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Bacterial Profile and Antibiotic Resistance Pattern of Aerobic Gram Positive Bacteria Isolated From Pus Sample.

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ABSTRACT

Infection of the wound or pus can be caused by a variety of microorganisms. Antibiotic resistance in the general population is burning issue in this decade. This study is aimed to determine the prevalence of bacteria and antibiotic resistance pattern of gram positive organism in pus sample. A 164 isolates was isolated from 190 pus and wound swab samples. Staphylococcus aureus (39%) was the predominant organism causing wound and pus infection, followed by Proteus spp. (16.7%). 80-90% of gram positive organism were resistant penicillin. 60-70% were resistant to amoxacillin, ofloxacin and ciprofloxacin.
Keywords: Antibiogram, Staphylococcus aureus.

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INTRODUCTION

Pus is a collection of thick, white or yellow fluid that accumulates around the source of infection. Pus is made up of dead tissue, white blood cells, and damaged cells. Breaking of the protective layer during trauma, accident, minor injury may induce variety of cell types by the host response leading to pus formation.

Infection of the wound or pus can be by various microorganisms ranging from bacteria to fungus and parasites. They can be gram negative and gram-positive microorganisms. Staphylococcus aureus and coagulase-negative staphylococci have been the predominant gram positive organisms isolated from both prospective, purpose-collected samples and retrospective analysis of clinical investigations [1].

The routine use of antibiotics has resulted in wide spread antibiotic resistance and development of antibiotic resistance genes especially within the gram negative organisms [2]. The aim of this study is to determine the prevalence of bacteria in pus and wound samples and antibiotic resistance pattern of gram positive isolates.

MATERIALS AND METHODS

Sample Collection

A 190 pus and wound swab samples were collected from various departments (general surgery, ICU, general medicine). The pus samples were examined for its odour, colour, presence of blood and tissues. The pus were initially processed in different plates, nutrient agar, blood agar and Mac Conkey agar. The isolated colonies were identified by appropriate biochemical test by conventional methods [3]. Gram positive organism were identified by gram stain, catalase, tube & slide coagulase .Antimicrobial susceptibility testing was performed by Kirby-Bauer disc diffusion method and the susceptibility to antibiotics was assessed based on the Clinical Laboratory Standards Institute (CLSI 2013)Guidelines[4] . The Antibiotics tested were penicillin G (PG), amoxicillin (AX), amoxicillin/clavulanicacid (AC), cotrimoxazole (CT), cephalothin (CP), cefazolin (CF), cefuroxime (CR), erythromycin (ER), chloramphenicol(CK),ciprofloxacin(CI), ofloxacin (OF), piperacillin / tazobactam (PC) , azithromycin (AZ) and tetracycline (TE). Escherichia coli ATCC 25922, Pseudomonas aeruginosa ATCC 27853 and Staphylococcus aureus ATCC 25923 were used for quality control.

RESULT AND DISCUSSION

A total of 190 pus and wound swab samples were collected in the microbiology department from April 2013 to June 2013 . 160 samples showed significant growth . Four showed mixed growth. In samples showing mixed growth the most common association was between Escherichia coli and Staphylococcus aureus [5].

Table 1: Number of isolates in pus sample

sno	Organism	No of isolates
1	Escherichia coli	15
2	Klebsiella pneumonia	14
3	Klebsiella oxytocoa	7
4	Pseudomonas aeruginosa	2
5	Pseudomonas spp	15
6	Proteus vulgaris	7
7	Proteus mirabilis	20
8	Staphylococcus aureus	64
9	CONS	12
10	Diphtheroids	5
11	Streptococcus spp.	1
		164

CONS – coagulase negative staphylococcus

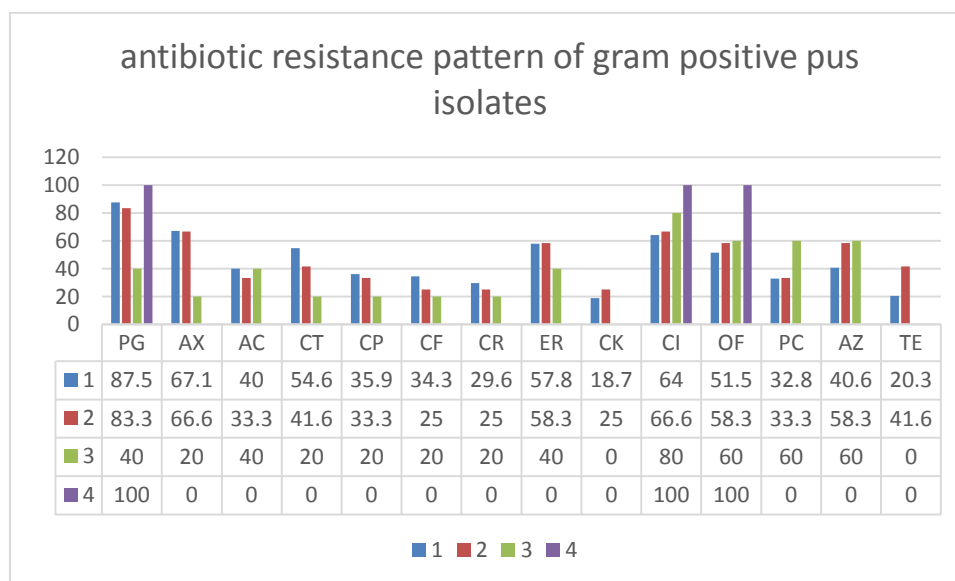**Table 2: Distribution of gram positive organism isolated in pus sample**

Sno	Organism	No of isolates
1	Staphylococcus aureus	64
2	CONS	12
3	Diphtheroids	5
4	Streptococcus	1
		82

Among them, 82 isolates were Gram negative isolates, in which majority (67 isolates) belonged to Enterobacteriaceae .82 isolates were gram positive isolates. Among all the isolates, S.aureus is major causative agent of wound and pus infection and constituted 39% of the isolates. This was consistent with other similar studies which also found a majority of Staphylococcus aureus isolates [5,6]. The next common isolate was Proteus spp,(16.4%) , followed by Klebsiella spp. (12.8%) (Table 1).

The distribution of gram positive organism in pus is shown in Table 2.

The antibiotic resistance pattern of gram positive organisms is shown in figure 1. S.aureus and CONS were the predominant organisms isolated. Both the species were highly resistance to penicillin, amoxicillin, cotrimoxazole and quinolones. The wide use of this group of antibiotic may be reason for resistance. 88% of S.aureus and CONS were resistant to penicillin.

Figure 1

	PG	AX	AC	CT	CP	CF	CR	ER	CK	CI	OF	PC	AZ	TE
1	87.5	67.1	40	54.6	35.9	34.3	29.6	57.8	18.7	64	51.5	32.8	40.6	20.3
2	83.3	66.6	33.3	41.6	33.3	25	25	58.3	25	66.6	58.3	33.3	58.3	41.6
3	40	20	40	20	20	20	20	40	0	80	60	60	60	0
4	100	0	0	0	0	0	0	0	0	100	100	0	0	0

In the present study, penicillin and amoxicillin, which are beta lactam antibiotics showed high level of resistance, this may be due beta lactamases producing S.aureus. This is consistent with other study [7].

Resistance to amoxicillin-clavulanic acid and piperacillin-tazobactam, cephalosporins was low.

Resistance is very lower for chloramphenicol & tetracycline, this indicates exposure to newer drugs, has eliminated the resistance to older drugs. The need of antibiotic recycling is indicated here.

CONCLUSION

This study revealed S.aureus is predominant cause of pus and wound infection, followed by Proteus and Klebsiella. It is concluded that majority of pus and wound samples showed mono-microbial infection. High level of resistance to penicillin G, amoxicillin, ciprofloxacin, ofloxacin among the gram positive isolates was observed, this may be due to the irrational use of antibiotics . Hence there is a need to emphasize rational use

of antimicrobials. Recycling of the antibiotics may help in preventing the development of resistance among the hospital strains.

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