Methicillin-susceptible Staphylococcus aureus (MSSA) strains in Universiti Kebangsaan Malaysia Medical Centre (UKMMC), Malaysia: association between agr groups and virulence genes

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Background: Staphylococcus aureus is an important pathogen in human disease where genetic regulatory elements and toxin-expressing genes are associated with its pathogenic potential. Special attention is being paid to methicillin-resistant S. aureus (MRSA); with fewer studies carried out on methicillin-susceptible S. aureus (MSSA) even though they are often more genetically variable and usually cause a higher incidence of infection in hospitals than their methicillin-resistant counterpart. We collected MSSA strains isolated in our university hospital (UKMMC) in 2009 and investigated the molecular characteristics of these strains.

Methods: A cross-sectional study on MSSA strains was performed in UKMMC in 2009. 880 cases of MSSA were selected for molecular typing was carried out using a multiplex PCR protocol. The association, if any, between agr group and presence of the 4 tested toxin genes was also determined in our tested strains.

Results: In our study, 58.9% (518) of MSSA strains harboured at least one of the 4 tested virulence genes: 51.6% (454) had cna, 21.8% (192) possessed seh, 10.2% (90) had PVL and 6.8% (60) harboured TSST-I. For agr group typing, 39.8% (350), 12.7% (112), 28.0% (246) and 4.3% (39) of our strains were detected as agr I, II, III or IV, respectively. Nevertheless, 15.2% (133) of the strains were untypeable for agr. Interestingly, we noticed that most of the agr group III strains were also positive for both cna and seh (P < 0.05).

Conclusion: In 2009, cna was commonly detected in our collection of UKMMC MSSA strains, whereas TSST-I was rarely detected. Most of the strains were detected as agr group I. We noticed a strong association between the presence of both cna and seh virulence genes and agr group III in our strains. The importance of this observation remains to be investigated.

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