

## **Taxonomic classification of *Vibrio harveyi* using 16S rDNA and atpA gene sequencing method**

### **Abstract**

Genotypic analyses could provide highly accurate information on taxonomic lineage and can be used to develop identification tool for fish bacterial pathogens. In this study, the nucleotide sequences of 16S rRNA and atpA genes in 15 strains of *V. harveyi* were analyzed to determine which of these genes provide high confident level in the identification of the bacterial pathogen. In addition, the phenotypic characteristics and antibiotic susceptibility of the bacterial strains were also determined. The phenotypic analysis classified *V. harveyi* strains into 5 phenotypic groups. Each of this phenotypic group also exhibited variable responses to antibiotics. The 16S rRNA gene sequence analysis grouped *V. harveyi* into two main groups. The grouping was due to the presence of two unique nucleotide sequences located at nt1004 – nt1013 (*V. harveyi* ATCC 35084 (GQ370528)). Unfortunately, these unique sequences were also found in other closely related *Vibrio* species. On the other hand, the atpA gene sequencing analysis clustered all the *V. harveyi* strains into a single group and differentiated from closely related species. The single clustering of *V. harveyi* was the result of the presence of one unique sequence at the nucleotide positions, nt1071 – nt1122 (*V. harveyi* ATCC 35084 (JF723525)). The present study shows that phenotypic characterization and antibiotic susceptibility test may not be able to identify *V. harveyi* strains with high degree of confidence. Although, 16S rDNA gene sequencing analysis has been widely accepted as the universal method for bacterial identification, it is less useful in taxonomic classification of *V. harveyi*. Hence our study suggests that atpA gene may be the best target for DNA sequencing analysis for the purpose of taxonomic classification of *V. harveyi*.