

Antibiogram and Plasmid profiling of clinical multidrug resistant *Escherichia coli*

Shrestha S¹, Mali NM¹, Tiwari KB², Adhikari N¹, Shrestha UT¹, Basnyat SR¹,

¹ Kantipur College of Medical Science, Tribhuvan University, Sitapaila, Kathmandu;

² Department of Biological Science, Illinois State University, Illinois, USA.

Email: upendrats@gmail.com

Abstract

Introduction: Multiple antibiotic resistances among common bacterial pathogens have been established as an alarming public health problem elsewhere. This study was aimed to explore prevalence of Extended-spectrum beta-lactamase (ESBL) producers among multi-drug resistant (MDR) and plasmid profiling patterns of *Escherichia coli* isolated in Kathmandu Model hospital, Nepal over three months period.

Methods: Altogether 49 isolates were randomly selected among the reported MDR *E. coli* and retested for their susceptibility pattern and ESBL production by Kirby-Bauer disc diffusion test. Minimum Inhibitory Concentration of the isolates towards (fluoro) quinolones was determined by agar dilution method. Plasmids from isolates were extracted by alkaline lysis method.

Results: All isolates were completely resistant to Amoxycillin but sensitive to Imipenem. A very high prevalence (44, 89.8%) of ESBL producers was detected. Most of the isolates were resistant to commonly used antibiotics such as Quinolones, Tetracyclines and Cotrimoxazole. Among Quinolones, the Minimum Inhibitory Concentration (MIC) range for Nalidixic acid, Ciprofloxacin and Ofloxacin were 512 - >4093, 8 - 4096 and 1 - 256 µg/ml respectively. All 31 (63.3%) plasmid-harboring isolates contained a >33.5 kb sized plasmid. Among them, seven isolates possessed multiple (2 – 7) plasmids. Overall, twelve different resistance patterns were observed among the bacteria. Based on the patterns, the high molecular weight plasmid seemed to contain most of the resistance genes.

Conclusion: It is suspected that multi drug resistance and ESBL production in *E. coli* with resistance to Quinolones may be due to their high molecular weight plasmids. So, continuous antibiotic susceptibility test and surveillance of the plasmid and chromosome of *E. coli* is essential as plasmid analysis has been applied to determine the evolution and spread of antibiotic resistance among isolates.

Keywords: *Escherichia coli*, Antibiotic resistance pattern, Multidrug resistant (MDR), Extended spectrum Beta-lactamases (ESBL), Plasmid profiling

Introduction

Prevalence of multidrug resistance (MDR) among clinical isolates varies greatly worldwide and in different geographic areas with increase in drug resistance over time because of the indiscriminate use of antibiotics in clinical practice¹. Among the bacteria, Gram negative bacteria including *Escherichia coli* have recently become more resistant to commonly used antibiotics. Those carrying R-plasmids

are the most serious problem among antibiotic resistant organisms because of their rapid spreading nature².

E. coli that exists as a normal flora in human intestine is an opportunistic gram-negative, facultative anaerobic pathogen of *Enterobacteriaceae* family. *E. coli* is major causes of nosocomial and community-acquired infections in humans as well as one of the most frequently isolated

organisms in clinical specimen. *E. coli* have been associated with a number of disease including severe and sometimes fatal infections such as pleonephritis, septicemia, meningitis, endocarditis, urinary tract infection, epidemic diarrhoea of adults and children^{3,4}.

Pathogenic isolates of *E. coli* that have a relatively large potential for developing resistance to multiple drugs is of main concern because of its ability to produce Extended spectrum Beta-lactamases (ESBL). ESBLs or Ultra-broad-spectrum β -lactamases are plasmid-mediated bacterial enzymes that confer resistance to a broad range of B-lactams (penicillins, first-, second-, and third generation cephalosporins, and aztreonam) by hydrolyzing these antibiotics. These enzymes are descended by genetic mutation from native B-lactamases found in gram negative bacteria. ESBLs are often acquired by transfer of genetic-related information from one organism to another and codes for resistance determinants to other antimicrobial agents; hence, multidrug (MD) resistance is expected of ESBL-producing isolates⁵.

In the present situation, the emergence of MDR *E. coli* isolates is a big threat for the antibiotic therapy. These MDR isolates are adding up resistance to antibiotics day by day. Therefore our prime research focus is to screen ESBL-positive resistance profile for β -lactamase, quinolones resistance and plasmid profiling of those emerging threats.

Methods

Bacterial strain: Out of many samples from urinary tract infected patients, forty-nine isolates were randomly selected among the reported MDR *E. coli* at Kathmandu Model Hospital, Kathmandu from February 2010 to April 2010. The samples were further retested in the Laboratory of Kantipur College of Medical Science by sub-culture in MacConkey agar, analyzing their colony characteristic as well as by Gram staining and biochemical tests. The pure culture of MDR isolates were preserved in 20% glycerol containing Tryptic Soya broth and kept at -70°C until subsequent tests were performed.

Antimicrobial susceptibility testing: Antimicrobial Susceptibility test was performed by kirby-Bauer disk diffusion method following Clinical and Laboratory Standard Institute guidelines.⁶ Isolates were introduced to 12 commonly used antibiotics namely Amoxycillin, Chloramphenicol, Ciprofloxacin, Cotrimoxazole, Doxycycline, Gentamycin, Imipenem, Nalidixic acid, Nitrofurantoin, Norfloxacin, Ofloxacin and tetracycline. Isolates showing resistance to three or more different classes of antibiotics were considered as MDR.

Screening and confirmation of ESBL producers: MDR isolates were screened for possible ESBL production using ceftazidime (30 μ g) and ceftriaxone (30 μ g) following CLSI, 2010. Confirmation of ESBL production was determined by combined disk (CD) assay using MASTDISCTM ID ESBL detection discs consisting of ceftazidime (30 μ g) and ceftazidime (30 μ g) plus clavulanic acid (10 μ g). Isolates with zone of inhibition diameter for either ceftazidime ≤ 22 mm or ceftriaxone ≤ 25 mm or both were considered as the possible ESBL producing strains and an increase in zone diameter of ≥ 5 mm in the presence of clavulanic acid was concluded as confirmed ESBL producers.

Determination of Minimum Inhibitory Concentration (MIC): Among quinolones, MICs of nalidixic acid, ciprofloxacin and ofloxacin were determined by agar dilution method following CLSI, 2010. Secondary antibiotics standards provided by Nepal Medicine Council, Babbarmahal were used for MIC determination.

Extraction and profiling of plasmid DNA: Plasmid DNA was isolated by alkaline lysis method⁷, separated on 0.8% agarose gel electrophoresis at 120 V for 1 hrs and stained by SYBR safe stain. Plasmid profile were created by grouping strains possessing the same number of plasmid bands and molecular mass or a part of profile containing a core plasmid³.

Data analysis: Data were analyzed by using WHONET 5.6.

Results

Of the 49 clinical MDR *E. coli* isolates screened for antimicrobial agents, all were found to be resistant to Amoxicillin (100%), Ciprofloxacin (100%) and Nalidixic acid (100%) but sensitive to Imipenem (100%). A higher percent of sensitivity was also found to Nitrofurantoin (97.95%). A very high prevalence (89.8%) of ESBL producers was detected among these MDR isolates. The MIC of fluoroquinolones showed that all isolates were resistant to nalidixic acid and ciprofloxacin where as only 2 (4.08%) isolates were susceptible to ofloxacin (Table 1).

Table 1. Minimum Inhibitory Concentrations for MDR E. coli isolates (n=49)

Antibiotic name		Ciprofloxacin	Nalidixic acid	Ofloxacin
Breakpoints		S≤1 R≥4	S≤16 R≥32	S≤2 R≥8
M	1µg/ml	0	0	1
I	2µg/ml	0	0	1
C	4µg/ml	0	0	1
	8µg/ml	1	0	0
V	16µg/ml	1	0	1
A	32µg/ml	5	0	6
L	64µg/ml	6	0	32
U	128µg/ml	6	0	4
E	256µg/ml	4	0	3
S	>256µg/ml	26	49	0
No of resistant isolates		49	49	47
MIC Range		8 to 4096	512 to >4096	1 to 256

Among these 49 isolates, 31 (63.27%) harbored plasmids ranging in molecular size from 2.05 kb to >33.5 kb. On the basis of plasmid band and number of visible bands, seven different plasmid profile groups for the antibiotic-resistant strains were identified. The number of strains per plasmid profile group vary from 1-11 (Table 2). The most common antibiotic resistance pattern was AmxNalNorCipOfiTetDoxCot followed by AmxGenNalNorCipOfiTetDoxCot, AmxNalNorCipOfiTetDoxCot and other R-type resistance patterns (Table 2). Strains showing the resistance pattern AmxGenNalNorCipOfiTetDoxCot contained the highest number of plasmids.

Table 2: Antibiotic resistance pattern, plasmid contents and plasmid size of MDR isolates

Antibiotic resistance pattern	Plasmid profile	No. showing pattern	Molecular weight
AmxGenNalNorCipOfiTetDoxCot	6	1	>33.50,>33.50,10.13,4.24,2.05,
	5	2	>33.50,9.39,6.68,5.06,2.05
	4	1	>33.50,>33.50,5.06,2.05
	3	1	>33.50,9.39,6.68
	2	1	>33.50,6.68
	1	3	>33.50
AmxNalNorCipOfiTetDoxCot	3	1	>33.50,9.39,6.68
	2	2	>33.50,6.68
	1	2	>33.50
AmxNalNorCipOfiTetDox	3	1	>33.50,9.39,6.68
	2	2	>33.50,6.68
	1	1	>33.50
AmxGenNalNorCipOfiTetDoxChlCot	6	1	>33.50,>33.50,9.39,6.68, 3.12,2.05
	2	1	>33.50,10.13
	1	1	>33.50
AmxNalNorCipOfiTetDoxCot	3	1	>33.50,10.13,6.68
	2	2	>33.50,10.13
AmxNalNorCipOfiTetDoxChlCot	2	1	>33.50,10.13
AmxNalNorCipTetDox	1	1	>33.50
AmxNalCipDoxTetCotChl	5	1	>33.50,9.39,6.68,5.06,4.24
AmxNalNorCipOfiTetCot	1	1	>33.50
AmxNalNorCipOfiTetDoxChlCot	1	1	>33.50
AmxNalNorCipOfiTetDoxCotNit	1	1	>33.50
AmxGenNalNorCipOfiTetDoxCot	2	1	>33.50,>33.50

Note: Lane 1 and Lane 7 super mix DNA Ladder (marker). Lane 4 >33.50, >33.50, 9.39, 6.68, 5.06, 4.24 (Eco 41); Lane 5 >33.50, 6.68 (Eco 29); Lane 11 (Eco 44) and Lane 13 >33.5 Kb (Eco 26) and Lane 2, Lane 3, Lane 6, Lane 8, Lane 9, Lane 10, Lane 12, Lane 14 and Lane 15 all are negative.

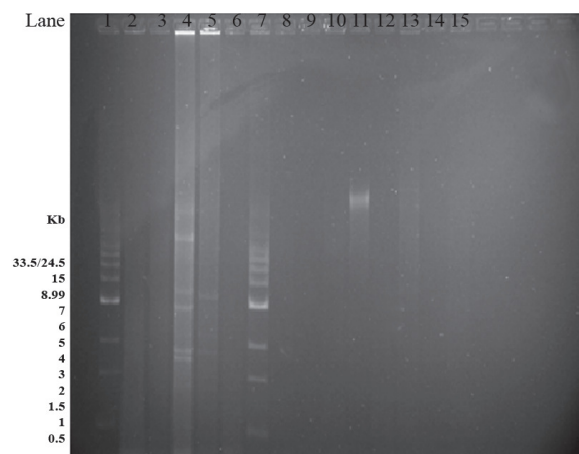


Figure 1. Agarose gel electrophoresis showing different plasmid bands

Discussion

Studies on antimicrobial sensitivities among commonly isolated microorganisms, mainly bacterial pathogens, has been conducting elsewhere. For developed countries, the advent and access of sophisticated molecular techniques accelerated them into new horizon of molecular biology of bacterial resistance. However, in our context, almost all of the basic researches used to focus on mere observations of antibiotic susceptibility tests. In these days, It's good that many of the published works these days are focusing on more specific microbial groups of clinical and non-clinical relevance. In this study, we tried to explore the relation between antibiotic susceptibility of multi-drug resistant *E. coli*, especially ESBLs, to their plasmid profiles in a hospital setting.

Randomly selected 49 MDR *E. coli* isolates were taken in to our research lab and retested for their antibiotic sensitivity response. Sixteen different resistance patterns were observed among the isolates with antibiotics that are commonly used in Nepal to treat *E. coli* infections.

All isolates were resistant to Amoxicillin, Nalidixic acid and Ciprofloxacin similar to recent studies conducted elsewhere^{3,8,9}. We observed more resistance patterns compared to that by Daini OA and Adesemowo A,

Gobernado et al., and Ozbakir G et al.^{3,10,11}. We included four commonly used quinolones, viz., Nalidixic acid, Norfloxacin, Ofloxacin and Ciprofloxacin. Except two, all isolates were resistant to those four quinolones. This finding elucidated that these bacteria are being resistant to all generations of quinolones tested. These antibiotics are used for years in Nepal and bacteria are gaining resistance to all gyrase inhibitors – broad spectrum antibiotics. Most of the isolates were resistant to Tetracyclines and Cotrimoxazoles too. This result is similar to other findings elsewhere that the ESBL producers are resistant to quinolones as well^{12,13,14}. Interestingly, most of them were sensitive to Chloramphenicol that is rarely used in these days and Nitrofurantoin to occasionally treat Urinary tract infections¹⁵. Only the drug of choice seemed to be Imipenem – a monolactam. However, it can easily be generalized that the ESBLs may gain resistance to the monolactam sooner or later similar to their aggressive response to the gyrase inhibitor – the quinolones. Therefore, this study explored an urgency of finding other effective anti-ESBL antibiotics in the area of clinical microbiology.

Comparatively higher prevalence (89.80%) of positive ESBL producers was found in the current research work. These ESBL producers showed highly resistance to quinolones (96-100%), tetracycline (68%), Doxycycline (93%) and Cotrimaxazole (77%), and low resistance to Gentamycin (32%) and Chloramphenicol (16%). All the isolates were susceptible to Imipenem and highly sensitive too Nitrofurantoin (98%). Ahmed *et al.*, 2010; Lagace-Wien *et al.*, 2007; and Vaidya, 2011 reported similar study of co-existence of ESBL with resistance to Cotrimoxazole, Tetracycline, Doxycycline, Gentamycin, Ciprofloxacin and degree of sensitivity to Imipenem and nitrofurantoin¹⁶⁻¹⁸.

In our study, plasmids of the molecular size ranging from 2.05 to >33.5 kb were isolated from 63.27 % of total MDR *E. coli*. Among them, seven isolates possessed multiple (2 – 7) plasmids. Overall, twelve different resistance patterns were observed among the bacteria. Plasmids of different molecular size ranging from 0.12 kb to 65 in clinical isolates of *E. coli* had reported in the work of Daini *et al.*, 2008 and Hamad, 2009^{3,19}. Daini *et al.*, 2008 concluded that different plasmids often coexisted in the same host cell³. Previous studies have demonstrated that multiple antibiotic resistances are associated with higher molecular weight plasmids^{20,21}. Plasmids of same molecular size can be found in many strains. Atmost isolates in this research showed a common higher molecular weight plasmid (>33.50 kb). Based on the resistance patterns, the high molecular weight plasmid seemed to contain most of the resistance genes.

Plasmids were not observed in 18 (36.73%) of our MDR isolates. The resistance in those isolates might probably be

chromosomal borne. In many bacteria, the mobile genetic elements, transposon carried resistance genes²². However, the broad spectrum of resistance can't be possessed by transposons alone. These plasmids less isolates might be Hfr strains.

In conclusion, MDR and ESBL-producing *E. coli* constitute a major health problem in Nepal. Drug resistant *E. coli* harbored plasmid of varying size and molecular weight. Higher molecular weight plasmid may be associated with MDR and ESBL-producing *E. coli*. So, increased periodic review and formulation of antibiotic policy to control acquisition of drug resistance and appropriate routine antimicrobial susceptibility testing with evaluation of phenotypic confirmatory ESBL by MIC and genotypic detection to confirm ESBL producers and detection of other β -lactamases, and surveillance of the plasmid and chromosome of *E. coli* is essential as plasmid analysis has been applied to determine the evolution and spread of antibiotic resistance among isolates.

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Conflict of interest: None declared

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