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Confirmation and molecular characterization of hospital and community acquired methicillin resistant *Staphylococcus aureus*

Purpose: Methicillin Resistant *Staphylococcus aureus* (MRSA) has spread globally in both hospital and community settings posing a major threat to global health. Increasing prevalence of healthcare-associated MRSA (HAMRSA) infections is most often based on wide dissemination of particular epidemic clonal lineages of the S. aureus population. Use of different methods of DNA-based molecular typing will reveal human-adapted MRSA and have been widely applied for studying MRSA.

Methods:

- This is a prospective study for 2 yrs. with a total target sample size of 600.
- Clinical S aureus isolates from inpatients/outpatients=200
- Corresponding nasal sampling from clinical MRSA positive patients =200
- Community nasal S.aureus isolates=200
- S.aureus isolates from clinical specimens like wound swabs, tracheal aspirates, bronchial lavage, cerebrospinal fluid, brain abscess pus, blood, shunt tips, central line tips etc submitted to Neuromicrobiology laboratory NIMHANS formed the study material
- Corresponding nasal sampling of the patients with MRSA isolates in the above clinical specimens was performed
- Isolation, identification and confirmation of the S aureus as MRSA was performed by phenotypic laboratory methods as per CLSI guidelines

Molecular characterization: PCR I - 16srRNA (Staphylococcus genus specific), nuc (S.aureus species specific) and mecA (determinant of methicillin resistance) genes PCR II - SCCmec typing: SCCmec typing of the MRSA isolates to classify them as HA (Type I, II,III) and CA (Type IV, V) MRSA.

Biography

Veena Kumari HB has completed M.D Microbiology, and been serving as Additional Professor in the Department of Neuro microbiology, NIMHANS, with more than15 years of experience in this discipline She has more than 20 papers in reputed journals and has been serving as Member Secretary, Hospital Infection Surveillance System of the Institute.

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