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Transforming Resistance Profile of ESBL-producing Klebsiella Pneumoniae in a Tertiary Care Hospital

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Author`s Contribution

[1,2]Substantial contributions to the conception or design of the work; or the acquisition, [1,3,6]Drafting the work or revising it critically for important intellectual content, [4,5]Active participation in active methodology, analysis, or interpretation of data for the work, [2]Final Approval

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ABSTRACT

Objective: To determine the transforming level of resistance in the Extended spectrum beta lactamase (ESBL) producing Klebsiella pneumoniae from clinical isolates in a tertiary care hospital.

Methodology: This was a descriptive cross sectional study, conducted at Department of Microbiology, Khyber Medical University and Department of Microbiology, Gajju Khan Medical College / Bacha Khan Medical Complex, Swabi from January 2025 to December 2025. Samples were received from different wards, mainly including blood, pus, urine, tissue, tracheal aspirate, sputum and CSF. The maximum number of samples were received from the neonatal and adult intensive care units. The received clinical samples were inoculated on appropriate culture media, followed by initial bacterial identification through colony morphology, Gram staining and biochemical testing. As per the Clinical and Laboratory Standards Institute guidelines, antibiotic susceptibility was performed using the Kirby-Bauer disc diffusion method, and for the phenotypic identification of the organisms as a beta lactamase producer the double disc synergy Test (DDST) was performed.

Results: Based on the antibiotic susceptibility out of the total 95 ESBL producing Klebsiella pneumoniae isolates, collected during the time of study, n=59(62.10%) were XDR and n=36(37.89%) were MDR. 100% co-resistance was observed against Amoxicillin-clavulanic acid Cefotaxime and Ceftriaxone in all 95 samples, followed by n=91(95.78%) resistance against Ciprofloxacin. n=57(60%) of the isolates were resistant to both Meropenem and Imipenem simultaneously. Out of a total of 19 urinary isolates, Nitrofurantoin showed comparatively better efficacy, with a sensitivity of n=10(52.63%) as compared to Fosfomycin, where the sensitivity was substantially reduced i.e. n=7(36.84%).

Conclusion: ESBL producing Klebsiella pneumoniae isolates showed very high level of resistance to most groups of antibiotics. Susceptibility was substantially reduced against the Carbapenems and Amikacin as well.

Keywords: Disc diffusion method, Extended spectrum beta lactamases (ESBLs), Klebsiella pneumoniae, MDR, XDR.

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Introduction

The threat of antimicrobial resistance is still on the rise globally, with *Klebsiella pneumoniae* being one of the important multidrug resistant organisms (MDROs) found in the healthcare settings, especially in intensive care units (ICUs). [1,2] *Klebsiella pneumoniae* is an important Gram-negative, non-motile rod belonging to the family Enterobacteriaceae and is recognized as an opportunistic pathogen. It commonly resides in the nasopharynx, oral cavity, and gastrointestinal tract as part of the normal human microbiome.[3,4] *Klebsiella pneumoniae* has been included in the group named as "ESKAPE" pathogens. In addition to it, *Enterococcus faecium, Staphylococcus aureus, Acinetobacter baumannii, Pseudomonas*

aeruginosa, and Enterobacter spp. are also included which have been given a "priority status", for which new antibiotics are urgently needed. *Klebsiella pneumoniae* is responsible for a wide spectrum of diseases starting from soft tissue infections, liver abscess, pneumonia, urinary tract infections, endophthalmitis and meningitis.[3] Adding to the current list of diseases, recent studies have confirmed *Klebsiella pneumoniae* as one of the major causes of neonatal sepsis in two major continents i.e. Africa[5] and Asia[6]. Similar trend was highlighted in a study conducted in Peru, South America, with ESBL producing *Klebsiella pneumoniae* identified in 73.3% of the neonates with blood stream infections.[7]

Although a considerable decrease in the infant mortality rate has been reported over the past 2 decades,[6] but the burden still remains substantial, based upon which, WHO has declared neonatal sepsis as a problem of global concern and the associated burden of neonatal infectious diseases a global challenge.[6] *Klebsiella pneumoniae* whether an ESBL or carbapenamase producer contributes majorly to the globally inclining problem of antimicrobial resistance.[8] Owing particularly to the ease of transmission of MDRs in healthcare environment, > 5 million deaths are expected to occur by 2030, which previously was considered responsible for over one million deaths.[9] Extended spectrum beta lactamase (ESBL) producing *Klebsiella pneumoniae* has also been included by CDC in its list of serious threats,[10] It has also been labelled as a bacterium of critical priority by the World Health Organization, [11] as it serves as a major driver of antimicrobial resistance (AMR) globally. In the report by CDC, it is stated, to stop referring to land up in a post antibiotic era, and that we are already living in it, with the most effective drugs being rendered ineffective. Rather than relying on the development of new antibiotics, which will also become ineffective one day, the strategies for infection prevention and control need to be implemented along with thorough antimicrobial stewardship.[10]

Klebsiella pneumoniae, first identified in the late nineteenth century as Friedländer's bacillus, has since emerged as a pathogen of significant global concern. [12] Two distinct types i.e. hypervirulent (hvKp) and classical (cKp), are known to exist, but the molecular diagnostics and microbiologic criteria for distinguishing between hvKp and cKp stays largely unestablished. [12] They have extensively acquired mobile genetic elements which encode antimicrobial resistance genes like for Extended spectrum beta lactamase (ESBL) and Carbapenamase, together called MDR-Kp are disseminated globally. [12] Especially associated with cKp, this is based on having gained the ability to accumulate mutations, thus enabling it to undergo extensive evolution, hence developing Pan drug resistant clones.[3] Grouped as multidrug resistant (MDR), showing resistance against three different drug classes, extensively drug resistant (XDR) showing resistance against at least one antibiotic from most of the antibiotic classes, and pandrug resistant (PDR) are the isolates showing resistance to each drug in all antibiotic groups.[3]

Both hypervirulence and drug resistance in *Klebsiella pneumoniae* is acquired through mutations and/or horizontal gene transfer via conjugative or/and mobilizable plasmids, integrative conjugative elements (ICE), integrons, insertion sequences and transposons.[3] This is also true for the β-lactamases that became mobilized on plasmids to become widespread, mainly due to the misuse of β-lactam antibiotics. Following the introduction of first and second generation cephalosporins, enzymes such as TEM-1 and SHV-1 arose, which were found to be highly related, with the difference in the variants being based on a few amino acid substitutions. On the contrary, CTX-M-family of ESBLs are reported to be genetically diverse. Today CTX-M type enzymes are the most prevalent with CTX-M-15 variant dominating worldwide.[13] with the same ESBL genes predominantly found in *Klebsiella pneumoniae* as well.[14] Inspite of the enormous number of diagnostic tests/tools available for phenotypic and genotypic identification of β-lactamses, unfortunately ESBLs are not identified timely, resulting in poor clinical outcomes.

Methodology

This was a descriptive cross sectional study, conducted at Department of Microbiology, Khyber Medical University and Department of Microbiology, Gajju Khan Medical College / Bacha Khan Medical Complex, Swabi from January 2025 to December 2025. After getting the ethical approval KMU/IPDM/IEC/2024/56 on 17th Dec, 2024, sample collection was carried out by non-probability convenience sampling. The sample size was calculated by formula $n= z^2pq/e^2$ used for descriptive studies,[15] where *n* is the sample size, whereas, *z* is the standard normal variate, with a value of 1.96 at 5% margin of error. *p* is the expected proportion in the population on the basis of previous studies (6.1% [16] overall average prevalence, *q* will be calculated as 1-*p* and *e* is the margin of error (0.05). The estimated sample size was calculated to be

88. The isolates from all clinical samples and all age groups were included in the study whereas the duplicate samples were excluded. For the phenotypic detection of an isolate to be an ESBL producer, the isolate showing resistance to the 3rd generation cephalosporins (a zone diameter of ≤ 22mm for Ceftazidime and ≤ 25mm for Ceftriaxone)[17] were included in the study whereas those found sensitive were excluded.

Received samples from the NICU, ICU and different wards were processed by inoculation on Blood, MacConkey and Chocolate agars, while Cystine Lactose Electrolyte Deficient agar (CLED) (Oxoid, UK), was used for the inoculation of the urine samples. The inoculated culture plates were incubated at 35°C ±2°C for 20-24 hours followed by observing growth and all the lactose fermenting, mucoid colonies resembling those of *Klebsiella pneumoniae* were subjected to further testing for initial identification by Gram staining. API 10S and 20E were used to identify up to the genus and species level. As per CLSI guidelines[17], the antimicrobial susceptibility testing was performed by Kirby Bauer disc diffusion method, for Amoxicillin clavulanic acid (20/10µg), Ceftazidime (30µg), Ceftriaxone (30µg), Amikacin (30µg), Sulbactam-cefoperazone (100/10µg), Piperacillin-tazobactam (100/10µg), Ciprofloxacin (5µg), Imipenem (10µg), Meropenem (10µg), Ertapenem (10µg), Fosfomycin (200µg) and Nitrofurantoin (300µg). Antimicrobial susceptibility pattern was noted accordingly. SPSS version 26 was used for the data analysis. For qualitative analysis, frequencies and percentages were used, and for quantitative analysis, means ± SD were used.

For phenotypic detection of ESBL production, Double disc synergy Test (DDST) was performed using the disc of Amoxicillin-clavulanic acid (20/10µg) along with those of third generation cephalosporins i.e. Cefotaxime (30µg) and/or Ceftriaxone (30µg), placed at a distance of 20 mm from each other on a lawn of the isolate made on Mueller-Hinton Agar[18]. Phenotypic detection of ESBL production was assessed through extension in the size of zone of inhibition towards amoxicillin clavulanic acid forming a keyhole like shape, [18] as shown in Figure 1. and the results were recorded accordingly.

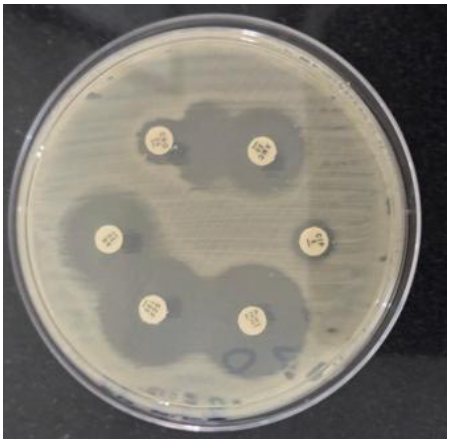


Figure 1. Phenotypic confirmation of ESBL production by DDST.

Results

Out of a total of 1584 samples that yielded growth, 1116(70.45%) were Gram negative rods. These included 572(51.25%) *Escherichia coli*, 165(14.78%) were *Klebsiella pneumoniae*, 151(13.53%) were *Salmonella typhi*, followed by *Pseudomonas aeruginosa*, which were 118(10.57%), 44(3.94%) were *Proteus mirabilis*, Acinetobacter were 31(2.77%), Enterobacter were 29(2.59%), both Burkholderia and *Strenotrophomonas* were 2 each (0.17%) and both Citrobacter spp. and *Salmonella paratyphi* were 01 each (0.08%). The remaining of the positive yields included 439(27.71%) Gram positive cocci and 1.83% i.e. 29 were identified as Candida species.

Out of 165 *Klebsiella pneumoniae* 95(57.57%) isolates were identified as ESBL producers, as showed a zone diameter of ≤ 22mm for Ceftazidime, ≤ 25mm for Ceftriaxone on Kirby Bauer disc diffusion method according to CLSI guidelines.[17] For further confirmation double disc synergy test was done, after which they were included in the study. It was a majority of males n=52(54.73%) that were affected whereas females were n=43(45.26%). Age group ranged from newborn to 80 years. Samples were received from the neonatal and adult intensive care units i.e. NICU and ICU mainly, as shown in Figure 2, with 50.52% of the isolates from blood, 20% each from pus and urine, 4.21% from tissue, 3.15% from tracheal aspirate and 1.05% each from sputum and cerebrospinal fluid as shown in Figure 3.

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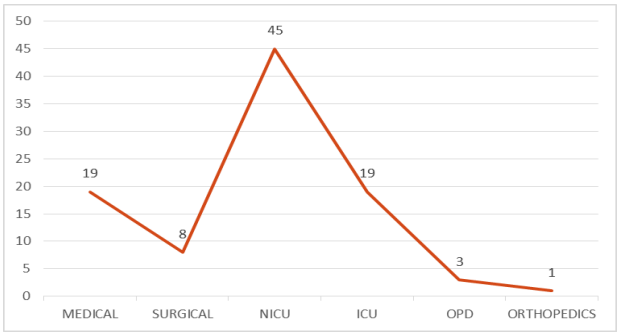


Figure 2: Ward wise distribution of the isolates

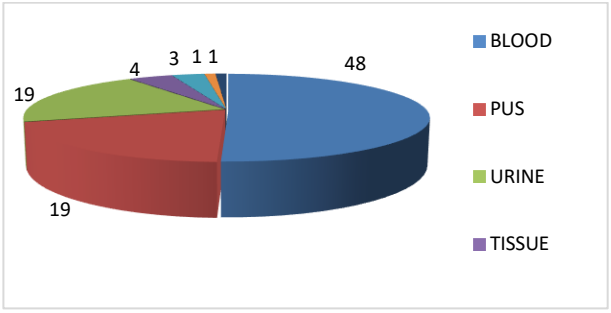


Figure 3. Sample wise distribution of the isolates.

Antibiotic susceptibility of the 95 ESBL producing *Klebsiella pneumoniae* isolates is shown in Figure 4, and based on the resistance pattern majority were XDR as shown in Figure 5. 100% co-resistance was recorded in all the isolates against Amoxicillin-clavulanic acid, Ceftriaxone and Cefotaxime, followed by 95.78% resistance against Ciprofloxacin. n=57(60%) of the isolates were resistant to Meropenem and Imipenem. Out of a total of 19 urinary isolates, Nitrofurantoin showed comparatively better efficacy, with a sensitivity of n=10(52.63%) as compared to Fosfomycin, where the sensitivity was substantially reduced i.e. n=7(36.84%).

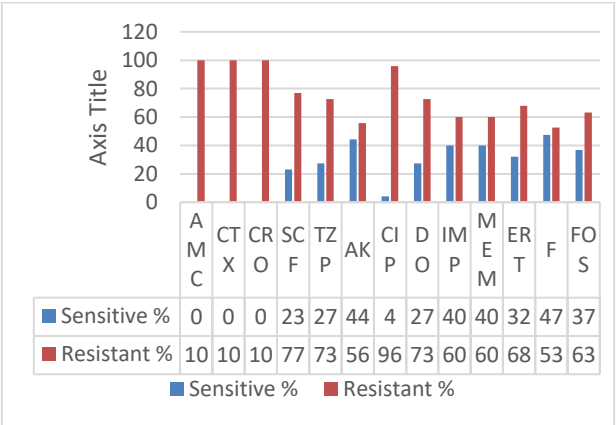


Figure 4. Antimicrobial susceptibility pattern of ESBL producing Klebsiella pneumoniae

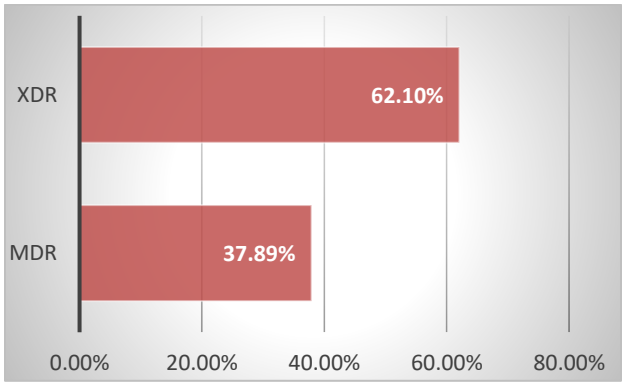


Figure 5. Distribution of the isolates as MDR (n=36) and XDR. (n=59)

Discussion

In the recent times, nosocomial infections pose a major threat to healthcare systems globally, mainly in developing countries. [19] *Klebsiella pneumoniae*, is included in the list of most common pathogens, responsible for causing a wide range of severe infections.[20] Being an important opportunistic pathogen especially in the nosocomial settings, it is continuously subjected to various groups of antibiotics, thus becoming multidrug resistant.[21]

Klebsiella pneumoniae, according to the annual epidemiological report on antimicrobial resistance in the EU/EEA (EARS-Net)[22] was reported as the third important bacterium after *Escherichia coli* and Methicillin resistant *Staphylococcus aureus* (MRSA) and second prevailing Gram negative bacillus which is the same order, as reported in our study. The pattern of resistance against different groups of antibiotics was also the same as reported in our study i.e. 100% co-resistance against Amoxicillin clavulanic acid, Cefotaxime and Ceftriaxone.[22] This was followed by 95.78% resistance against Ciprofloxacin, with increasing resistance levels against the Carbapenems and Amikacin, comparable with the results in another study.[18]

Another pertinent finding common in the said report and our study was the increasing prevalence majorly in the NICUs and ICUs.[22] This increasing prevalence in the intensive care units was also reported in other studies as well reported from different parts of the world. [5,6,7,18,23]

Klebsiella pneumoniae, being capable of persisting on the environmental surfaces, human skin, within the respiratory tract and urinary tract allows ease of transmission among patients by touching the surfaces and patients during examination, thus making it responsible for causing frequent outbreaks in intensive care units.[24] It

has also been referred to low hygiene standards and understaffing on one side whereas the factors like prematurity with low birth weight, and prolonged hospitalization together contribute to the entire process especially in LMICs.[7]

Since another important finding in our study, in addition to antimicrobial resistance was the increased incidence of blood stream infections(BSI) with resistant organisms, it was the same concern stressed upon in the annual epidemiological report on antimicrobial resistance in the EU/EEA. [22] but inconsistent with the results of studies where majority was of the isolates were from the urinary samples.[18,23] an important reason of the high rates of BSI especially in the lower and middle income countries are the financial constraints making effective management of sepsis not always possible. Hence this leads to a constant increase in the rates of antimicrobial resistance (AMR) globally which further compromises the management for sepsis.[6]

With the advent of increasing resistance, Carbapenems had emerged as the drugs of choice for the treatment of serious infections caused by ESBL producing *Klebsiella pneumoniae*, but the results of our study showed a much higher level of resistance against this group as compared to the previous studies that reported it to be 28% [20]and 25.7%. [25,26]

Another important finding was increasing level of resistance against Fosfomycin in the urinary isolates, which as recorded in our study was much higher than in the previous studies showing a resistance level of 16% and 10.9%.[23] This increase can be attributed to the ability of the organisms to modify enzymes, altered target site and/or reduced permeability. Further adding to this, Fosfomycin has been increasingly used in both Europe and Asia to treat infections caused by highly resistant organisms, leading to the spread of resistant isolates, with high levels of resistance against Fosfomycin reported as 61.9% in China, 36.4% in Taiwan 32%in Germany and 15% in USA.[23]

Aminoglycosides, yet another important group of antibiotics has been used massively for treating the infections caused by MDR *Klebsiella pneumoniae*. In our study, 55.78% of the isolates were resistant to Amikacin, which is higher than the percentage reported by Kashelfieh *et al*.,[25] and by Hesam *et al*., [27] further limiting the options.

This study aimed at highlighting the importance and implementation of thorough surveillance systems for MDROs and verifying the effectiveness of the empirical therapies, thus minimizing therapeutic failures. Continuous surveillance strategies are crucial in order to save limited treatment options available, along with spreading awareness about the prevention strategies amongst which maintaining hygiene is an important and effective measure to control the spread of infections in the healthcare settings.

Conclusion

ESBL producing *Klebsiella pneumoniae* isolates showed very high level of resistance to most groups of antibiotics. Susceptibility was substantially reduced against the Carbapenems and Amikacin as well, which stresses upon the importance of treatment based on empirical with antimicrobial stewardship in true spirit.

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