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Emergence of a Microbe in a New Geographic Area

Vibrio metschnikovii M1 isolated from a chronic venous leg ulcer from Montevideo, Uruguay and a mini-review of human cases from Latin America

Rosario Palacio [a], Gabriela Otero [b], Florencia Peñalba [c], Daniela Costa [c], María Magdalena Portela [d,g], Lucia Ferraz [b], Steven Tapia-Villacis [e], Cecilia Portela [f], Evangelina Costa [a], Bernardina Rivera [d], Nadia Riera [c,f,*]

[a] *Academic Unit Clinical Laboratory Microbiology Hospital de Clínicas, Montevideo, Uruguay*
[b] *Academic Unit of Dermatology. Hospital de Clínicas, Montevideo, Uruguay*
[c] *Microbial Genomics Laboratory, Institut Pasteur de Montevideo, Montevideo, Uruguay*
[d] *Analytical Biochemistry and Proteomics Unit. Institut Pasteur de Montevideo e Instituto de Investigaciones Biológicas Clemente Estable, Montevideo, Uruguay*
[e] *Academic Unit of Infectious Diseases, Universidad de la República, Montevideo, Uruguay*
[f] *Center for Innovation in Epidemiological Surveillance, CiVE. Institut Pasteur de Montevideo, Montevideo, Uruguay*
[g] *Instituto de Química Biológica, Facultad de Ciencias, UdelaR, Uruguay*

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ABSTRACT

We report a leg ulcer infection caused by *Vibrio metschnikovii* in a patient with chronic venous leg ulcers in Montevideo, Uruguay. Shotgun MS/MS combined with long-read whole-genome sequencing confirmed species assignment to *V. metschnikovii*. In addition, we incorporate a mini-review of the previous reported cases in Latin America.

While *Vibrio metschnikovii* is primarily considered an opportunistic pathogen, its clinical history in Latin America is intermittently documented alongside major diarrheal outbreaks (Table 1). Early reports include the isolation of the bacteria from five infants with watery diarrhea in Arequipa, Peru, in 1994, followed by six cases in healthy individuals in Recife, Brazil, in 1996. More recently, a 2008 case in Spain involving a leg ulcer in a patient recently emigrated from Uruguay further highlights its pathogenic potential in the region's population. Despite a lack of recent human clinical reports, environmental surveillance confirms its persistence; for instance, it was identified in bivalve mollusks in Venezuela in 2012, and recent CONICET research in Argentina has found significant presence in both local and imported shrimp. Because regional epidemiological surveillance in countries like Chile typically prioritizes *V. parahaemolyticus*, *V. vulnificus*, and *V. cholerae,* the lack of current human records likely reflects a gap in routine clinical reporting rather than an absence of risk, emphasizing the need for strengthened monitoring to track both food safety and the spread of antimicrobial resistance.

In this report, a 55-year-old woman with a 20-year history of a chronic venous ulcer involving the distal left leg circumferentially (Fig. 1) and multiple prior skin grafts had a medical history of hypertension, type 2 diabetes mellitus, and dyslipidemia. A biopsy performed in June 2023 excluded malignancy. Eighteen months later, she presented with marked ulcer enlargement, increased pain, abundant exudate, and foul odor, without systemic symptoms.

An exudate sample from the lesion was collected for microbiological analysis. Gram staining revealed abundant polymorphonuclear leukocytes and curved Gram-negative bacilli. Primary cultures showed abundant growth on blood agar, CHROMagar (Uriselect 4, Bio-Rad), and MacConkey agar (Oxoid). Colonies were grayish, opaque, 1–3 mm with complete β-hemolysis on blood agar after 24 hours, lactose non-fermenting on MacConkey, and beige on CHROMagar. The isolates were oxidase-negative.

Species identification was performed by Vitek MS® MALDI-TOF,

* Corresponding author. Microbial Genomics Laboratory, Institut Pasteur de Montevideo, Montevideo, Uruguay.
E-mail address: nriera@pasteur.edu.uy (N. Riera).

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Table 1
V. metschnikovii cases reported in Latin America.

Study	Region	Comments	Year
Dalsgaard et al. [9]	Arequipa, Peru	five infants with watery diarrhea	1994
Magalhães et al. [10]	Recife, Brasil	six cases of diarrhea	1996
Pariente Martin [5]	Albacete, Spain	isolated from a leg ulcer in a woman from Uruguay living in Spain for five months	2008
Muñoz et al. [11]	Sucre State, Venezuela	Bivalve mollusks	2012

yielding a 99.9% confidence score for *Vibrio metschnikovii*. As this species had not been previously reported in Uruguay, the isolate was considered clinically significant and referred to the National Reference Laboratory, where identification was confirmed. Antimicrobial susceptibility testing was performed using the Vitek 2 System® (AST cards 422 and 402). The minimum inhibitory concentration (MIC) for doxycycline was determined by gradient strip (Liofilchem®). Method and results were interpreted according to CLSI guideline M45 [1] (Table 2).

Table 2
Antimicrobial susceptibility of the isolate *Vibrio metschnikovii* M1.

	MIC	Interpretation
Amikacin	16 μg/ml	S
Ampicillin	≥32 μg/ml	R
Ampicillin Sulbactam	8 μg/ml	S
Cefazolin	≤4 μg/ml	S
Cefepime	≤0,12 μg/ml	S
Cefotaxime	≤0,25 μg/ml	S
Ceftazidime	≤0,12 μg/ml	S
Ceftriaxone	≤0,25 μg/ml	S
Ciprofloxacin	≤0,06 μg/ml	S
Doxycycline	2 μg/ml	S
Gentamicin	≤4 μg/ml	S
Imipenem	≤0,5 μg/ml	S
Meropenem	≤0,25 μg/ml	S
Piperacillin Tazobactam	≤4 μg/ml	S

S- Susceptible, R- Resistant, MIC- Minimum Inhibitory Concentration.

Although only a superficial exudate sample was obtained, abundant polymorphonuclear leukocytes, heavy bacterial growth in all quadrants, and worsening local symptoms supported infection. The patient was

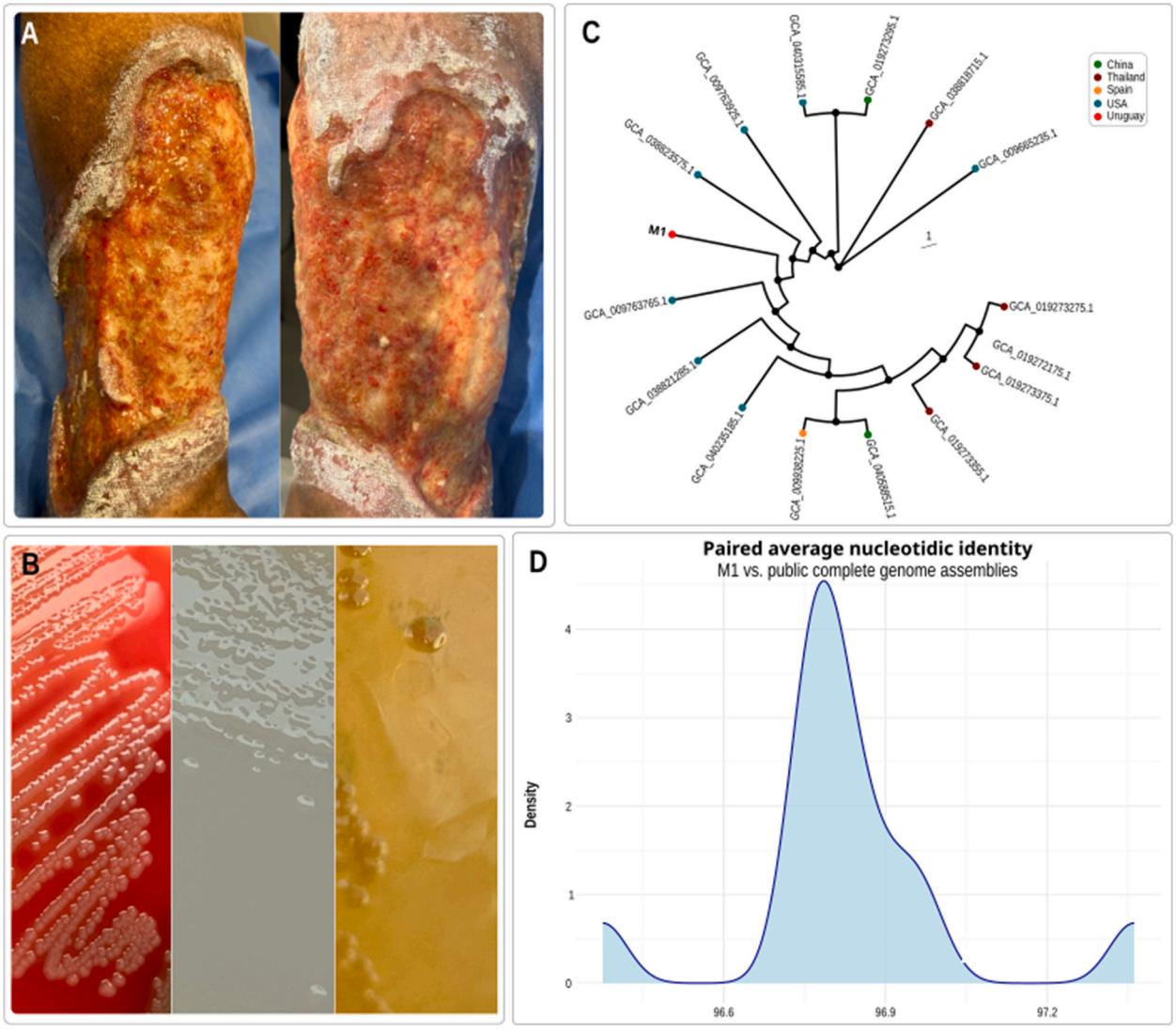

Fig. 1. (A) Chronic Venous Leg Ulcer (CVLU). Left leg chronic circumferential ulcer with fibrinous ulcer bed, exudate, and prominent borders. **(B)** *Vibrio metschnikovii* on blood agar showed beta-hemolytic colonies; colonies on cromoagar; lactose negative colonies on MacConkey agar. **(C)** Phylogenetic analysis based on the core genome of isolate M1 (in red) and 13 complete *V. metschnikovii* reference genomes. **(D)** Density plot with pairwise Average Nucleotide Identity (ANI) values of isolate M1 against the 13 complete genomes retrieved from NCBI.

treated with ciprofloxacin 500 mg every 12 h for two weeks. A follow-up culture obtained one month later was negative for *V. metschnikovii* and the patient showed progressive clinical improvement.

For proteomic confirmation, whole-cell extracts from a single colony were analyzed by shotgun nanoLC–MS/MS. A total of 5576 MS/MS spectra corresponding to 462 proteins uniquely mapped to *Vibrio metschnikovii*, providing strong peptide-level support for species identification. Genomic DNA was extracted using the PureLink™ Genomic DNA Mini Kit and sequenced using Oxford Nanopore technology (GridION platform, Flongle R9 flow cell). Library preparation was performed with the SQK-LSK109 ligation sequencing kit. De novo genome assembly was carried out using Flye v2.9 following contamination screening with Kraken2 v2.4.1 [2]. Taxonomic classification using GTDB-Tk (v2.4.1) [3] confirmed the isolate (M1) as *V. metschnikovii*, with an average nucleotide identity (ANI) of 96.83% and 81% genome coverage relative to the reference genome (GCF_000176155.1). Comparative genomic analysis with thirteen complete genomes retrieved from NCBI placed M1 within a lineage that includes previously described clinical and food-associated strains. Genome annotation identified the virulence-associated gene hcp2, encoding a Type VI secretion system (T6SS) component, as well as the antimicrobial resistance genes blaCARB-4 and qnrVC6. Despite the presence of these determinants, no phenotypic resistance to quinolones or β-lactams was observed. These results provided independent proteomic and genomic confirmation of species identification.

1. Discussion

V. metschnikovii is a rare human pathogen considered an environmental and zoonotic microorganism, with a presumed fecal–oral transmission route [4]. It has been isolated from aquatic environments (fresh, brackish, and marine waters), sewage, shellfish, birds, and poultry [5]. Several infections have occurred without reported seafood or water exposure. Identification of *Vibrio* spp. may be challenging. In oxidase-negative isolates, differential diagnosis is limited, as only two species are oxidase-negative: *V. metschnikovii* and *V. gazogenes*. Regionally, reports remain scarce. A recent review by Carrozzo et al. (2025) described cases only from Brazil and Peru, highlighting its rarity in Latin America. Our findings contribute to understanding its geographic distribution and raise awareness of its circulation in the region [6].

Active surveillance is important, as detection in clinical samples suggests a wider distribution than previously recognized. In this case, the patient had a self-limited course and responded well to ciprofloxacin. Despite detection of β-lactam and fluoroquinolone resistance genes, the isolate remained phenotypically susceptible.

Previous studies have reported antimicrobial resistance in *Vibrio* spp. Falco et al. found resistance to third-generation cephalosporins and aminoglycosides in 22% of isolates, without multidrug resistance [7]. Similarly, Wong et al. reported lower mortality with quinolone-based regimens than with β-lactam therapy in severe *Vibrio* infections [8].

Integration of proteomic and genomic approaches enabled reliable species identification and genomic characterization. This multimodal strategy facilitates detection of rare or underrecognized microorganisms not easily identified by conventional methods. Isolation of *V. metschnikovii* from a chronic venous ulcer suggests chronic wounds may serve as niches for environmental pathogens. To our knowledge, this is the first report of *V. metschnikovii* from a human clinical sample in Uruguay. Tracking *Vibrio* spp. and *V. metschnikovii* in Uruguay and Latin America, in new human cases, the environment and seafood is vital for understanding the spread of antimicrobial resistance and its underlying genetic mechanisms.

CRediT authorship contribution statement

Rosario Palacio: Writing – review & editing, Writing – original draft, Resources, Project administration, Methodology, Investigation, Funding acquisition, Formal analysis, Data curation, Conceptualization. **Gabriela Otero:** Writing – original draft, Resources, Project administration, Methodology, Investigation, Funding acquisition, Formal analysis, Data curation, Conceptualization. **Florencia Peñalba:** Writing – original draft, Visualization, Software, Methodology, Formal analysis, Data curation. **Daniela Costa:** Writing – review & editing, Visualization, Methodology, Formal analysis, Data curation. **María Magdalena Portela:** Methodology, Data curation. **Lucia Ferraz:** Investigation, Formal analysis, Data curation, Conceptualization. **Steven Tapia-Villacis:** Investigation, Formal analysis, Data curation, Conceptualization. **Cecilia Portela:** Methodology, Data curation. **Evangelina Costa:** Methodology, Investigation, Formal analysis, Data curation. **Bernardina Rivera:** Writing – original draft, Visualization, Software, Resources, Project administration, Methodology, Investigation, Funding acquisition, Formal analysis, Data curation, Conceptualization. **Nadia Riera:** Writing – review & editing, Writing – original draft, Visualization, Supervision, Software, Resources, Project administration, Methodology, Investigation, Funding acquisition, Formal analysis, Data curation, Conceptualization.

Ethics approval

Written informed consent was obtained from the patient for the publication of this case report and any accompanying images or data.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.nmni.2026.101754.

Data availability

The complete genome sequence and raw sequencing reads for the isolate reported in this study, have been deposited in the NCBI database under the following accession numbers: BioProject PRJNA1312815, BioSample SAMN50874118, and SRA SRS2634154.

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