Documents

Sapri, H.F.[a] , Ismail, M.A.H.[b] , Sani, N.A.M.[a] , Noordin, A.[a] , Tan, T.L.[c] , Hussin, S.[a d] , Neoh, H.-M.[b]

Molecular surveillance of methicillin-susceptible staphylococcus aureus (MSSA) isolated over a one-year period from a malaysian teaching hospital
(2020) *GERMS*, 10 (2), pp. 104-111.

DOI: 10.18683/germs.2020.1191

[a] Department of Medical Microbiology and Immunology, Faculty of Medicine, Universiti Kebangsaan Malaysia, Cheras, Kuala Lumpur, 56000, Malaysia
[b] UKM Medical Molecular Biology Institute (UMBI), Universiti Kebangsaan Malaysia, Cheras, Kuala Lumpur, 56000, Malaysia
[c] Department of Emergency Medicine, Faculty of Medicine, Universiti Kebangsaan Malaysia, Cheras, Kuala Lumpur, 56000, Malaysia
[d] Medical Science Division, Faculty of Medicine, University of Cyberjaya, Cyberjaya, Selangor 63000, Malaysia

Abstract
Introduction We report the results of a molecular surveillance study carried out on methicillinsusceptible Staphylococcus aureus (MSSA) isolated in a one-year duration from Hospital Canselor Tuanku Muhriz (HCTM), a tertiary hospital located in Kuala Lumpur, Malaysia. Methods The first strain isolated from each MSSA infection in HCTM during the year 2009 was included into the study. Antimicrobial susceptibility testing and agr group typing were carried out for all strains; virulence gene (cna, seh, TSST-1 and PVL) typing results of the strains were obtained from a previous study. Pulsed-field gel electrophoresis (PFGE) was done on selected strains from the orthopedic ward. Relationship(s) between different typing methods used in the study was investigated, where a p value of <0.05 indicated significant association between typing methods. Results A total of 880 MSSA strains were included into the study. The strains were generally susceptible to most antibiotics, with most of them carrying cna and agr-I (51.6%, n=454; 39.8%, n=350, respectively). A total of 17 PFGE pulsotypes were identified using an 80% similarity cut-off value, where the main pulsotype (pulsotype E) consisted of 24 isolates (23.5%). agr-III strains were found to be usually positive for both cn and seh (p<0.05). In addition, some PFGE pulsotypes were also characteristic of certain virulence genes or agr groups. Conclusions We did not identify a dominant MSSA clone circulating in HCTM in 2009. Nevertheless, results from this molecular surveillance will provide good baseline data for the hospital's second S. aureus surveillance planned for the year 2020. © GERMS 2020.

Author Keywords
Agr typing; Aureus (MSSA); Methicillin-susceptible S; Molecular surveillance; PFGE; Virulence gene typing

Index Keywords
bacterial DNA, cefoxitin, ciprofloxacin, erythromycin, fusidic acid, gentamicin, penicillin derivative; antibiotic resistance, antibiotic sensitivity, Article, bacterial gene, bacterial strain, bacterial virulence, bacterium isolate, disease surveillance, DNA isolation, genetic profile, genotype, human, methicillin susceptible Staphylococcus aureus, methicillin susceptible Staphylococcus aureus infection, molecular typing, multiplex polymerase chain reaction, nonhuman, pulsed field gel electrophoresis

Correspondence Address
Neoh H.-M.; UKM Medical Molecular Biology Institute (UMBI), Cheras, Malaysia; email: huimin@ppukm.ukm.edu.my

Publisher: European Academy of HIV/AIDS and Infectious Diseases

ISSN: 22482997
Language of Original Document: English
Abbreviated Source Title: GERMS
2-s2.0-85086039508
Document Type: Article
Publication Stage: Final
Source: Scopus