
Molecular characterization of *Vibrio cholerae* O1 and non-O1 from human and environmental sources in Malaysia

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SUMMARY

A total of 31 strains of *Vibrio cholerae* O1 (10 from outbreak cases and 7 from surface water) and non-O1 (4 from clinical and 10 from surface water sources) isolated between 1993 and 1997 were examined with respect to presence of cholera enterotoxin (CT) gene by PCR-based assays, resistance to antibiotics, plasmid profiles and random amplified polymorphic DNA (RAPD) analysis. All were resistant to 9 or more of the 17 antibiotics tested. Identical antibiotic resistance patterns of the isolates may indicate that they share a common mode of developing antibiotic resistance. Furthermore, the multiple antibiotic resistance indexing showed that all strains tested originated from high risk contamination. Plasmid profile analysis by agarose gel electrophoresis showed the presence of small plasmids in 12 (7 non-O1 and 5 O1 serotypes) with sizes ranging 1·3–4·6 MDa. The CT gene was detected in all clinical isolates but was present in only 14 (6 O1 serotype and 8 non-O1 serotype) isolates from environmental waters. The genetic relatedness of the clinical and environmental *Vibrio cholerae* O1 and non-O1 strains was investigated by RAPD fingerprinting with four primers. The four primers generated polymorphisms in all 31 strains of *Vibrio cholerae* tested, producing bands ranging from < 250 to 4500 bp. The RAPD profiles revealed a wide variability and no correlation with the source of isolation. This study provides evidence that *Vibrio cholerae* O1 and non-O1 have significant public health implications.

INTRODUCTION

Vibrio cholerae is an important cause of cholera in humans causing in its severe forms, profuse diarrhoea, vomiting and muscle cramps. Transmission of this organism is associated with consumption of contaminated foods and often with contaminated water and person-to-person transmission [1–3]. The pathogenicity of cholera is mainly associated with their ability to produce a cholera enterotoxin (CT), encoded by two contiguous genes that form the *ctxAB* operon

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[4]. Since not all *Vibrio cholerae* strains are toxigenic, regular examination of isolates for their potential to produce CT are needed to obtain a better understanding of the public health hazard caused by toxigenic strains. Differentiation of *V. cholerae* will be required to ascertain the incidence, prevalence and diversity of strains. Epidemiologic investigation of cholera requires the characterization of *V. cholerae* isolates by typing systems which allow determination of isolates relatedness. It is common to use phenotypic and genotypic techniques for the characterization of organisms, and among them plasmid profiles, anti-