

Available online at http://www.journalcra.com

INTERNATIONAL JOURNAL OF CURRENT RESEARCH

International Journal of Current Research Vol. 13, Issue, 11, pp.19709-19712, November, 2021 DOI: https://doi.org/10.24941/ijcr.42610.11.2021

RESEARCH ARTICLE

IMPORTANCE OF THE BACTERIAL EXTENDED-SPECTRUM BETA LACTAMASES

Canul-Chulim L.E.,¹ Flores-Encarnación, M.,^{1*} Aguilar-Gutiérrez G.R.,² Carreño-López R.,³ and García-García S.C.³

¹Laboratorio de Microbiología Molecular y Celular, Biomedicina, Facultad de Medicina, Benemérita Universidad Autónoma de Puebla, Puebla, Puebla, México

²Centro de Investigación sobre Enfermedades Infecciosas, Instituto Nacional de Salud Pública, Cuernavaca, Morelos, México

³Centro de Investigaciones Microbiológicas, Benemérita Universidad Autónoma de Puebla, Puebla, Puebla, México

ARTICLE INFO

ABSTRACT

Article History: Received 25th August, 2021 Received in revised form 19th September, 2021 Accepted 24th October, 2021 Published online 30th November, 2021

of a new drug with antibacterial properties, strains of bacteria resistant to that new drug emerge. Extended spectrum beta lactamases are a group of bacterial enzymes that can inactivate different antibiotics. They have been found in different examples of Gram positive and negative pathogenic bacteria.

Antibiotic resistance is a global public health problem. Bacteria have developed different strategies

that have allowed them to cope with the action of antibiotics, thus in a few years after the appearance

Keywords

Bacteria, Antibiotic, Beta-Lactamase, Extended-Spectrum.

*Corresponding author: Flores-Encarnación, M.

Copyright © 2021. Canul-Chulim et al. This is an open access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Citation: Canul-Chulim L.E., Flores-Encarnación, M., Aguilar-Gutiérrez G.R., Carreño-López R., and García-García S.C. "Importance of the bacterial extended-spectrum beta lactamases", 2021. International Journal of Current Research, 13, (11), 19709-19712.

INTRODUCTION

Within a few years, microbial resistance to antibiotics will become the leading cause of mortality worldwide, since it is estimated that up to 10 million in 2050 will be directly related to this problem. Within the wide range of microorganisms, viruses and bacteria are the ones that trigger epidemiological alerts due to their ability for damage and transmission (Chávez-Jacobo et al., 2020). Despite advances in the knowledge and description of the various antibacterial resistance mechanisms, today there are several examples of with increasingly superbacteria complex survival One of characteristics. these resistance mechanisms corresponds to the production of extended spectrum betalactamases (Morejón, 2013). This enzymes have been described from long ago, initially for coding genes of proteins againts penicillins, however in a short time new enzymes were appearing and their effects were observed in other families of

beta-lactam drugs for example cephalosporins. The extendedspectrum beta lactamases are produced by Gram positive and negative bacteria highlighting found in the genera *Streptococcus* sp., *Staphylococcus* sp. and in different species of the *Enterobacteriaceae* family. The resistance to extendedspectrum beta lactamases is conferred by intrinsic and acquired pathways. The latter are linked to indiscriminate use of antibiotics, self-medication and other bad practices (Olaitan and Rolain, 2014). Therefore, this work shows the most relevant aspects of the bacterial extended-spectrum beta lactamases and the medical importance.

THE BACTERIAL EXTENDED-SPECTRUM BETA LACTAMASES: There is an alarming increase of antibiotic resistance in bacteria that cause community infections or hospital acquired infections. Many of these multidrug pathogens are of particular interest such as, *Escherichia coli, Klebsiella pneumoniae, Acinetobacter baumannii*, methicillinresistant *Staphylococcus aureus*, penicillin-resistant Streptococcus pneumoniae, vancomycin-resistant Enterococcus, and extensively drugs resistant Mycobacterium tuberculosis (Alekshun and Levy, 2007; Nagshetty et al., 2021). The extended-spectrum beta lactamases are bacterial enzyme complex that promote resistance to multiple antibiotics, calling them "broad spectrum", unlike "the betalactamases" that only confer to bacteria a limited resistance (Biutifasari, 2018; Rawat and Nair, 2010). The breaking of the amide ring of penicillines, cefalosphorines and cephamycins is the main mechanism of action of extendend-spectrum beta lactamases (Pilmis et al., 2014). These peculiarities allow bacteria to increase survival against different antimicrobials, representing a therapeutic challenge priority in current health care and for the years to come. The extended-spectrum beta lactamases genes have chromosomal and plasmid location, being this the main mechanism of acquisition of multiresistence and producing a high mutagenic rate (Päivärinta et al., 2020; Vaidya, 2011; Zhou et al., 2021). On the other hand, at present the extended-spectrum beta lactamases can be classified into 4 important groups (A, B, C, D) according to their molecular characteristics such as the arrangement of amino acids. So A, C and D groups are in serine extendedspectrum beta lactamases class. For example, the A and C groups include the TEM (name of the Athenian patient SHV Temoniera), (sulfhydryl variable), CTX-M (cephotaximase) and AmpC (amoxicillin) varieties (Nagshetty et al., 2021). The group D include the OXA-type (oxacillinase). It has been established that A, C and D groups are homologous with a common origin. The group B corresponds to metallo extended-spectrum beta-lactamases, which are sensitive to chelating agents such as ethylenediamine tetraacetic acid (EDTA) and they are resistant to clavulanic acid and tazobactam (Hall and Barlow, 2005). Currently, extendend-spectrum beta-lactamases are classified in 16 groups according to the criteria of Bush-Jacoby-Medeiros, which include particular characteristics of each group, the molecular classes and subclasses and the substrate affinity (Bush and Jacoby, 2010). For example: the group 1 includes different lactamase enzymes such as AmpC, P99, ACT (ampC type 3), CYM-2, FOX-1, MIR⁻¹, GC1, CMY-37, which act on cephalosporins and have been found in Escherichia coli, Enterobacter cloacae, Serratia marcescens, Pseudomonas aeruginosa and Acinetobacter baumannii. The group 2 includes different lactamase enzymes such as PC1, TEM-1, TEM-2, SHV-1, TEM-3. SHV-2, CTX-M-15, PER-1, VEB-1, TEM-30, SHV-10, TEM-50, which act on penicillins, cephalosporines, carbenicillins, cloxacicline, carbapenems, and have been found in Staphylococcus sp., other Gram-positive cocci, Kluyvera sp., P. aeruginosa, Klebsiella pneumoniae and and other bacteria in the family Enterobacteriaceae (Bush and Jacoby, 2010).

IMPORTANCE OF EXTENDED-SPECTRUM BETA LACTAMASES FOR HUMAN HEALTH: Bacterial resistance is a global public health problem. Due to the austerity of new and more powerful antibiotic molecules available on the market, the presence of multidrug resistance in bacteria is becoming more and more frequent among the population (Nikaido, 2009). *E. coli* is the microorganism most frequently implicated in nosocomial and community bacteriemia. The extended spectrum beta-lactamasesproducing strains of *E. coli* are increasing more and more, having multi-resistant strains that circulate day by day among the population (Kayastha *et al*,. 2020; Sangama and Pereyra, 2018).

Infections with strains of E. coli that possess extended spectrum beta-lactamases have undergone important epidemiological changes in recent times (Terlizzi et al., 2017). Thus, infection and colonization by these strains have increased in community patients, especially in health institutions where CTX-M variants predominate compared to other types of extended-spectrum beta-lactamases (Varela et al., 2017). The presence of these enzymes in bacteria associated with nosocomial and community infections has increased the mortality in patients, thus bacteriemia caused by E. coli containing extended-spectrum beta-lactamases have complicated seriously when patients receive inadequate treatment (Chang et al., 2020). Therefore, it is important to identify the presence of extended-spectrum beta-lactamasesproducing strains in order to provide better treatment to patients as soon as possible. Regarding the measures to control the spread of extended-spectrum beta-lactamases, as an immediate measure, it has been proposed to implement the correct and responsible use of antibiotics (Hall and Barlow, 2005).

Staphylococcus aureus is a Gram-positive bacterium that causes a large number of nosocomial infections associated with surgical and postsurgical complications. It has the ability to cause accumulation of purulent material, which can migrate to neighboring structures and deepen systemically through the circulatory stream, and consequently, can produce systemic infections (Echevarría and Iglesias, 2003). Penicillin initially promised to be an effective treatment against bacterial infections, however in less than twenty years, resistance cases by extended-spectrum beta-lactamases have been reported in S. aureus strains (Lyon and Skurray, 1987; Abarca and Herrera, 2001). To counteract the observed resistance to penicillins, methicillins began to be used, however, the case of resistance was presented again, giving rise to a new variety known as MRSA (Methicillin-Resistant Staphylococcus aureus), which has increased its incidence and it has been reported as a serious problem in hospitals due the therapeutic ineffectiveness has been extended to cephalosporins and carbapenems (Grema et al., 2015). Methicillin-resistant strains of staphylococci are also resistant to the action of beta-lactams, and resistance to glycopeptides has recently been reported (Castro-Orozco et al., 2018; Del Río et al., 2016). S. epidermidis is also an infectious agent that can cause hospital infections. This bacterium can adhere and colonize surfaces, vascular and parenteral access routes, as well as medical devices (such as surgical implants) causing infectious processes. It is considered less virulent than S. aureus, however it has been reported that it has the same resistance profile to antibiotics (Echevarría and Iglesias, 2003). On the other hand, it has been reported that bacteria of the ESKAPE group such as Acinetobacter baumannii, are responsible for nosocomial infections, especially in patients with prolonged hospital stays and associated with circulatory conditions (Smiline et al., 2018). This bacterium produces extended-spectrum beta-lactamases of group D as OXA-5 (oxacillinases). Metallo beta-lactamases such as IMD, VIM, SIM, SPM and NDM (resistant to aminoglycosides) have also been found in A. baumannii. These extended-spectrum betalactamases cannot be inactivated with beta-lactam inhibitors, so these strains of A. baumannii have been reported to be resistant to almost all types of antibiotics (Vanegas-Múnera, 2014; Zarabadi-Pour et al., 2021). E. coli is another infectious agent that in decades has been related to various infectious processes due to the fact that it presents many pathotypes that adapt to any organ in the host (Miranda-Estrada et al., 2017;

Sarowska *et al.*, 2019). It also causes hospital and community infections and cases of the presence of extended-spectrum beta-lactamases have been reported among these strains, especially in uropathogenic *E. coli* (Salame-Khouri *et al.*, 2018).

CONCLUSION

The rapid emergence of resistance to antibiotics (such as extended-spectrum beta-lactamases) among hospital and community pathogens, represents a serious threat to the management of infectious diseases in the world. Therefore, strategies to control and to prevent the development of antibiotic-resistant bacteria require the participation of all, as well as surveillance in hospitals and environmental monitoring as important aspects for a policy to control infectious diseases.

ACKNOWLEDGEMENTS

Thank to Facultad de Medicina-BUAP for the facilities provided for the development of this work.

REFERENCES

- Abarca G. and Herrera M.L. (2001). Betalactamasas: su importancia en la clínica y su detección en el laboratorio. Rev. Méd. Hosp. Nac. Niños Dr. Carlos Sáenz Herrera. 36:77-104.
- Alekshun M.N. and Levy S.B. (2007). Molecular mechanisms of antibacterial multidrug resistance. Cell. 128:1037-1050.
- Biutifasari V. (2018). Extended spectrum beta-lactamase (ESBL). Oceana Biomed. J. 1:1-11.
- Bush K. and Jacoby G.A. (2010). Updated functional classification of β-lactamases. Antimicrob. Agents Chemother. 54:969-976.
- Castro-Orozco R., Villafañe-Ferrer L., Rocha-Jiménez J. and Alvis-Guzmán N. (2018). Resistencia antimicrobiana en Staphylococcus aureus y Staphylococcus epidermidis: tendencia temporal (2010-2016) y fenotipos de multirresistencia, Cartagena (Colombia). Rev. Biosalud. 17:25-36.
- Chang K., Rattanavong S., Mayxay M., Keoluangkhot V., Davong V., Vongsouvath M., Luangraj M., Simpson A.J.H., Newton P.N. and Dance D.A.B. (2020). Bacteremia caused by extended-spectrum beta-lactamase-producing Enterobacteriaceae in Vientiane, Lao PDR: a 5-year study. Am. J. Trop. Med. Hyg. 102:1137-1143.
- Chávez-Jacobo V.M. (2020). La batalla contra las superbacterias: no más antimicrobianos, no hay ESKAPE. Rev. Especial. Ciencias Químico-biológicas. 23:1-11.
- Del Río A., Garcia-De-La-Maria C., Entenza J.M., Gasch O., Armero Y., Soy D. and Hospital Clinic Experimental Endocarditis Study Group. (2016). Fosfomycin plus βlactams as synergistic bactericidal combinations for experimental endocarditis due to methicillin-resistant and glycopeptide-intermediate Staphylococcus aureus. Antimicrob. Agents Chemother. 60:478-486.
- Echevarria-Zárate J. and Iglesias-Quilca D. (2003). Estafilococo meticilino resistente, un problema actual en la emergencia de resistencia entre los Gram positivos. Rev. Méd. Herediana. 14:195-203.

- Grema H.A., Geidam Y.A., Gadzama G.B., Ameh J.A. and Suleiman A. (2015). Methicillin resistant *Staphylococcus aureus* (MRSA): a review. Adv. Anim. Vet. Sci. 3:79-98.
- Hall B.G. and Barlow M. (2005). Revised Ambler classification of β -lactamases. J. Antimicrob. Chemother. 55:1050-1051.
- Kayastha K., Dhungel B., Karki S., Adhikari B., Banjara M.R., Rijal K.R. and Ghimire P. (2020). Extended-spectrum βlactamase-producing *Escherichia coli* and *Klebsiella* species in pediatric patients visiting international friendship children's hospital, Kathmandu, Nepal. Infect. Dis. Res. Treat. 13:1-7.
- Lyon B.R. and Skurray R. (1987). Antimicrobial resistance of *Staphylococcus aureus*: genetic basis. Microbiol. Rev. 51:88-134.
- Miranda-Estrada L. I., Ruíz-Rosas M., Molina-López J., Parra-Rojas I., González-Villalobos E. and Castro-Alarcón N. (2017). Relación entre factores de virulencia, resistencia a antibióticos y los grupos filogenéticos de *Escherichia coli* uropatógena en dos localidades de México. Enferm. Infec. Microbiol. Clín. 35:426-433.
- Morejón García M. (2013).Extended spectrum beta-lactamase (ESBL). Rev. Cub. Med. 52:272-280.
- Nagshetty K., Shilpa M., Patil S.A., Shivannavar C.T. and Manjula N.G. (2021). An overview of extended spectrum beta lactamases and metallo beta lactamases. Adv. Microbiol. 11:37-62.
- Nikaido H. (2009). Multidrug Resistance in Bacteria. Annu. Rev. Biochem. 78:119–146.
- Olaitan A.O., Morand S. and Rolain J.M. (2014). Mechanisms of polymyxin resistance: acquired and intrinsic resistance in bacteria. Frontiers Microbiol. 5:1-18.
- Päivärinta M., Latvio S., Fredriksson-Ahomaa M. and Heikinheimo A. (2020). Whole genome sequence analysis of antimicrobial resistance genes, multilocus sequence types and plasmid sequences in ESBL/AmpC *Escherichia coli* isolated from broiler caecum and meat. Internat. J. Food Microbiol. 315:108361.
- Pilmis B., Parize P., Zahar J.R. Lortholary O. (2014). Alternatives to carbapenems for infections caused by ESBL-producing Enterobacteriaceae. Eur. J. Clin. Microbiol. Infect. Dis. 33:1263-1265.
- Rawat D. and Nair D. (2010). Extended-spectrum β -lactamases in Gram negative bacteria. J. Global Infect. Dis. 2:263-274.
- Salame-Khouri L., Contreras-Pichardo B., Arias-Rodríguez S., Mondragón-Soto M., Cataneo-Serrato J.L., Núñez-Martínez M. and Valente-Acosta B. (2018). Epidemiología de las bacteriemias por *Escherichia coli* en dos hospitales de tercer nivel de la Ciudad de México. Anales Méd. Asoc. Méd. Centro Médico ABC. 63:91-95.
- Sarowska J., Futoma-Koloch B., Jama-Kmiecik A., Frej-Madrzak M., Ksiazczyk M., Bugla-Ploskonska G. and Choroszy-Krol I. (2019). Virulence factors, prevalence and potential transmission of extraintestinal pathogenic *Escherichia coli* isolated from different sources: recent reports. Gut Pathog. 11:1-16.
- Smiline A.S.G., Vijayashree J.P. and Paramasivam A. (2018). Molecular characterization of plasmid-encoded blaTEM, blaSHV and blaCTX-M among extended spectrum βlactamases [ESBLs] producing *Acinetobacter baumannii*. British J. Biomed. Sci. 75:200-202.
- Terlizzi M.E., Gribaudo G. and Maffei M.E. (2017). Uropathogenic *Escherichia coli* (UPEC) infections: virulence factors, bladder responses, antibiotic, and non-

antibiotic antimicrobial strategies. Frontiers in Microbiol. 8:1-23.

- Vaidya V.K. (2011). Horizontal transfer of antimicrobial resistance by extended-spectrum β lactamase-producing enterobacteriaceae. J. Lab. Physicians. 3:37-42.
- Vanegas-Múnera J., Roncancio-Villamil G. and Jiménez-Quinceno J.N. (2014). Acinetobacter baumannii: clinical importance, resistance mechanisms and diagnosis. CES Med. 28:233-246.
- Varela Y., Millán B. and Araque M. (2017). Diversidad genética de cepas extraintestinales de *Escherichia coli* productoras de las betalactamasas TEM, SHV y CTX-M asociadas a la atención en salud. Biomédica. 37:209-217.
- Zarabadi-Pour M., Peymani A., Habibollah-Pourzereshki N., Sarookhani M.R. Karami A.A. and Javadi A. (2021). Detection of extended-spectrum β-lactamases among *Acinetobacter Baumannii* isolated from Hospitals of Qazvin, Iran. Ethiop. J. Health. Sci. 31:229-236.
- Zhou Z.C., Shuai X.Y., Lin Z.J., Liu Y., Zhu L. and Chen H. (2021). Prevalence of multi-resistant plasmids in hospital inhalable particulate matter (PM) and its impact on horizontal gene transfer. Environ. Pollution. 270:116296.
