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Spread of Pacific Northwest *Vibrio parahaemolyticus* Strain

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To the Editor

Globally, *Vibrio parahaemolyticus* is a leading cause of seafood-associated gastroenteritis. Historically, the *V. parahaemolyticus* serotypes O4:K12 and O4:KUT, which have been shown to be more virulent than other pathogenic *V. parahaemolyticus* strains, have been unique to the Pacific Northwest region.[1] These strains, which were first identified in the Pacific Northwest in 1988, caused large U.S. outbreaks in 1997 and 2004.[2] The outbreaks were linked to consumption of Pacific shellfish, but these strains have not been linked to illness or isolated outside the Pacific Northwest until recently.

During the summer of 2012, outbreaks of *V. parahaemolyticus* infection caused by these serotypes occurred on the Atlantic coasts of the United States and Spain. The U.S. Centers for Disease Control and Prevention received reports of 28 cases of infection from 9 states, and regional health authorities in Galicia in northwest Spain received reports of 51 cases, of which 9 were subsequently confirmed by laboratory tests.

The U.S. outbreak was linked to consumption of shellfish harvested from Oyster Bay Harbor, New York, between April and August 2012. The Spanish outbreak occurred in August 2012 on a cruise ship in Galicia and was epidemiologically linked to cooked seafood cooled with ice produced from untreated local seawater.

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Clinical isolates obtained from U.S. and Spanish patients were highly similar to Pacific Northwest strains on serologic tests, polymerase-chain-reaction assays for virulence factors, pulsed-field gel electrophoresis, and multilocus sequence typing (Table 1). The specificity of these subtyping methods used in combination indicates commonality among outbreak strains. The initial arrival and overall environmental distribution of, as well as the mechanism for the introduction of, the *V. parahaemolyticus* strains to the Atlantic coasts of the United States and Spain are unknown. However, importation and storage of live contaminated bivalve shellfish in local waters, ballast water movement,[3] and long-distance oceanic transportation of strains into new regions[4] are possible mechanisms. Both New York and Galicia have previously had outbreaks of *V. parahaemolyticus* infection caused by other strains, and both cities are near major ports. Both the U.S. and Spanish outbreaks corresponded temporally and spatially with higher-than-normal surface seawater temperatures, which have been associated with an increase in both the environmental prevalence of *V. parahaemolyticus* and illnesses.[5]

These strains were associated with illnesses on the U.S. Atlantic coast again this year; however, it is uncertain whether these strains will continue to persist or spread to other regions. Europe currently lacks systematic surveillance for noncholera vibrio species; this limits the identification of new strains and estimates of the burden of illness. We advocate continued and improved national and international collaboration and data sharing to help recognize and respond to future outbreaks of *V. parahaemolyticus* infection.

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Table 1

Vibrio parahaemolyticus Strains from Outbreaks in 2012 in the United States and Spain and Closely Matching Pacific Northwest Isolates.*

Strain	Year of Isolation and Characterization	Source	Location	Serotype
F11–3A	1988	Environmental	Washington State	O4:K12
48057	1990	Clinical	Washington State	O4:K12
10296	1997	Clinical	Washington State	O4:K12
029–1(b)	1997	Environmental	Oregon	O4:K12
10329	1998	Clinical	Washington State	O4:K12
CDC_2012V-1109	2012	Clinical	Oyster Bay Harbor, New York	O4:K12
CDC_2012V-1108	2012	Clinical	Oyster Bay Harbor, New York	O4:K12
CDC_M12–108 G	2012	Clinical	Oyster Bay Harbor, New York	O4:KUT
CDC_2012V-1131	2012	Clinical	California	O4:KUT
CDC_2012V-1132	2012	Clinical	California	O4:K12
CDC_2012V-1134	2012	Clinical	Oyster Bay Harbor, New York	O4:KUT
G35	2012	Clinical	Spain	O4:K12
G36	2012	Clinical	Spain	O4:K12
G37	2012	Clinical	Spain	O4:K12

* All isolates, which were positive for thermostable direct hemolysin and thermostable direct-related hemolysin, were multilocus sequence type 36.