Int.J.Curr.Microbiol.App.Sci (2018) *7*(5): 2881-2891

International Journal of Current Microbiology and Applied Sciences
***ISSN: 2319-7706* Volume 7 Number 05 (2018)**
Journal homepage: http://www.ijcmas.com

Original Research Article https://doi.org/10.20546/ijcmas.2018.705.336

Clinical Importance of Emerging ESKAPE Pathogens and Antimicrobial Susceptibility Profile from a Tertiary Care Centre

Jagadevi, B. Saipriya*, D.S. Shubha, K.S. Sudhindra, A. Sumantha and K.R. Madhuri

Department of Microbiology, Basaveshwara Medical College and Hospital, Chitradurga, Karnataka, India

**Corresponding author*

Keywords

Antimicrobial resistance, ESKAPE pathogens, Multidrug resistant (MDR) bacteria

Article Info

Accepted:
20 April 2018
Available Online:
10 May 2018

A B S T R A C T

Bacterial species from the ESKAPE group (*Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa* and *Enterobacter species*) have high resistance rates by escaping the action of the antimicrobials and are responsible for two third of all health care associated infections. Aim of our study was to find out the bacterial profile and characterize the antimicrobial resistance in ESKAPE pathogens isolated from various specimens. A three year retrospective study was undertaken. Urine samples, pus/wound swabs, respiratory samples, blood samples received in the microbiology laboratory were included &processed as per standard techniques and bacteria identified. Antibiotic susceptibility was determined according to Clinical & Laboratory Standards Institute (CLSI) guidelines. 41.5% of S. aureus isolates were confirmed to be methicillin resistant and 5.9% vancomycin resistant enterococci (VRE) were identified. A high multidrug resistance was observed for *Acinetobacter* and *P. aeruginosa* than Enterobacteriaceae. For carbapenem group, resistance varied from 8 to 27%. Resistance to amikacin and netilmycin was lower (4-11%) for gram negative ESKAPE pathogens. Antimicrobial resistance surveillance reports on regular basis can provide valuable insight into resistance trends at a particular medical facility to assist in guidance in the appropriate choice of empiric therapy in diseases due to ESKAPE pathogens.

Introduction

Antimicrobial resistance has been on the rise in the past few years in all parts of the world and has become a challenge to health care system. Although the overall global mortality has decreased in the last three decades due to infections, it is still the most important cause of disability (Lozano *et al.*, 2010; Murray, 2010) and India is no exception which shows the same trends. Antimicrobial resistance is particularly worrying in India, where hospital standards are inconsistent and antibiotics are readily available over the counter at pharmacies. Antibiotic use is unnecessary or inappropriate in as many as 50% of cases and this creates unnecessary pressure for the selection of resistant species (John *et al.*, 2011).

Infectious Diseases Society of America (IDSA), has highlighted a group of antibiotic

resistant bacteria as "ESKAPE pathogens", because they effectively escape the effects of antibacterial drugs (Jack N. Pendleton *et al.,* 2013). ESKAPE is an acronym for the group of bacteria, encompassing both Gram-positive and Gram-negative species, made up of *Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter species*.

ESKAPE bacteria are common causes of severe and often deadly infections such as bloodstream infections, pneumonia and urinary tract infections. They can cause serious life threatening infections amongst critically ill and immunocompromised individuals and their clinical importance relies on their virulence, ability in developing mechanisms to decrease susceptibility to antimicrobials, increasing inappropriate therapy and affecting negatively on ICU patients' outcome (Sandiumenge *et al.,* 2012).

The incidence of ESKAPE pathogens as etiologic agents of human disease has increased with time, and infections resulting from antimicrobial-resistant ESKAPE pathogens have been observed to be associated with poorer patient outcomes than infections arising from similar antimicrobial-susceptible isolates (Pogue Jmkaye *et al.,* 2015; James A. Karlowsky *et al.,* 2017). Importantly, patients infected with antimicrobial-resistant ESKAPE pathogens more frequently receive inappropriate empirical antimicrobial therapy than do patients with antimicrobial-susceptible pathogens leading to higher case fatality rates and opportunities for spread to neighbouring patients (Bodro *et al.,* 2013, James A. Karlowsky *et al.,* 2017).

Emergence of multidrug resistant organisms leading to treatment failure is of concern. It is necessary that studies trace periodically the bacterial resistance profile, to contribute for both local and global epidemiological data. These data assist in therapeutic management, since they consider the prevalence of resistance locally, adding it to the clinical effectiveness and cost of the antimicrobial. The aim of the current study is to satisfy this need by reporting the bacterial profile and antimicrobial susceptibility pattern of culture positive ESKAPE pathogens isolated in various clinical specimens.

Materials and Methods

A three year retrospective study from September 2013 to August 2016was carried out in a tertiary care Centre at Basaveshwara medical college and hospital, Chitradurga. During this period, urine samples (3989), pus/wound samples (2293), respiratory samples (2397) and blood samples (1434) received at our microbiology laboratory were included in the study.

All the above samples were processed as per standard microbiological techniques and isolates identified based upon gram staining characteristics, colony morphology, motility, oxidase test, catalase test and a panel of standard biochemical tests.

Following identification of the bacterial isolates, antibiotic susceptibility testing was performed on Mueller- Hinton agar plates by Kirby- Bauer disk diffusion method as per Clinical and Laboratory Standard Institute guidelines (CLSI 2013). The antibiotics tested included beta-lactam group (penicillins and cephalosporins), aminoglycosides, macrolides, clindamycin, glycopeptides, colistin, carbapenem, fluoroquinolones, cotrimoxazole and nitrofurantoin. However, some modification was done based on the organism. For example, for gram negatives, glycopeptides like vancomycin (which are specific for gram positives) were not tested.

The antibiotics discs and their concentrations for gram positive bacteria included; Ampicillin (10µg), Cotrimoxazole (1.25/23.75 µg), Ciprofloxacin (5µg), Gentamicin (10µg), High level Gentamicin (120 µg), Erythromycin (15µg), Clindamycin (2µg), Clarithromycin (15µg), Cefoxitin (30µg), Tetracycline (30µg), Amoxycillin/Clavulanic acid (20/10µg), Vancomycin (30µg) and Linezolid (30µg). For Gram negatives bacteria included; Ampicillin (10µg), Cotrimoxazole (1.25/23.75 µg), Gentamicin (10 µg), Amikacin (30 µg), Netilmycin (30 µg), Ciprofloxacin(5µg), Levofloxacin(5µg), Nitrofurantoin(300µg), Cefepime (30µg), Ceftriaxone(30 µg), Ceftazidime (30 µg), Cefaperazone – Sulbactum (75 µg), Piperacillin – Tazobactum (100/10 µg), Imipenem (10 µg), Meropenem (10 µg), Amoxycillin/Clavulanic acid(20/10µg), Aztreonam(30 µg), Colistin (10 µg)discs were used. All the antimicrobials used for the study were obtained from Himedia, India. The reference strains used as control were E. coli (ATCC 25922) and *S. aureus* (ATCC 25923). In this study multi-drug resistance was defined as simultaneous resistance to two or more antimicrobial agents.

Detection of MRSA: Methicillin resistance was detected by Cefoxitin disk diffusion test. Lawn culture was done onto Mueller-Hinton agar plate. A 30 µg cefoxitin disc was placed and incubated at 3°C for 24 hrs. The zone of inhibition of *S. aureus* ≤ 21 mm were considered as methicillin resistant.

Results and Discussion

During the study period a total of 10, 113 various clinical samples were examined, 29.64% (2998/10, 113) were culture positive. Of this culture positive samples, maximum growth was seen from pus/wound swabs, 42.25% (985/2293) followed by 30.99% (743/2397) respiratory samples, 28.95% (1156/3989) from urine samples and 7.94%(114/1434) from blood samples. Overall growth of Gram negative bacilli (GNB) were 69.44% (2082/2998) and Gram positive cocci (GPC) were 29.35 % (880/2998). These findings are consistent with Anuradha S De *et al.*, 2017; Daniely M. Silva *et al.*, (2017). The global scenario shows that Gram- positive infections are more prevalent in the Western world, however, Gram- negative bacterial infections dominate in India and Asia- Pacific region (DhruvaChaudhry *et al.*, 2016).

In this study, it is seen that, of the total 2998 positive cultures (Table 1), 2, 107(70.28%) were ESKAPE pathogens and 891(29.72%) were non ESKAPE pathogens. Among the ESKAPE pathogens, the most prevalent microorganism isolated was *Staphylococcus aureus* 19.17% (575), followed by *Klebsiella pneumoniae* 16.14% (484), *Pseudomonas aeruginosa* 10.97% (329), *Acinetobacter* species 9.67%(290), *Enterococcus* species 7.30% (219) and *Enterobacter species* 7.00% (210). Our study results correlated with other workers Anuradha S. De *et al.*, (2017), Jorge Martín L. laca-Díaz *et al.*, (2017), Dhruva Chaudhry *et al.*, (2016). A study from Brazil by Daniely M. Silva *et al.*, (2012), also reported similar isolation rate of ESKAPE pathogens, they documented the *Klebsiella pneumoniae* (41%) as most prevalent microorganism followed by *Staphylococcus aureus* (22%), *Pseudomonas aeruginosa* (14%), *Enterobacter* spp. (11%), *Acinetobacter baumannii* (8%) and *Enterococcus faecium* (4%).

Among non ESKAPE pathogens Escherichia coli was the most predominant microorganism isolated in 19.31% (579 samples), followed by NFGNB 4.46% (134), Coagulase Negative *Staphylococcus* (CONS) 1.90% (57), *Citrobacter* species 1.06% (32), *Streptococcus* species 0.96% (29), *Proteus* species 0.70% (21), *Salmonella typhi* 0.10%(3) and *Candida*

albicans 1.20% (36). Our study results correlated with other workers (Razia Khatoon *et al.,* 2016; Rudrajit Paul *et al.,* 2017; Sugantha Valli *et al.,* 2017).

Majority of isolates from urine and respiratory samples were gram negative bacilli, 81.92% (947/1156) and 82.23% (565/743) respectively while from pus/wound swabs and blood cultures the majority of isolates were gram positive cocci 50.4% (497/985) and 57.8% (66/114) respectively. In urine and respiratory samples the microorganism most commonly isolated was *Klebsiella pneumoniae* 49.17% (238/484) and 42.35% (205/484) respectively and in pus/wound swab and blood cultures, *Staphylococcus aureus* was the most commonly isolated microorganism 72.17% (415/575) and 8%(46/575) respectively. Our study results correlated with Daniely M. Silva *et al.,* (2017), Anuradha De *et al.,* (2015). The main problem across most sites of infections as shown above is Gram Negative bacillary infections. This is the scenario in most centers in India. This is quite different from the Western setting where the major share of hospital associated infections since the 1980's are Gram positive coccal organisms like *Staphylococcus aureus* and Enterococci. (George K. Varghese *et al.,* 2010; Gaynes *et al.,* 2005).

Antimicrobial susceptibility in ESKAPE pathogens

Enterococci were traditionally regarded as low-grade pathogens, but have emerged as an increasingly important cause of health care infections in recent years (Sood *et al.,* 2006). Vancomycin resistant Enterococci (VRE) has been increasingly reported from all parts of the world. In present study 5.93% (13/219) isolates were resistant to vancomycin. 1.4 - 8 % resistance to vancomycin has been reported in India by Kapoor *et al.,* (2005), Shah *et al.,* (2012), Taneja *et al.,* (2004), Karmarkar *et al.,* (2004) in separate studies, but Preeti Srivastava *et al.,* (2013) reported a prevalence of 27% VRE.

In the present study, *Enterococci* showed highest resistance to ampicillin(98.6%), followed by erythromycin (62.7%), ciprofloxacin (56.3%), Tetracycline(54.6%), clindamycin (51.6%), nitrofurantoin (29.7%) and linezolid showed lowest resistance(0%), these findings are consistent with studies done by Preeti Srivastava *et al.,* (2013), Kapoor *et al.,* (2005). 21.4% High level Gentamicin resistance (HLAR) of *Eneterococci* was detected in our study, similar resistance rate was reported by Anuradha S. De *et al.,* (2015). More than 50% resistance with gentamicin was reported by Butch *et al.,* (2011) and Nepal *et al.,* (2013).

Among Gram-positive pathogens of ESKAPE group, the majority were *S. aureus* strains (19.1%). The following resistance rates of *S. aureus* were identified in the descending order to: ampicillin (97.2%), cotrimoxazole (78.2%), tetracycline (71.4%) gentamicin (66.2%), erythromycin (59.6%), ciprofloxacine (51.8%), levofloxacine (46.7%), and amoxicillin-clavulanate (36.4%). Inducible clindamycin resistance was (42.8%). These finding correlated with Sangeeta Joshi *et al.,* (2013) and Sathish *et al.,* (2017). *S. aureus* isolates exhibited 100% sensitivity with vancomycin and linezolid which is similar to study done by Abbas *et al.,* (2015).

Reports of methicillin-resistant *Staphylococcus aureus* (MRSA)emerged in the 1960s, and currently, MRSA isolates are estimated to account for 25% of *S. aureus* isolates, with a prevalence of up to 50% or more in some areas (Sirijan Santajit *et al.,* 2016). In our study, prevalence of MRSA was 41.5% which correlated with studies done by Sangeeta Joshi *et al.,* (2013) who reported 42% MRSA. In India, the incidence of MRSA

is increasing, with prevalence rates varying from 23.6% to as high as 59.3% (Tiwari *et al.*, 2006; Boucher *et al.*, 2009; Lockhart *et al.*, 2007).

In recent years, many *K. pneumoniae* strains have acquired a massive variety of *β* lactamase enzymes, which can destroy the chemical structure of *β*-lactam antibiotics such as penicillins, cephalosporins and carbapenems (SirijanSantajit *et al.*, 2016). Because carbapenems are conventionally used to treat persistent infections caused by Gram-negative bacteria, the increasing prevalence of carbapenem-resistant *K. pneumoniae* (CRKP), with resistance encoded by blaKPC, presents a significant challenge for physicians (Queenan *et al.*, 2007; Bush *et al.*, 1995). In addition, the emergence of the *K. pneumoniae* super enzyme, known as NDM-1 and encoded by blaNDM-1, has increased the proportion of carbapenem-resistant *K. pneumoniae* isolates and may pose a threat to other antibiotics such as *β*-lactams, aminoglycosides, and fluoroquinolones (Kumarasamy *et al.*, 2010; Yong *et al.*, 2009).

When analyzing the susceptibility profile for *Klebsiella pneumoniae*, in our study it was possible to observe that this strain presented the highest resistance rates to the following antimicrobials: to Ampicillin (100%), Trimethoprim-sulphamethoxazole (89.4%), Ciprofloxacine (87.3%) levofloxacin (86.9%), nitrofurantoin (79.8%) amoxycillin–clavulanate (72.5%), aztreonam (49.2%) and the lowest rate of resistance to colistin (1%), imipenem (18.4%), meropenem (15.6%), amikacin (4.1%), netilmycin (3.8%) these findings correlated with the other workers (Daniely M. Silva *et al.*, 2017; Anuradha S. De *et al.*, 2015).

Table.1 Showing ESKAPE bacteria and Non- ESKAPE bacteria isolated from different samples

Bacteria (Total no.)	Pus No (%)	Respiratory No (%)	Urine No (%)	Blood No (%)
ESKAPE bacteria (2, 107)				
Enterococcus species (219)	55 (25.11)	67(30.59)	83(37.89)	14((6.39)
Methicillin sensitive *Staphylococcus aureus* (MSSA) (336)	237 (70.53)	35(10.41)	37((11.01)	27(8.03)
Methicillin Resistance *Staphylococcus aureus* (MRSA) (239)	178 (74.47)	18(7.53)	24(10.04)	19(7.94)
***Klebsiella pneumoniae* (484)**	36 (7.43)	205(42.35)	238(49.17)	05(1.03)
***Acinetobacter* species (290)**	97(33.48)	113(38.96)	67(23.10)	13(4.48)
***Pseudomonas aeruginosa* (329)**	153(46.50)	97(29.48)	73(22.18)	06(1.82)
***Enterobacter* species (210)**	72(34.28)	47(22.38)	82(39.04)	09(4.28)
Non- ESKAPE bacteria (891)				
***Escherichia coli* (579)**	80(13.18)	76(13.12)	419(72.36)	04(0.69)
***Citrobacter* species(32)**	09(28.12)	07(21.87)	14(43.75)	02(6.25)
***Proteus* (21)**	07(33.33)	04(19.04)	08(38.09)	02(9.51)
NFGNB (134)	31(23.14)	53(39.55)	46(34.32)	04(2.98)
***Salmonella typhi* (03)**	00	00	00	03(100)
CONS (57)	13(22.80)	00	39(68.42)	05(8.77)
***Streptococcus* species(29)**	14(48.27)	O9(31.03)	05(17.24)	01(3.44)
***Candida albicans* (36)**	03(8.33)	12(33.33)	21(58.33)	00

Table.2 Antimicrobial resistance pattern of culture positive ESKAPE bacteria

Antimicrobial drugs	Resistant Pattern of bacterial isolates (%)					
	Enterococci spp, N=219	*S. aureus* N=575	*K. pneumoniae* N=484	*Acinetobacter* spp, N=290	*P. aeruginosa* N= 329	*Enterobacter* Spp, N= 210
Ampicillin	98.6%	97.2%	100%	-	-	100%
Cotrimoxazole	-	78.3%	89.4%	72.6%	76.2%	88.4%
Ciprofloxacin	56.3%	51.8%	87.3%	90.5%	86.8%	83.1%
Levofloxacin	49.1%	46.7%	86.9%	89.2%	85.7%	82.8%
Gentamicin	-	66.2%	69.7%	53.6%	49.3%	65.6%
High level Gentamicin	21.4%	-	-	-	-	-
Clarithromycin	60.6%	58.3%	-	-	-	-
Erythromycin	62.7%	59.6%	-	-	-	-
Clindamycin	51.6%	42.8%	-	-	-	-
Cefoxitin	-	41.5%	-	-	-	-
Tetracycline	54.6%	71.3%	-	-	-	-
Vancomycin	5.93%	0 %	-	-	-	-
Linezolid	0 %	0 %	-	-	-	-
Amoxycillin/Clavulanic acid	-	36.4%	72.5%	78.4%	76.2%	74.9%
Nitrofurantoin	29.7%	50.9%	79.8%	81.2%	80.6%	76.3%
Amikacin	-	-	4.1%	10.7%	9.3%	8.6%
Netilmycin	-	-	3.8%	9.2%	8.6%	5.4%
Ceftriaxone	-	-	80.4%	87.3%	78.4%	81.9%
Cefepime	-	-	71.5%	84.6%	76.2%	70.2.%
Ceftazidime	-	-	62.7%	87.3%	79.6%	69.6%
Cefaoperazone–Sulbactum	-	-	61.3%	19.6%	16.8%	65.3%
Piperacillin – Tazobactum	-	-	78.6%	62.9%	61.4%	79.2%
Imipenem	-	-	18.4%	27.2%	10.4%	16.7%
Meropenem	-	-	15.6%	21.7%	8.2%	14.3%
Aztreonam	-	-	49.2%	46.2%	49.6%	39.5%
Colistin			1.0%	2.5%	1.0%	1.5%

Table.3 Multidrug resistant (MDR) Gram negative bacilli isolated between 2013 and 2016

Year	Gram negative bacilli (No)	Total MDR No. (%)
2013-2014	Enterobacteriaceae (427)	113(26.4%)
	Non-fermenters (304)	179(58.8%)
	Total (731)	292(39.9%)
2014-2015	Enterobacteriaceae (504)	172(34.1%)
	Non-fermenters (198)	91(47.3%)
	Total (702)	263(37.4%)
2015-2016	Enterobacteriaceae (397)	117(29.4%)
	Non-fermenters (252)	136(53.9%)
	Total (649)	253(38.92%)

Rates of susceptibility of *Klebsiella pneumoniae*, for cephalosporinsin our study were Ceftriaxone (80.4%), Ceftazidime (62.5%) cefoperazone -sulbactam (61.3%), cefepime (71.5%). Karlowsky *et al.,* (2017), Daniely M. Silva *et al.,* (2017) and Rudrajit Paul *et al.,* (2017) also reported similar rate of resistance.

Recently, the emergence of carbapenemase producing *A. baumannii* strains carrying imipenem metallo β-lactamases, encoded by blaIMP, and oxacillinase serine βlactamases, encoded by blaOXA, has been reported. These strains show resistance to both colistin and imipenem, and the combination of resistance genes makes them capable of evading the action of most traditional antibiotic compounds (Vila *et al.,* 2007; Bradley *et al.,* 2009).

In the present study *Acinetobacter baumannii* presented the most worrying susceptibility profile, presenting a higher resistance frequency of 90.5% to ciprofloxacin, 89.2% to levofloxacin, 87.3% to ceftazidime and cefotaxime, 84.8% to cefepime, 87.3% to piperacillin tazobactam and Lower resistance frequency to colistin (2.5%) amikacin (10.7%), netilmycin (9.2%), cefoperazone-sulbactam (19.6%), meropenem (21.7%)and imipenem (27.2%). These frequencies of resistance to *Acinetobacter* correlated with other workers (Daniely M. Silva *et al.,* 2017; Anuradha S De *et al.,* 2015; Rudrajit Paul *et al.,* 2017) (Table 2).

Many *P. aeruginosa* strains show an intrinsic reduced susceptibility to several antibacterial agents, as well as a propensity to develop resistance during therapy especially in carbapenem-resistant (chiefly imipenem) strains. The combination of these leads to high rates of carbapenem resistance amongst P. aeruginosa isolates and also to the emergence of fluoroquinolone-resistant strains as the corresponding mechanisms of resistance may be carried by the same plasmid (Livermore *et al.,* 2002; Bush *et al.,* 1998).

In our study *P. aeruginosa* was found highly resistant to ciprofloxacin (86.8%), levofloxacin (85.7%), ceftazidime (79.6%), cefepime (76.2%), Amoxycilline-clavulanate (76.2%) and piperacillin-tazobactam (61.4%) and lower resistance to colistin (1%) amikacin (9.3%), netilmycin (8.6%), imipenem (10.4%) and meropenem (8.2%). Daniely M. Silva *et al.,* (2017), Anuradha S De *et al.,* (2015), Jorge Martín L laca-Díaz *et al.,* (2012), Rudrajit Paul *et al.,* (2017) also reported similar rate of resistance.

As observed for *K. pneumoniae*, in general, *Enterobacter* spp. were less susceptible to the antimicrobials tested. *Enterobacter* spp., showed higher rate resistance to ampicillin (100%), ciprofloxacin (81.3%), levofloxacin (82.8%), ceftriaxone (81.9%), piperacillin-tazobactam (79.2%), cefepime (70.2%) and lower resistance to amikacin (8.6%), netilmycin (5.4%), imipenem (16.7%), meropenem (14.3). Similar resistance rate was reported by Anuradha S. De *et al.,* (2015), Daniely M. Silva *et al.,* (2017), Jorge Martín L laca-Díaz *et al.,* (2012) and Rudrajit Paul *et al.,* (2017).

Overall multidrug resistant gram negative bacilli (MDR-GNB) isolated in our study in three years 2013-2014, 2014-2015 and 2015-2016 was 39.9%, 37.4% and 38.9% respectively. In general, a high MDR was observed for *A. baumannii* and *P. aeruginosa* (Non-fermenting bacilli) than Enterobacteriaceae (Table 3). 81.7% (237/290) of *A. baumannii* isolates were MDR, as were 85.9% (98/210) of *Enterobacter* spp., 65.2% (316/484) of *K. pneumoniae* and 59.8% (197/329) of *P. aeruginosa*. *E. coli* deserves special attention because it also showed a high level of MDR

62.8% (364/579), even though this bacterial species is not included within the ESKAPE group. Jorge Martín L. laca-Díaz *et al.,* (2012) and Anuradha S De *et al.,* (2015) also reported similar rate of MDR-GNB.

Both infection and MDR results in a considerable clinical and economic burden and the presence of MDR boosts the deleterious impact of health care associated infection (Salgado *et al.,* 2005). Compared with infections not caused by MDR microorganisms, the additional cost of multidrug resistance in hospitalized patients with infections has been estimated to be much higher per patient (Cosgrove, 2006; DhruvaChaudhry *et al.,* 2016). The continuous increase of MDR isolates presents a complicated situation for antimicrobial therapy; however, colistinis still effective in most cases (Boucher *et al.,* 2009).

Present study indicates a serious problem in the treatment of infections and current resistance pattern emphasizes the importance of strict antibiotic policy to prevent emergence and spread of antibiotic resistance. In this tertiary care hospital, the ESKAPE pathogens were responsible for a considerable number of infections and represented the majority of isolates for which resistance to multiple antimicrobial agents reduces therapeutic alternatives for physicians. The awareness of residential antimicrobial resistance pattern can support the selection of convenient empirical treatment in which infections occur due to ESKAPE pathogens.

In view of high drug resistance, caution should be exercised and wide spread use of antibiotics should be avoided to minimize the potential development of multidrug and sometimes pan drug resistant pathogens. Every health‐ care institution must develop its own antimicrobial stewardship program which should be based on the local epidemiological data and standard guidelines, to optimize the antimicrobial use among the hospitalized patients, to improve the patient outcomes, to ensure a cost‐ effective therapy, to reduce the adverse consequences of the antimicrobial use and to limit the emergence and transmission of drug resistant bacteria. Preventive measures such as a continuous surveillance of the health care centers and treatment based on antibiogram and a strict implementation of infection control practices are essential in containing the threat of drug resistance in the health‐ care settings.

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How to cite this article:

Jagadevi, B. Saipriya, D.S. Shubha, K.S. Sudhindra, A. Sumantha and Madhuri, K.R. 2018. Clinical Importance of Emerging ESKAPE Pathogens and Antimicrobial Susceptibility Profile from a Tertiary Care Centre. *Int.J.Curr.Microbiol.App.Sci.* 7(05): 2881-2891.
doi: https://doi.org/10.20546/ijcmas.2018.705.336