

ESKAPE Pathogens: Bad Bugs with No Drugs- A Study in Tertiary Care Hospital

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Abstract

ESKAPE pathogens Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, and Enterobacter species are currently the cause of majority of hospital infections globally and they also effectively “escape” the effects of antibacterial drugs. The UNSTOPPABLE SUCCESS of these SUPERBUGS will lead to UNWINNABLE WAR. It has been suggested that resistance by these organisms are due to mutations, modification of LPS. As the crisis of antibiotic resistance continues to grow, the latest IDSA (Infectious disease society of America) "Bad Bugs, No Drugs" report examines the trickle of new antibiotics in the research and development (R&D) pipeline and proposes steps to tackle the shortage. The aim of the study was to characterize the antimicrobial resistance in ESKAPE pathogens isolated from 430 culture positive clinical sample like urine, pus, blood, wound swab and sputum,. Antibiotic resistance was determined by VITEK 2 and manual Kirby Bauer method. MIC was determined by VITEK 2 and E Test according to Clinical and Laboratory Standards Institute (CLSI). ESKAPE pathogens account for 63%. Except for S. aureus multiple drug resistance (MDR) index of ESKAPE pathogens revealed an increasing trend. The statistical analysis was done for hospital acquired and community acquired MDR infections. Extended spectrum betalactamase (ESBL), Klebsiellaspp., carbapenem resistant, A. baumannii and P. aeruginosa were identified mainly in hospital acquired than in community acquired infections. In conclusion, ESKAPE pathogens are commonly identified in alarming frequency and knowledge of antimicrobial resistance will be aided for empirical treatment.

Keywords: Multi drug Resistant, ESKAPE pathogens, Infections, antibiotics.

Introduction

Infections caused by antibiotic-resistant bacteria continue to challenge physicians from last decade. We face growing resistance among Gram-positive and Gram-negative pathogens that cause infection in the hospital and in the community [1–3]. IDSA (Infectious disease society of America) reported these as the “ESKAPE” pathogens Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, and Enterobacter species) to emphasize that they currently cause the majority of hospital infections and effectively “escape” the effects of antibacterial drugs. Data from the Centers for Disease Control and Prevention (CDC) show rapidly increasing rates of infection due to methicillin-resistant S. aureus (MRSA), vancomycin-resistant E. faecium (VRE), and fluoroquinolone-resistant P. aeruginosa [4].

Infections caused by Multi drug resistant organisms have been reported with increasing frequency, thereby limiting the choice of effective antimicrobial agents available to clinicians. In addition the aging population and frequent referrals of patients from and to acute care facilities also add for the prevalence of multi drug resistant organisms.

Multidrug resistant (MDR) organisms especially Gram negative bacilli have become a pivotal of long term care facilities in the hospitals and vice versa[5]. In contemporaneous the

aging population and frequent referrals of patients from and to acute care facilities also add as the reservoir for the MDR(1). The unstoppable success of these SUPERBUGS will lead to the crisis called “UNWINNABLE WAR”[6]. Data from the National Nosocomial Infection Surveillance (NNIS) System (2003 versus 1998– 2002) showed that, in the nine selected antimicrobial-resistant pathogens associated with nosocomial infections in intensive care unit patients, there is increase in the prevalence of resistance to third-generation cephalosporins (either ceftriaxone, cefotaxime or ceftazidime) The recent emergence of resistant organisms to other drug classes serves to highlight the important therapeutic role of polymyxins such as colistin. No new antibiotic classes against multi drug resistant Gram-negative bacteria are expected to be commercially available within the next several years. Even more worrying, the emergence of resistance to colistin, the only available active antibiotic against multidrug-resistant Gram-negative bacteria[7]. Our therapeutic options for these pathogens are so extremely limited that clinicians are forced to use older, previously discarded drugs, such as colistin, that are associated with significant toxicity and for which there is a lack of robust data to guide selection of dosage regimen or duration of therapy [8]. The growing number of elderly patients and patients undergoing surgery, transplantation, and chemotherapy and dramatic increases in population in neonatal intensive care units will produce an even greater number of immunocompromised individuals at risk of these infections [9]. MDR organisms are commonly hospital acquired. Hospital acquired infections defined as the infections that was not present nor incubating at the time of admission in the hospital.

The study focuses on the antibiotic resistant organisms. It will be useful in implication of the antibiotic policy and also guide the physicians for treatment.

Methodology

The research done was applied, analytical type of case study research. The samples were collected by direct observational method. All the ESKAPE PATHOGENS isolated samples was be included in the study (probability sampling).

To avoid multiple entries from a single patient, only the first positive MDR culture for a given patient was included. The patients Identification number, age, sex, type of sample, recent significant treatment history with antibiotics, provisional diagnosis, duration of hospital stay and any other history related to the research was collected in observational design from the administrative data base. All the clinical samples received for Bacteriological culture in Microbiology section of the laboratory were processed and analyzed for the research. All clinical samples(Urine, pus, wound swab, sputum) were inoculated in the respective media and methods as per standard guidelines and incubated. The blood culture bottles will be placed in Bac T/ Alert 3 D and the positive culture bottle will be processed by Grams stain and in routine bacteriological media for inoculation and incubated. The samples with significant growth was processed by VITEK Compact for identification. All the ESKAPE pathogens isolated from all the clinical samples will be subjected for determining the MIC and Sensitivity by Vitek 2 and Kirby Bauer method as per CLSI

Isolates that were collected within 2 days after admission were considered to be acquired prior to the hospitalization, or “nonnosocomial”; Isolates acquired after day 2 were considered “nosocomial.”Total of 1000 samples were included in the study after the ethical committee approval by the institution.

Results

In total 1000 samples, 430 culture positive clinical sample. Among 430 Positive samples, 271 pathogens were identified as ESKAPE pathogens. The Enterococcus faecium accounted for 28, 72 samples isolated MRSA. In 64 and 39 samples Pseudomonas aeruginosa and

acinetobacter were isolated respectively.46 samples isolated Klebsiella pneumonia and 22 isoated Enterobacter.

The samples which were resistant to more than 3 groups of antibiotic were considered as Multidrug Resistant Organisms (MDRO). Out of 1000 samples 6.9% were MDR.

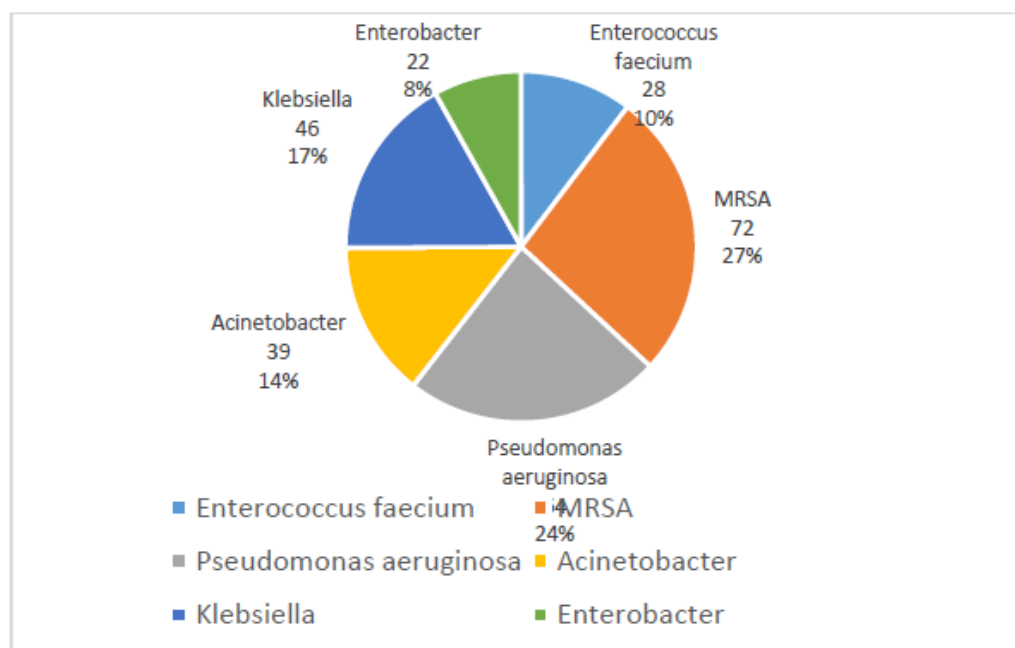


Figure 1. Distribution of ESKAPE

Discussion

Due to the ability of bacteria to rapidly gain resistance along with overuse and misuse of antibiotics, we are now in an age of multidrug-resistant (MDR) and pan-drug-resistant (PDR) bacterial pathogens leading to the situation like the pre-antibiotic era. This burden of antimicrobial resistance has resulted in increase in the length of hospital stays, patient mortality, and health care costs(10). Of more recent concern is the emergence of MDR Gram negative bacilli (GNB) in long term care facilities; Several studies have shown that the carriage prevalence of MDR GNB has far exceeded that of methicillin-resistant Staphylococcus aureus (MRSA) and vancomycin-resistant enterococci (VRE)(4).

A retrospective study states that there is an increase in the resistance pattern organisms in the past one year. Few studies have been focused on Pandrug resistant organisms especially Acinetobater and Pseudomonas species. Acinetobacter baumannii, Pseudomonas and Enterobacteriaceae were considered to be Pan drug resistant (PDR) if isolates were resistant to all classes of anti pseudomonal agents(11,12). This study focuses on the resistance pattern of the most commonly isolated MDR organism and emergence of antimicrobial stewardship to be followed by the physicians. This study has the pervelence of 6.9 of MDR organisms which was similar to other studies.

The Enterococcus species develops drug resistance by chromosomal mediated while Staphylococcus acquires resistance by plamid mediated. The Pseudomonas and Acinetobacter species transferred easily from one patient to other and prevalent in ICU patients. In the study it was observed chronic hospitalized patients developed drug resistance to which it was sensitive previously. Many carbapenamase resistant pseudomonas were also been isolated. Enterobacter acquired resistance by Amp C gene and it was found that the patients treated with

third generation cephalosporins to *Enterobacter* developed resistance in few weeks for the same drug due to Amp C production.

Conclusion

In the study there were significant isolation of MDR organisms. The study mainly concerns of resistance pattern in the ESKAPE pathogens which is the major threat to hospital as well as community acquired infections. There should be a strict antibiotic stewardship to be followed in each hospitals and restricted use of antibiotics as per sensitivity pattern.

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