SKIN, SOFT TISSUE INFECTIONS AND THEIR MICROBIOLOGICAL PROFILE FROM A TERTIARY CARE HOSPITAL

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ABSTRACT

Background: Skin and soft tissue infections (SSTIs) are considered as diverse group of infections which may vary in microbial etiology and clinical presentation and ranges from simple, uncomplicated infections to severe, complicated picture. Causative organisms with antimicrobial resistance may worsen the situation.

Objectives: The aim of present study was to check the frequency and antibiotic sensitivity pattern of bacterial isolates causing SSTIs.

Methods: A retrospective study performed over a period of 3 years. Pus and wound samples were collected and were processed by using standard microbiological procedures. Confirmation of bacterial species was done by different biochemical tests. Antimicrobial susceptibility pattern (AST) was checked on Mueller-Hinton (MH) agar by disc-diffusion method according to CLSI guidelines.

Results: Among 2345 total samples, 63.1% were cultured positive. Percentage of gram-negative bacteria was 51.3% while 48.7& were gram positive. *E. coli* (33.7%) was most common organism among gram-negative and *S. aureus* (34.5%) was more prevalent among gram positive organisms. Linezolid and glycopeptides showed excellent susceptibility against gram-positive organism, while maximum resistance was observed against Co-trimoxazole and Fluoroquinolones among gram-negative isolates.

Conclusion: Changing trend of bacterial spectrum causing SSTIs along with increasing antimicrobial resistance becomes a serious health problem which limits the treatment options for such infections.

Key words: Skin and soft tissue infections, antimicrobial sensitivity testing, Clinical and Laboratory standard institutes, *Escherichia coli*, *Staphylococcus aureus*.

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INTRODUCTION

Skin and soft tissue infections (SSTIs) are considered as the main cause of morbidity, visits to emergency departments and increased in length of hospital stay.[1,2] Infections of skin and soft tissue usually results from invasions of microbes in skin and its surrounding structures. SSTIs are a communal and diverse group of infections and it usually ranges from superficial uncomplicated to complicated SSTIs. Consequently, this type of infection ranked third among various causes of sepsis in perspective of its frequency. Additionally, 24% of hospital acquired infections are because of this varied group of infections. SSTIs may vary in clinical demonstration, microbial spectrum, and complications. Risk factors which lead to hospital admission may include a history of some unusual exposures, speedily spreading infection, broader involvement site, non-responsive oral antibiotics, requirement of surgical debridement, comorbidities, or risk of systemic infection and sepsis. *Staphylococcus aureus* is an eminent causative microorganism responsible for purulent cellulitis.[3] *S. aureus* resistant to Methicillin (MRSA) accounted for more than 60% of skin and soft tissue infections which are usually community-associated.[4,5] It is difficult to assess the accurate incidence and rate of prevalence of SSTIs resulting from MRSA because in many patients, culturing of skin infections is not processed. Severity of infection and clinical presentation can vary from patient to patient.[6] Among gram-negative bacteria, *P. aeruginosa* and *E. coli*, are considered as the important causative agents of soft tissue infections. Additionally, it is also the point to ponder that such kinds of infection are mostly polymicrobial is respect of their causative agents.[7-9] Currently, it is observed that different gram-negative isolates which were not considered to cause any noteworthy infections are more common causative agents for SSTIs along with increasing antibiotic resistance.[10,11] Etiological agents causing SSTIs tends to change its diversity from MRSA which is a gram-positive coccus towards gram-negative organisms with considerable drug resistance profiles.[12,13] Therefore, the current study was designed to check the bacterial spectrum and antimicrobial sensitivity pattern of skin and soft tissue infections.

METHODS

This retrospective study was done at Pathology Department of Allama Iqbal Medical College, Lahore. The study duration was of three years, from 1st January 2020 to 30th April 2023. Inclusion Criteria: Only pus and wound swabs from both genders were included in the study. Exclusion criteria: Clinical samples other than pus and wound swabs were excluded from the study. Repetitive samples from the same patient were also excluded. Pus and wound swabs were taken from each patient who were suffering from skin and soft tissue infections by experienced staff nurses. Then the collected samples were sent to the microbiology laboratory for processing. Samples were cultured on blood agar, chocolate agar, and MacConkey agar. Inoculated culture plates were then incubated overnight aerobically at 37˚C. On the next day, the isolates were identified by using standard microbiological methods. Identification of gram-negative bacteria was done by using different biochemical tests including indole, citrate utilization, urease test, lysine decarboxylase test, motility tests, triple sugar iron agar, and API 20E. Meanwhile, gram-positive bacteria were identified based on Gram reaction, catalase test, hemolytic pattern, and coagulase test. Antibiotic sensitivity testing of isolated bacteria was done by Modified Kirby-Bauer disc diffusion method by using Mueller Hinton agar and interpretation was done according to the Clinical & Laboratory Standards Institute guidelines.

RESULTS

Total 2345 pus and wound swabs were collected over the study period of 3 years. Out of 2345 samples, (n=1481, 63.1%) yield positive growth. Among 1481, (n=759, 51.3%) were gram negative organisms while (n=722, 48.7%) were gram positive organisms.

Most common organism among gram negative bacteria were found to be *E. coli* (n=256, 33.7%), followed by *P. aeruginosa* (n=196, 25.8%) and *klebsiella* species (n=134, 17.7%). Minor gram-positive organisms accounted for (n=11, 1.4%) which included *Achromobacter, Aeromonas hydrophila, Morganella morganii* and *Pantoea* species (Figure 1)

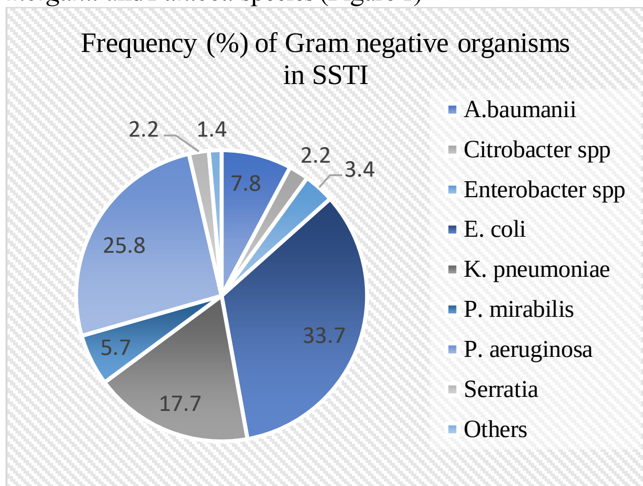

Figure 1: Distribution of Gram-negative organisms causing skin and soft tissue infections

Among gram positive organisms, *S. aureus* was found to be most common organism which accounted for (n=249, 34.5%), followed by MRSA (n=207, 28.6%) and *Enterococcus faecalis* (n=98, 13%). Minor organisms accounted for (n=10, 1.4%) which included Group F *Streptococci, S. epidermidis* and *S. pneumoniae* (Figure 2).

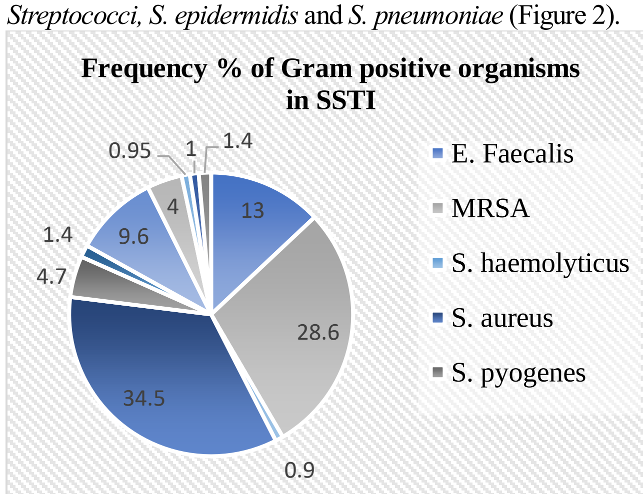

Figure 2: Distribution of Gram-positive organisms causing skin and soft tissue infections

Antibiogram of gram-negative organisms showed 54.5% susceptibility against Aminoglycosides while the maximum resistance was observed against Cephalosporins (73.4%), followed by Co-trimoxazole (71.1%) and Fluoroquinolones (65.9%) (Figure 3).

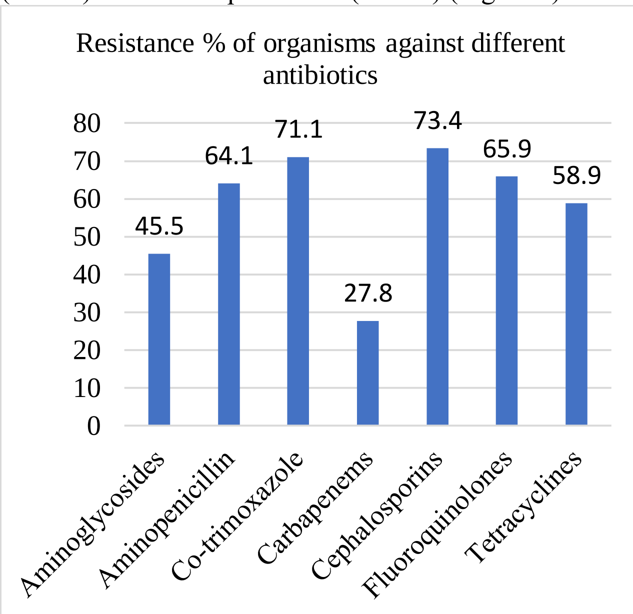

Figure 3: Sensitivity pattern of Gram-negative organisms

Among gram-positive organisms, Linezolid showed 100% sensitivity, followed by Glycopeptides (82.4%). While the maximum resistance was observed against Co-trimoxazole (72.9%), followed by Macrolides (70.2%) and Fluoroquinolones (59.1%) (Figure 4).

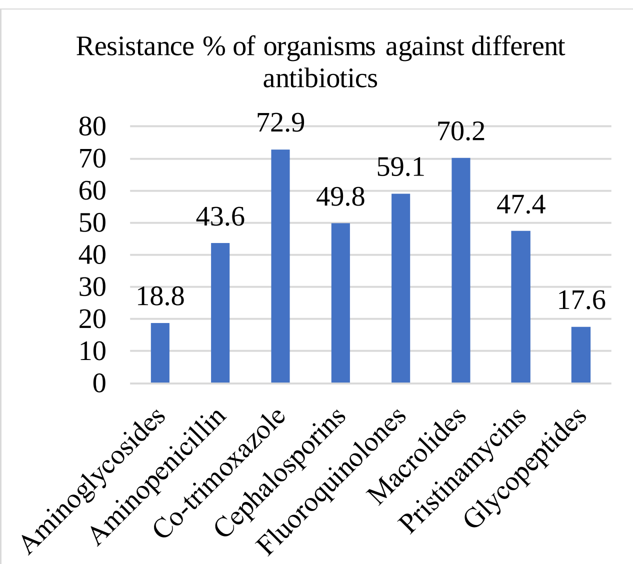

Figure 4: Sensitivity pattern of Gram-positive organisms

DISCUSSION

Ambulatory care visits for the treatment of skin and soft tissue infections have augmented to significant level over the past 20 years as reported by various studies.[14] The rate of incidence of SSTIs varied geographically with highest percentage in Spain and lowest in Russia and the reason of this variation may be the differences in diagnostic criteria and hospitalization policies among different countries.[15] In the current study, 2345 samples of pus and wound swabs were collected over the study period of three years. 63.1% samples yield positive growth which were in accordance with the study conducted in 2022 in which 54.9% positivity ratio were reported among skin and soft tissue infections.[16] Among 1481, 759 (51.3%) were gram negative organisms while 722 (48.7%) were gram positive organisms. Similar to our results, a study from Kazakhstan in 2020 also reported the gram-negative bacteria as the most common cause of SSTIs as compared to Gram-positive in a ratio of 5:3.[17]

In gram negative bacteria, 33.7% infections were caused by *E. coli* while *P. aeruginosa* accounted for 25.8% infections. Similar results were reported by Ioannou *et al*,[18] in which *E. coli* and *P. aeruginosa* were found to be most common causative agents causing SSTIs and these were also significantly linked with increasing rate of mortality, especially when they possess antimicrobial resistance.[19] Another study in 2022 also reported the *E. coli* and *pseudomonas* as the most frequent cause of bacterial SSTIs among gram negative bacteria.[17]

Among gram positive organisms, *S. aureus* was found to be most common organism which accounted for 34.5% infections of skin and soft tissue while 28.6% infections were caused by MRSA. S. Esposito, *et al* in 2022 reported 38.2% infections were caused by *S. aureus* which were similar to our results.[20] Another study done in 2020 also reported a higher frequency of SSTIs caused by *S. aureus* in 2 to 5 years of children in Colombia.[21] Though, there are few studies which stated dissimilar results in which Methicillin Resistant *S. aureus* were the main organisms causing SSTIs.[16,22]

When evaluating the changing trends of the sensitivity pattern of isolated bacterial strains against antibacterial drugs, it was observed that gram-negative bacteria showed 54.5% sensitivity to aminoglycosides, while 73.4% isolates were resistant to Cephalosporins, followed by Co-trimoxazole (71.1%) and Fluoroquinolones (65.9%). In accordance to our study, Sholpan S. Kaliyeva *et al* in 2022 reported the antimicrobial sensitivity pattern of gram-negative bacteria and reported about one-third of *Pseudomonas* strains were found to be resistant to fluoroquinolones while 60% resistance was experiential against cephalosporins. Likewise, *E. coli* showed decreased sensitivity against tetracyclines which were in accordance to our results in which 58.9% resistance were reported against tetracyclines.[17]

Among gram-positive organisms, Linezolid showed 100% sensitivity, followed by Glycopeptides (82.4%). While the maximum resistance was observed against Co-trimoxazole (72.9%), Macrolides (70.2%) and Fluoroquinolones (59.1%). Similar results were reported in 2022 in which 100% sensitivity was reported against Linezolid, while Glycopeptides also showed excellent susceptibility against gram positive organisms.[16] However, there is gradual increase in antibiotic resistance against commonly used antibiotics including cephalosporins and tetracyclines were observed in our study which were similar to various previous studies.[23-25]

LIMITATIONS

This was a retrospective, single-center study. The sources from where the data was collected are not consistent, and documentation may be varying or incompletely available. This may border the generalizability of our study findings.

CONCLUSION

Currently, an increasing trend in antibiotic resistance possess a serious threat. In current study, it was determined that *E. coli, Pseudomonas, S. aureus* and MRSA were the most frequent organisms causing SSTIs and the susceptibility rate of commonly used antibiotics for the treatment of such types of infections gradually declines over time. Because of this trend, the treatment options for SSTIS becomes limited. It is the need of an hour to revise national guidelines on the judicious antibiotic's usage, along with to increase awareness regarding sensible usage of antibiotics.

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AUTHOR'S CONTRIBUTIONS

FR: Concept, study design, reviewing manuscript, supervision lab work
IJ: Manuscript writing
GF: Supervision lab work
AS: Statistical analysis, reviewing manuscript
MB: reviewing manuscript
JNK: Performed lab work