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Emergence of Methicillin-Resistant *Staphylococcus aureus* ST239 with High-Level Mupirocin and Inducible Clindamycin Resistance in a Tertiary Care Center in Chennai, South India

Methicillin-resistant *Staphylococcus aureus* (MRSA) ST239 is probably the most predominant clone of MRSA causing hospital-acquired infections (4). Different clones of MRSA ST239 have been reported: Hungarian, Brazilian, Portuguese, and Viennese clones (4). MRSA ST239 is an invasive clone of multidrug-resistant (MDR) MRSA producing potential exotoxins, causing a wide range of life-threatening infections. It is reported that MRSA ST239 strains from Asian countries are resistant to additional antibiotics compared to their counterparts in Western countries. MRSA ST239 strains with varying resistances and susceptibilities to mupirocin, amikacin, and cotrimoxazole have been reported from different parts of the world (4). There is paucity of data on MRSA ST239 from India, where the prevalence of MRSA is high (6). We studied the prevalence, antibiotic resistance, and virulence of MRSA ST239 among clinical isolates of MRSA causing skin and soft tissue infections in a tertiary-care hospital in Chennai, South India.

A total of 50 nonrepetitive isolates of MRSA causing various skin and soft tissue infections (cellulitis [$n = 18$], infected wound [$n = 12$], furuncle and carbuncle [$n = 9$], abscess [$n = 9$], and impetigo [$n = 2$]) collected between January and March 2011 were included in the study. The study was approved by the Institutional Ethical Committee. High-level mupirocin resistance was detected by using mupirocin (200 μg) disc diffusion test, the agar dilution MIC method, and *ileS2* gene PCR (9). Inducible clindamycin resistance was detected by the disc approximation test (D-test). Staphylococcal cassette chromosome *mec* element (SCC*mec*) typing (1) and *spa* typing (5) were done for all MRSA isolates. MRSA isolates with SCC*mec* III and *spa* type t037 were tested for multilocus sequence type (MLST) (3). MRSA ST239 isolates were further tested for an array of virulence genes (8). Standard strains of *S. aureus* (ATCC 43300, ATCC 25923, COL, N315, JCSC2724, MW2, and WIS) were used as controls for detection of SCC*mec* types and virulence genes.

The major SCC*mec* type was found to be SCC*mec* V-25 (50%), followed by the SCC*mec* III-16 (32%), SCC*mec* I-8 (16%), and SCC*mec* IV-1 (2%). All the MRSA isolates tested were sensitive to vancomycin and linezolid. Resistance was observed for other classes of antibiotics, including tetracycline (78%), cotrimoxazole (66%), ofloxacin (38%), rifampin (34%), and amikacin (32%). All the 16 MRSA isolates with SCC*mec* III were found to be t037 and ST-239. The other major *spa* types found in this study were t064 ($n = 16$) and t657 ($n = 9$). All MRSA ST239 isolates showed high-level mupirocin resistance (MIC > 512 mg/liter/*mupA*$^+$), inducible clindamycin resistance, and high-level methicillin resistance (MIC = 256 mg/liter). The AST results of MRSA ST239 isolates revealed that they were MDR (Table 1). They were found to cause all kinds of skin infections included in this study, except abscesses, and were positive for an array of virulence genes (Table 1). Although there have been individual reports of mupirocin resistance (7) and inducible clindamycin resistance (2) among MRSA, this is the first report on emergence of hospital-acquired MRSA with both mupirocin and inducible clindamycin resistance. The increasing efficacy of MRSA in extending its resistance to the effective antibiotics makes treatment challenging and expensive.

In conclusion, to the best of our knowledge, HAMRSA with both mupirocin and inducible clindamycin resistance has not been reported elsewhere. The emergence of such invasive MDR MRSA with extended antibiotic resistance has to be addressed to prevent increasing morbidity and mortality.

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TABLE 1 Characteristics of mupirocin-resistant MRSA ST239 isolates ($n = 16$) in this study

Characteristic	Description
Clinical manifestations	Skin and soft tissue infections: wound infection ($n = 6$), carbuncle ($n = 3$), furuncle ($n = 3$), impetigo ($n = 2$), and cellulitis ($n = 2$)
Patient age and category	All ages, inpatients (HAMRSA)
Antibiotic resistance profile	Sensitive to vancomycin, fusidic acid, and linezolid; resistant to amikacin, cotrimoxazole, erythromycin, mupirocin, netilmicin, ofloxacin, oxacillin, rifampin, and tetracycline; erythromycin induced clindamycin resistance (iMLSB); oxacillin MIC, 256 mg/liter; mupirocin MIC, ≥512 mg/liter[a]
Virulence gene profile	Enterotoxins: *sea* and *sek*; hemolysins: *hla*, *hld*, and *hlg*; leucocidins: none; innate immune evasions: *chp*, *scn*, and *sak*
Resistant determinants	*mec*A; SCC*mec* type III (HAMRSA); *ileS2*[a] (*mup*A) gene, mupirocin-resistant gene; *erm*A, erythromycin resistance and inducible clindamycin resistance
Molecular typing	Accessory gene regulator (*agr*), type I; *spa* type, t037; MLST, ST239

[a] High-level mupirocin resistance.

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