

## Identification of clonal lineages of *S. aureus* isolates from diabetic foot ulcer

**Kavitha S**

Manipal University, India

*Staphylococcus aureus* is known to cause a range of human diseases and is typically associated with skin infections, bacteremia, endocarditis, and wound and joint infections. Antibiotic resistant clones of *S. aureus* are a major cause of public health concern and MRSA (Methicillin Resistant *S. aureus*) have emerged as an important pathogen identified in hospitalized patients. In particular, certain clones armed with potential virulence factors and drug resistance are prone to cause more invasive diseases than others. Molecular methods are now universally applied to determine genetic diversity among pathogens to effectively characterize the strains as accurate strain typing is crucial in studies pertaining to clinical microbiology and epidemiology, especially while establishing national and global databases. Strain differences among the *S. aureus* isolates at the molecular level has been demonstrated using various molecular typing tools including pulsed-field gel electrophoresis (PFGE) and Multilocus sequence typing (MLST), *spa* typing and Multiple-locus variable number tandem repeat analysis (MLVA) in humans, animals, food sources and other environmental settings. MLST elucidates taxonomic relationship between strains based on sequence similarities, provides unambiguous and comparable sequence information across different laboratories and hence considered to be an operational genotyping technique especially for *S. aureus*. DNA sequence information from seven housekeeping genes are compared with reference sequences available in public database to arrive at sequence types in MLST analysis. In this study, we characterized thirteen *S. aureus* isolates associated with diabetic foot ulcer based on their antibiogram profile, Minimum Inhibitory Concentration (MIC) values, biofilm formation and genotyping methods including MLST and MLVA. One of the genes associated with biofilm formation (*icaAB* gene) was amplified using polymerase chain reaction and methicillin resistance was confirmed by detection of *mecA* gene. The results from MLST and MLVA analysis are compared and the effectiveness of these in discriminating *S. aureus* isolates from diabetic foot ulcer will be discussed.

kavithamicro11@gmail.com