DISTRIBUTION AND SEQUENCE ANALYSIS OF VIRULENCE ASSOCIATED GENES IN *VIBRIO CHOLERAE* O1, O139 AND NON-O1/NON-O139 ISOLATES FROM THAILAND

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Abstract. Virulence-associated genes of *Vibrio cholerae* including O1, O139 and non-O1/non-O139 from an outbreak in Songkhla Province and sporadic cases occurred in Thailand during 1993 - 2002 were investigated. One hundred eighty-five *V. cholerae* strains were examined for the presence of virulence-associated genes including *ctxA, tcpA, zot, toxR, toxS, toxT,* and *ace* by polymerase chain reaction. DNA sequences of *ctxA, tcpA, zot* and *toxR* also were investigated in 8 selected isolates. Results showed that the virulence factors genes were distributed in the majority of *V. cholerae* O1 biotype Inaba and Ogawa strains (85-97%). All 6 strains of the O139 harbored *toxR, toxS* and *toxT* whereas *ctxA, tcpA, zot* and *ace* were detected only 50-67%. Toxins genes found in non-O1/non-O139 strains ranged 8-30% except *toxR* (73.5%). Results of multiple sequence alignments among the isolates compared with *V. cholerae* O1 in database (embl M21249), showed that *ctxA, tcpA* and *zot* sequences in all 8 isolates were conserved, but base changes were found in *toxR* sequence. These molecular characteristics of *V. cholerae* isolated from Thailand will provide detailed information for facilitating future studies on the development and design of appropriate vaccine providing protection against local strains.

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