Thesis Title Antibiogram and Plasmid DNA Analysis to Characterize *Staphylococcus aureus* Strains

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## ABSTRACT

Antibiogram and plasmid DNA analysis were used to characterize 231 *Staphylococcus aureus* of both methicillin-susceptible (MSSA) and methicillin-resistant (MRSA) isolated from patient clinical specimens of 8 hospitals and from environmental wastewater samples at various time of collection during July to September 1993.

Their susceptibilities to 8 antistaphylococcal agents by agar disc diffusion method showed that all isolates were susceptible to vancomycin. More than 90% of isolates were resistant to penicillin, 56.7% to tetracycline, and 27-34% to other drugs. Frequency distribution of resistance determinants were varied from 0 to 7 drugs ( $\bar{X}$ 2.98, S.D. 2.52). Single drug resistant strains were commonly detected, and 6.1% of isolates were not resistant to antibiotics. All *S. aureus* demonstrated 16 different resistance patterns and 127 different plasmid patterns or 188 different types after plasmid digestion with *Eco*RI enzyme. Their plasmid distributions were in the range 0-9 ($\bar{X}$ 4.0, S.D. 1.9), and 3.5% of isolates lacked plasmid. The plasmid DNA analysis was more specific and powerful to discriminate *S.aureus* strains than resistance patterns (antibiograms). However, it could not determine whether these plasmid patterns were related to resistance patterns or not, because of wide variety of *S.aureus* strains in this study.

When *S.aureus* isolates were divided into 2 groups of 63 MRSA and 168 MSSA. All were susceptible to vancomycin. The MRSA were highly (>95%) resistant to all antibiotics that were significantly different from MSSA which 90.5% of isolates were resistant to penicillin, 42.9% to tetracycline and 1-5% to other drugs. Resistance determinant distributions of MRSA isolates were in the range 4-7 ($\bar{X}$ 6.9, S.D. 0.6) that were significantly different from MSSA which in the range 0-5 ($\bar{X}$ 1.5, S.D. 0.9). The MRSA isolates showed 4 different resistance patterns, while the MSSA showed 12 patterns. The most common patterns of MRSA were resistant to all antibiotics except vancomycin, while the MSSA were double or single drug resistance patterns. All MRSA produced beta-lactamase that were significantly different from MSSA which 90% of isolates produced this enzyme. More than 95% of both groups harboured plasmid and 4 plasmid harboured strains were commonly detected; however the plasmid distributions between MRSA and MSSA were significantly different. (MRSA, $\bar{X}$ 4.2, S.D. 2.0; MSSA, $\bar{X}$ 3.4, S.D. 1.4). Plasmid DNA patterns gave 22 different types in MRSA, and 112 types in MSSA; and increased to 37 patterns in MRSA and 151 patterns in MSSA after *Eco*RI digestion.

In summary, plasmid DNA analysis were more helpful to discriminate *S.aureus* strains than resistance patterns. This method was rapid, easy to perform, stable and reproducible to use for the epidemiological study.