CTX-M-15 in Gram-Negative Bacteria Isolated from Afghaninan Refugees in Iran (2012-2013)

Hamedani P*, Fallah F, Goudarzi H

Abstract—CTX-M beta-lactamases are enzymes were named for their greater activity against cefotaxime than other oxyimino-beta-lactam substrates (e.g., ceftazidime, ceftriaxone, or cefepime). The main aim of this study was to determine CTX-M-15 in gram-negative bacteria isolated from Afghaninan refugee in Iran. From August 2012 to February 2013, 100 non-duplicate non-consecutive K. pneumoniae and Escherichia coli were isolated from subjects of study. DNA was extracted using PCR method. Our findings showed that 32 isolated samples had CTX-M-15 gene and other genes were not observed. Of 32 samples containing CTX-M-15 gene, 24 samples belonged to E. coli and 8 samples belonged to Klebsiella pneumonia.

Keywords—CTX-M-15, Gram-negative Bacteria, Afghaninan Refugee, Iran

I. INTRODUCTION

The Enterobacteriaceae are a large family of Gram-negative bacteria including pathogens, such as: Salmonella, Escherichia coli, Yersinia pestis, Klebsiella and Shigella. Other disease-causing bacteria in this family include Proteus, Enterobacter, Serratia, and Citrobacter. Members of the Enterobacteriaceae can be trivially referred to as entrobacteria or "enteric bacteria", as several members live in the intestines of animals [1].

Many members of this family are a normal part of the gut flora found in the intestines of humans and other animals, while others are found in water or soil, or are parasites on a variety of different animals and plants. Escherichia coli is one of the most important model organisms, and its genetics and biochemistry have been closely studied. Most members of Enterobacteriaceae have peritrichous, type I fimbriae involved in the adhesion of the bacterial cells to their hosts. Some enterobacteria produce endotoxins. Endotoxins reside in the cell cytoplasm and are released when the cell dies and the cell wall disintegrates. Some members of the Enterobacteriaceae produce endotoxins that, when released into the bloodstream following cell lysis, cause a systemic inflammatory and vasodilatory response. The most severe form of this is known as endotoxic shock, which can be rapidly fatal. Enterobacteriaceae are also the most common cause of urinary tract infections (UTIs) in both community and healthcare settings [2].

Among gram-negative bacteria, escherichia coli remains one of the most frequent causes of several common bacterial infections in humans and animals. E. coli is the prominent cause of enteritis, urinary tract infection, septicaemia and other clinical infections, such as neonatal meningitis. E. coli is also prominently associated with diarrhoea in pet and farm animals [3].

Klebsiella pneumoniae is the causative agent of a variety of diseases, including pneumonia, urinary tract infections, septicemia, and the recently recognized pyogenic liver abscesses (PLA) [4].

Bacteria have also the genetic ability to transfer and acquire drug resistance factors. In recent years, inappropriate use of antibiotics has led to drug resistance among bacteria, which is the cause of untreatable "superbugs" and high death rates in clinics throughout the world, particularly among patients with suppressed immunity. The increasing prevalence of hospital and community-acquired infections caused by multidrug-resistant (MDR) bacterial pathogens is limiting the options for effective antibiotic therapy. Moreover, this alarming spread of antimicrobial resistance has not been paralleled by the development of novel antimicrobials. Resistance to the scarce new antibiotics is also currently known. CTX-M-14, CTX-M-3, and CTX-M-2 are the

Abstract—CTX-M beta-lactamases are enzymes were named for their greater activity against cefotaxime than other oxyimino-beta-lactam substrates (e.g., ceftazidime, ceftriaxone, or cefepime). The main aim of this study was to determine CTX-M-15 in gram-negative bacteria isolated from Afghaninan refugee in Iran. From August 2012 to February 2013, 100 non-duplicate non-consecutive K. pneumoniae and Escherichia coli were isolated from subjects of study. DNA was extracted using PCR method. Our findings showed that 32 isolated samples had CTX-M-15 gene and other genes were not observed. Of 32 samples containing CTX-M-15 gene, 24 samples belonged to E. coli and 8 samples belonged to Klebsiella pneumonia.

Keywords—CTX-M-15, Gram-negative Bacteria, Afghaninan Refugee, Iran

I. INTRODUCTION

The Enterobacteriaceae are a large family of Gram-negative bacteria including pathogens, such as: Salmonella, Escherichia coli, Yersinia pestis, Klebsiella and Shigella. Other disease-causing bacteria in this family include Proteus, Enterobacter, Serratia, and Citrobacter. Members of the Enterobacteriaceae can be trivially referred to as entrobacteria or "enteric bacteria", as several members live in the intestines of animals [1].

Many members of this family are a normal part of the gut flora found in the intestines of humans and other animals, while others are found in water or soil, or are parasites on a variety of different animals and plants. Escherichia coli is one of the most important model organisms, and its genetics and biochemistry have been closely studied. Most members of Enterobacteriaceae have peritrichous, type I fimbriae involved in the adhesion of the bacterial cells to their hosts. Some enterobacteria produce endotoxins. Endotoxins reside in the cell cytoplasm and are released when the cell dies and the cell wall disintegrates. Some members of the Enterobacteriaceae produce endotoxins that, when released into the bloodstream following cell lysis, cause a systemic inflammatory and vasodilatory response. The most severe form of this is known as endotoxic shock, which can be rapidly fatal. Enterobacteriaceae are also the most common cause of urinary tract infections (UTIs) in both community and healthcare settings [2].

Among gram-negative bacteria, escherichia coli remains one of the most frequent causes of several common bacterial infections in humans and animals. E. coli is the prominent cause of enteritis, urinary tract infection, septicaemia and other clinical infections, such as neonatal meningitis. E. coli is also prominently associated with diarrhoea in pet and farm animals [3].

Klebsiella pneumoniae is the causative agent of a variety of diseases, including pneumonia, urinary tract infections, septicemia, and the recently recognized pyogenic liver abscesses (PLA) [4].

Bacteria have also the genetic ability to transfer and acquire drug resistance factors. In recent years, inappropriate use of antibiotics has led to drug resistance among bacteria, which is the cause of untreatable "superbugs" and high death rates in clinics throughout the world, particularly among patients with suppressed immunity. The increasing prevalence of hospital and community-acquired infections caused by multidrug-resistant (MDR) bacterial pathogens is limiting the options for effective antibiotic therapy. Moreover, this alarming spread of antimicrobial resistance has not been paralleled by the development of novel antimicrobials. Resistance to the scarce new antibiotics is also currently known. CTX-M-14, CTX-M-3, and CTX-M-2 are the
most widespread. CTX-M-15 is the most widespread type in E. coli the UK and is widely prevalent in the community [7]. The main aim of this study was to determine CTMX-15 in gram-negative bacteria isolated from Afghanian refugee in iran.

II. MATERIAL AND METHODS

From August 2012 to February 2013, 100 non-duplicate non-consecutive K. pneumoniae & Escherichia coli were isolated. Out of total samples, 50% were from Afghanian refugee in Iran. Resistance to β-lactams among Gram-negatives is a worldwide issue. Increased prevalence of extended spectrum β-lactamases (ESBLs), the blaCTX-M genes, and aminoglycoside modifying enzymes genes in clinical isolates of Klebsiella pneumoniae (K. pneumoniae) was also determined in Tehran- Iran. The results show that CTX-M-15 is the dominant type of CTX-M, which associates with entities that have high aminoglycoside resistance [10]. A recent study also reports the first examples of bla(CTX-M-15) in UK river sediment; the prevalence of bla(CTX-M-15) was dramatically increased downstream of the waste water treatment plant [11].

V. CONCLUSION

We determined CTX-M15 in our study for a considerable number of subjects suffering E. coli and Klebsiella pneumonia isolated from Afghanian refugee in Iran.

ACKNOWLEDGMENT

We appreciate all who helped us to exert the present study.

REFERENCES


http://dx.doi.org/10.15242/IICBE.C1214124 52