

中文關鍵詞(至少三個)：霍亂，分型，資料庫

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Project Title: Genotyping for *Vibrio Cholerae*
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Executing Institute: Centers for Disease Control
Principal Investigator(P.I.):
P.I. Position Title:Rsearch Associate Fellow
P.I. Institute: Centers for Disease Control

Abstract:

Genome-based bacterial typing is essential for determining phylogenetic relationship and epidemiological and forensic investigation. In this study, we employed two methods for molecular typing of *Vibrio cholerae*: PFGE (pulse field gel electrophoresis) and MLVA (multilocus variable number tandem repeat analysis). A total of 54 *Vibrio cholerae* clinical isolates (23 of O1 serogroup, 27 of O139 serogroup, and 4 of non O1/non O139) were analyzed by PFGE and partitioned into 4 clades with 85% similarity, O139 could not be separated from O1 within this similarity, clustered in the same clade. A total of 9 VNTR loci were used for fine typing of 54 *Vibrio cholerae* clinical isolates. This MLVA enables the partitioning to 5 clades with $p < 0.01$ and $p < 0.05$. MLVA could discriminate not only O139 from O1 but also all ctxA (+) isolates from ctxA (-). Our data indicated that MLVA has higher degree of resolution than PFGE in discriminating of *Vibrio cholerae* isolates.

Keyword: Cholerae,typing, database