

***Vibrio cholerae* in ships' ballast tanks—toxic genes and antibiotic resistance**

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Ships' ballast has been implicated as a vector in the dispersal of invasive species into new environments. Numerous cases have been documented for the introduction of metazoans via ballasting operations; much less known is the role of ballast water and tanks' residual sediments in the spread of potentially harmful microbes, especially with reference to novel genotypes. Of particular interest are genes conferring antibiotic resistance, many of which are carried on mobile genetic elements, and genes responsible for human disease. A four-year sampling effort yielded over 300 putative isolates of *Vibrio cholerae* from ships' ballast tanks and various environmental sources, and subsets of these isolates were profiled for antibiotic susceptibility and the presence of genes that encode for the cholera toxin (CTX) and toxin co-regulated pili (TCP).

Of 284 isolates tested, 11% were positive for serotype O1 and 21% for serotype O139. PCR assays were used to test for the presence of *ctxA* and *tcpA* genes in the O1 and O139 isolates; none contained *ctxA* and only 2% contained *tcpA*. The dearth of these genes is expected in environmental isolates from areas not undergoing a cholera pandemic.

Antibiotic susceptibility of 189 isolates was determined using 12 diverse antibiotics. There was widespread resistance to beta-lactam antibiotics (67% of isolates), especially in nearshore isolates compared to those derived from ships' ballast tanks. Plasmid extractions and restriction enzyme analyses showed evidence of plasmids of approximately 38 and 23 kbp in many of these isolates, suggesting the potential for horizontal gene transfer. Additional work using restriction fragment length polymorphisms and PCR for specific antibiotic resistance genes has yet to reveal the genetic source of the observed antibiotic resistance.