GENOTYPE AND DRUG RESISTANCE OF CLINICAL AND ENVIRONMENTAL VIBRIO CHOLERAE NON-O1/ NON-O139 IN NORTHEASTERN THAILAND

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Abstract. A total of 124 \textit{V. cholerae} non-O1/non-O139 isolates were collected in Khon Kaen, Thailand from diarrheal patients, asymptomatic carriers and environmental water. The presence of virulence-associated and regulatory genes including \textit{ctxA}, \textit{tcpA}, \textit{zot}, \textit{ace}, \textit{ompU}, \textit{stn}, \textit{hlyA} and \textit{toxR}) were examined using multiplex PCR. The genomic diversity of the various \textit{V. cholerae} isolates were differentiated using the random amplified polymorphic DNA (RAPD) method. Antimicrobial susceptibility was tested using disk diffusion. All of \textit{V. cholerae} non-O1/non-O139 isolates carried \textit{hlyA} and \textit{toxR} and none carried \textit{ctxA} and \textit{tcpA}. The \textit{zot}, \textit{ace} and both genes together were found in 1.6%, 4.7% and 4.7% of 64 clinical \textit{V. cholerae} non-O1 isolates, respectively, while the environmental ones did not. The \textit{stn} gene was found in 3.1% (2/64) of the clinical and 3.3% (2/60) of the environmental isolates. The RAPD patterns were differentiated into 45 types (A to 2S). RAPD type A (32.3\%) was the most frequently found in both clinical and environmental \textit{V. cholerae} non-O1 strains (34.4\% and 30.0\%, respectively); indicating that there was a clonal relationship between some clinical and environmental isolates whereas almost all of the environmental isolates belonged to different clones. All strains were sensitive to ciprofloxacin and norfloxacin. The environmental isolates (30\%) were more resistant than the clinical ones (21.9\%). Resistance to sulfamethoxazole/trimethoprim and tetracycline among the clinical isolates occurred in 9.4\% (6/64) in 2007, during which period the prevalence of \textit{V. cholerae} O1 increased. We conclude that \textit{V. cholerae} non-O1/non-O139 from the aquatic environment are potentially pathogenic and this same aquatic environment may be a source of antimicrobial resistance in \textit{V. cholerae}.

Keywords: \textit{V. cholerae} non-O1/non-O139, genotype, environment, RAPD, drug resistant