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 157episodes 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

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