

Investigation of Antibigram and Aerobic Bacteria in Pus Specimens

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Abstract

Introduction: The advent of antibiotic resistant bacterial species has made pyrogenic wound infection a significant source of morbidity. In order to identify the proper antibiotics for the patient's therapy, it is crucial to understand the antibiotic sensitivity pattern of the isolates from pus samples. In order to separate the aerobic bacteria from pus samples and analyse the pattern of their antibiotic sensitivity.

Method: 200 samples were received by the Department of Medicine, Apollo Hospital, Bhubaneswar, and they were processed in the lab in accordance with the prescribed procedures. The Kirby Bauer disc diffusion method was used to determine the antibiotic sensitivity of each and every bacterial isolate, and CLSI guidelines were followed for interpretation.

Result: Out of 200 samples examined, 140 (90.7%) had a positive culture and 40 (9.1%) had a negative culture. Gram negative bacilli made up 73.6% of the 140 culture-positive samples, whereas Gram positive cocci made up 26.2%. *Klebsiella pneumoniae* (29.4%), *Pseudomonas* (23.2%), *Escherichia coli* (14.3%), and *Proteus* (3.4%) made up the majority of GNB. Coagulase negative staphylococci (3.7%) and *Staphylococcus aureus* (21%) were identified. 88.1% of cultures were obtained as pure, while 11.7% were mixed. The majority of GNB were sensitive to fluoroquinolones, third-generation cephalosporins, piperacillin tazobactam, carbapenems, and aminoglycosides. 26 percent of *Staphylococcus aureus* isolates were MRSA.

Conclusion: Antibiotics must be used empirically and appropriately if multidrug resistant bacteria are to be avoided. Therefore, these investigations are necessary to understand the current situation of bacterial aetiology and their antibiogram.

Keywords: Pus, Antibiogram, Aerobic bacteria, *Klebsiella spp*, *Pseudomonas*, MRSA

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Introduction

A pyogenic infection results in localised inflammation, the production of pus that is typically brought on by one of the pyogenic bacteria, and the aggregation of dead leukocytes and the pyogenic bacteria that are collectively known as pus [1]. A wound infection caused by colonisation and bacterial flora growth can be serious and occasionally fatal [2]. Numerous

organisms, including bacteria, viruses, fungi, and protozoa, can cause wound infection. These organisms may coexist as polymicrobial communities, particularly in the wound margins and in chronic wounds [3]. There is frequently a mixed illness involving multiple bacterial species [4]. The most frequent bacteria that create pus are *Staphylococcus aureus*, *klebsiella*

species, *Pseudomonas*, *Escherichia coli*, and streptococci, with *Staphylococcus aureus* being the most prevalent [5]. Most of the countries where Methicillin-resistant *Staphylococcus aureus* (MRSA) is sought after have a high prevalence of the bacteria. One of the significant bacteria in hospital-acquired infections is MRSA [6].

Method

The Department of Medicine, Apollo Hospital, Bhubaneswar is where the current study was carried out. The study included 200 pus samples from diverse departments of the government hospital. Samples from people who are known to have diabetes and those who are currently taking antibiotics

were excluded. All of the samples underwent gramme stain processing before being inoculated on Blood, Chocolate, and Macconkey agar. The organism was isolated and identified in accordance with the lab's established protocol. The Kirby Bauer disc diffusion method was used for the antibiotic sensitivity test, and the zones were interpreted in accordance with CLSI recommendations.

Results

Out of 200 samples evaluated in the current investigation, 147 (90.7%) were culture-positive and 53 (9.2%) were culture-sterile. Table 1 presents the bacterial cultures.

Table 1: Organisms isolated in the culture

Organsims	Percentage of occurrence
<i>Klebsiella pneumoniae</i>	29.4%
<i>Pseudomonas aeruginosa</i>	23.2%
<i>Escherichia coli</i>	14%
proteus species	3.4%.
<i>Staphylococcus aureus</i>	21%
coagulase-negative <i>Staphylococci</i>	3.7%

86 (73.6%) of the 140 culture-positive samples were GNB, while 54 (26.1%) were GPC. *Klebsiella pneumoniae* (29.4%) made up the majority of the gram-negative bacilli, followed by *Pseudomonas aeruginosa* (23.2%), *Escherichia coli* (14%) and proteus species (3.4%). *Staphylococcus aureus* (21%) and coagulase-negative *Staphylococci* (CONS 3.7%) were the most prevalent gram-positive cocci. 200 culture-positive samples were tested, and of them, 140 (88.1%) contained only pure bacterial isolates, while 60 (11.7%) had mixed cultures including multiple bacterial isolates.

Aminoglycosides (Amikacin 88.3%, Gentamicin 71%) and carbapenems (Imipenem (86.1%), Piperacillin Tazobactam (85%), third-generation Cephalosporins (78%) and Fluoroquinolones (63%) were the antimicrobials that had the most effect on gram-negative bacteria. The following

antibiotics are effective against *Pseudomonas aeruginosa*: colistin (91%), aminoglycosides (88%), meropenem (77%) and piperacillin tazobactam (76.7%). Vancomycin and Linezolid, two antibiotics for Gram-positive cocci, were the most effective against *Staphylococcus aureus* (95% each), followed by Teicoplanin (91%), Clindamycin (83%), Quinolones (68.3%), and Erythromycin (65%). MRSA made for 26% of *Staphylococcus aureus*.

Discussion

The problem of bacterial antibiotic resistance is getting worse and worse all across the world. According to some, the development of bacteria toward medication resistance, particularly multidrug resistance, is inevitable since it is a specific manifestation of the irreversible evolution of bacteria as a whole [8].

Patients receiving empiric antimicrobial medication therapy frequently develop

antibiotic resistance. The selection of one antimicrobial agent over another is heavily influenced by the microbiology laboratory. When the patient specimens are delivered to the microbiology lab, the first causal organism is recognised and isolated. One can rationally select the class of antibiotics most likely to help the patient once the microbiological species causing the ailment has been identified [9]. In the current study, out of 524 samples cultured, 90.7% were culture positive and 9.1% were culture sterile, which is consistent with Rao et al. [1] who reported 89.47%, Vijetha Sharma et al. [10] (93% and 7%), Swathi Duggan et al. [11] (92% and 8%), whereas Asmabegaum Biradar et al. [12] (66.01% and 33.9%) Gram negative bacilli were isolated in 73.6% of our study's culture-positive samples and Gram positive cocci in 26.2% of these samples, which is consistent with the findings of Asmabegaum Biradar et al. [12] (58.01% and 41.98%), Jain et al. [7], Ghosh et al. [14], and Hanumanthappa et al. [13] (58.01% and 41.98%). According to Vijetha Sharma et al. [10], Dr. R. Sarathbabu et al. [15], Rajeshwar rao et al. [16], Kritu panta et al. [17] and K N Ravichitra et al. [18] who found *Klebsiella* species as the predominant organism present in wound infection, *Klebsiella pneumoniae* was the predominant isolate among gramme negative bacilli. *Pseudomonas* was the second most frequent isolate in the current investigation, which is consistent with the findings of Vijetha Sharma et al. [10] (20%), A. Ananth and S. Rajan et al. [19], Sankarankutty J. et al. [20] and Aizza Zafar et al. [21], while Farzana R. et al. [22] and Ehmer Alebram et al [23,24].

Conclusion

Antibiotics must be used empirically and appropriately if multidrug resistant bacteria are to be avoided. Therefore, these investigations are necessary to understand the current situation of bacterial aetiology and their antibiogram.

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