應用 rep-PCR 作為院內感染 MRSA 菌株快速分型比對之研究

Use of rep-PCR for Rapid Molecular Genotyping among Nosocomial Infection Associated MRSA Isolates

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Nosocomial infections caused by Methicillin-resistant *Staphylococcus aureus* (MRSA) remain a global challenge for healthcare professionals. Identifying the source of MRSA is an important task to halt the nosocomial transmission. Molecular subtyping is a powerful tool for determining the source of infection by their genetic relatedness among isolates. However, conventional method, namely pulsed-field gel electrophoresis (PFGE), is time consuming and requires highly skilled technicians for interpretable results. Currently repetitive-sequence-based PCR (rep-PCR) technique has been developed to an automated procedure that may provide a rapid and reliable method for molecular subtyping of MRSA. Such rapid method provides same-day genotyping results and enables infection control practitioners to timely eliminate further nosocomial MRSA transmission. Thus, the objective of this study is to use the rep-PCR for MRSA typing. Twelve distinct clinical isolates of *S. aureus* (8 MSSA, 4 MRSA), which were previously subtyped by PFGE, were used in this study. A rep-PCR assay and a capillary electrophoresis system (Agilent 2100 Bioanalyzer, bioMerieux) were used for molecular analysis. We followed the standardized procedures for analysis including: (1) extract DNA from the isolated cultures; (2) amplify samples using rep-PCR and the appropriate commercially available fingerprinting kits; (3) separate fragments via electrophoresis performed in a microfluidics DNA LabChip; and (4) analyze data using dendrogram, similarity matrix, and overlay analysis. Our results showed that the 12 isolates were successfully distinct by rep-PCR method. The signal-base electrophoresis by rep-PCR provide more reproducible results than the analog image-base results by PFGE. Times to results were 6 to 8 hr for rep-PCR compared to 3 to 5 days for PFGE. Rapid, standardized results and high reproducibility make the rep-PCR a valuable tool for use in MRSA outbreak investigations.

必填資料-------

※ 論文性質：

☐ AM (應用微生物) ☐ BM (基礎微生物)

■ CM (臨床微生物) ☐ V (病毒)

※ 發表方式：■ Oral ■ Poster

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