

# Study of Aerobic Bacterial Isolates and Their Antibiogram from Pus Sample in Government General Hospital, Guntur

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## ABSTRACT

**Introduction:** Pyogenic wound infection is a major cause of morbidity because of emergence of multidrug resistant bacterial strains. Hence it is important to know the antibiotic sensitivity pattern of the isolates from pus samples to choose right antibiotics for the management of patient.

**Aim:** To isolate the aerobic bacteria from pus samples and study their antibiotic sensitivity pattern.

**Methods:** 524 samples received in the Department of Microbiology, Guntur medical college were processed as per the standard guidelines in the laboratory. All the bacterial isolates obtained were tested for antibiotic sensitivity by Kirby Bauer disc diffusion method and interpretation was done as per CLSI guide lines.

**Results:** Out of 524 samples tested 476 (90.8%) were culture positive and 48 (9.2%) were culture sterile. Out of 476 culture positive samples 73.7% were Gram negative bacilli and 26.3% were Gram positive cocci. Majority of GNB were *Klebsiella pneumoniae* (29.5%) followed by *Pseudomonas* (23.3%), *Escherichia coli* (14.4%) and *Proteus* (3.5%). *Staphylococcus aureus* (22%) and Coagulase negative staphylococci (3.8%) were isolated. Pure cultures were obtained in 88.2% and mixed cultures in 11.8%. Most of the GNB were sensitive to aminoglycosides, carbapenems, Piperacillin Tazobactam, third generation cephalosporins and fluoroquinolones. MRSA were isolated in 27% of *Staphylococcus aureus* strains.

**Conclusion:** Empirical and appropriate use of antibiotics is very crucial in preventing emergence of multidrug resistant bacteria.

Hence there is a need for such studies to know the current status of bacterial etiology and their antibiogram.

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

## INTRODUCTION

Pyogenic infection causes local inflammation, formation of pus generally caused by one of the pyogenic bacteria, which results in aggregation of dead leukocytes as well as pyogenic bacteria commonly known as pus<sup>1</sup>.

Colonization with proliferation of bacterial flora may lead to wound infection which may be serious even sometimes leads to death<sup>2</sup>. Wound infection can be caused by variety of organism like bacteria, virus, fungi and protozoan and may coexist as polymicrobial communities especially in wound margins and in chronic wounds<sup>3</sup>. In many cases there is a mixed infection with more than one bacterial species<sup>4</sup>.

The most common pus producing bacteria are *Staphylococcus aureus*, *klebsiella* species, *Pseudomonas*, *Escherichia coli* and streptococci in which *Staphylococcus aureus* is the most common bacteria that produce pus<sup>5</sup>.

Methicillin resistant *Staphylococcus aureus* (MRSA) is prevalent in majority of the countries where it is sought for. MRSA is one of the important pathogens in hospital acquired infections<sup>3,6</sup>.

The spread of multidrug resistant bacterial pathogens has added as new angle

to the problem of wound infections. This is particularly worse in resource poor countries where sale of antibiotics is under poor control<sup>7</sup>.

The present study is conducted to isolate and identify aerobic bacteria from pus samples and to study antibiotic susceptibility pattern of the isolated organism.

## **MATERIALS & METHODS**

The present study was conducted in the department of Microbiology Guntur medical college, Guntur, Andhra Pradesh. A total of 524 samples of pus from various departments of the govt hospital were included in the study. Samples from known diabetic patients and those who are already on antibiotics were excluded.

All the samples were processed for gram stain and inoculated on Blood agar, chocolate agar and Macconkey agar. Isolation and identification of the organism was done as per the standard protocol in the lab. The antibiotic sensitivity test was performed by Kirby Bauer disc diffusion method and the zones were interpreted as per CLSI guidelines.

## **RESULTS**

In the present study out of 524 samples tested 476 (90.8%) were culture positive and 48 (9.2%) were culture sterile. Out of 476 culture positive samples 351 (73.7%) were GNB and 125(26.3%) were GPC. In gram negative bacilli majority of them were *Klebsiella pneumoniae* (29.5%) followed by *Pseudomonas aeruginosa* (23.3%), *Escherichia coli* (14.4%) and proteus species (3.5%). Among gram positive cocci *Staphylococcus aureus* (22%) and coagulase negative *Staphylococci* (CONS 3.8%). Out of 476 culture positive samples 420 (88.2%) were pure bacterial isolates and 56 (11.8%) were mixed cultures with more than one bacterial isolates.

Gram negative bacilli were more sensitive to aminoglycosides (Amikacin 88.4%, Gentamicin 72%) followed by carbapenems - Imipenem (86.2%),

Piperacillin Tazobactam (86%), third generation Cephalosporins (79%) and Fluoroquinolones (64%). *Pseudomonas aeruginosa* strains are sensitive to colistin (92%), aminoglycosides (89%), Meropenem (78%) and Piperacillin Tazobactam (76.8%).

Among Gram positive cocci *Staphylococcus aureus* were most sensitive to Vancomycin and Linezolid (96% each) followed by Teicoplanin (92%), Clindamycin (84%), Quinolones (68.4%) and Erythromycin (66%). Among *Staphylococcus aureus* 27% were MRSA.

## **DISCUSSION**

Antibiotic resistance among bacteria is becoming more and more serious problem throughout the world. It is said that evolution of bacteria towards resistance to antimicrobial drugs including multidrug resistance is unavoidable because it represents a particular aspect of general evolution of bacteria that is unstoppable<sup>8</sup>.

Antibiotic resistance emerges commonly when patients are treated with empiric antimicrobial drugs.

The microbiology laboratory plays a central role in the decision to choose a particular antimicrobial agent over others. First causative organism is identified and isolated when the patient specimens are sent to the microbiology laboratory. Once the microbial species causing disease have been identified, a rational choice of the class of antibiotics likely to work on the patient can be made<sup>9</sup>.

In the present study out of 524 samples cultured 476 (90.8%) were culture positive and 48 (9.2%) were culture sterile which correlate with Rao et al<sup>1</sup> who reported 89.47% and Vijetha Sharma et al<sup>10</sup> (93% and 7%), Swathi Duggan et al<sup>11</sup> (92% and 8%) whereas Asmabegaum Biradar et al<sup>12</sup> (66.01% and 33.9%) and Hanumanthappa et al<sup>13</sup> (56% and 44%) reported lower incidence.

In our study Gram negative bacilli were isolated in 73.7% and Gram positive cocci in 26.3% of culture positive samples

which correlate with Asmabegaum Biradar et al<sup>12</sup> (58.01% and 41.98%), Jain et al<sup>7</sup>, Ghosh et al<sup>14</sup> and Hanumanthappa et al<sup>13</sup>.

Among gram negative bacilli *Klebsiella pneumoniae* was the predominant isolate (29.5%) which correlates with Vijetha Sharma et al<sup>10</sup>, Dr R Sarathbabu et al<sup>15</sup>, Rajeshwar rao et al<sup>16</sup>, Kritu panta et al<sup>17</sup> and K N Ravichitra et al<sup>18</sup> who have found *Klebsiella* species as the predominant organism present in wound infection.

*Pseudomonas* was the second most common isolate (23.3%) in the present study which correlates with Vijetha Sharma et al<sup>10</sup> (20%), A. Ananth and S Rajan et al<sup>19</sup>, Sankarankutty J et al<sup>20</sup> and Aizza Zafar et al<sup>21</sup> whereas Farzana R et al<sup>22</sup>, Ehmer Al-ebaram et al<sup>23</sup> showed it as the most predominant organism.

Among gram positive cocci, *Staphylococcus aureus* was isolated in 22% of samples which correlates with Iffat Javeed et al<sup>24</sup> (23.2%), Swathi Duggal et al<sup>11</sup>, Tiwari et al<sup>25</sup>, Lee C Y et al<sup>26</sup> whereas Asmabegum Biradan et al<sup>12</sup> reported 41.9% and Vijetha Sharma et al<sup>10</sup> reported 8% only.

In the present study 88.2% were pure bacterial isolates and 11.8% were mixed bacterial isolates (polymicrobial) which correlates with Asmabegum Biradan et al<sup>12</sup>, Prajuli et al<sup>3</sup> (92% and 8%) and Mohanty et al<sup>27</sup> (85.8% and 14.2%) whereas Vijetha Sharma et al<sup>10</sup> reported 20% of mixed growth in their study.

The antibiotic pattern of GNB and GPC in the present study correlates with Vijetha Sharma et al<sup>10</sup>, Soumya Kaup et al<sup>20</sup>, Rajeshwar et al<sup>16</sup>, Balan et al<sup>28</sup> Asmabegum Biradan et al<sup>12</sup>, Swathi Duggal et al<sup>11</sup>.

In the present study MRSA was isolated in 27% of *Staphylococcus aureus* which correlates with Swathi Duggal et al<sup>11</sup> (35.9%) and Asmabegum Biradan et al<sup>12</sup> (39.47%). In the present study most of the gram positive and gram negative isolates were resistant to penicillin and cephalosporin group similar to the study done by Rao et al<sup>1</sup>.

## CONCLUSION

Pyogenic wound infection is the most important cause of morbidity. Empirical and appropriate use of antibiotics is very crucial in preventing emergence of multidrug resistant bacteria. Hence there is a need for such studies to know the current status of bacterial etiology and their antibiotic sensitivity pattern to help the clinician to choose proper antibiotics for the management of pyogenic infections.

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