Helsinki. Ethical approval was obtained from the Ethics Committee of Fuxin Central Hospital (Approval No.EC-RT-2026-039). Written informed consent was obtained from the patient's legal surrogate for the publication of this case report and any accompanying images.

Consent for publication

Written informed consent was obtained from the patient’s legal surrogate for the publication of this case report and associated clinical images/data. A copy of the written consent is available for review by the Editor-in-Chief of this journal.

Conflict of interest

The authors declare no conflicts of interest.

Funding

This research received no specific grant from any funding agency in the public, commercial, or not-for-profit sectors.

Acknowledgments

This work was supported by the 'Medical Experts' program of the Xingliao Talent Project in Liaoning Province (Grant No. XLYC2512068).

Author Contribution

Xuehua Li and Zeng Lu collected data; Shisong Yang drafted the manuscript; Qianqian Liu assisted with literature; Zhongyan Li supervised and revised. All authors approved the final version.

References

1. Morris JG. Cholera and Other Types of Vibriosis: A Story of Human Pandemics and Oysters on the Half Shell. Clin Infect Dis. 2003;37(2):272–80. https://doi.org/10.1086/375600.
2. Su LD, Chiu CY, Gaston D, Hogan CA, Miller S, Simon DW, Thakur KT, Yang S, Piantadosi A. Clinical Metagenomic Next-Generation Sequencing for Diagnosis of Central Nervous System Infections: Advances & Challenges. Mol Diagn Ther. 2024;28(5):513–23. https://doi.org/10.1007/s40291-024-00727-9.
3. Chen Y-Y, Guo Y, Xue X-H, Pang F. Application of Metagenomic Next-Generation Sequencing in the Diagnosis of Infectious Diseases of the Central Nervous System after Empirical Treatment. *WJCC* 2022, *10* (22), 7760–7771. https://doi.org/10.12998/wjcc.v10.i22.7760

4. Miller S, Naccache SN, Samayoa E, Messacar K, Arevalo S, Federman S, Stryke D, Pham E, Fung B, Bolosky WJ, Ingebrigtsen D, Lorizio W, Paff SM, Leake JA, Pesano R, DeBiasi R, Dominguez S, Chiu CY. Laboratory Validation of a Clinical Metagenomic Sequencing Assay for Pathogen Detection in Cerebrospinal Fluid. Genome Res. 2019;29(5):831–42. https://doi.org/10.1101/gr.238170.118.
5. Wilson MR, Sample HA, Zorn KC, Arevalo S, Yu G, Neuhaus J, Federman S, Stryke D, Briggs B, Langelier C, Berger A, Douglas V, Josephson SA, Chow FC, Fulton BD, DeRisi JL, Gelfand JM, Naccache SN, Bender J, Dien Bard J, Murkey J, Carlson M, Vespa PM, Vijayan T, Allyn PR, Campeau S, Humphries RM, Klausner JD, Ganzon CD, Memar F, Ocampo NA, Zimmermann LL, Cohen SH, Polage CR, DeBiasi RL, Haller B, Dallas R, Maron G, Hayden R, Messacar K, Dominguez SR, Miller S. Chiu, C. Y. Clinical Metagenomic Sequencing for Diagnosis of Meningitis and Encephalitis. N Engl J Med. 2019;380(24):2327–40. https://doi.org/10.1056/NEJMoa1803396.