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Dhvani Goti
Research Scholar, Bhagwan Mahavir College of Basic and applied Sciences, Bhagwan mahavir University, Surat, Gujarat, India

Dr. Sumita Dasgupta
Assistant Professor, Bhagwan Mahavir College of Basic and Applied Sciences, Bhagwan Mahavir University, Surat, Gujarat, India

Correspondence
Dhvani Goti
Research Scholar, Bhagwan Mahavir College of Basic and applied Sciences, Bhagwan mahavir University, Surat, Gujarat, India

Prevalence and distribution of etiological agent from open wound drainage

Dhvani Goti and Dr. Sumita Dasgupta

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Abstract
Wound infection due to various pathogenic microorganisms and the development of resistance to antibiotics is one of the major problems in the medical sector. This study aimed to identify the etiological agents of wound infection along with their antibiotic susceptibility. A total of 94 wound etiological agents were isolated from patients at microbiological laboratories for six months and analysed for the prevalence of bacterial as well as fungal isolates. The data was then compared with the survey data of the previous six months' bacteriological analysis reports.
Seven different bacterial strains were isolated from the wounds and also seven bacterial and 1 fungal strain were mentioned in the survey report. The prevalence of the microorganisms was then compared.

Keywords: Microorganisms, bacteria, prevalence, wound, resistance

Introduction
The human body's primary organ and first line of defense, the skin covers the exterior of the body. Illnesses related to skin account for 34% of occupational problems worldwide. Skin diseases are the most common sort of disorder that afflicts people of all ages (Koshta and Sharma, 2023) [8]. The microbial pathogens triggering problems related to infected inflammatory diseases, human skin and soft tissue infections (SSTIs) after or while undergoing trauma, burn injuries, and surgical procedures forming pus or purulent wound drainage are of major concern. Wound drainage can be characterized as white to yellow fluid composed of necrotic tissues, cellular debris, and dead white blood cells (Hatlen and Miller, 2021; Ziesmer, 2023) [1, 2]. The etiological agents will remain commensal till the skin remains intact. Any abrasion on the skin surface provides an open door for bacterial invasion leading to infection (Maharjan and Mahawal, 2020) [9]. Both anaerobic and aerobic microbes have been associated with wound infections, which are frequent in healthcare facilities and can lead to serious morbidity, prolonged hospital stays, and infections that are resistant to multiple drugs (Puca *et al*., 2021) [3]. Furthermore, drains alone may not be effective, leading to discomfort and an extended hospital stay (Muthu *et al*., 2020) [4]. The rapid emergence of antibiotic resistance among potentially hazardous bacterial isolates and its appearance are regarded as serious dangers to public health globally (Chinemerem Nwobodo *et al*., 2022) [5]. There are a plethora of infectious bacteria as well as fungi, which can not only cause purulent infections but make them incurable hence creating major problems for patients as well as for clinicians (Dhara *et al*., 2023) [7]. Due to widespread misprescription and insufficient antibiotic dosage regimens, multidrug-resistant Gram-negative bacterial strains such as extended-spectrum beta-lactamases producing *Enterobacteriaeae*, *Enterococcus spp*., *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *E. coli*, *Pseudomonas aeruginosa* and Gram-positive methicillin-resistant *Staphylococcus aureus* (MRSA) have been linked to pus infections in hospital settings across the past few decades (Prasanth *et al*., 2022) [6]. The objective of this study is to characterize the pyogenic bacteria from pus samples and to determine prevalence among all other species.

Materials and Methodology
Research design
We conducted a retrospective survey from records for microbial culture results reported in regional laboratories as well as isolated and identified the prevalence of the microorganisms from the purulent wound drainage (Shimekaw *et al*., 2022; Stout *et al*., 2023). No inclusion and exclusion criteria were put in the application.

Bacterial identification and characterization

Specimens from regional laboratories were transported to the microbiology department laboratory at our University campus, for analysis within 2 h of collection in sterile swab tubes filled with 1 ml of brain heart infusion broth (Duzyol *et al*., 2020) [2]. Standard microbiological methods of cultivation have been employed to isolate and characterize fungi and bacteria. The media has been prepared following Cheesbrough guidelines. About 0.1 mL of purulent wound drainage from the open wound site of patients, respectively were inoculated into Brain heart infusion broth medium and incubated for 24 h (Bobai *et al*., 2022) [14]. Positive cultures were gram-stained and sub-cultured onto MacConkey agar plates or Mannitol salt agar plates respectively (Karah *et al*., 2020) [15]. Isolates were identified and processed according to standard techniques by Vitek 2 analysis (Al-Gburi and Mohammed, 2020) [16]. Data was interpreted according to the CLSI guidelines. Major bacterial isolates were evaluated for their percentage prevalence and compared with prevalence data obtained from the survey analysis.

Data analysis

Data was analysed using Excel (Microsoft office, USA). Graphs or pie chart were used to show the prevalence and distribution of the isolated bacterial and fungal etiological agents against specimens (Pus, ear swab, sputum, stool, abscess, throat swab).

Results and Discussion

The results of the survey analysis are represented here in Figure 1. The inner pie chart indicates the percentage of the pus sample reported in the six months survey of the percentage of the various samples reported in the survey during the phase of 6 months, the percentage of the pus sample reported was 68%, which is higher than any other clinical samples. In support of our results, Barai *et al*., 2021 [18] also reported 30.2% wound/pus swab from the samples collected between the 2001 to 2021. Whereas study of Jangla and Naidu (2018) [17] reported only 5.5% of wound swab and pus samples. The results of the prevalence analysis among the bacterial and fungal isolates indicates the incredible prevalence of the *Staphyloccus auerus* (306), followed by the *Escherichia coli (137), Pseudomonas aeruginosa* (119), *Klebsiella spp.*(62), *Candida spp.* (27), *Streptococci spp*. (20), Coagulase negative S*taphylococcus aureus* (12), Methicillin resistant *Staphylococcus aureus* (6), *Aspergillus niger* (1), (Figure 1). Whereas, Out of all 94 isolated bacterial strain, we observed the 57 *Staphylococcus aureus*, 12 *Klebsiella pneumoniae*, 11 *Escherichia coli*, 11 *Pseudomonas aeruginosa*, 1 *Enterococcus faecalis*, 1 *Strenotrophomonas maltophilia*, 1 *Burkholderia spp.*, which again show the prevalence of the *Staphylococcus spp.* But have a distinct diversity among the etiology. Figure 2 is representing the percentage prevalence obtained from the experimental method.

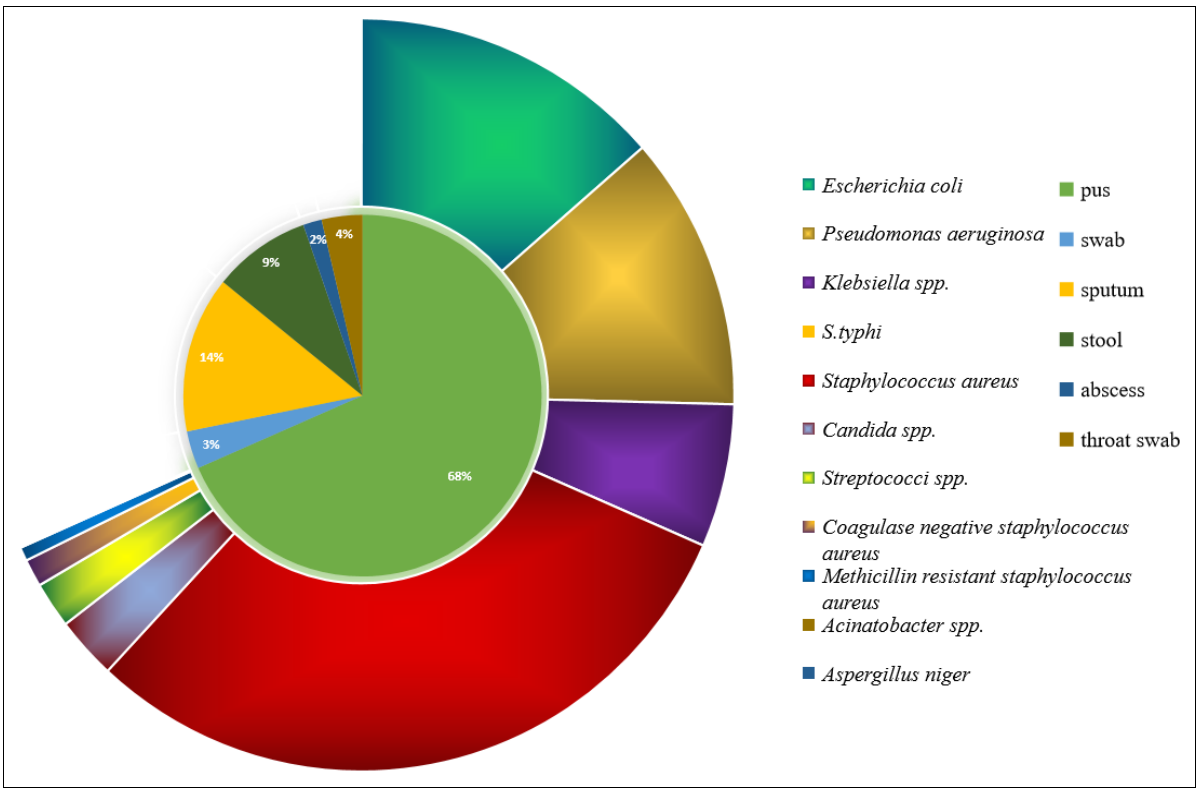

Fig 1: Prevalence analysis of etiological agents from pus by survey method

The study of Biswas *et al*., 2021 [19] on prevalence of methicillin resistant *Staphylococcus aureus* in pus samples in a tertiary care hospital of eastern India reported the 4.6% to 54.4% prevalence of methicillin resistant *Staphylococcus aureus*. Quayum *et al*., 2022 [20] reported the 93.4% proportion of *Staphylococcus aureus* followed by the *Klebsiella pneumoniae*.

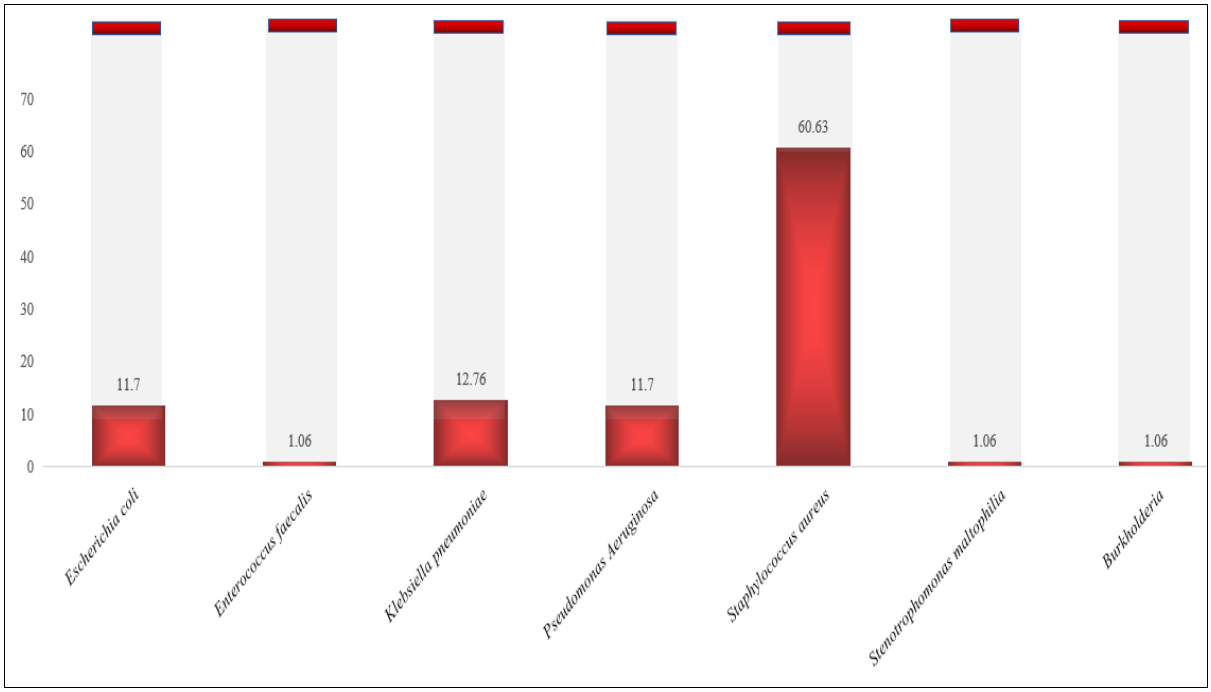

Fig 2: Prevalence analysis of etiological agents from pus by experimental method

Prevalence of multidrug-resistant (MDR) among the gram-negative bacteria causing pyogenic infections from June 2022-January 2023 reported *Pseudomonas aeruginosa* (42.9% cases), *Escherichia coli* (25.7%), and *Enterobacter* (7.1%) as the prevalent isolate, which is irreconcilable to our findings (Devi *et al*., 2023) [21].

Conclusion

Results of the present study showed the significant prevalence of microbial strains within the pyogenic organisms. Particularly prominent among them is *Staphylococcus aureus* isolates responsible for purulent wound drainage and soft skin and tissue infections. Findings of the present study will be helpful for the clinician and researchers for identifying the highly prevalent strain, responsible for frequent incurable infectious wound drainage. Specific drug can be used to target the particular strains to cure such infections. This also highlights the urgency of specialized antibiotic to treat such persistent infections before it reaches the chronic stage.

Conflict of Interest

The authors declare that no conflict of interests exist

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