

## A fatal case of *Vibrio cholerae* bloodstream infection

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### Introduction

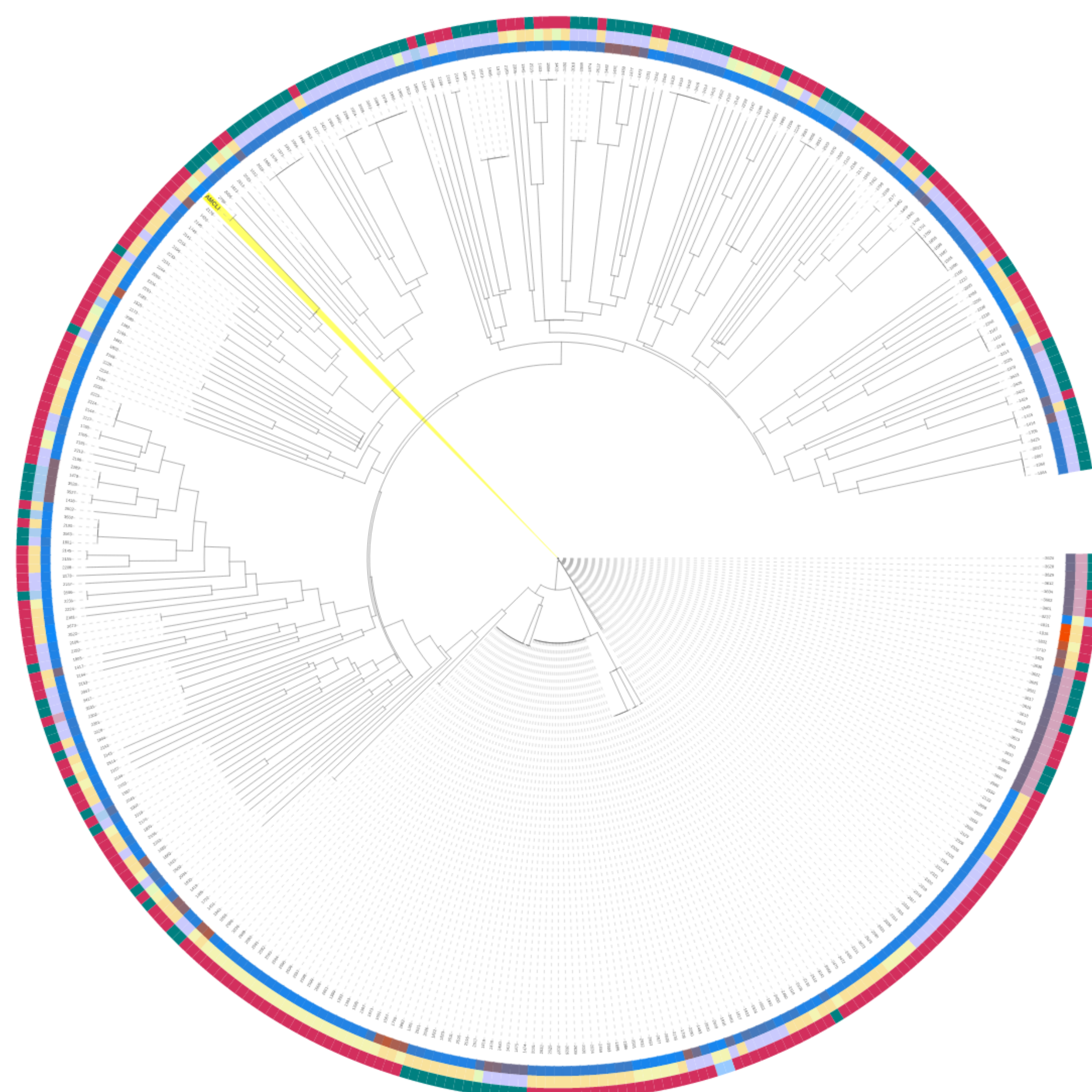
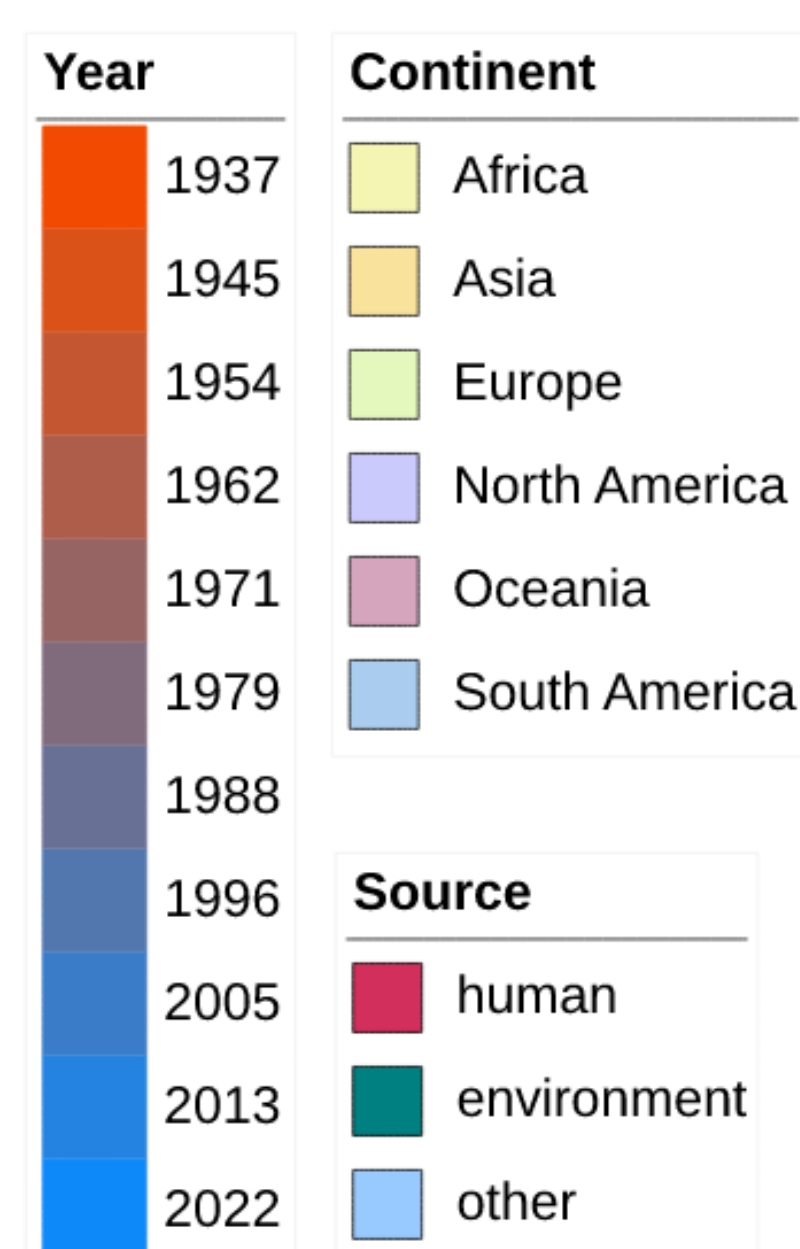
*Vibrio* spp. are gram-negative rods causing gastroenteritis and rarely extraintestinal infections in humans. *Vibrio cholerae* serogroups O1 and O139 are known to be associated with cholera epidemics, the strains not belonging to these serogroups (NOVC) don't produce toxins causing the disease. However, in recent years an increased number of infections involving NOVC was reported, particularly in immunocompromised or oncological patients.

This study reports a case of NOVC bloodstream infection. On August 21, 2022, a 78-year-old male patient was admitted to the Department of Internal Medicine of Scorrano Hospital (Lecce, Apulia, Italy) for severe lower limb phlebitis. Prior to admission (on August 18, 2022), he had fever without gastrointestinal symptoms. A week before admission, the patient, had accidentally injured himself while working in the countryside on his left leg, already affected by massive edema due to a previous phlebitis. The patient also has an oncological disease and cardiopathy. Death occurred 3 days after admission, due to septicemia. Epidemiological investigation showed that the patient in the days before the onset of symptoms had not consumed mussels and had drunk water from an uncontrolled well. Analysis of the well water yielded negative results for *V. cholerae*.

### Materials and methods

Blood cultures showed Gram-negative rods. Subculture in TCBS agar revealed oxidase-positive yellow colonies, similar to *V. cholerae*. The strain species was subsequently confirmed by MALDI-TOF-MS with a 99% confidence level. Genomic DNA was extracted from the isolate (TS: This Study isolate) using a DNeasy Blood & Tissue Kit, according to the manufacturer's instructions. Whole genome sequencing (WGS) of the DNA was performed on Illumina MiSeq platform. Reads were assembled with Galaxy platform. Taxonomic identification was performed on the genomic sequence using ribosomal MultiLocus Sequence Typing (rMLST) database. Analysis of resistome and virulence factors was determined using ABRicate v1.0.1 software, that includes different pre-downloaded databases.

Tree scale: 1

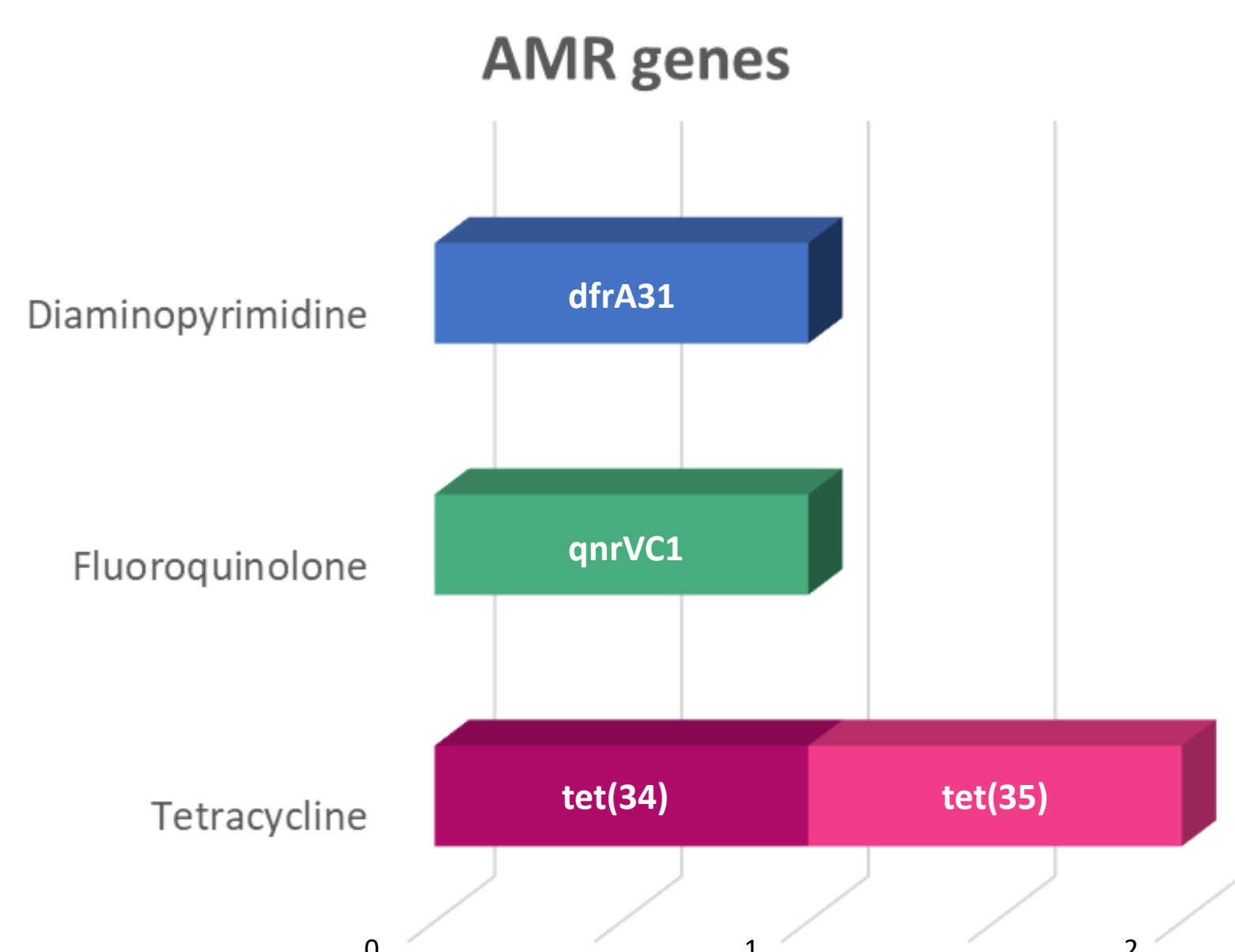


**Figure 1:** Phylogenetic tree with MLST profiles of all *V. cholerae* genomes in PubMLST database. TS isolate is highlighted in yellow.

### Results

The predicted taxa provided by rMLST analysis was *Vibrio cholerae*, in accordance with the MALDI-TOF MS identification. Thirty-two virulence genes were predicted, but in silico analysis showed the absence of the cholera toxin virulence genes (*ctxA*), the O139 (*rfbA*) and the O1 (*rfbB*) antigen genes, classifying the strain as NOVC. MLST analysis allowed a genetic comparison of the isolate with *V. Cholerae* genomes in the PubMLST database, and the finding of only one other strain with the same ST (ST947), isolated in China in 2016 (**Figure 1**). The ABRicate analysis predicted the antimicrobial resistance (AMR) genes to tetracycline, fluoroquinolones and diaminopyrimidine (**Figure 2**).

The clinical case highlights how untreated cases of infection sustained by virulent pathogens such as *V. cholerae* can evolve with death. In order to identify the sources of infection, it would be crucial to investigate the epidemiology of such cases.



**Figure 2:** Antimicrobial-resistant genes detected for the TS *V. Cholerae* genome sequence.