0803

High-risk ST772-MRSA lineage in South Asia: potential for global dissemination

Y.D. Bakthavatchalam[1,*], K. Vasudevan[2], P. Babu[3], E. Munusamy[3], B. Veeraraghavan[4]

[1] *Christian Medical College, Clinical Microbiology, Vellore, Tamil Nadu, India*
[2] *Christian Medical College, Vellore, India*
[3] *Christian Medical College, Clinical Microbiology, Vellore, India*
[4] *Christian Medical college, Clinical Microbiology, Vellore, India*

Background: Methicillin resistant *Staphylococcus aureus* (MRSA) is a clinically important pathogen with an abundance of virulence factors and multi-drug resistance, that are essential for survival within host. In recent decades, a community-acquired lineage, ST772-MRSA are being frequently reported cause of hospital-onset infections and outbreak. ST772-MRSA is currently circulating in South Asia, Australia and Europe. We hypothesis that the presence of multiple resistance determinants in ST772-MRSA, is the driver for potential adaptation and evolution. Genome-wide association study was conducted to understand the evolutionary events within ST772-MRSA and propensity for dissemination.

Methods and materials: Whole genome sequencing was performed for ST772-MRSA ($n = 33$), isolated from blood culture during 2013-2018. Global collection ST772 *S. aureus* genome ($n = 120$) were retrieved from National Center for Biotechnology Information (NCBI) and European Nucleotide Archive (ENA) databases. Core genome alignment and variant calling analysis were carried out using parsnp and snippy pipeline respectively. Divergence and evolution of ST772 *S. aureus* were estimated using phylogenetic BEAST analysis.

Results: ST772-MRSA was emerged in the early 1970s. In this lineage, *mec*A gene was identified on a short variant (5C2) or composite (5C2&5) SCC*mec* V element. Among the investigated genome, 90% carried Panton Valentine leukocicidin (PVL) toxin, which is encoded by the prophage Φ-IND772PVL. vSaα, vSaβ and vSaγ pathogenicity islands carrying exotoxins, enterotoxin gene cluster and exfoliative toxin were identified on all ST772-MRSA genome. Mutation in *par*C (S80Y) and *gyr*A (S82L), contributed for quinolone resistance in 72% of the genome. A copy of *dfr*A gene, encoding for trimethoprim resistance was identified on all the core genome. An integrated resistance plasmid (IRP) containing resistant determinants for beta-lactam (*bla*Z), aminoglycosides (*aph*A3-*sat*-*aad*E), macrolide (*msrA*, *mphC*), and bacitracin (*bac*A, *bac*B) was found in all MRSA genome. Another landmark event, is the acquisition of IRP, in the early 1990s, resulted in a highly distinct uniform clade comprised of multi-drug resistant variant. Most of this variant mediated intercontinental transmission is typically associated with travel from South Asia.

Conclusion: Acquisition of IRP contributed for the emergence of ST772-MRSA lineage, as a multi-drug resistant variant. Genetic changes associated with the adaptation and increasing multi-drug resistance in ST772-MRSA, represents the potential threat for global dissemination.

https://doi.org/10.1016/j.ijid.2020.09.868

0804

Knowledge, attitude and practice of influenza vaccination among adults attending Pusat Kesihatan Universiti (PKU) UPM

N. Mohd Taib[1,*], E.M. Mohd Mundir[2], S.N.A. Abdul Manan Ponan[2], H.Y. Kuay[2], S.N. Masri[1], T.Z.M. Tengku Jamaluddin[1]

[1] *Universiti Putra Malaysia, Medical Microbiology and Parasitology, Serdang Malaysia*
[2] *Universiti Putra Malaysia, Medical Doctor Programme, Serdang, Malaysia*

Background: Influenza is a contagious respiratory illness caused by influenza viruses which range from mild to severe illness. It is one of the leading causes of communicable disease in Malaysia. Despite awareness campaigns regarding the disease and its prevention, the vaccination rates are still low. This study aimed to evaluate knowledge, attitude and practice levels among attendees at Pusat Kesihatan Universiti (PKU) UPM.

Methods and materials: A cross-sectional study was conducted among adults in Pusat Kesihatan Universiti (PKU) UPM. Attendees to PKU were randomly sampled and were required to fill in a self-administered questionnaire. Data was analysed by IBM Statistical package for Social Science (SPSS) Version 25. Chi-square bivariate analysis were used to measure the association between the variables.

Results: A total of 235 adults participated in this study. Most respondents were female ($n = 147$, 62.6%), within the age group 18-29 years old ($n = 144$, 61.3%), Malays ($n = 194$, 82.6%) and Muslim ($n = 196$,83.4%). The study revealed respondents had good knowledge ($n = 181$, 77.0%), good attitude ($n = 163$, 69.4%) but poor practice ($n = 105$, 44.7%) towards influenza and vaccination. More than 80% had correct knowledge regarding influenza and the severity of the disease, availability of influenza vaccine, effectiveness of influenza vaccine against the disease and the risk of non-vaccinated. There is a significant association between knowledge towards attitude regarding influenza and vaccination ($p < 0.05$). There is no significant association between knowledge towards practice regarding influenza and vaccination ($p > 0.05$). However, there is a significant association between attitude towards practice regarding influenza vaccination ($p < 0.05$).

Conclusion: These results indicate good knowledge influences attitude towards influenza vaccination and good attitude influences practice towards influenza vaccination. The uptake of influenza vaccine in this study was not influenced directly by the level of knowledge. Attitude modification towards influenza vaccination is necessary to improve the vaccine uptake.

https://doi.org/10.1016/j.ijid.2020.09.869