

Molecular epidemiology: a valuable tool for determination of emerging and clonality of methicillin resistant *Staphylococcus aureus* (MRSA)

ABSTRACT

Methicillin-resistant *Staphylococcus aureus* (MRSA) is one of the leading nosocomial pathogen that is also emerging as a zoonotic pathogen. In this review, it was observed that rapid emergence of new MRSA clones at a higher frequency has ushered in a new knowledge on the clonality and epidemic potentials of MRSA. Secondly, the success of treatment and management of MRSA infection is threatened by the diversity in the clonal types. This is because different clones harbours different antibiotics resistance characteristics and as such respond differently to treatment. Furthermore, clonal replacement of hospital-acquired MRSA with community -acquired MRSA has also been observed. Thirdly, the transmission of MRSA even though previously thought to be exclusively within the hospital setting through hand contact and nasal colonization has now spread to the community and in addition human to animal and animal to human transmission has also been observed. Similarly, pet owners, veterinarians and farmers have been described as high-risked group with potentials of becoming reservoirs of MRSA. Furthermore, the adoption of hand hygiene in healthcare setting have to a great extent reduced the incidence of MRSA in the hospital. And lastly, the advent of molecular typing such as Pulsed Field Gel Electrophoresis (PFGE), Multi Locus Sequence Typing (MLST), Staphylococcal protein A typing (Spa typing) and Double Locus Sequence Typing (DLST) have proven to be a useful tool in providing valuable information on the evolution and clonal diversity of MRSA. These in turn help researchers to answer some pertinent questions on the epidemiology of MRSA.

Keyword: Clonality; Emergence; epidemiology; Methicillin resistant *Staphylococcus aureus*; Molecular typing