Phylogenetic study and identification of human pathogenic Vibrio species based on partial hsp60 gene sequences

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Abstract:

The use of hsp60 gene sequences for phylogenetic study and identification of pathogenic marine vibrios was investigated. A 600-bp partial hsp60 gene was amplified by PCR and sequenced from 29 strains representing 15 Vibrio species within the family Vibrionaceae. Sequence comparison of the amplified partial hsp60 gene revealed 71 82% sequence identity among different Vibrio species and 96 100% sequence identity among epidemiologically distinct strains with the same species designation. This degree of discrimination allows unambiguous differentiation of all Vibrio species included in the current study from each other, as well as from Aeromonas hydrophila and Plesiomonas shigelloides, which are often misidentified as Vibrio species by conventional biochemical methods. Based on the hsp60 gene sequences, two previously unidentified shrimp isolates were found to be more closely related to Vibrio alginolyticus (93 94% sequence identity) than to Vibrio parahaemolyticus (89% sequence identity), whereas 16S rRNA gene analysis was unable to differentiate among these closely related species (95 97% sequence identity). Our results indicate that the hsp60 gene may be a useful alternative target for phylogenetic analysis and species identification of marine Vibrios to complement more conventional identification systems.Key words: Vibrio, hsp60, 16S rRNA, phylogenetic analysis, species identification.