

# Cause of Maryland food poisoning outbreak traced to Asia

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*Vibrio parahaemolyticus* caused an outbreak of food poisoning in Maryland in 2010. The pathogen strain sequenced from patients proved to be the same strain as one of those found in raw oysters from local restaurants, strong evidence that the oysters were the source of the illness. That particular strain of *V. parahaemolyticus* was not local, but was traced to Asia. The research is published March 18 in *Applied and Environmental Microbiology*, a journal of the American Society for Microbiology.

The [outbreak](#) involved two individuals who became ill after eating [raw oysters](#) at two different restaurants in Baltimore, MD. According to the Centers for Disease Control and Prevention, two individuals is sufficient to constitute an outbreak since it is likely there were other cases that went unreported. Bolstering the evidence that local oysters were responsible for the outbreak, neither patient had traveled outside of the state in the previous week; nor did either have risk factors for *Vibrio* infections.

The outbreak offered an unusual opportunity, as disease-causing strains are rarely isolated from food sources. That made it possible for the investigators to identify the culprit strain of *V. parahaemolyticus*, called "sequence type 8," with a high degree of certainty, because that was the only strain among 10 strains found in the oysters that was also present in the patients' stools.

The authors then discovered that the culprit strain had previously been

found only in Asia. The Asian origin is important in demonstrating that a [pathogenic strain](#) may be introduced from afar, and have a public health impact, said coauthor Jessica L. Jones, PhD, Research Microbiologist and Acting Chief, Microbiological Hazards Science Branch, FDA, Gulf Coast Seafood Laboratory, Dauphin Island, Alabama.

The investigators suggested several ways in which an Asian strain could have arrived in the Chesapeake Bay area: via ballast water from ships arriving from Asia, or due to the introduction of exotic [oysters](#) or fish carrying the strain.

*V. parahaemolyticus* is the most important cause of seafood poisoning in the US. Approximately 4,500 cases occur annually in the United States, according to the Center for Disease Control and Prevention. The number of cases has risen in recent years, possibly do to the warming climate.

This research is important in demonstrating the crucial role that techniques including whole genome sequencing, and whole genome multi-locus sequence typing play in enabling a detailed retrospective study of outbreak and non-outbreak strains of the pathogen. Studies such as these allow resesarchers to pinpoint the culprit strain, and its likely origination point. In particular, whole genome multi-locus sequencing was easy to perform, and could easily be scaled up to identify multiple [strains](#) of *V. parahaemolyticus* in future investigations of outbreaks.

**More information:** Julie Haendiges et al. A non-autochthonous US strain of isolated from Chesapeake Bay oysters caused the outbreak in Maryland in 2010 , *Applied and Environmental Microbiology* (2016). [DOI: 10.1128/AEM.00096-16](https://doi.org/10.1128/AEM.00096-16)

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