

Letter to Editor

Asian Pacific Journal of Tropical Medicine

apjtm.org

doi: 10.4103/apjtm.apjtm_626_25

Whole genome analysis of a Non-O1, Non-O139 *Vibrio cholerae* isolate from a bacteremia case in Ho Chi Minh City

Tuan-Loc Le[1], Ngoc-Lan Nguyen[2], Duc-Khai Luong[3], Hieu Vu-Quang[4]✉

[1]*Department of Biomedical Sciences, Faculty of Applied Science and Technology, Nguyen Tat Thanh University, Vietnam*

[2]*University of Medicine and Pharmacy at Ho Chi Minh City, Vietnam*

[3]*Thong Nhat Hospital, Ho Chi Minh city, Vietnam*

[4]*Department of Biomedical Sciences, Faculty of Applied Science and Technology, Nguyen Tat Thanh University, Vietnam*

Non-O1/non-O139 *Vibrio (V.) cholerae* (NOVC) has emerged as a potential pathogen in patients with compromised health conditions[1]. We report the whole genome sequencing (WGS) of a rare NOVC sepsis isolate (GenBank Accession: GCF_051906115.1) from an 89-year-old male admitted to the Intensive Care Unit (ICU) with septic shock (lactate 6.61 mmol/L) digestive illness. The patient's severe underlying cardiovascular comorbidities, including chronic mesenteric ischemia (superior mesenteric artery stenosis), significantly compromised his intestinal barrier, enabling rapid pathogen translocation and systemic infection.

WGS identified the isolate as closest to Sequence Type (ST)-1565/cgST-1986, a lineage circulated in South East Asia[2]. Its NOVC status was confirmed by the absence of the *ctxA/B* operon and *O1/O139* clusters. Core genome single nucleotide polymorphism (SNP) phylogenetic dendrogram (Figure 1A, Supplementary Table 1) revealed clustering within a major monophyletic clade encompassing regional clinical strains and, significantly, all classical O1 and O139 pandemic reference strains. This suggests that our isolate shares a recent evolutionary background with highly virulent *V. cholerae* lineages, highlighting the broad pathogenic potential within this common ancestral pool.

The functional analysis, summarized in the Circos map (Figure 1B) and virulence table (Table 1), provides the basis for virulence evaluation. The isolate possessed a potent pathogenic payload, including genes for RTX toxins and hemolysins, factors that facilitate tissue damage and epithelial breach. Crucially, complete Type Ⅲ (T3SS) and Type Ⅵ (T6SS) Secretion Systems were detected. T3SS, known for degrading epithelial barriers, likely drove the widespread tissue damage and subsequent septic shock observed in our patient whose immunity and gut health has been compromised[3]. Further analysis indicated that the gene for the adherence protein MSHA pili (*mshA*) was structurally truncated, suggesting the isolate relies on alternative or compensatory adhesion mechanisms.

The isolate exhibited intermediate resistance to ciprofloxacin on phenotypic testing (Supplementary Table 2). This reduced susceptibility was supported by WGS detection of the plasmid-mediated quinolone resistance gene *QnrVC5* and mutations in *parC* and *parE* genes[4,5]. Although resistance genes associated with meropenem and trimethoprim were present, the isolate remained phenotypically susceptible, underscoring the importance of combined genotype and phenotype assessment.

In conclusion, our report provides WGS characterization of a highly virulent NOVC isolate linked to severe Intensive Care Unit infection. The presence of T3SS/T6SS and the close phylogenetic relationship to pandemic strains demonstrate that this isolate possesses high pathogenic potential, particularly when combined with patient vulnerability. We emphasize that WGS is essential for rapidly identifying and differentiating such highly virulent NOVC strains for clinical surveillance.

✉To whom correspondence may be addressed. E-mail: vqhieu@ntt.edu.vn

This is an open access article distributed under the terms of the Creative Commons Attribution-Non-Commercial-No Derivatives License 4.0 (CCBY-NC-ND), where it is permissible to download and share the work provided it is properly cited. The work cannot be changed in any way or used commercially without permission from the journal.

For reprints contact: reprints@medknow.com

©2026 *Asian Pacific Journal of Tropical Medicine* Produced by Wolters Kluwer-Medknow.

How to cite this article: Le TL, Nguyen NL, Luong DK, Vu-Quang H. Whole genome analysis of a Non-O1, Non-O139 *Vibrio cholerae* isolate from a bacteremia case in Ho Chi Minh City. Asian Pac J Trop Med 2026; 19(2): 94-96.

Article history: Received 29 October 2025 Revision 16 January 2026
Accepted 21 January 2026 Available online 27 January 2026

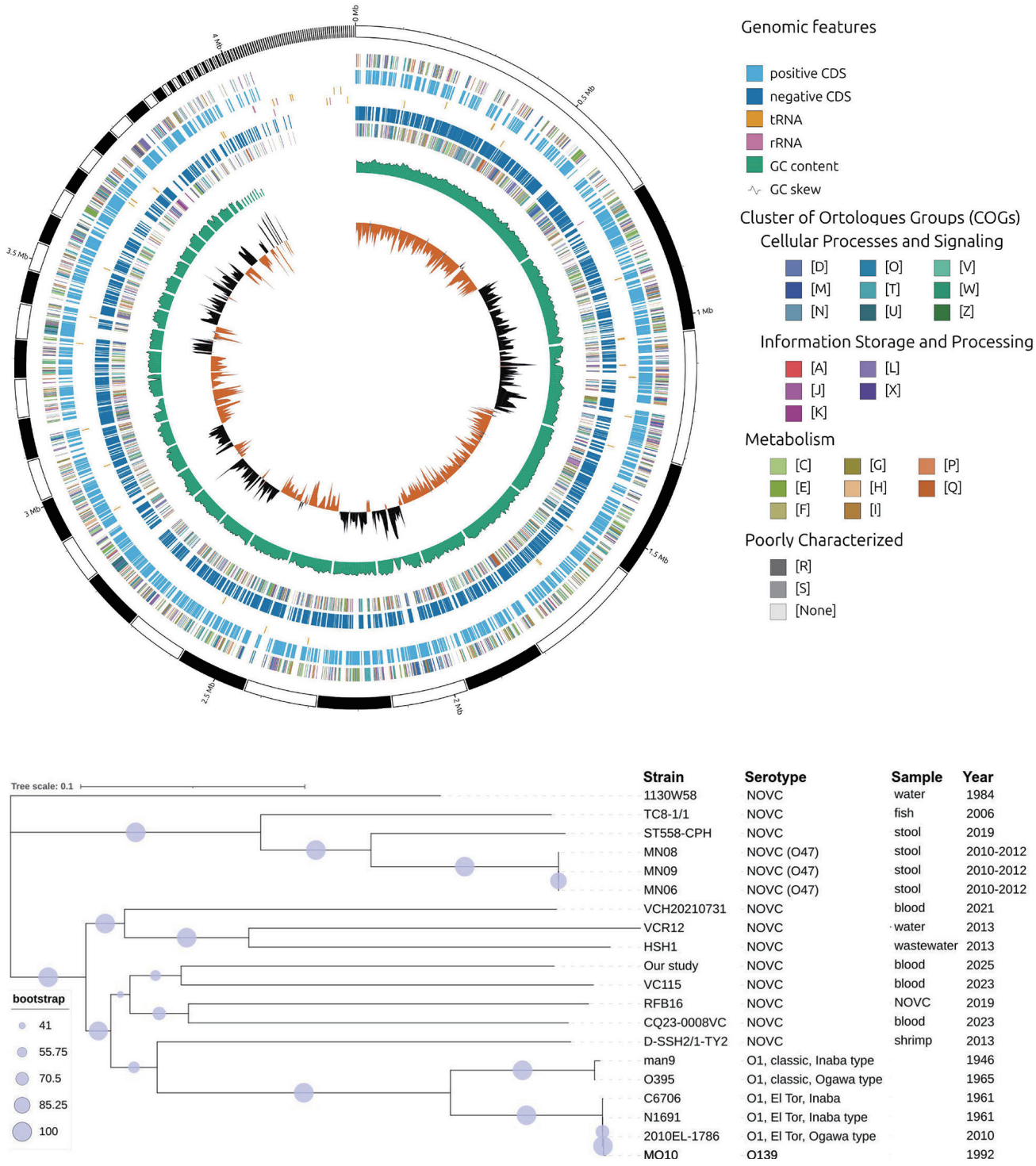


Figure 1. A: Gene circle map of *Vibrio cholerae* isolate from an 89-year-old male patient with septic shock complicated by digestive disease. B: Phylogenetic dendrogram of *Vibrio cholerae* strains in this study versus reference strains. J: Translation; A: RNA processing and modification; K: Transcription; L: Replication, recombination and repair; B: Chromatin structure and dynamics; D: Cell cycle control, cell division, chromosome partitioning; Y: Nuclear structure; V: Defense mechanisms; T: Signal transduction mechanisms; M: Cell wall/membrane/envelope biogenesis; N: Cell motility; Z: Cytoskeleton; W: Extracellular structures; U: Intracellular trafficking, secretion, and vesicular transport; O: Posttranslational modification, protein turnover, chaperones; X: Mobilome: prophages, transposons; C: Energy production and conversion; G: Carbohydrate transport and metabolism; E: Amino acid transport and metabolism; F: Nucleotide transport and metabolism; H: Coenzyme transport and metabolism; I: Lipid transport and metabolism; ribosomal structure and biogenesis; P: Inorganic ion transport and metabolism; Q: Secondary metabolites biosynthesis, transport and catabolism; R: General function prediction only; S: Function unknown.

Table 1. Virulence factor genes identified in the study.

Virulence function		Gene name
Toxin and hemolysin	RTX toxin	*rtxA-D*
	Hemolysin/cytolysin	*hlyA, tlh*
Secretion system	Type Ⅱ	*gspC-L, gspB, exeA*
	Type Ⅲ	*vopB2,D2,vcrD2, vscC2,N2,R2,S2,T2,U2, VP_RS21705, VP_RS21585, VPA1353*
	Type Ⅵ	*vasA-L, vipA-B, vrgG-2, VCA0109, VCA0122, tagH(*)*
Adherence and biofilm	MSHA pili	*mshA(**), mshB-N*
	Pilus assembly and processing	*pilB, pilD/vcpD*
	VPS synthesis	*vpsC-I, P, Q, U*
	Capsular synthesis	*cpsA-D,F, wbfU, wbjD, wecC*
	Quorum sensing	*cqsA, luxS, hapR, aphA*
	Biofilm factors	*bap1, rbmA,C*
	N-Acetylglucosamine-binding	*gpbA*
	Hemagglutinin/protease	*hapA*
	Sialidase	*nanH*
Iron acquisition		*vibA-H, viuA-P, irgA, hutR, hasR*
Motility	*Flagella*	*flaA-E,G,I, fleN/G,R/C,S/B, flhA,B,F,G, flgA-I,T, fliA,D-R, motA,B,Y*
	Chemotaxis	*cheA,B,R,V,W,Y,Z*

(*) detected by reference gene on NCBI database; (**) partially matched.

Conflict of interest statement

The authors declare that they have no conflict of interest.

Ethical approval and patient's consent to participate

The research project is approved by Ethics Committee for Biomedical Research of Thong Nhat Hospital pursuant to Decision No. 462/QĐ-BVTN dated 8 April 2024 by the Director of Thong Nhat Hospital regarding the establishment of the Institutional Review Board (IRB) for Biomedical Research, and Approval Certificate no. 18/2025/CN-BVTN-HĐĐĐ signed on 10 March 2025. Participants provided written informed consent prior to taking part in the study.

Acknowledgements

We are deeply grateful to the Nguyen Tat Thanh University, Thong Nhat Hospital in Ho Chi Minh city, University of Medicine and Pharmacy at Ho Chi Minh City for providing invaluable assistance to our study.

Funding

The authors received no extramural funding for the study.

References

[1] Carr ER, Estepa A, Colson J, Ayoade F. *Vibrio cholerae* Skin and soft tissue infection complicated by sepsis in an immunocompromised patient: A rare case report. *Clin Case Rep* 2025; **13**(1): e70086.

[2] Liang KYH, Orata FD, Islam MT, Nasreen T, Alam M, Tarr CL, et al. A *Vibrio cholerae* core genome multilocus sequence typing scheme to facilitate the epidemiological study of cholera. *J Bacteriol* 2020; **202**(24). doi: 10.1128/JB.00086-20.

[3] Mathieu-Denoncourt A, Giacomucci S, Duperthuy M, Mathieu-Denoncourt A, Giacomucci S, Duperthuy M. The secretome of *Vibrio cholerae*. *Infect Sepsis Develop* 2021; doi: 10.5772/intechopen.96803.

[4] Zhang Y, Zheng Z, Chan EWC, Dong N, Xia X, Chen S. Molecular characterization of *qnrVC* genes and their novel alleles in *Vibrio* spp. isolated from food products in China. *Antimicrob Agents Chemother* 2018; **62**(7): e00529-e00518.

[5] Zhou YY, Ma LY, Yu L, Lu X, Liang WL, Kan B, et al. Quinolone resistance genes and their contribution to resistance in *Vibrio cholerae* serogroup O139. *Antibiotics* 2023; **12**(2): 416.

Publisher's note

The Publisher of the *Journal* remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Edited by Pan Y, Lei Y, Zhang Q

Supplementary

Table S1. V. cholerae isolates and strains used for phylogenetic dendrogram built in our study

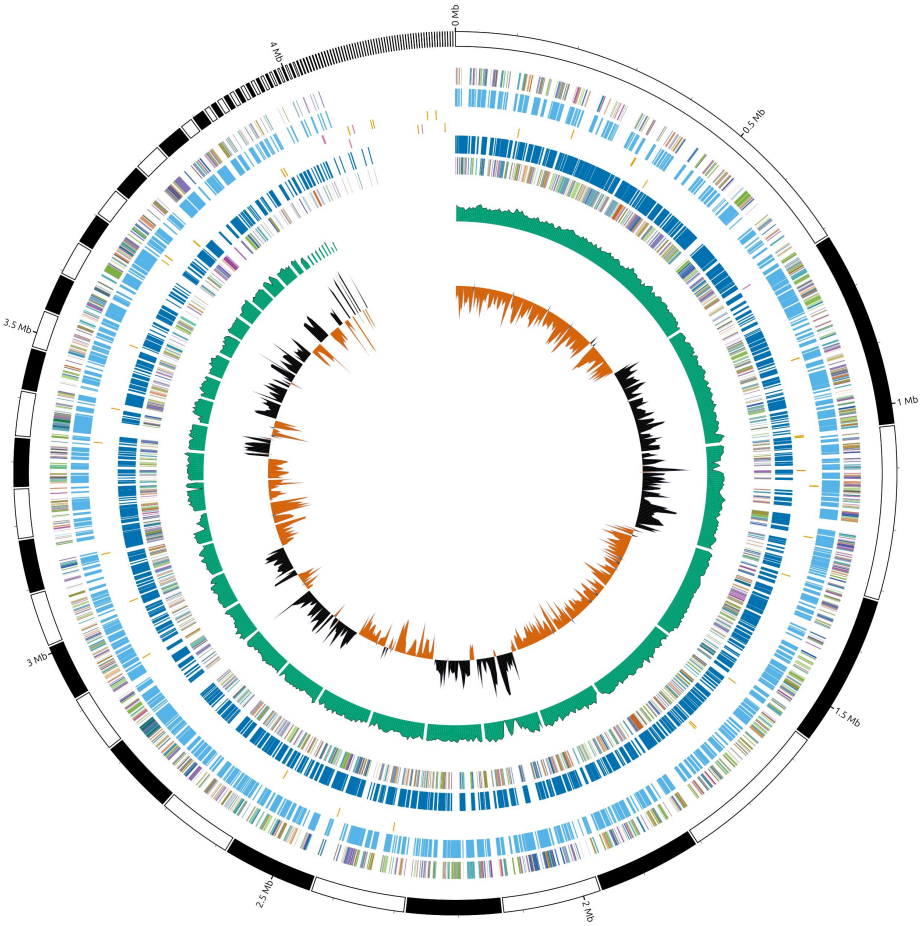
Strain/Isolate	Serotype	Location	Accession number (*)
Our study	NOVC	HCMC, Vietnam	GCF_051906115.1 (N)
N1691	O1, El Tor, Inaba type	Sulawesi, Indonesia	GCA_900205735.1 (N)
C6706	O1, El Tor, Inaba	Peru	GCA_009763945.1 (N)
2010EL-1786	O1, El Tor, Ogawa type	Haiti	GCA_000166455.2 (N)
O395	O1, classic, Ogawa type	India	GCA_009646135.1 (N)
man9	O1, classic, Inaba type	Sasebo, Japan	GCA_030295265.1 (N)
MO10	O139	Bengal	GCA_017948345.1 (N)
RFB16	NOVC-environment	Pennsylvania	GCA_008369605.1 (N)
VC115	NOVC	Mianyang, Sichuan, China	GCA_029906585.1 (N)
VCH20210731	NOVC	Taizhou, Zhejiang, China	GCA_021228575.1 (N)
CQ23-0008VC	NOVC	Xiushan, Chongqing, China	GCA_039581465.1 (N)
1130W58	NOVC	Thailand	ERR1485320 (E)
D-SSH2/1-TY2	NOVC	Thailand	ERR1485318 (E)
TC8-1/1	NOVC	Thailand	ERR1485330 (E)
VCR12	NOVC	Thailand	ERR1485346 (E)

HSH1	NOVC	Thailand	ERR1485338 (E)
ST553-CHP	NOVC	Vietnam	ERZ25371650 (E)
MN06	NOVC (O47)	Bangladesh	GCA_047830805.1 (N)
MN08	NOVC (O47)	Bangladesh	GCA_047830785.1 (N)
MN09	NOVC (O47)	Bangladesh	GCA_047830825.1 (N)
(*) N: NCBI database; E: ENA-EMBL database			

Table S2. Antibiogram test results and resistance genes detected by CARD database and Cholerae Finder 1.0.

Antibiotics	MIC	Resistance Phenotype	Genes detected
Beta-lactams			
Ampicillin	8	S	
Amoxicillin/Clavulanic acid	4	S	
Piperacillin/Tazobactam	<=4	S	
Cefazolin	<=4	S	
Cefotaxime	<=0.25	S	
Ceftazidime	<=0.12	S	
Cefepime	<=0.12	S	
Ertapenem	0.25	S	

Imipenem	0.5	S	
Meropenem	<=0.25	S	*varG*
Aminoglycosides			
Amikacin	2	S	
Gentamicin	<=1	S	
Tobramycin	<=1	S	
Fluoroquinolones			
Ciprofloxacin	0.5	I	*QnrVC5*, *parC*, *parE*
Others			
Nitrofurantoin	<=16	S	
Trimethoprim	<=20	S	*dfrA31*
Vancomycin	Not tested	Not tested	*vanY*, *vanT*
Colistin	Not tested	Not tested	*almG*, *almF*, *almE*
General regulator			CRP (Global transcriptional regulator)



Genomic features

- positive CDS
- negative CDS
- tRNA
- rRNA
- GC content
- GC skew

Cluster of Ortologues Groups (COGs)

Cellular Processes and Signaling

[D] [O] [V]
[M] [T] [W]
[N] [U] [Z]

Metabolism

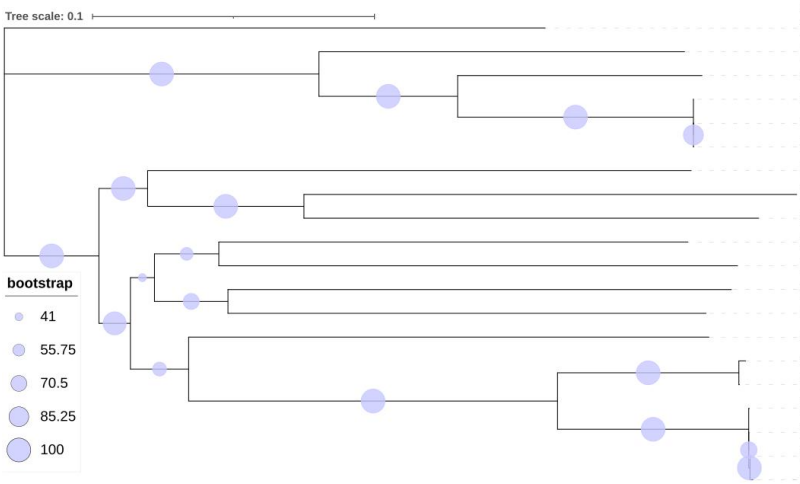
[C] [G] [P]
[E] [H] [Q]
[F] [I]

Information Storage and Processing

[A] [L]
[J] [X]
[K]

Poorly Characterized

[R]
[S]
[None]



Strain	Serotype	Sample	Year
1130W58	NOVC	water	1984
TC8-1/1	NOVC	fish	2006
ST558-CPH	NOVC	stool	2019
MN08	NOVC (O47)	stool	2010-2012
MN09	NOVC (O47)	stool	2010-2012
MN06	NOVC (O47)	stool	2010-2012
VCH20210731	NOVC	blood	2021
VCR12	NOVC	water	2013
HSH1	NOVC	wastewater	2013
Our study	NOVC	blood	2025
VC115	NOVC	blood	2023
RFB16	NOVC	NOVC	2019
CQ23-0008VC	NOVC	blood	2023
D-SSH2/1-TY2	NOVC	shrimp	2013
man9	O1, classic, Inaba type		1946
O395	O1, classic, Ogawa type		1965
C6706	O1, El Tor, Inaba		1961
N1691	O1, El Tor, Inaba type		1961
2010EL-1786	O1, El Tor, Ogawa type		2010
MO10	O139		1992