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A COMPARITIVE STUDY OF COMMUNITY – AND HEALTH CARE ASSOCIATED METHICILLIN RESISTANT *STAPHYLOCOCCUS AUREUS* INFECTIONS

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ABSTRACT

Methicillin resistant *Staphylococcus aureus* (MRSA) is now a worldwide phenomenon. The exceptional ability of this pathogen to colonize patients and staff has resulted in widespread epidemics in hospitals. Nowadays reports of community associated MRSA (CA-MRSA) in patients without identifiable risk factors point to an ongoing epidemiological shift. The present study was conducted in the department of Microbiology, Pt BD Sharma, PGIMS, Rohtak. During one year study period, 575 *S.aureus* strains were isolated from various clinical samples out of which 185(32.17%) were MRSA. Out of these 34(18.38%) were CA-MRSA and 151(81.38%) were hospital acquired MRSA (HA-MRSA). Previous exposure to antimicrobial agents, presence of invasive devices and past history of similar disease were important risk factors for HA-MRSA and CA-MRSA cases. In HA-MRSA, most common underlying chronic disease was diabetes mellitus (27.8%). A high rate of multidrug resistance was seen in HA-MRSA in comparison to CA-MRSA strains. Therefore, there is a clear need to keep track of the MRSA infections and to formulate guidelines for empirical therapy to minimize spread of MRSA before situation worsens.

KEYWORDS: **MRSA,CA-MRSA,HA-MRSA**

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INTRODUCTION

Multidrug resistance is now the norm among common pathogens. *S.aureus* is perhaps the pathogen of greatest concern because of its intrinsic virulence, its capacity to adapt to different environmental conditions.[1]

Methicillin – resistant S.aureus (MRSA) first emerged as a nosocomial pathogen in early 1960's.[2,3] MRSA is now a worldwide phenomenon and its incidence continues to rise. The exceptional ability of this pathogen to colonize patients and staff has resulted in widespread epidemics in hospitals. Established risk factors for MRSA infection include recent hospitalization, residence in a long term care facility and injection drug usage.[4,5]

Nowadays MRSA can no longer be regarded as a purely nosocomial pathogen.[6] Recent reports of community associated MRSA (CA-MRSA) in patients without identifiable risk factors point to an ongoing epidemiological shift. Dissemination of MRSA in the community can lead to an expanding reservoir for this pathogen making these infections difficult to control and eradicate. Thus antibiotic policies of CA- MRSA are equally important.[7]

The present study was carried out to compare community and health care associated MRSA infections among patients attending this institute and to determine the antimicrobial sensitivity pattern of both CA-MRSA and HA-MRSA.

MATERIALS AND METHODS

The study was conducted in the department of Microbiology, Pt BDS PGIMS, Rohtak. Staphylococcal isolates obtained by standard microbiological procedures from various clinical samples of patients attending OPD and admitted in various wards were included in the study over a period of one year. Relevant clinical history of the patient was taken and routine clinical examination was carried out. The various samples taken were pus, urine, blood, and respiratory samples like sputum, throat swabs, BAL, endotracheal aspirates, vaginal swabs, CSF and other drain fluids. All the samples were collected using sterile aseptic precautions. Culture and identification was done by standard conventional techniques.[8]

Cases were classified as CA-MRSA and HA-MRSA depending on the risk factors. HA-MRSA cases were identified as patients with:

1. An MRSA infection identified after 48 hrs of admission to the hospital.
2. A history of hospitalization, surgery, dialysis or residence in a long term care facility within one year of MRSA culture date.
3. A permanent indwelling catheter or percutaneous medical device (e.g tracheostomy tube, gastrostomy tube or Foley's catheter) present at the time of culture.
4. A known positive culture for MRSA prior to study period.

Cases that had none of the above features were classified as CA-MRSA.

All the isolates obtained from various samples were subjected to antibiotic susceptibility testing using Kirby-Bauer disc diffusion method on Muller Hinton Agar.[10,11] The antimicrobial susceptibility was done in two stages. In the first stage oxacillin (1mcg) and cefoxitin (30mcg) were included. Cefoxitin was used as a surrogate marker for detection of mecA gene mediated methicillin resistance.[10]In the second stage all the MRSA isolates were further tested for the antimicrobial agents by Kirby-Bauer disc diffusion method approved by CLSI guidelines[10]. *S.aureus* ATCC 25923 was employed as standard control strain.

RESULTS

During the study period of one year from various clinical samples 575 S.*aureus* strains were isolated. Out of them 185 (32.17%) were MRSA. Of these 34(18.38%) were CA-MRSA and 151(81.62%) were HA-MRSA. More number of CA-MRSA(61.76%) were isolated from out patients while HA-MRSA were isolated in more number (86.11%) from

in-patients. The isolation rate of CA-MRSA and HA-MRSA is shown in Table 1.

Table I
Isolation rate of CA-MRSA and HA-MRSA from various specimen

SPECIMEN	No(%) of CA-MRSA isolates	No.(%)of HA-MRSA isolates
Pus	21(61.76)	59(39)
Urine	4(11.76)	32(21.19)
Blood	3(8.82)	40(26.49)
Sputum	2(5.88)	8(5.29)
Throat swab	1(2.94)	0(0)
BAL/tracheal aspirates	0(0)	6(3.97)
CSF	0(0)	3(1.98)
Pleural/ascitic fluid/drain fluid	3(8.82)	3(1.98)

In HA-MRSA cases, diabetes mellitus was found to be the most common underlying chronic disease (27.8%) followed by chronic dermatological conditions (25.16%). Among all the risk factors, previous exposure to antimicrobial agents was found in maximum number of patients(97.35%) followed by presence of invasive devices (70.19%) while CA-MRSA cases had only past history of similar diseases and previous exposure to antimicrobial agents as risk factors. Table 2 shows the susceptibility pattern of CA-MRSA and HA-MRSA to various antimicrobial agents.

Table II
Antimicrobial susceptibility of CA-MRSA and HA-MRSA to various antibiotics

ANTIMICROBIAL AGENTS	No.(%) of CA-MRSA Susceptible	No.(%) of HA-MRSA Susceptible
Erythromycin	21(61.76)	69(45.69)
Clindamycin	30(88.23)	66(43.7)
Quinopristin/Dalfopristin	31(91.17)	131(86.75)
Gentamycin	30(88.25)	102(67.54)
Amikacin	29(85.29)	113(74.83)
Ofloxacin	29(85.29)	92(60.9)
Levofloxacin	30(88.23)	108(71.52)
Gatifloxacin	28(82.35)	117(77.48)
Sparfloxacin	28(82.35)	113(74.83)
Pefloxacin	30(88.23)	92(60.9)
Norfloxacin	4(100)	28(87.5)
Doxycyclin	25(73.52)	108(71.52)
Trimethoprim/sulfamethoxazole	28(82.35)	91(60.26)
Rifampicin	30(88.23)	131(86.75)
Mupirocin	32(94.12)	136(90)
Fusidic acid	29(85.29)	112(74.17)
Nitrofurantoin	4(100)	29(90.62)
Vancomycin	34(100)	151(100)
Linezolid	34(100)	151(100)

DISCUSSION

S.aureus is an important bacterial pathogen and a major cause of nosocomial infections including pneumonias; post operative wound infections, infections of the skin and soft tissue, bacteraemia and other infections. Widespread outbreaks of nosocomial infections by MRSA have renewed the interest in this species.[2]

The epidemiology of MRSA has continued to evolve since its first appearance more than four decades ago. Initially there were sporadic reports of methicillin resistance amongst nosocomial *S.aureus* isolates but later MRSA became a well established hospital acquired pathogen with a few reports of community acquired isolates.[12] Recent studies report an increased prevalence of community acquired MRSA with different risk factors compared to the earlier investigations from Detroit which first reported community acquired MRSA.[13]

Our study showed the prevalence of MRSA to be 32.17% among all *S.aureus* isolates from various clinical samples. Many workers have found out the prevalence of MRSA from various parts of the world at different times. In 1990, Wenzel et al reported 15% of all *S.aureus* isolates to be resistant to methicillin. Similar reports have been cited by various authors from different parts of the world.[14]

In the cohort with *S.aureus* infection studied by Groom et al 55% had an MRSA infection. They have also shown that proportion of MRSA isolates in the same population increased substantially from 1989 to 1997. The high prevalence of MRSA might be due to the fact that the study was conducted only on the American Indian population. Low socio-economic condition, crowded housing condition and limited access to healthcare, which contribute to the high background rate of skin infections in this population.[15]

Dietrich et al had also found that the proportion of S.aureus cases attributable to MRSA steadily increased over the 5 years (1997-2001) from 2.7% to 9.3%. The lower isolation rate of MRSA as compared to our study may be due to the study population that they had considered in their study. They had reviewed the data of only the patients below 18 years, but in our study we have included patients of all age groups.[16]

In the study of Mathur et al in 1991 the prevalence of MRSA in a tertiary care hospital in Lucknow was found to be 32.8% which is consistent with our findings.[17]

In 1998, Chaudhary et al had reported that 23.8% were MRSA out of 400 strains of *S.aureus* isolated from various clinical samples in our institute. In these 12 years, there is a rise in prevalence rate of MRSA in our hospital from 23.8 % to 32.17%.[18]

The MRSA strains isolated from the patients were categorised as CA-MRSA and HA-MRSA on the basis of risk factors. The present study revealed that 18.38% of MRSA were CA-MRSA while 81.62% were HA-MRSA. The prevalence of CA-MRSA which was very low previously, has emerged as a pathogen causing infections among a large population both in community and hospitals.

Groom et al reported a very high prevalence rate of CA-MRSA (74%) among the MRSA isolated from American Indian Community.[15]Naimi et al in 2000 had a prospective comparison of CA and HA-MRSA cases in the United States. Among the MRSA infections 12% were classified as community associated, 85% were classified as health care associated and 3% could not be classified. Our data is very much closer to theirs.[9] Our study is also in concordance with the study by Gupta et al[19] and Vidhani et al.[20]

In our study we found that skin and soft tissue infections (SSTI) were the most common clinical syndromes associated with CA-MRSA (67.64%) and HA-MRSA (41.72%).Similar trends have been observed by Niami et al[9], Deitrich et al[16] and Huang et al.[21]

Among all the risk factors, past exposure to antimicrobial agents (97.35%) topped the list where HA-MRSA was concerned followed by history of hospitalization in the past one year (68.88%). Almost similar findings have been shown by Groom et al[20] and Srinivasan et al.[22]

Among CA-MRSA cases past history of similar disease and exposure to antimicrobial agents were found in 16% and 14%.

CA-MRSA and HA-MRSA differ significantly in their antimicrobial susceptibility pattern. In contrast to CA-MRSA strains HA-MRSA strains tend to be resistant to multiple classes of antimicrobial agents other than beta-lactams, since they possess the SCC MecII and III gene which is responsible for resistance to other classes of antimicrobials. In our study both CA and HA-MRSA were uniformaly sensitive to vancomycin and linezolid. A significant difference in the sensitivity to clindamycin was found i.e 83.23% vs 43.7% in CA and HA-MRSA respectively. Similar patterns have been shown by other studies also.[9,16,21]

Resistance to macrolide, lincosamide, streptogramin B (MLSB) antibiotics most commonly results from acquisition of erythromycin resistant methylase gene (erm gene) which encode enzymes that methylate the 23 SrRNA. The overlapping binding sites of macrolides,lincosamides and streptogramin B in 23 SrRNA account for cross resistance to the three classes of drugs.

For other groups of antibiotics also, the CA-MRSA was more sensitive in comparison to HA-MRSA strains. In our study, multidrug resistance was encountered in 67.54% of HA-MRSA and only 14.7% of CA-MRSA.

Many authors from India and abroad have reported multidrug resistance among HA-MRSA isolates.[9,16,21,23,24]

The phenomenon of MRSA has swept worldwide within a few decades. There is a clear need to keep track of the MRSA infections and to formulate guidelines for empirical therapy to minimize spread of MRSA before situation worsens. It is equally important to focus on antibiotic stewardship in order to reduce the evolutionary pressure for generation of yet more resistant pathogenic organism.

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