

## Virulence genes of *Vibrio harveyi* and their association with pathogenicity

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Shrimp aquaculture has been steadily progressing across the globe in the last two decades and intensified shrimp farming has led to increased incidence of bacterial infections resulting serious losses. Virulent *Vibrio harveyi* causes high mortality in the shrimp farming systems and its larval production. In order to understand molecular virulence mechanisms of *V. harveyi* to *Penaeus monodon* vibrio isolates were collected from shrimp farming systems and infected shrimps of the coastal waters of south India and were investigated. Of the eleven species of vibrios identified, *Vibrio harveyi* constituted 30.8 % of the isolates.

Representative luminescent isolates from each sample were studied for their molecular characteristics and the pathogenicity. The isolates were confirmed as *Vibrio harveyi* by the PCR detection of *gyrB* gene and 16S rDNA. The isolates were fingerprinted using IS and (GTG)<sub>5</sub> PCR and strain variations were established. Gene specific analysis was carried out for *vhh*, *lux L*, *lux N*, *tox R*, elastase, type III secretion system and metalloprotease.

Pathogenicity of the isolates was investigated in *Penaeus monodon* postlarvae by LD<sub>50</sub> values of the isolates, which ranged from  $1.56 \times 10^4$  to  $4.02 \times 10^9$ /ml. DNA fingerprinting although differentiated the isolates into different genogroups, was not conclusive enough to distinguish high and low pathogenic ones. Analysis of *vhh*, metalloprotease and type III secretion system genes indicated that these genes partially correlated with pathogenicity. Sequence analysis of *vhh* gene showed 99 % similarity with published sequences. Analysis also indicated that *tox R*, *lux L*, *lux N*, elastase genes did not correlate with virulence of *V. harveyi* isolates towards *Penaeus monodon*.