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Molecular determinants of B-lactamase producing *Klebsiella pneumoniae* in Mansoura University Neonatal Intensive Care Unit

Abstract

Background: The emergence of β-lactamase- producing *Klebsiella pneumonia*, represents a significant diagnostic and therapeutic challenge to the management of infections caused by this organism. This prospective study aimed to study the frequency of β-lactamase production by *K. pneumoniae* in neonatal intensive care unit (NICU) of Mansoura University Children's Hospital in Egypt.

Methods: This study was conducted over a period of 36 months from September 2010 to August 2013, where 684 samples were collected from different body sites of neonates in the NICU. Microbial isolation, identification and antimicrobial susceptibility testing were carried out. β -lactamase production by *K. pneumoniae* isolates was confirmed by phenotypic methods and PCR amplification of related genes using a sixgene panel for the amplification of the bla_{CMY-2} , bla_{DHA} , bla_{ACC} , bla_{SHV} , bla_{TEM} and bla_{CTX-M} genes. In vitro transformation and conjugation were carried out to detect plasmid mediated *AmpC* β - lactamase resistance by transmission to *E. coli*.

Results: *K. pneumoniae* was isolated at a rate of 12.6% and β-lactamase production was detected in 62.8% of the isolates. The most commonly detected β-lactamase gene was bla_{SHV} (51.9%), followed by Bla_{CMY-2} (16.7%), bla_{DHA} (13%), bla_{TEM} (9.2%), bla_{CTX-M} (7.4%) and bla_{ACC} (1.9%). Additionally, some strains carried combinations of two or three genes. The plasmid carrying bla_{CMY-2} was 100% successfully transformed

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into the competent *E. coli* LE392, while conjugation was only 77.8% successful using the same *E. coli* strain.

Conclusion: This study demonstrates that *K. pneumoniae* is a common multidrug resistant isolate in neonatal ICU and associated with production of β-lactamases in a significant number of those isolates. This feature could represent a real risk for failure of therapeutic options.

Key words: K. pneumoniae, ESBL, Egyptian neonates.

Introduction

Beta-lactamase producing *K. pneumoniae* has been increasingly noticed as a problematic pathogen in different hospital settings. Moreover, the widespread and misuse of antibiotics, continues to increase resistance in Beta-lactamase drugs and to reduce the chance for cure and hamper infection control measures in hospitals worldwide (1,2).

Beta-lactamases are a group of enzymes that inhibit ß- lactam drugs by breaking their active ring structure. The most important ß-lactamases are those produced by *Enterobactericae*. These enzymes are mostly responsible for therapeutic failure to this crucial group of drugs (3).

Two types of Ampler class A ß-lactamases are known to inhibit third generation cephalosporins, and these spread rapidly through chromosomal and plasmid mediated enzymes in Gram-negative bacteria. The plasmid mediated process is more critical being transferable among different species of *Enterobactericae*. Extended spectrum ß-lactamases (ESBLs) resist all ß-lactams, except cephamycin and carpabenems and include a classical type that is a mutant of TEM and SHV and especially the CTX-M type (4). Moreover, Ampler class C (AmpC) β-lactamases are clinically important, since these mediate resistance to broad range cephalosporins including cephamycins and being resistant to clavulanates (5). Chromosomal AmpC enzymes are inducible and non-transferable. The transferable plasmid mediated AmpC genes favored their dissemination among *Enterobacteriaceae*. Plasmidencoded bla_{CMY} , bla_{DHA} , and bla_{ACC} determinants producing class C enzymes are described with increasing frequencies (6).

This work aimed to investigate the prevalence of *K. pneumoniae* as a nosocomial pathogen and its molecular resistance determinants in the NICU of Mansoura University Children's Hospital.

Patients and Materials

Study population

This prospective study included neonates suspected of having nosocomial infection (NI) after 48 hours of admission to the NICU. A thorough history, clinical monitoring and laboratory tests were performed and documented on standard forms.Clinical sepsis evaluation was performed and divided into five categories as described by Grether

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and Nelson (7); (1) Frequent episodes of apnea and bradycardia; (2) seizure or change in the level of consciousness; (3) tachycardia, dyspnea or increase in respiratory support; (4) signs of septic shock; and (5) fever or temperature instability. Neonates diagnosed with early-onset sepsis were excluded. A case was defined as any neonate who developed *K. pneumoniae* nosocomial infection diagnosed by a positive culture. Parents of neonates have signed informed consent and the study protocol was approved by the ethics committee at Mansoura Faculty of Medicine.

Sample collection

Samples from different body sites; blood, urine, cerebrospinal fluid, endotracheal aspirate of mechanically ventilated neonates and wounds of surgically operated neonates were collected. Processing of the samples was done according to standard protocols used in the Microbiology Diagnostic and Infection Control Unit (MDICU)/ Department of Medical Microbiology and Immunology, Mansoura faculty of medicine. K. pneumoniae isolates were identified by colonial morphology, Gram-stained smears, culturing the isolates on MacConkey's agar (Oxoid, UK) at different temperatures 4°C, 10°C and 42°C to differentiate K. pneumoniae from other Klebsiella spp.(8), and using biochemical reactions (oxidase, gelatin liquefaction test, catalase, DNAase production and IMVC). Further identification to the species level was carried out using API 20E. Isolates were stored with50% sterile glycerol at -80°C.

Antimicrobial susceptibility testing

Susceptibility tests were performed using the Kirby–Bauer disc diffusion method and Muller-Hinton agar (Oxoid, UK) according to the Clinical Laboratory Standards Institute guidelines (CLSI) (9). The following antibiotics were used; gentamicin (10 μ g), ceftazidime (30 μ g), cefpime (30 μ g), aztreonam (30 μ g), imipenem (10 μ g) and ampicillin/

sulbactam (20 µg) (Oxoid, UK).

Screening for extended spectrum β-Lactamases production

All *K.pneumoniae* isolates that showed resistance to any of the β -lactam drugs were tested for the presence of ESBL. Detection of ESBL was performed using double disk synergy (DDS) test on Mueller-Hinton agar. It was defined as an increase in the zone of inhibition of \geq 5 mm with cefotaxime discs when they were tested in combination with discs containing clavulanic acid (10). The class C β -lactamase resistance of AmpC phenotype was detected by the AmpC disc test and is defined as a flattening or indentation of the cefoxitin inhibition zone in the vicinity of a sterile disc of 6 mm moistened with 20µl of sterile saline and inoculated with multiple colonies of the tested organism after overnight incubation at 37°C (11). A negative test showed undistorted zone. E. coli ATCC 25922 was used as a control strain.

Plasmid content and transmissibility

Plasmid DNA was extracted from the β-lactamase producing K. Pneumoniae isolates using the alkaline lysis method described by Birnhoim and Doly (1979) (12). E. coli LE392 strain was made competent using calcium chloride. Plasmid DNA (0.1-1mg in water) was mixed with (100ml of fresh or 200ml of competent cells stored at -80° C) and placed on ice for 30 minutes. The cells were then heat shocked by incubation at 42°C for 90-120 seconds and then back to ice for another 2 minutes (13). Conjugation was carried out by broth mating (at a ratio of 1:4) to test the transmissibility of bla_{CMY-2} plasmid from the K. pneumoniae isolates harboring this plasmid as donors to a recipient E. coli LE392 strain which was made competent using calcium chloride E. coli ATCC 25922 strain (14). The transformants and transconjugants were selected on Luria-Bertani agar containing ceftazidime (10 µg/ml) (Oxoid, UK).

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Characterization of the transformants and transconjugants

Detection of beta-lactamase production in transformants and transconjugants, was confirmed phenotypically by the ability to grow on Luria-Bertani agar containing ceftazidime (10 μ g/ml) and genotypically by isolation of the bla_{CMY-2} plasmid, comparing its size with that of the donor strain. PCR amplification of bla_{CMY-2} gene was accomplished using primers listed in **Table 1**.

PCR for β**-lactamase genes**

For those isolates that met the criteria for either the ESBL resistance or the AmpC phenotype, PCR was carried out using a six-gene panel for the amplification of the bla_{CMY} , bla_{DHA} , bla_{ACC} , bla_{SHV} , bla_{TEM} and bla_{CTX-M} genes. The following thermal cycling program was used: 95° C for 5` followed by 35 x [95°C for 1`; 55°C for 1`; 72°C for1` then 72°C for 10`. The amplified DNA fragments were visualized after electrophoresis of 10µl of the PCR samples using a 1% agarose gel (15, 16).

Results

Out of the 684 collected samples, 86 (12.6%) yielded positive culture results for *K. pneumoniae* isolates. These were recovered from 35 blood samples (40.7%), 20 wound swabs (23.3%), 16 urine samples (18.6%) and 15 endotracheal aspirates (ETA) (17.44%). All isolates were sensitive to imipenem while none of them showed sensitivity to ampicillin. B-lactamases production was

<i>bla</i> gene		Oligonucleotide sequence	Product size (bp)	Reference
bla _{CMY2}	F	TGG CCA GAA CTG ACA GGC AAA	461	(15)
	R	TTT CTC CTG AAC GTG GCT GGC	401	(13)
bla _{DHA}	F	AAC TTT CAC AGG TGT GCT GGG T	405	(15)
	R	CCG TAC GCA TAC TGG CTT TGC	405	
bla _{ACC}	F	AAC AGC CTC AGC AGC CGG TTA T	346	(15)
	R	TTC GCC GCA ATC ATC CCT AGC	540	(61)
bla _{tem}	F	ATA AAA TTC TTG AAG ACG AAA	867	(16)
	R	GAC AGT TAC CAA TGC TTA ATC A	007	
bla _{SHV}	F	GGG TTA TTC TTA TTT GTC GC	930	(16)
	R	TTA GCG TTG CCA GTC CTC	550	(10)
bla _{CTX-M}	F	CGA TGT GCA GTA CCA GTA A	585	(17)
	R	TTA GTG ACC AGA ATC AGC GG	505	(, , , ,

Table 1. Specific primers used for molecular amplification of the bla genes

Table 2. Distribution of 62 phenotypically
detected beta-lactamase producing
K. pneumoniae from different clinical
samples.

	K. pneumonia isolates		No. (%)lactamases producing	
Sample site	No.	%	K. pneumoniae isolates	
			ESBL	AmpC
Blood	31	50	26	5
Wound	15	24.2	09	6
Urine	10	16.1	05	5
ETA	06	9.7	03	3
Total	62	100	43 (69.4)*	19 (30.6)

*Represent 50% of the total K. pneumoniae isolates

phenotypically detected in 62/86 (72%) isolates as shown in **Table 2.**

The distribution of b-lactamase producing K. pneumoniae according to different body sites is shown in Table 2. The results revealed a higher detection among blood sample isolates; 31 (50%), followed by wound swab samples 15 (24.2%). Ten isolates (16.1%) were from urine samples and 6 samples (9.7%) were isolated from ETA samples. ESBL production was found in 43/86 of the total isolates (50 %). The frequencies of ESBL genes varied among isolates with 28, 5 and 4 isolates being positive for bla_{SHV} , bla_{TEM} and bla_{CTX-M} genes respectively. Two of these isolates contained dual resistance determinants for bla_{SHV} and bla_{CTX-M} . Class C (AmpC) b - lactamases were detected in 19 (22.1%) isolates. Molecular genetic basis for AmpC production determinants were as follows: 9, 7 and 1 isolates producing bla_{CMY-2} , bla_{DHA} and bla_{ACC} , respectively.

Table 3. Distribution of gene resistancedeterminants in the 54 beta lactamaseproducing K. pneumoniae

	lecular resistance determinants Beta lactamase	No. (%)
1.	bla _{sHV}	28 (51.9%)
2.	bla _{TEM}	5 (9.2%)
3.	bla _{CTX- M}	4 (7.4%)
4.	bla _{CMY-2}	9 (16.7)
5.	bla _{DHA}	7 (13%)
6.	blaACC	1 (1.9%)
7.	bla _{SHV} + bla _{CTX-M}	2*
8.	bla _{TEM} + bla _{CMY-2}	2*
9.	$bla_{TEM} + bla_{DHA}$	1*
10.	bla_{SHV} + bla_{ACC}	1*
11.	$bla_{CMY-2} + bla_{SHV} + bla_{CTX-M}$	2*

*Combined genes were already calculated among the individual genes in cells 1-6

Two isolates contained both bla_{CMY-2} and bla_{TEM} , one isolate had both bla_{TEM} and bla_{DHA} resistance genes, one more isolate possessed bla_{SHV} and bla_{ACC} . Two isolates possessed triple resistance genes (bla_{CMY-2} , bla_{SHV} , and bla_{CTX-M}) **(Table 3).** The (9) *K. pneumoniae* isolates carrying isolated bla_{CMY-2} plasmid were used as donors for both transformation and conjugation experiments. Transmissibility of antibiotic resistance plasmid bla_{CMY-2} was 100% successful by transformation to the competent *E. coli* LE392. Conjugation experiment was (77.8%) successful, 7 of the 9 *K. pneumoniae* isolates which were selected as donors.

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Discussion

Klebsiella pneumoniae has a feature of being one of the most common species harboring beta lactamases. Extensive use of antibiotics has contributed greatly to the emergence of multidrug resistant *Klebsiella* strains that cause hospital infections (18).

This study indicated that K. pneumoniae was responsible for 12.6% of nosocomial infection and (50%) of those isolates were ESBL produces. Higher ESBL production of *K. pneumoniae* clinical isolates (67%) was also reported by Abdel-Hady et al.(19) in Egyptian neonates hospitalized in ICU. However, a much lower incidence (2.97%) was reported by Romero et al.(20) in Spanish patients and healthy person. Therefore, wide range of incidence of ESBL production among organisms including K. pneumoniae can be attributed to the source of isolates, different antibiotic policies, empirical treatment and the age of patients enrolled in different studies. A study in an Egyptian University Hospital in 2010 reported the ESBL production rate of 76.5% in K. pneumoniae (21). The high rate of ESBL producers among clinical isolates in the developing world is troublesome due to lack of financial support for effective infection control and limited sources of effective antimicrobials. These factors have a clear impact on the morbidity and mortality related to infections caused by ESBL producers

This study demonstrated that bla_{SHV} was the most common resistance determinant accounting for 51.9% of the *K. pneumoniae* isolates, followed by bla_{CMY} , blaDHA, bla_{TEM} and bla_{CTX-M} at rates of 16.7%, 13 %, 9.2% and 7.4%, respectively,

These findings are lower than the results reported by Guiqing Wang and co-workers in USA (22) who detected bla_{SHV} and bla_{TEM} genes at rates of 84.3% and 50.4%, respectively In contrast, the study of Parveen *et al.*(2011) in India, reported bla_{CTX-M} as the most common ESBL-type among *K. pneumonia* isolates from blood, and 92% of their strains were ESBLs-producers, including high rates prevalence of bla_{TEM} (82%) and bla_{SHV} 46% (23).

The present study showed that the occurrence rate of class C beta lactamases (Amp C) is (30.6. %) among our Klebsiella isolates, and this figure is much higher than reports from other countries like Korea (3.1%) (24) and the United States (1.2%) (25). Additionally, our result was also less than those reported recently from Cairo (34.8%) and Korea (39.3%), respectively (26, 27). While this study demonstrated that bla_{CMY-2} is the most prevalent gene (51.9%), followed by bla_{DHA} (13.2%). The study of Al-Agamy (28) in Egypt, reported less prevalence rate of $bla_{CMY-2}(5\%)$ and slightly more rate of *bla_{DHA}* (23.5%). Furthermore, a second Egyptian study by the same author demonstrated bla_{CMY} , as a sole gene among AmpCB- lactamase genes in the Klebsiella isolates (29), whereas a Turkish study has found that all their K. pneumoniae isolates carried MOX group genes but bla_{DHA} and bla_{ACC} genes were not detected (30). All these results confirm the fact that these ESBL types are widely different within the same and each country.

In conclusion, this study demonstrates that the majority of *Klebsiella* isolates are multidrug resistant and producers of beta lactamases. The potential of these isolates in horizontal spread of resistance genes represent a real risk for failure of therapy by third generation cephalosporins.

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