ABSTRACT

*Staphylococcus* is known for its inherent ability to live in harmony with the human host and also to switch from the life style of a commensal to that of a pathogen under various host-driven conditions. On account of its uniqueness in acquiring resistance to virtually all the antibiotics employed in clinical practice, *Staphylococcus* has become a subject of immense clinical and research interests. The present investigation was an attempt towards evaluating the scenario of drug resistance in clinical isolates of staphylococci from the city of Mysuru, Karnataka state, South India. Our study conducted with the participation of three major hospitals in Mysuru documents many disturbing trends in the epidemiology of drug-resistant staphylococci from this geographical region. We report a very high rate (86.9%) of methicillin resistance among the staphylococcal isolates analyzed in the study. Epidemiological typing of a cluster community-associated methicillin resistant *Staphylococcus aureus* (CA-MRSA) identified four sequence types (ST2371, ST22, ST772 and ST8). The majority of the isolates were of ST2371-t852-SCCmecIV [sequence type-*spa* type-SCCmec type], a lineage which has not been reported previously from Asia. We also document for the first time, the appearance of the pandemic CA-MRSA clone, USA300 (ST8-t008-SCCmec IV) from India. Furthermore, multidrug resistance (MDR) was conspicuous (77.8%) among CA-MRSA isolates which are traditionally known for their susceptibility to non-beta-lactam drugs. This indeed signifies a growing challenge for the therapeutic options for treating CA-MRSA infections.

With regard to coagulase negative staphylococci, we observed ‘true significance’ of *S. haemolyticus* isolated from cases of neonatal septicaemia. This reiterates the increasing importance of coagulase negative staphylococci in causing bacterenmia in infants. The other important highlight of the study is the characterization of a collection of linezolid-resistant isolates. Linezolid is an entirely synthetic antibiotic and a drug of last resort for the treatment of infections caused by MDR strains of Gram-positive bacteria. We have come across *S. haemolyticus* strains with transmissible and multiple mechanisms of linezolid-resistance. The strains harbored the multiantibiotic resistance gene, *cfr* and mutations (G2576T in 23S rDNA and Met156Thr in L3 ribosomal protein)
which confer linezolid-resistance. This is for the first time $cfr$-carrying clinical isolates are reported from India. It is of great concern as the low fitness cost of this gene makes bacterial cells to retain it even in the absence of the selection pressure imposed by the antibiotic. Moreover, the unstable genetic environment of this gene can facilitate its easy spread to susceptible population and other pathogenic bacteria. Our study emphasizes the need for strict surveillance of $cfr$-carrying strains in the healthcare settings in India. Judicious use of linezolid in clinical practice is important to preserve its clinical utility.