

Molecular detection and epidemiological analysis of staphylococcus aureus from Malaysian hospitals using random amplified Polymorphic DNA-typing.

ABSTRACT

Staphylococcus aureus is among the most prominent pathogen in both community acquired and nosocomial infection. The epidemiology analysis of Staphylococcus aureus isolates will be required to ascertain the incidence, prevalence and diversity of strains. To investigate the epidemiological of S. aureus in Malaysia, a highly reliable typing method-Randomly amplified polymorphic DNA was applied to 50 S. aureus isolates obtained from 3 different hospitals in Malaysia namely Hospital Tunku Ampuan Afzan Kuantan, Hospital Besar Seremban and Hospital Miri Malaysia. The results obtained from this study showed that the isolates can be clustered into 8 different clones. All members of the respective clones are of the same origin. In addition, there were 2 clonal grouping of isolates for each hospital. However, the clonal groupings are not in accordance to the geographical distribution. To understand the epidemiology of these isolates in depth it is very important to have information about the patient's history. The Nei and Li's genetic distances obtained from this study ranged from 0.0803922-0.11111. Two genetic markers a band of size 500 bp when amplified with primer OPAE-14 and another marker band of size 750 bp amplified with primer OPAE-15 was identified and this band can be used as diagnostic marker for the rapid identification of S. aureus. Apart from the genetic markers, an epidemiological marker of 1200 bp was also identified for the Miri isolates. This marker can be used as the epidemiological marker for the identification of the isolates from Miri in the future outbreaks. From this study, RAPD has proved to be an useful aid to epidemiological investigations of S. aureus.

Keyword: Random amplified polymorphic DNA; Staphylococcus aureus; Primer; Human; Pathogen; Malaysia.