

Isolation of Gram Positive and Gram Negative Bacteria from operation theaters of Tertiary Care Hospital and Molecular Detection of *Staphylococcus Aureus* Genes

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ABSTRACT

Aim: To identify the microorganisms in different operation theaters in tertiary care hospital and characterization of isolates on the basis of biochemical test and molecular level.

Methodology: Microbial contamination of five different operation theaters were selected including General surgery (OT1), gynecology (OT2), urology (OT3), orthopedics (OT4) and cardiac (OT5). Air samples of five different operation theatres were collected by Settle Plate Method. Sterile plates of nutrient, blood and Macconkey's agar were kept open for 15 min at four different places in operation theatres for air sampling.

Result: *Staph. aureus* was commonly found in OT's and to confirm this bacteria, molecular identification was done by amplifying TStAG gene.

Conclusion: Microbial burden is too much high in operation theatres and proper sterilization and fumigation is required.

Keywords: Hospital Acquired Infection, Operation Theatre, *Staphylococcus aureus*

INTRODUCTION

Nosocomial Infections are life-threatening problem in developing countries. A survey revealed that rate of Hospital Acquired Infection (HAI) ranges from 2.5 to 14.8%.¹ Surgeries play a major role in preventing death and disabilities for those who are suffering from tumors, obstetrical complications, injuries, emergency abdominal or non-abdominal conditions which can affect the quality of life i.e. cataract.² Successful surgeries improve the quality of life and prevent transmission of infectious diseases like Hepatitis, AIDS. Surgical conditions usually put the people out of work and put them into poverty i.e. a survey in Pakistan, blindness due to cataract was associated with poverty.³ Such type of infections are called nosocomial infections. These infections are not related to the original disease, which brings patient to the hospital.⁴ Operation theatre contamination is severely life threatening for the Transplantation, Cardiac, Neurosurgeries, Bladder and Tumor operations⁵.

METHODOLOGY

Bacterial contamination in operation theatre air was evaluated by settle plate method. Petri plates containing sterile media i.e. Nutrient agar, Blood agar, MacConkeys agar were opened at four different places (entrance, OT table, window and instrument table) for 15 minutes. 12 plates were opened in each operation theatre at different levels and incubation for 24 hours at 37°C. When incubation is done, colonies with different morphology were carefully streaked on fresh nutrient agar plates. Gram

staining was done for well-isolated colonies on nutrient agar, blood agar and MacConkeys agar. Spore staining was performed for gram positive rods.

Biochemical properties: Bacteria that appeared as Staphylococci or Streptococci were further tested for catalase and coagulase test. All Staph. species were catalase positive hence were differentiated from catalase negative Strept. species. Micrococcus species found in the form of tetrad or diplococcus. Catalase test is performed for Micrococcus species. Coagulase test is specifically performed to identify *S. aureus* and grown on Mannitol Salt Agar (MSA).

DNA Extraction of S. Aureus: DNA extraction was done by chemical method. Isolated colonies of *S. aureus* were cultured in LB broth and incubated for 24 hr at 37°C. Now 1.5ml of cultured broth poured into sterile eppendorf and performed Isopropanol method and gets DNA and then stored at -20°C for further used.

RESULTS

Molecular identification of isolated bacteria: For molecular identification of *S. aureus*, 16 samples among 53 isolated *S. aureus* samples were picked for molecular identification. 14 out of 16 samples were amplified TStAG (370 bp) gene specific for *S. aureus* hence positive for this gene. For methicillin resistant *S. aureus* strains, *mecA* gene amplification was done and all 8 samples picked among *S. aureus* confirmed by TStAG gene amplification were positive for methicillin resistance gene as well. While for vancomycin resistant strains of *S. aureus* *vanA* gene was amplified for TStAG positive *S. aureus* isolates but none of the sample amplified *vanA* gene. Hence no vancomycin resistant *S. aureus* was present. *B. cereus* confirmed by 16srRNA gene amplification. Out of 7 bacteria

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for Vancomycin resistant gene, one bacteria showed bands in PCR product of 500 and 900bp size. Required band was 1032 but it showed at 900 and 500bp size in the table.

Operation Theater 1 (General Surgery): Total 71 bacteria were isolated from OT-1 at different level and among them, %age of *S.aureus* were 22.5%, CoNS species 10.9%, *Micrococcus* species 8.8%, *Enterococcus* species 9.3%, *Bacillus .cereus* 13.2%, other bacilli species 9.8%, *listeria monocytogenes* 9.4%, *E. coli* 2.8 % and *Pseudomonas .aeruginosa* 13.4%.

Operation Theater 2 (gynecology): Total 61 bacteria were isolated from OT-2 at different level and among them %age of *S. aureus* were 19.5 %, CoNS species 11.4%, *Micrococcus* species 10.4%, *Enterococcus* species 10.2%, *Bacillus.cereus* 9.3%, Other bacilli 14.8%, *listeria monocytogenes* 6.5%, *E.coli* 7.8% and *P.aeruginosa* 10.2%.

Operation Theater 3 (Urology): 50 bacteria were isolated from OT-3 at different level and among them %age of *S.aureus* were 18.1%, CoNS species 11.4%, *Micrococcus* species 12.1%, *Enterococcus* species 16.9% *Bacillus .cereus* 16.6%, Other bacilli species 10 % and *E.coli* 14.2%.

Operation Theater 4 (Ortho): Total 42 bacteria were isolated from OT-4 at different level and among them %age of *S. aureus* were 20.5%, CoNS species 13.4%, *Micrococcus* species 6.5%, *Enterococcus* species 8.6%, *B. cereus* 22.6%, Other bacilli species 17.8%, *E. coli* 2.9%, *Streptococcus* species 7.7%.

Operation Theater 5 (Cardiac): Total 31 bacteria were isolated from OT-5 at different level and among them %age of *S.aureus* were 16.5% CoNS 9.8%, *Micrococcus* 15.4%, *B. cereus* 18.9%, Other bacilli 22.3% *E.coli* 1.8%, *P.aeruginosa* 15.4%.

Morphological and Biochemical tests: Fig 1, 2 and 3 show morphological changes and biochemical tests of *S. Aureus*.

Fig 1:
(A): Gram positive cocci in the form of chains (Streptococci)
(B): Small pinpoint colonies of staph aureus
(C): Spore staining of gram +ve rods by malachite green
(D): Gram –ve rods showing pink color by Gram staining.

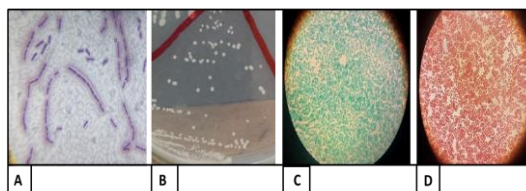


Fig 2:
(A) Different growth morphologies on Nutrient agar
(B) *S.aureus* showing β hemolysis on blood agar.
(C) *S.aureus* showing yellow growth on MSA

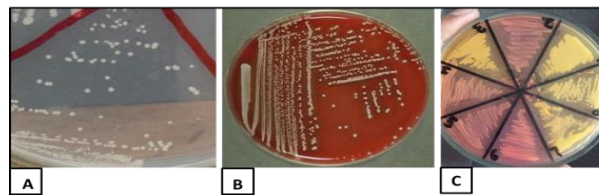


Fig 3:
(A) *S.aureus* showing coagulase test +ve by clump formation.
(B): Bubble formation showing +ve catalase test

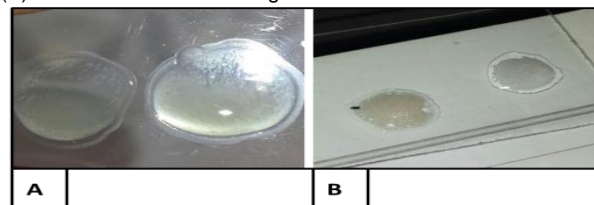


Table 1: Primer sequence for *S. Aureus* identification, methicillin and vancomycin resistant genes

Targeted gene.	5' to 3' primer sequence	References
TStaG422	F- GG. CC. GT. GT. TG. AA. CG. TG. GT. CA. A A. TC. A R- TT. AC. CA. TT. TC. AG. TA. CC. TT. CT. G G. TA.A	(McClure & Zhang, 2017)
mecA	F- AA. AA. TC. GA. TG. GT. AA. AG. GT. TG. G C R- AG. TT. CT. GG. AG. TA. CC. GG. AT. TT. G C	(Pournajaf et al 2014)
vanA	F- AT. GA. AT. AG. AA. TA. AA. AG. TT.GC R- TC. AC. CC. CT. T T. AA. CG. CT. AA.TA	(Saadat et al., 2014).

Table 2: Primers used for PCR

Targeted gene of Staph. aureus	Amplicon size (bp)	+ve samples
TStaG	370 bp	14/16
mecA	533 bp	8/8
vanA	1032 bp	0/7

DISCUSSION

The evaluation was done by using settle plate method at different level of OTs. Among the isolated bacteria gram positive cocci i.e. *Staph aureus*, CoNS species and *Micrococcus* species were the common, isolated from every OT. From above mentioned results it is obvious that gram positive cocci was the leading contaminant of OT environment as almost 55% of isolated samples were of

gram positive cocci in all 5 OTs. Among gram positive cocci, *S. aureus* was the leading contaminant of OT environment in individual OT ($\geq 16.46\%$ and $\leq 22.46\%$) as well as collectively in all OTs (19.4%). Although in number of previous studies⁶. *S. aureus* was reported but in what is unusual in present study was the fact that pathogenic *S. aureus* was the leading contaminant of OT air. Coagulase negative Staphylococci were second leading contaminant of OT environment among gram positive cocci with

percentage between ($\geq 9.8\%$ and $\leq 13.4\%$) at individual OT level and well as an overall percentage of 11.4%. Similar kind of results was observed in the studies⁷. Other gram positive cocci isolated were micrococcus, enterococcus and streptococci species. In present study streptococci was only isolated specie from orthopedic OT and is in accordance with findings where Streptococci was isolated from a few OTs i-e from surgery and eye OT. Enterococci and micrococci species were isolated from almost all OTs⁶.

For the Molecular identification of vancomycin resistant *S.aureus* strain genus specific gene TStAG of *S. aureus* was amplified. 14 out of 16 randomly selected samples were positive for the TStAG gene, producing 370bp product. Similar result was observed in previous studies of hence confirming *S. aureus*. For detection of MRSA strain *mecA* gene was amplified for 8 *S. aureus* isolates. All 8 *S. aureus* strains were positive for *mecA* gene producing 533 bp band as observed in previous study⁸.

CONCLUSION

S.aureus is major pathogen isolated and it is involved in skin, systemic infections and surgical site infections. Vancomycin was the most effective drug but now showing intermediate resistance which is real threat.

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