EVOLUTION AMONG O1 HYBRID AND EL TOR VARIANT *VIBRIO CHOLERAE* O1 STRAINS IN THAILAND

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Abstract. *Vibrio cholerae* O1 belonging to hybrid and El Tor variant biotypes were first reported in Bangladesh in 2002. Subsequently, these new variants were detected in various countries including Thailand. The study investigated possible events and period associated with emergence of these *V. cholerae* O1 variants in Thailand. Ribotyping and pulsed-field gel-electrophoresis (PFGE) were used to analyze *V. cholerae* O1 clinical isolates ($n = 173$) collected during 1973-2013, resulting in identification of 12 ribotypes and 29 pulsotypes, with implication of four periods of genotypic drift. From 1973-1989 the majority of isolates had ribotype A with pulsotype 23, 32 or 33; from 1990-1998 isolates carried a variety of genotypes with bias towards ribotype A or D and pulsotype 5 or 22; from1999-2002 isolates carried ribotypes H and G with pulsotypes 8 and 11 being predominant; and from 2003-2013 isolates with ribotype B or J and pulsotype 34 or 2b were in the majority. Ribotyping and PFGE analyses suggested each genotypic drift period comprised of a limited set of distinct *V. cholerae* O1 clones, and minor genetic changes generated novel indigenous clones observed in the subsequence period. Thus, the emergence of hybrid and El Tor variant strains found in Thailand during the later half of study period were the results of genetic evolution of Thai indigenous clones. No difference in vibriocidal titer against these *V. cholerae* O1 strains compared to reference strains suggests lack of change in cholera vaccine efficacy against the emerging new variant *V. cholerae* O1 strains in Thailand.

Keywords: *Vibrio cholerae* O1, evolution, pulsed-field gel-electrophoresis, ribotyping, hybrid and El Tor variant biotype, Thailand

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