MOLECULAR EVOLUTION OF MRSA IN A TERTIARY HOSPITAL

Lim King Ting 1,2, Yasmin Abu Hanifah3, Mohd Yasim Mohd Yusof 3; Thong Kwai Lin 1,2*

1Microbiology Division, Institute of Biological Science, Faculty of Science, University of Malaya, 50603 Kuala Lumpur.
2Biomedical Science and Molecular Microbiology Laboratory, UMBIO, A407, Institute of Graduate Studies, University of Malaya, 50603, Kuala Lumpur.
3Department of Medical Microbiology, Faculty of Medicine, University of Malaya, 50603 Kuala Lumpur.
*Corresponding authors. E-mail address: thongkl@um.edu.my

Methicillin-resistant Staphylococcus aureus (MRSA) is one of the main bacterial pathogens responsible for nosocomial infections in Malaysia. The objective of this study was to investigate the MRSA trends and their evolution in University Malaya Medical Centre (UMMC) between the years 2003, 2004, 2007 and 2008. One hundred fifty-four MRSA strains were characterized by MLST, spa and mec-associated dru typing. Among the 154 strains, 29 different dru, 15 spa and 8 MLST types were identified. Seven sequences types (STs) (ST239, ST22, ST5, ST6, ST80, ST573 and ST241) were identified among 2007-08 strains, although only ST239 and ST20 were observed among 2003 strains. Ten dru types (dt11am, dt13j, dt15n, dt13q, dt13n, dt13p, dt13f, dt13ao, dt12j, dt7v) shared the same MLST-spa types with dt13d, suggesting that these MRSA clones might have evolved from ST239-t037-dt13d. In conclusion, our data showed that ST239-t037-dt13d clone and other MRSA clones in 2003 were replaced by ST239-t037-dt13g and other new emerging spa and dru types.