Fatal Vibrio vulnificus Infection Associated with Eating Raw Oysters, New Caledonia
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Peripheral blood aerobic–anaerobic samples were taken from all patients, stored in BacT/Alert FA vials (bioMérieux, Marcy-l’Etoile, France), and incubated in the BacT/Alert 3D system (bioMérieux). Curved mobile gram-negative bacilli were isolated from blood samples cultured on conventional media without additional salt within 24 h after incubation at 37°C in a 5% CO₂-enriched atmosphere. *V. vulnificus* was identified through the Vitek2 system (bioMérieux) and confirmed by using the Api 20E system (bioMérieux).

Strains were sent to the Centre National de Référence des Vibrons et du Choléra, (Institut Pasteur, Paris, France), which by PCR confirmed the gene encoding virulence-associated hemolysin, a species-specific marker (3). Molecular typing by pulsed-field gel electrophoresis was performed to assess possible clonality of the strains.

Several studies have shown the genomic diversity among environmental and clinical *V. vulnificus* isolates. The use of genotyping methods has identified >100 *V. vulnificus* strains in a single oyster (4) and notable heterogeneity among clinical isolates from multiple patients, even if a unique pathogenic strain causes the infection in each patient. Thus, *V. vulnificus* infections within a large population at risk may result from rare events controlled more by the host than by the bacterial strain (5).

Pulsed-field gel electrophoresis genotype analysis enabled us to divide the strains into 2 groups. One group included the isolate from patient 1, and the other group included isolates from patients 2 and 3, which despite having slightly different NcoI and SphiI patterns reflecting genetic rearrangement, clearly belonged to a single clone. Isolation of strains with such a high degree of homogeneity is not common, raising the question of the existence of *V. vulnificus* clones that are particularly virulent or adapted to humans. Currently, however, reliable markers for determining *V. vulnificus* virulence do not exist. Thus, no genotyping system is likely to be useful for rapidly identifying strains that affect public health (6). *V. vulnificus*–related analysis requires the assumption that all strains are virulent.

Epidemiologic information collected from patients’ families indicated recent consumption of raw oysters. Two of the 3 cases occurred within a short time frame and were associated with eating local oysters harvested on the west coast of New Caledonia.

The literature mentions few cases of *V. vulnificus* infection in the South Pacific. Cases described were isolated, rarely fatal, and involved infection through the skin (7–10). The *V. vulnificus* infections we report may be related to the emergence of a new clone or to changes in the climate or environmental conditions. New Caledonia experienced unusual weather conditions during the first half of 2008 (heavy rains and exceptionally high temperatures). These specific conditions may have favored higher sea surface temperatures, lower salinity, increased turbidity, and subsequent multiplication of *V. vulnificus* in seawater.

A range of projects were implemented to train practitioners to recognize potential *V. vulnificus* infections. Local health authorities issued criteria for defining suspected cases of *V. vulnificus* infection and recommendations for early medical care of patients with clinical symptoms. Methods of detecting the bacterium in human and animal health laboratories were improved, particularly by the systematic use of selective media in the event of suspected clinical *V. vulnificus* infection and standardized reporting of *V. vulnificus* isolation. Preventive measures, such as improving microbial surveillance and warning consumers about risks associated with eating raw seafood, are essential to help reduce the risk for *V. vulnificus*–induced illness.
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References


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Vibrio vulnificus

[Vib’re-o vůl-nif’i-kah]

From the Latin vibrio (to move) and vulnificus (causing wounds). Vibrio vulnificus is a virulent, gram-negative, comma-shaped, motile bacterium that belongs to the family Vibrionaceae. In 1976, researchers at the Centers for Disease Control identified it as a Vibrio sp. and possible emerging pathogen. Because of its association with blistering skin infections, the bacterium was named Vibrio vulnificus in 1979.