

Volume 6, No. 1 (Supplement)

June 2011

ISSN 1823-2140

The National University
with an INTERNATIONAL REACH



UNIVERSITI
KEBANGSAAN
MALAYSIA
National University of Malaysia

MEDICINE & Health

The Official Journal of The Faculty of Medicine UKM

7th Malaysia Indonesia Brunei Medical Sciences Conference "TOWARDS A HOLISTIC AND INTEGRATIVE APPROACH IN HEALTHCARE"



22nd - 24th July 2011

Equatorial Hotel, Bangi, Selangor,
MALAYSIA

officiated by

Y.B Datuk Rosnah Haji Abdul Rashid Shirlin
Deputy Minister of Health Malaysia

Organised by



STAPHYLOCOCCAL VIRULENCE GENES AND INFECTION: THE METHICILLIN-SUSCEPTIBLE *STAPHYLOCOCCUS AUREUS* (MSSA) EXPERIENCE IN AN ORTHOPAEDIC WARD

Hassriana FS¹, Azirah NMS¹, Ainihayati N¹, Hui-min N², Salasawati H¹

¹Department of Medical Microbiology and Immunology, Universiti Kebangsaan Malaysia Medical Centre, Kuala Lumpur, Malaysia

²UKM Medical Molecular Biology Institute (UMBI), Universiti Kebangsaan Malaysia (UKM), Kuala Lumpur, Malaysia.

Background:

Staphylococcus aureus has been known to produce several toxins that contribute to its virulence. Many studies on methicillin resistant *S. aureus* (MRSA) virulence have been done, however, reports on its methicillin susceptible counterpart (MSSA) are few.

Materials and methods:

We collected MSSA strains isolated in our university medical centre's orthopaedic ward during 2009 and determined the presence of four virulence genes (collagen binding adhesion, *cna*; staphylococcal enterotoxin H, *seh*; Panton-Valentine leukocidin, PVL and toxic shock syndrome toxin-1, TSST-1) in these strains by multiplex PCR. Type of MSSA infection for each corresponding patient was also recorded. Statistical analysis was performed to investigate the presence, if any, of association between staphylococcal virulence gene carriage and MSSA infection.

Results:

Ninety-nine MSSA infections were included in this study. A total of 62 (62.6%) cases from these infections were due to MSSA which harboured virulence genes (either one of *cna*, *seh*, PVL, TSST-1 or in combination), where 54.5% (54/99) had *cna*, 23.2% (23/99) possessed *seh*, 13.1% (13/99) carried PVL and 3.0% (3/99) were positive for TSST-1. Most of the orthopaedic patients (65.6%, 62/99) had skin and soft tissue infections, followed by surgical site infection (16.2%, 16/99). In our study, we could not find any association between staphylococcal virulence gene carriage with MSSA infection ($P > 0.05$).

Conclusion:

Among the four virulence genes detected in this study, the most common virulence gene found in our medical centre's orthopaedic ward MSSA isolates was *cna*. Even though MSSA infections are generally easier to manage as they are commonly susceptible to most available antibiotics, infections with MSSA should be treated with caution as they could still serve as reservoirs of virulence factors which might introduce complications into patients' clinical course.

Keywords:

MSSA, virulence gene, patient's diagnosis