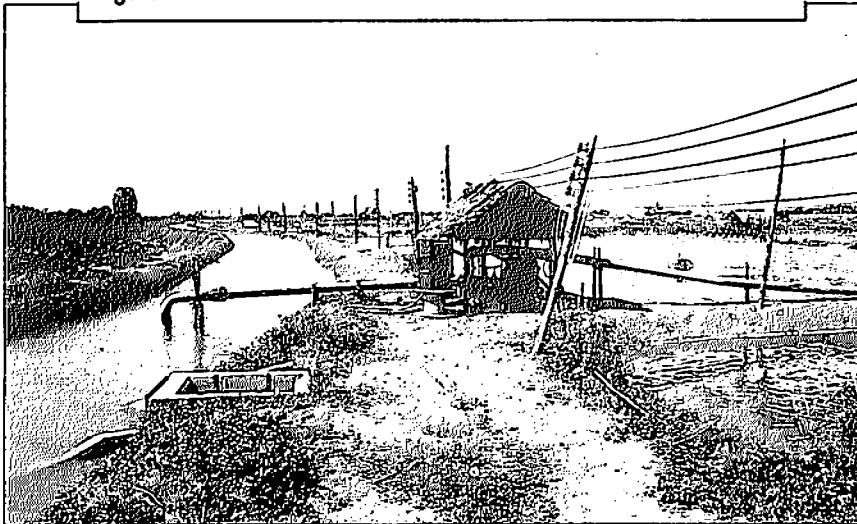


Shrimp culture is a major industry in South east Asia and the export of cultured shrimp is important for earning foreign currency. Most importing countries will not accept *Salmonella* and *Vibrio cholerae* in imported shrimp, and failure to meet these bacteriological standards may cause severe economic losses. In 1992/1993, we studied a major shrimp production area in Thailand—to determine the prevalence and significance of bacterial human pathogens, especially *Salmonella* and *V. cholerae*.

We collected some 200 samples from 16 shrimp farms, including coastal water (28), pond water (28), pond sediment (26), shrimp (25), feed (26), shrimp gut (15) and chicken manure (50). Using traditional and molecular-based methods, *Salmonella* was recovered from one chicken manure sample only despite the presence of high numbers of total and fecal coliform bacteria in water, sediment and shrimp samples. These results indicate that *Salmonella* did not constitute a normal part of the microbial flora in the marine environment where shrimp culture was practised, and that the application of dry pelleted chicken manure as an organic fertilizer in shrimp ponds was unlikely to have been a source of *Salmonella*.

The recovery of *V. cholerae* non-O1 was not significantly influenced by the proximity of the shrimp farms to suspected pollution sources and did not correlate with presently used indicator organisms. *V. cholerae* serotypes O1 and non-O1 were isolated from 2% and 33% of all samples studied, respectively. None of the strains contained genes encoding cholera toxin (CT) whereas 10% of the non-O1 strains hybridized with a heat-stable enterotoxin (NAG-ST) gene probe. Thus toxigenic *V. cholerae* O1 did not appear to be ubiquitous in the area studied.

Any presence of bacterial human pathogens in shrimp products may be of public health concern. This note by Danish expert Anders Dalsgaard concludes that *Salmonella* do not appear to constitute a part of the microbial flora where shrimp culture is practised in Thailand. *Vibrio cholerae* O1, the cause of cholera, was rarely recovered from the environment with no isolates containing genes encoding cholera toxin. Further studies are needed to describe the prevalence of bacterial human pathogens in shrimp culture, especially determination of possible postharvest cross-contamination with these pathogens.



Shrimp farms such as this one in Thailand need to meet bacteriological standards.



Typical shrimp harvest size in farms in Thailand.

Surveying Bacterial Human Pathogens in Shrimp Culture in Thailand

ANDERS DALSGAARD

The public health significance of the NAG-ST positive non-O1 strains remains to be clarified. Characterization of 93 *V. cholerae* non-O1 isolates by their antibiotic susceptibility patterns and plasmid profiling revealed a low degree of resistance with no significant difference in antibiotic susceptibility between isolates recovered from coastal waters and isolates obtained from shrimp farms, and with no relationship between resistance and the presence of plasmids. Hence, any previous use of chemotherapeutics in the area investigated does not appear to have influenced antibiotic resistance among the *V. cholerae* non-O1 studied.

Out of 483 *V. cholerae* isolates recovered from individuals with diarrhea in Thailand, Indonesia, the Philippines and Peru, only isolates from Thailand belonged to serotype O139 (122/364). Ninety-eight per cent of these isolates contained genes encoding a virulence gene complex including CT, zonula occludens toxin (Zot), accessory cholera enterotoxin (Ace), and repetitive sequence (RS1). *V. cholerae* O139 was not recovered from any samples obtained at the 16 shrimp farms studied. Ribotyping using a digoxigenin-labeled DNA probe was useful discriminating among 143 non-O1 and 47 O139 strains presenting 64 and 4 different *Bgl*I ribotypes, respectively. Correlation between ribotypes and serotypes were shown among 36 non-O1 strains studied. Restriction fragment length polymorphisms (RFLP) using CT and NAG-ST probes showed a varying degree of genetic diversity among clinical O139 and environmental non-O1 strains, respectively.



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