Session: Bacterial Infections

Title: Genetic diversity of Malaysian methicillin resistant *Staphylococcus aureus* strains based on virulotypes, pulsed-field gel electrophoresis and PCR-RFLP of coa gene

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Abstract: **Background:** *Staphylococcus aureus* is a persistent human pathogen responsible for a variety of infections ranging from soft-tissue infections to bacteremia. The objective of this study was to determine the prevalence of a repertoire of toxin genes among Malaysian MRSA strains isolated over a four years period and the genetic relatedness of MRSA strains.

**Methods:** One hundred eighty-eight strains (2003, 2004, 2007 and 2008) of methicillin-resistant *S. aureus* (MRSA) isolated from a tertiary hospital were screened for 20 genes encoding for extracellular virulence determinant (*sea, seb, sec, sed, see, seg, seh, sei, sej, tst, eta, etb, etd*) and adhesins (*cna, etb, fnbA, fnbB, hlg, ica, sdr*) via PCR. The genetic relatedness of these strains was determined by PFGE, PCR-RFLP of *coa* gene and *agr* grouping.

**Results:** Majority of the strains were tested positive for *efb* and *fnbA* (96% each), *ica* (78%) and *hlg* (59%) genes. A total of 101 strains were positive for at least one type of staphylococcal enterotoxin genes with *sea* being the predominant. Genes for *seb, sed, see, seh, sej, eta* and *etb* were not detected in any of the MRSA strains. The prevalence of *sea, sec* and *ica* among strains isolated in 2008 was increased significantly (p < 0.05) compared to 2003. Most of the strains were of *agr* type I (97.5%) followed by *agr* type II (1.2%) and *agr* type III (0.6%). Subtyping by PFGE and PCR-RFLP of *coa* gene produce 88 different pulsed-field profiles (F=0.51-1.0) and 47 different patterns (F=0.24-1.0), respectively.

**Conclusion:** No direct correlation between virulotypes, PFGE and PCR-RFLP profiles was observed. Strains with identical PFGE and PCR-RFLP profiles frequently belonged to different virulence patterns. Increase of MRSA strains with virulence factors over the years signal the potential loss of the usage of antimicrobial agents in treating MRSA infections as MRSA strains with virulence factors are normally resistant to host immune systems and other antimicrobial agents. The MRSA clinical strains from this tertiary hospital were genetically related, suggesting that few predominant clones of the species are involved in infections.