Shrimp culture is a major industry in Southeast 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.

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 0139 (122/364). Ninety-eight per cent of these isolates contained genes encoding a virulence gene complex including CT, zona occludens toxin (Zot), accessory cholera enterotoxin (Ace), and repetitive sequence (RS1). V. cholerae 0139 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 0139 strains presenting 64 and 4 different BglII 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 0139 and environmental non-O1 strains, respectively.

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