

Nosocomial Wound Infections in Intensive Care Unit at Tertiary Care Center Review of Microbiologic Analysis Over 5-Years Period (2013-2017)

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ABSTRACT

Study design: Chart review.

Background: Sepsis following traumatic and surgical intervention increases morbidity, mortality, cost and length of patient stay in hospital. The aim of this study was to identify the major pathogens associated with wounds infection and to review their antimicrobial reactions.

Methods: A 5-year review of nosocomial wound infection and colonization in patients admitted to the intensive care unit of tertiary care Hospital southern region of Saudi Arabia from January 2013 to August 2017. Patients of all ages and gender who required ICU attention at some point and defined as nosocomial infection using standard CDC criteria and presented with various degrees of wound and bed sore infections were included in the study. Data on bacterial isolates (n= 536) and reactions to antimicrobials (n= 51) were analyzed.

Results: There were 379 episodes of wound and 157 episodes of bedsore infections. The most common organisms *Klebsiella pneumoniae* (22.8%) followed by *Proteus mirabilis* (15.1%); *Acinetobacter baumannii* (12.7%); *Escherichia coli* (10.8%); *Pseudomonas aeruginosa* (10.1%); *Morganella morgani* (7.6%); *Providencia stuartii* (3.4%); *Staphylococcus aureus* (3.0%); *Enterobacter aerogenes* (1.5%) and Methicillin-resistant *Staphylococcus aureus* (MRSA) (1.3%) figure 1. The percentage sensitivity of the 536 organisms to the 51 antimicrobial agents was 39.2%; intermediate sensitivity was 3.3% and resistant was 57.5% figure 2.

Conclusion: Data from this and other studies supports the hypothesis that high incidence of gram negative bacilli (91.4%) in particular *Klebsiella pneumoniae*, *Proteus mirabilis* and *Acinetobacter baumannii* are more common in tropical regions compared to gram positive bacteria. This requires strong infection control actions to enhance patient care.

Key words: Nosocomial infections, Intensive care unit, Gram positive bacteria, Gram negative bacteria

INTRODUCTION

In adult critical care unit, health care associated infections remain a major risk factor related to mortality, morbidity and length of hospital stay¹. Device-Associated Healthcare- Associated Infection (DA-HAI) contribute to the majority of nosocomial infections in ICU². Multidrug resistance and gram-negative bacteria are common causative pathogen among critical ill patients³.

Wound is considered a major source of infection as the main barrier against bacterial infection is disrupted. Different sites and types of wounds including traumatic, surgical, burn and pressure wound injuries are risk factor to develop HAI with the potential adverse outcome⁴.

Little is known about healthcare associated wound infections in critical care unit. In fact, there is limited evidence related to the common isolated pathogens from different sites of wound among adult patients admitted to the ICU⁴. One cohort study has shown the high incidence of surgical site infection with multidrug resistance pathogen in patient with secondary peritonitis required admission to ICU⁵. However, the incidence of healthcare associated wound infections in critical

ill patients along with the predominant causative organisms and the influence of this type of infections in the outcome has been poorly addressed in the literature.

Therefore, we conducted a retrospective cross-sectional study aimed to address this knowledge gap. Our objectives were to assess the incidence of nosocomial wound infection in adult medical and surgical ICU at tertiary care center and to determine the antimicrobial resistance profile for the causative pathogens.

METHODS

The present study is a cross-sectional study in which a 5-year review of nosocomial wound infection and colonization in patients admitted to the intensive care unit of tertiary care Hospital southern region of Saudi Arabia from January 2013 to August 2017. Patients of all ages and gender who required ICU attention at some point and defined as nosocomial infection using standard CDC criteria and presented with various degrees of wound and bed sore infections were included in the study. Non wound specimen was excluded from the analysis. In our microbiology laboratory the Isolates identification using selected

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phenotypic criteria and confirmed using the Vitek 2 automated system. Antibiotics and their strength used were according to the Clinical and Laboratory Standards Institute guidelines.

Descriptive statistics were used to describe the characteristics of various wound infection causative agents. Analyses were performed using the IBM SPSS Statistics (version 21).

Data on bacterial isolates (n= 536) and reactions to antimicrobials (n= 51) were analyzed.

RESULTS

There were 379 episodes of wound and 157 episodes of bedsores infections. The most common organisms are Klebsiella pneumoniae

(22.8%) followed by Proteus mirabilis (15.1%); Acinetobacter baumannii (12.7%); Escherichia coli (10.8%); Pseudomonas aeruginosa (10.1%); Morganella morganii (7.7%); Providencia stuartii (3.4%); Staphylococcus aureus (3.0%); Enterobacter aerogenes (1.5%) and Methicillin-resistant Staphylococcus aureus (MRSA) (1.3%) (Figure 1). The percentage sensitivity of the 536 organisms to the 51 antimicrobial agents was 39.2%; intermediate sensitivity was 3.3% and resistant was 57.5% (Figure 2 and Table 1).

DISCUSSION

This cross-sectional study provides data on the incidence of wound infection in a mixed (medical and surgical) adult critical care unit. We found the bedsores infection contribute to almost a third of all wounds related nosocomial infections.

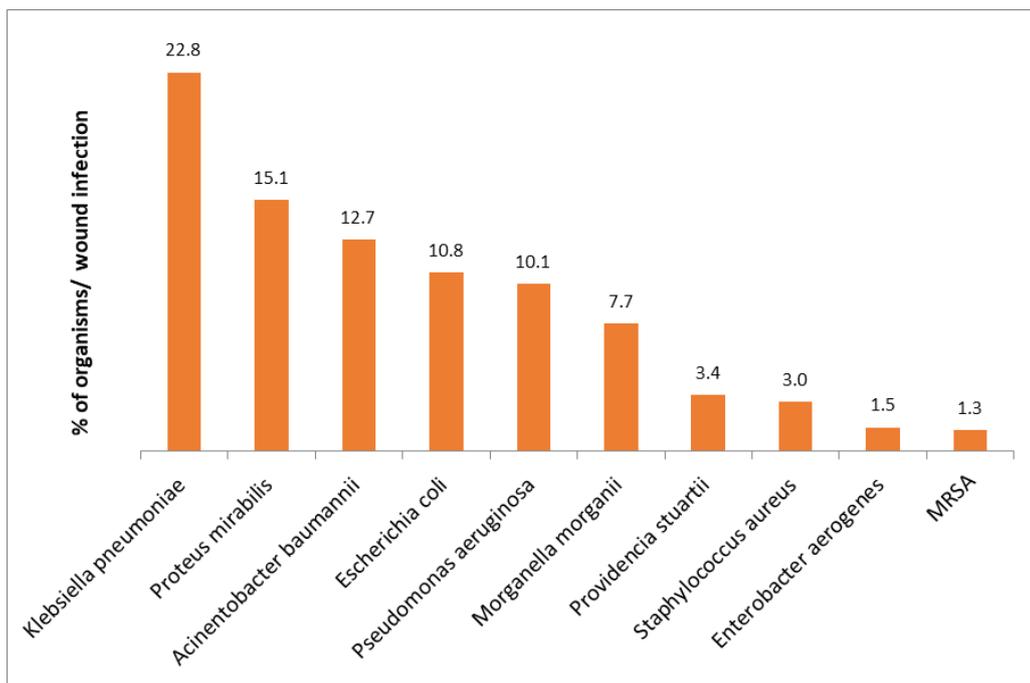


Figure 1: Major organisms (%) causing wound infections in ICU, (2013-2017)

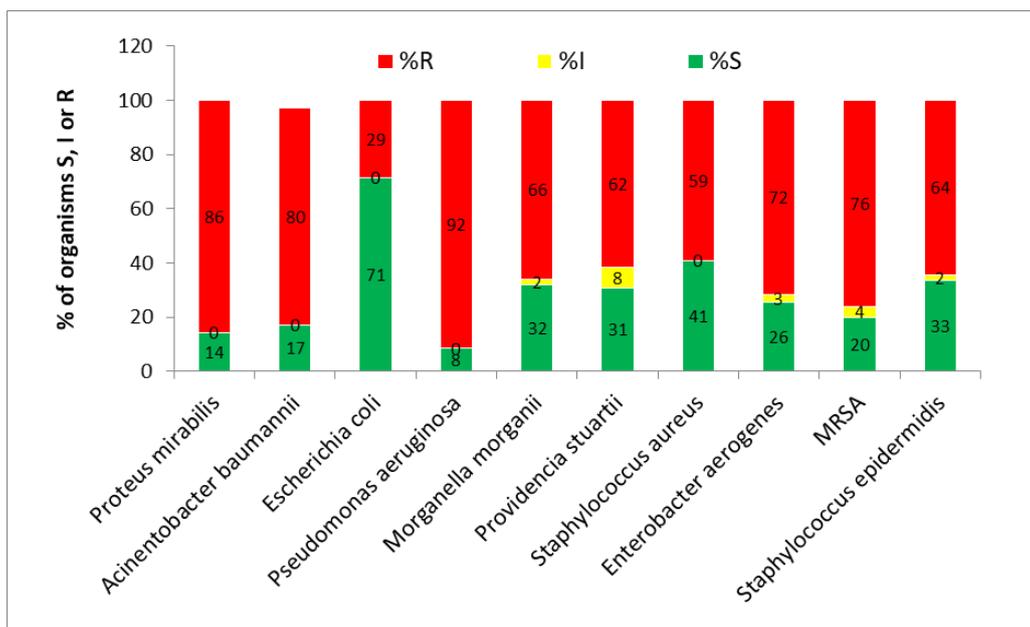


Figure 2: Sensitivity pattern of the major organism causing wound infection in ICU

Table 1: Bacterial isolates causing nosocomial wound infection at ICU 2013-2017 and results of their antimicrobial assay

Organism	Number (%) of strains testes	Antimicrobial assay		
		% Sensitive	% Intermediate	% Resistant
1. Klebsiella pneumoniae	122 (22.8%)	18	11	71
2. Proteus mirabilis	81 (15.1%)	14	0	86
3. Acinetobacter baumannii	68 (12.7%)	17	0	80
4. Escherichia coli	58 (10.8%)	71	0	29
5. Pseudomonas aeruginosa	54 (10.1%)	8	0	92
6. Morganella morganii	41 (7.6%)	32	2	66
7. Providencia stuartii	18 (3.4%)	31	8	62
8. Staphylococcus aureus	16 (3.0%)	41	0	59
9. Enterobacter aerogenes	8 (1.5%)	26	3	72
10. MRSA	7 (1.3%)	20	4	76
11. Staphylococcus epidermidis	6 (1.1%)	33	2	64
12. Serratia marcescens	5 (0.9%)	20	0	80
13. Serratia liquefaciens	5 (0.9%)	28	0	72
14. Enterobacter cloacae	5 (0.9%)	41	4	56
15. Acinetobacter baumannii/ haemolyticus	4 (0.7%)	37	0	63
16. Coagulase - negative Staphylococcus spp.	4 (0.7%)	71	0	29
17. Staphylococcus hominis	4 (0.7%)	31	5	65
18. Gram positive bacilli	3 (0.6%)	90	0	10
19. Acinetobacter sp.	3 (0.6%)	46	0	54
20. Citrobacter freundii	2 (0.4%)	37	4	59
21. Serratia odorifera 1	2 (0.4%)	29	5	65
22. Enterbacter sp.	2 (0.4%)	35	0	65
23. Klebsiella oxytoca	1 (0.2%)	29	0	71
24. Proteus penneri	1 (0.2%)	31	5	64
25. Proteus sp.	1 (0.2%)	73	7	20
26. Staphylococcus hominis subsp. hominis	1 (0.2%)	47	6	47
27. Klebsiella sp.	1 (0.2%)	50	0	50
28. Enterococcus sp.	1 (0.2%)	80	10	10
29. Staphylococcus xylosus	1 (0.2%)	18	18	64
30. Staphylococcus haemolyticus	1 (0.2%)	57	2	41
31. Providencia rettgeri	1 (0.2%)	68	4	28
32. Acinetobacter lowffii	1 (0.2%)	14	0	86
33. Citrobacter species	1 (0.2%)	33	8	58
34. Staphylococcus sciuri	1 (0.2%)	33	5	62
35. Citrobacter braakii	1 (0.2%)	79	1	20
36. Pseudomonas sp.	1 (0.2%)	42	2	55
37. Sphingomonas paucimobilis	1 (0.2%)	31	6	63
38. Serratia ficaria	1 (0.2%)	47	2	51
39. Enterococcus faecium	1 (0.2%)	38	8	54
40. Pseudomonas fluorescens/putida	1 (0.2%)	20	0	80
Total	536 (100.0%)	39.2%	3.3%	57.5%

The main finding of the study is that the gram-negative organisms attributed to more than 90% of the causative organisms where Klebsiella pneumoniae was the most identified pathogens. Around 60% of the identified pathogen were multidrug resistance organisms. In agreement with the literature, this finding confirms the gram-negative organisms are the most common cause of nosocomial infections in ICU⁶⁻⁸. However, the percentage may vary according to certain risk factors and different sites and types of wounds⁹. But correlation of this finding with available evidence cannot be assessed due to limited evidence related to nosocomial wound infection in ICU. reducing the infection rate in the critical care setting is needed although trial of eliminating it is a hard and difficult task¹⁰.

Although the total elimination of SSI is not possible, a reduction in the rate of infection to a minimum should be achievable, even in critically ill patients

This is the first study to address the incidence of healthcare associated wound infections in adult patients admitted to critical care unit.

Limitations include the limited available evidence related to nosocomial wound infections in ICU. Further studies are required to determine the incidence and risk factors of healthcare associated wound infections in critical ill patients along with the mortality and morbidity outcome and preventive measures.

CONCLUSION

Data from this and other studies supports the hypothesis that high incidence of gram-negative bacilli (91.4%) in particular *Klebsiella pneumoniae*, *Proteus mirabilis* and *Acinetobacter baumannii* are more common in tropical regions compared to gram positive bacteria. This requires strong infection control actions to enhance patient care.

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Potential Conflict of Interest: None

Competing Interest: None

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