Science Journal of Public Health
2015; 3(5): 797-803
Published online October 16, 2015 (http://www.sciencepublishinggroup.com/j/sjph)
doi: 10.11648/j.sjph.20150305.39
ISSN: 2328-7942 (Print); ISSN: 2328-7950 (Online)

Beta-lactamases and Their Global Health Implications-Two: Resistance Profile and Global Health Risk

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To cite this article:
Sunday Akidarju Mamza, Godwin Onyemaechi Egwu, Gideon Dauda Mshelia. Beta-lactamases and Their Global Health Implications-Two: Resistance Profile and Global Health Risk. *Science Journal of Public Health*. Vol. 3, No. 5, 2015, pp. 797-803.
doi: 10.11648/j.sjph.20150305.39

Abstract: Beta-lactamases are enzymes produced by some bacteria, which make them resistant to β-lactam antibiotics such as penicillins, cephalosporins, cephamycins and carbapenems. In this article, global health implications, resistance profile and treatment options were reviewed. Extended-spectrum β–lactamases produced by enterobacteria and methicillinases produced by Staphylococci have been shown to constitute the growing strains of bacteria that confer resistances to all β–lactam agents and many non–β–lactam antimicrobials, including fluoroquinolones. Their continued detection in animal species and food products poses a great challenge to diagnosis and treatment of resulting infections, thus, emanating to serious global health implications. Although a lot of works on β-lactamases have been directed towards the search for molecules which can inhibit these enzymes, the beta-lactamase producting bacteria are not leaving any stone to chance. Investigations targeted at identifying the carriers of these enzymes and intercepting their transmission will help curb the emergence and spread of the β–lactamases and their menace to public health.

Keywords: Beta-lactamase, *Escherichia coli*, *Staphylococcus aureus*, Epidemiology, Resistance, Health Implications

1. Introduction

One of the most important mechanisms of resistance in bacteria is the production of β –lactamases, which inhibit protein transpeptidases and carboxypeptidases participating in bacterial cell wall synthesis, thereby disrupting cell wall formation of the pathogen (Pitout *et al*., 1998; Ritu *et al*., 2006; Kolar *et al*., 2010).

Much of work on β-lactamases over the past decades has been directed to the search for molecules that can resist β-lactamase-producing organisms, or which can inhibit these enzymes (Brad and Edward, 2008). β-lactam antibiotics have recently been on the list of the most frequently prescribed drugs used worldwide in the control of *S. aureus* and *E. coli* infections, but the efficacy of these antimicrobials have suffered set back by the growing trend of multidrug resistant (MDR) strains of these β-lactamase-producing bacteria (Jensen and Lyon, 2009).

The present paper focused on resistance profiles and global health implications of β-lactamases, with overview of the control options. There was a relieve in the therapy of bacterial infections during the late nineteenth century when the third-generation cephalosporin were first introduced into clinical practice in both human and veterinary medicine. But sooner than realised, after the development and widespread use of these oxyimino-cephalosporins there was an emergence of extended-spectrum beta–lactamases (ESBLs) in bacteria that hydrolyze both penicillins and the extended-spectrum cephalosporins and aztreonam (Ritu *et al*., 2006; Brad and Edward, 2008; Mirzaee *et al*., 2009). These emergent resistant ESBLs in various bacterial organisms, is creating a huge public health concern worldwide. Resistance by β-lactamase-producing strains of Enterobacteriaceae against the extended-spectrum cephaolosporins have widely been studied and documented in human isolates, and increasing reports in isolates from food-producing animals (Paterson and Bonomo, 2005), companion animals (Sidjabat *et al*., 2007) and wildlife (Carmen and Myrian, 2007; Pinto *et al*., 2010). Resistance to β-lactam antibiotics by *E. coli* is by the production of ESBLs and AmpC type β-lactamases that

confer resistance to the penicillins, cephalosporins and aztreonam, and cephamycins (Ritu *et al*., 2006). The extended-spectrum cephalosporins-resistant strains of *E. coli* often carry integrons that encode resistance to fluoroquinolones and many newer antibiotics (Lorena and Alvaro, 2007), which further sabotages therapeutic options.

S. aureus exhibit resistance to β-lactam antibiotics by the expression of a low-affinity penicillin-binding protein (PBP2a) encoding the resistance gene, *mec*A, or by the production of the chromosomally-mediated β-lactamases (Ritu *et al*., 2006; Kolar *et al*., 2010). The ability of β-lactamase-producing strains of *S. aureus* to exhibit multi-resistance to antibiotics is largely determined by the location, kinetics, quantity, Physiochemical conditions and interplay of the produced enzyme or expressed PBP2a (McCallum *et al*., 2010), as well as, the capacity of the enzyme to hydrolyze the ß-lactam ring of ß-lactam antibiotics and inactivates them, thereby rendering the cells resistant to ß-lactam antibiotics (Bywater, 1991).

2. Health Implications

The production of β–lactamase enzymes has been reported to be the most common cause of bacterial resistance to β–lactam antibiotics in both humans and animals. β –lactam antibiotics are widely used in humans and veterinary medicine to treat human and animal infections (Briñas *et al*., 2002). This wide spread use of these antibiotics could be associated with the selection of antibiotic resistance mechanisms in both pathogenic and nonpathogenic bacteria, as well as, the production of β–lactamases.

There are now well over 200 recognized ESBLs in a variety of Gram-negative bacteria, conferring resistance to penicillins, cephalosporins, monobactams and even carbapenems (Brad and Edward, 2008). The ESBLs represents an impressive example of the ability of Gram-negative bacteria to develop new antibiotics resistance mechanisms in the face of introduction of new ones (Paterson and Bonomo, 2005). Plasmids responsible for ESBLs production frequently carry genes encoding resistance to other drug classes such as aminoglycosides, sulfanamides, chloramphenicol, rifampin, aminoquinolones or quinolones (Paterson and Bonomo, 2005; Ferran and Elisanda, 2007). The resistance plasmids can also be transferred to other bacteria, not necessarily of the same species, conferring resistance to them. Resistance plasmids or transposons have been reported to transmit multiple resistance traits among Enterobacteriaceae (Carattoli, 2001). This implies that therapeutic options in the treatment of ESBLs–producing organisms are extremely limited (Paterson and Bonomo, 2005; Cuzon *et al*., 2010). The use of extended–spectrum antibiotics have been said to exert a selective pressure for the emergence of ESBLs–producing bacteria. Involvement of many bacteria organisms producing ESBLs and the emergence of multiple β–lactamases–producing strains of some bacteria are of grave global health implication (Thomson, 2001; Kim *et al*., 2009). Organisms resistant to multiple antibiotics pose a special threat particularly among transplant patients (Mlynarczyk *et al*., 2009). The intestine of healthy animals is a reservoir for bacteria carrying CTX–M, mainly *E. coli*, and transmission to humans through the food chain have been emphasized (Carmen and Myrian, 2007). The enzymes of CTX–M and SHV–12 family are implicated mainly in urinary tract infections (Lorena and Alvaro, 2007). Epidemic clones of these enzymes and their dissemination from a specific group of enzymes have been described to be through the mobile elements called integrons (Lorena and Alvaro, 2007). This implies possible dissemination of these β–lactamases from food animals to humans can occur, since both enzymes have been reported in healthy animals destined for human consumption including chickens (Carmen and Myrian, 2007). Integrons are important, both in terms of the mechanisms of resistance and the dissemination of resistance genes within or outside the health care setting (Gupta, 2007). Integrons are also known to be associated with multiple-drug resistance in enteric organisms (Zhao *et al*., 2001) and have been reported to be implicated in the dissemination of ESBLs in gram-negative bacteria (Jacoby and Munoz-Price, 2005; Poirel *et al*. 2010). The transmission of resistance between bacteria haboured within the gut can occur both horizontally through the movement of these mobile genetic elements (integrons), and vertically through proliferation and subsequent dissemination of resistant bacterial strains (Deborah *et al*., 2005). These mobile elements can thus diffuse resistance genes to many other antibiotics (Ferran and Elisanda, 2007).

Resistance in bacteria isolated from food animals is in itself not a problem, but the possible transfer of resistance elements to zoonotic pathogens within the gut has serious public health implications (Deborah *et al*., 2005). The strain of *E. coli* producing CTX–M has been described as the most frequent cause of community–acquired urinary tract infections, and its increase is mostly due to the dissemination of Inck plasmids among *E. coli* isolates (Aránzazu *et al*., 2009). CTX–M β–lactamases, which show a high cefotaxime hydrolytic activity, constitute the most prevalent ESBL type found among clinical isolates of *E. coli* (Angela *et al*., 2008), and these enzymes have emerged as the most common type of ESBLs globally (James *et al*., 2010), and are therefore, of global health risk. TEM–52, SHV–2 and CTX–M–1 isolated from chickens and SHV–12 isolated from swine were observed to exhibit high clonal diversity, and contain transferable blaESBL genes which might be acquired by humans via the food chain (Elisabete *et al*., 2008). Infections caused by ESBL–producing strains of gram-negative bacteria have been on the increase, and were associated with higher morbidity and mortality in humans (Lorena and Alvaro, 2007; Cuzon *et al*., 2010), particularly the worldwide growing carbapenemase-producing organisms (Dortet *et al*., 2008). Treatments of such infections have been reported to be associated with high failure rates (Paterson and Bonomo, 2005). The possession of additional fluoroquinolones resistance by

some ESBLs-producing bacteria has further undermined therapeutic options.

Clonal outbreaks of CTX–M–15–producing Enterobacteriaceae, most frequently involving *E. coli* have been reported in France, Italy, Spain, Portugal, Austria, Norway, the UK, Tunisia, South Korea and Canada (Teresa *et al*., 2008). Plasmids encoding [bla.SubCTX–M–15] have been reported from clinical isolates of *E. coli* in France, Spain, Portugal, UK, Canada, India, Pakistan, south Korea, Taiwan, The United Arab emirates and Honduras (Noyais *et al*., 2007).

Infection caused by plasmid AmpC–producing isolates was said to significantly increase treatment failure at 72 hrs and that prior use of an oxyimino–cephalosporins is said to be a risk factor for infections caused by plasmid AmpC–producing Enterobacteriaceae (Park *et al*., 2009). AmpC β–lactamases are typically associated with broad–spectrum multi-drug resistance, which usually is a consequence of genes for other antibiotics resistance mechanisms residing on the same plasmids as the ESBL and AmpC genes (Thomson, 2001).

Methicillinase-producing *S. aureus* strains have gradually become resistant to almost all hospital disinfectants, and bacteria which survive attacks by biocides are becoming ultra-resistant super bugs (Ippolito *et al*., 2010). Molecular studies of animal isolates of β–lactamase–producing *S. aureus* has demonstrated that MRSA producing the *mec*A gene had similar nucleotide substitutions at same positions in their *mec*I genes as those described previously in humans (Lee, 2006). These alterations within the *mec* genes of animal MRSA strains which are homologous to that occurring in human MRSA strains, signals a transfer of such genes between humans and animals, possibly through the food chain. The risk of transfer of MRSA from animals and animal products has been described (Kwon *et al*., 2006), and the transfer of both resistance and genetic markers from poultry to humans has been reported (Saeed *et al*., 2000), as well as, the transmission of MRSA between dogs and humans (Mamian, 2003) and between humans and horses (Seguin *et al*., 1999). MRSA infections thus have zoonotic potential to portend serious human health dangers. Although Staphylococci isolated from animals are generally thought to be host-adapted, the MRSA similar to human epidemic cluster 257 was isolated from fistula of a dog in The Netherlands (van Duijkeren *et al*., 2004). The MRSA transmitted to the community by foodstuffs such as chicken meat and cow milk, still has the potential of causing human infections (Kwon *et al*., 2006).

A serious challenge facing clinical laboratories is that clinically relevant ESBLs–mediated resistance is not always detectable in routine susceptibility tests (Thomson, 2001); and most hospitals in rural settlements do not even use routine diagnostic tests for detecting resistant organisms, especially ß–lactamase–producers (Stevenson *et al*., 2003). Such laboratories may also lack the resources to prevent the spread of these resistance mechanisms. This lack of resources according to Thomson (2001) is particularly responsible for a continuous failure to address the rapid global spread or dissemination of pathogens producing these enzymes.

3. Treatment and Control

ESBL-producing bacteria have shown some susceptibility level to cephamycins and carbapenems *in vitro* (Jacoby and careras, 1990). Some TEM and SHV type ESBL-organisms have *in vitro* susceptibility to cefepime and piperacillin/tazobactam, but both drugs have exhibited diminished susceptibility alongside inoculum effect (Thomson and Moland, 2000). Bacterial strains possessing some CTX–M–type and OXA–type ESBLs were found to be resistant to cefepime on testing, despite the use of a standard inoculum (Ritu *et al*., 2006; Brad and Eward, 2008; Mirzae *et al*., 2009). AmpC–producing strains typically shown to resist oxyimino–cephalosporins and cephamycins were initially susceptible to carbapenems, but were however, shown resistant to the carbapenems due to loss of membrane porins (Briñas *et al*., 2002). Strains possessing IMP–, VIM– and OXA– type carbapenemases are said to be susceptible to aztreonam whilst resistance to non–ß–lactam antibiotics is said to be common in strains producing any of these enzymes, such that alternative options for non–ß–lactam therapy needed to be determined by direct susceptibility testing (Pfaller and Segreti, 2006). Infections caused by ESBL–producing *E. coli* and *K. pneumoniae* have been treated with the best outcomes in terms of survival and bacteriologic clearance using imipenem or meropenem (Jonathan *et al*., 2006); whilst *in vitro* resistance to cefotaxime, ceftazidime and aztreonam have been shown in some strains of ESBLs (Pitout *et al*., 1998). But KPC–producing bacteria have been shown to inactivate carbapenems and other ß–lactam antibiotics, and have also demonstrated typical resistance to trimethoprim-sulfamethoxazole, quinolones, and aminoglycosides, thereby making these pathogens truly multi-drug resistant (Jonathan *et al*., 2006). Some resistance profiles are shown in table 1 below.

Similarly, the ß–lactamases produced by *S. aureus* have shown resistance to a wide variety of ß–lactam antibiotics and many non-ß–lactam antibiotics as well (Mansouri and khaleghi, 1997; Kwon *et al*., 2006; Mamza *et al*. 2010). However, some strains have shown *in vitro* sensitivity to vancomycin and teicoplanin (van Duijkeren *et al*., 2004; Lee, 2006), but surprisingly, however, several newly discovered strains of methicillinase-producing *S. aureus* have been reported to resist vancomycin and teicoplanin (Diep *et al*., 2006). This new evolution of ß–lactamase *S. aureus* have been dubbed vancomycin–intermediate resistant *Staphylococcus aureus* or VISA (Diep *et al*., 2006). Monitoring and control of extended–spectrum cephalosporins usage, and regular surveillance of antibiotics resistance patterns, as well as efforts to decrease the use of empirical therapy have been recommended to help curb (control) the spread of ß–lactamase–producing organisms. The need for extensive research into plant materials that could elicit

permanent activity against these growing ß–lactamase–producing strains of bacteria is also a prerequisite.

Table 1. *Antibiotics resistance profiles of some beta-lactamases previously reported.*

Bacterial species	Beta-lactamases	Resistance profile (*)	Reference
E. coli	CTX-M-1,CTX-M-2, CTX-M-	A,Ac,Ce,Cx,No,Fx,St,K,T,C,G, At, Ct,Cp,Cz, CT,An	Vo *et al*., 2007 Woodford *et al*., 2004
	14, CTX-M-15	A,Ac,Cx,Cz,Cz,Ce,Pi,Tz,I,M	Park *et al* 2009
	CTX-M-9-like	I,M,ce,Cz,Cx,Ct,At,Tz,G,A, Cp,Tg,Fx, ,Ax,Ti, Pi	Monteiro *et al.*, 2009
K. Pneumoniae	TEM-1, TEM-2	Fx,Cx,Cz,At,C,G,S,T,St,	Mirzae *et al*., 2009
	OXA-1 to OXA-10	CT,cp,A,Ti,Pi,I,M,Ce,CtTz,	Jacoby and Sutton, 1985
	SHV-1, SHV-11, SHV-12	Fx,CT,Cx,Cz,Ce,An,G,Cp I,M,Ct,At,Tz,G, Cp,Tg,Fx,A,Ti, Pi,A,CT,Cx,Ce	Moland *et al*., 2002 Briňas *et al*., 2002
	KPC-2, KPC-3	Cz,At,I	Luzzaro *et al*., 2009
Salmonella spp	DHA-1, CMY-1, CMY-2,CMY-16 ESBL-K. pneumoniae	Fx,CT,Cx,Cz,G,Cp,A,Ce,No, Pi,Tz,St,G,K,T,Ac,At,I	Song *et al*., 2005
	AmpC-E. Coli	P,A,Co,Ct,Ce,G,T,C,O, Cd,A, Fx,Ct, Cz, At, Ce, Tz,	Akindele *et al*., 2010 Yu *et al*., 1999
S. aureus	ß–lactamase-S. aureus (not characterized)	A,Ti, Ac, Cf, Fx, Cz,P,A,Co, Ct,G,Ce,T,C,Ox,Ax,Cn,Cm,Cp	Mamza *et al*., 2010

(*) A: ampicillin, Ac: amoxiclav, Ce: cefepime, Cx: cefotaxime, Fx: cefoxitin, No: norfloxacin, St: sulfamethoxazole-trimethoprim, K: kanamycin, T:tetracycline, C: chloramphenicol, G: gentamicin, Cz: ceftazidime, Ct: ceftriazone, CT: cefotatan, At: aztreonam, P: penicillin, pi: piperacillin, Tz: piperacillin/tazobactam, I: imipenem, M: meropenem, Cp: ciprofloxacin, Ax: amoxicillin, S: streptomycin, An: andriamycin, Ox: oxacillin, Co: cloxacillin, Cd: cefamandole, Cf: cefazoline, Cn: cephalexin, Cm:c efuroxime

4. Conclusion

Bacterial organisms have adapted to both broad–spectrum and ß–lactam antibiotics by modifying substrate spectrum of common plasmid–mediated ß–lactamases, and by mobilizing resistance–promoting chromosomal ß–lactamase genes into plasmids, thereby enhancing their spread to new hosts. The persistence of β–lactamase–producing bacteria in our healthcare centres and the emergence of same in the Veterinary field is a global threat to both therapeutic and healthcare services. Although the precise cause and route of β–lactamase-producing strains into the Veterinary field could not be determined, it is clear that β–lactamases-producing bacterial strains do exist, and are being transmitted regardless of the use of ß–lactam antibiotics in this field. Also, the relative ease with which these bacteria organisms become resistant to newly developed antibiotics and the alarming global dissemination of β–lactamases highlights the need for continued epidemiological monitoring of these enzymes and prudent use of antibiotics. Investigations aimed at identifying the carriers of ß–lactamases and intercepting their transmission will play a vital role in curbing the emergence and spread of these β–lactamases and further enzymes, and their menace to global health.

Acknowledgement

We are grateful to our well wishers for encouraging us to pursue this review to its logical end. We acknowledge the typesetting work.

References

[1] Akindele, A. A., Adewuyi, I. K., Adefioye, O. A., Adedokun, S. A. and Olaolu, A. O. (2010) Antibiogram and ß–lactamase production of *Staphylococcus aureus* isolates from different human clinical specimens in tertiary health institutions in Ile-Ife, Nigeria. *American-Eurasian Journal of Scientific Research* 5(4): 230 – 233.

[2] Angela, N., Rafael, C., Teresa, M. C., Andrés, M., Fernando, B. and Juan-Carlos, G. (2008) Mutational Events in Extended–spectrum beta–lactamase cefotaximases of the CTX–M–1 Cluster involved in ceftazidime Resistance. *Antimicrobial Agentsand Chemotherapy*52: 2377 – 2782.

[3] Aránzazu, V., Rafael, C., Pilar, G. B. M., Angela, N., Juan, C. G., Andres, A., de la Fernando, C., Fernando, B. and Teresa, M. C., (2009) Spread of blaCTX–M–14 is mainly driven by Inckpalsmids disseminated among A (ST10), B1 (ST155/ ST359) and D *Escherichia coli* phylogroups in Spain. *Antimicrobial Agents and Chemotherapy*53: 5204 – 5212.

[4] Brad, M. W. and Edward, H. E. (2008) Current Perspectives on Extended-Spectrum Beta–lactamase–Producing Gram-negative Bacilli. *Journal of Pharmacy Practice* 21: 338-345.

[5] Briñas Laura, B., Myrian, Z., Yolanda, S., Fernanda, R. and Carmen, T. (2002) Beta–lactamases in ampicillin-resistant *Escherichia coli* isolates from food, humans and healthy animals. *Antimicrobial agents and Chemotherapy* 46: 3156-3166.

[6] Bywater, R. J. (1991) Beta-lactamases and beta-lactamase inhibitors. In: applied veterinary pharmacology and therapeutics 5th ed., (G. C. Brander, D. M. Pugh *et al* eds.), Pp 449 – 451, Bailliere Tindal.

[7] Carattoli, A. (2001) Importance of integrons in the diffusion of resistance. *Veterinary Research*32: 243 – 259.

[8] Carmen, T. and Myrian, Z. (2007) Extended-spectrum beta-lactamase in animals and their importance in transmission to humans

[9] *Enfermedades Infecciosas Microbiologia Clinica* 25 (suppl2): 29 – 37.

[10] Cuzon, G., Naas, T. and Nordmann, P. (2010) KPC carbapenemases: what issue in Clinical Microbiology? *Pathologie Biologie (Paris*) 58: 39 – 45.

[11] Deborah, V. H., Catherine, M. Y., Margo, E. C., George, J. G., Mark, E. J. W. and Sebastein, G. B. A. (2005) Molecular epidemiology of antimicrobial-resistant commensal *Escherichia coli* strains in a cohort of newborn calves. *Applied Environmental Microbiology*71: 6680 – 6688.

[12] Diep, B., Carleton, H., Chang, R., Sensabaugh, G. and Perdreau-Remington, F. (2006). Roles of 34 virulence genes in the evolution of hospital – and community – associated strains of methicillin-resistant *Staphylococcus aureus*. *Journal of Infectious Diseases*193: 1495 – 1503.

[13] Dortet, L., Radu, I., Gautier, V., Blot, F., Chachaty, E. and Arlet, G. (2008) Intercontinental travel of patients and dissemination of plasmid-mediated carbapenemase (KPC-3) associated with OXA-9and TEM-1. *Journal of Antimicrobial Chemotherapy*61, 455–457.

[14] Elisabete, M., Teresa, M. C., Rafael, C., Joâo, C. S. and Luisa, P. (2008) Antibiotic resistance integrons and extended-spectrum {beta}-lactamases among Enterobacteriaceae isolates recovered from chickens and swine in Portugal. *Journal of Antimicrobal Chemotherapy*62: 296 – 302.

[15] Ferran, N. and Elisanda, M. (2007) The genetic environment of ESBL: Implications in transmission. *Enfermedades Infecciosas Microbiologia Clinica*25(suppl 2): 11 – 17.

[16] Gupta, V. (2007) An update of newer ß-lactamases. *Indian Journal of Medical Research*126: 417 – 427.

[17] Ippolito, G., Leone, S., Lauria, F. N., Nicastri, E. and Wenzel, R.P. (2010) Methicillin-resistant *Staphylococcus aureus*: the superbug. *International Journal of infectious diseases* 14 (S4): S7 – S11.

[18] Jacoby, G. A. and Carreras, I.(1990) Activities of beta-lactam antibiotics against

[19] *Escherichia coli* strains producing extended-spectrum beta-lactamases. *Antimicrobial Agents and Chemotherapy*34: 858 – 862.

[20] Jacoby, G. A. M. D. and Munoz-Price, L. S. M. D (2005) Mechanisms of diseases: The new ß-lactamases. *New England Journal of Medicine*352: 380 – 391.

[21] Jacoby, G. A. and Sutton, L. (1985) ß–lactamases and ß–lactam resistance in *Escherichia coli*. *Antimicrobial Agents and Chemotherapy* 28 (5): 703 – 705.

[22] James, H. J., McElmeel, M. L., Fulcher, L. C. and Zimmer, B. L. (2010) Detection of CTX–M type extended-spectrum beta-lactamases by testing with microscan overnight and extended-spectrum beta-lactamase confirmation panels. *Journal of Clinical Microbiology*48: 120 – 123.

[23] Jensen, S. O. and Lyon, B. R. (2009) Genetics of antimicrobial resistance in *Staphylococcus aureus. Future Microbiology* 4(5): 565-582.

[24] Jonathan, P., Adams, J., Doi, Y., Szabo, D. and Paterson, D. L. (2006)KPC – type beta–lactamase, Rural Pennsylvania. *Emerging Infectious Diseases*12: 1613- 1614.

[25] Kim, J., Jeon, S., Rhie, H., Lee, B., Park, M., Lee, H. M. D., Lee, J. M. D. and Kim, S. (2009) Rapid detection of extended spectrum beta –lactamase (ESBL) for Enterobacteriaceae by use of a multiplex PCR –based method. Infection and Chemotherapy41: 181 – 184.

[26] Kolar, M., Bardon, J., Chiroma, M., Hricova, K., Stosova, T., Sauer, P. and Koulalova, D. (2010) ESBLs and AmpC beta-lactamase-producing Enterobacteriaceae in poultry in the Czech Republic. *Veterinarni Medicina*55: 119 – 124.

[27] Kwon, N. H., Park, K. T., Jung, W. K., Youn, H. Y., Lee, Y., Kim, S. H., Bae, W., Kim, J. Y., Kim, J. Y., Kim, J. M., Hong, S .K. and Park, Y. H. (2006) Characteristics of methicillin–resistant *Staphylococcus aureus* isolated from chicken meat and hospitalized dogs in Korea and their epidemiological relatedness. *Veterinary Microbiology*117: 304 – 312.

[28] Lee, J. H. (2006) Occurrence of methicillin-resistant *Staphylococcus aureus* strains from cattle and chickens, and analyses of their mecAmecR1 and mecI genes. *Veterinary Microbiology*114: 155-159.

[29] Lorena, L-C. and Alvaro, P. (2007) Epidemiology of exteneded-spectrum beta-lactamase in the community: An increasing problem.

[30] *Enfermedades Infecciosas Microbiologia Clinica* 25 (suppl2): 23 – 28.

[31] Luzzaro, F., Brigaute, G., D'andrea, M. M., Pini, B., Cuani, T., Mantengoli, E., Rossolini, G. M. and Toniolo, A. (2009) Spread of multidrug-resistant *Proteus mirabilis* isolates producing an AmpC-type beta-lactamases: epidemiology and clinical management. *International Journal Antimicrobial Agents*33: 328 – 333.

[32] Mamian, F. A. (2003) Asymptomatic nasal carriage of mupirocin-resistant methicillin–resistant *Staphylococcus aureus* (MRSA) in a pet dog associated with MRSA infection in household contacts. C*lincal Infectious Diseases*36: e26 – e28.

[33] Mamza, S. A., Egwu, G. O. and Mshelia, G. D. (2010) Beta-lactamase *Escherichia coli* and *Staphylococcus aureus* isolated from chickens in Nigeria. *Veterinary Italiana*46:155 – 165.

[34] Mansouri, S. and Khaleghi, M. (1997) Antibacterial resistance pattern and frequency of methicillin-resistant *Staphylococcus aureus* isolated from different sources of south-eastern Iran. *Iranian Journal of Medical Science*22: 89 – 93.

[35] McCallum, N., Berger-bächi, B. and Senn, M. M. (2010) Regulation of antibiotics resistance in *Staphylococcus aureus*. *International Journal of Medical Microbiology*300: 118 – 129.

[36] Mirzaee, M., Pourmand, M. R., Chitsaz, M. and Mansouri, S. (2009) Antibiotic resistance to third generation cephalosporins due to CTX – M – type ESBLs in isolates of *Escherichia coli*. *Iranian Journal of Public Health*38: 10 – 17.

[37] Mlynarczyk, A., Szymanek, K., Sawicka-Grzelak, A., Pazik, J., Buczkowska, T., Durlik, M.,

[38] Lagiewska, B., Pacholczyk, M., Chmura, A., Paczek, L. and Mlynarczk, G. (2009)

[39] CTX–M and TEM as predominant types of Extended-spectrum beta-lactamases among *Serratiamarcescens* isolated from solid organ recipients. *Transplantation Proceedings*41: 3252 – 3255.

[40] Moland, E. S., Black, J. A., Ourade, J., Reisbig, M. D., Hanson, N. D. and Thomson, K. S. (2002) Occurrence of newer beta-lactamases in *Klebsiellapneumonia*e isolates from 24 US hospitals. *Antimicrobial Agents and Chemotherapy* 46(2): 3837 – 3842.

[41] Monteiro, J., Asensi, M. D. and Gales, A. C. (2009) First report of KPC-2-producing *Klebsiellapneumoniae* strains in Brazil. Antimicrobial Agents and Chemotherapy 54(1): 333 – 334.

[42] Noyais, A., Canton, R., Moreira, R., Peixe, L., Baquero, F. and Coque, T.M. (2007) Emergence and dissemination of Enterobacteriaceae isolates producing CTX – M–1 – like enzymes in Spain are associated with IncFII (CTX–M–15) and broad-host-range (CTX–M–1, – 3, and – 32) plasmids. *Antimicrobial Agents and Chemotherapy*51: 796 – 799.

[43] Park, Y. S. Sunmi, Y., Mi-Run, S., Jin, Y. K., Yong, K. C. and Pai, H. (2009) Risk factors and clinical features of infections caused by plasmid-mediated AmpC beta-lactamase-producing Enterobacteriaceae. *International Journal of Antimicrobial Agents* 16: 38 – 43.

[44] Paterson, D. L. and Bonomo, R. A. (2005) Extended-spectrum beta-lactamases: A clininal update. *Clinical Microbiology Reviews*18: 657 – 686.

[45] Pfaller, M. A. and Segreti, J. (2006) Overview of the epidemiological profile and laboratory detection of extended-spectrum beta-lactamases. *Clinical Infectious Diseases*42 (Suppl 4): S153 – S163.

[46] Pinto, L., Radhouani, H., Coelho, C., Martins da Costa, P., Simoes, R., Brandao, R. M., Torres, C., Igejas, G. and Poeta, P. (2010) Genetic detection of extended-spectrum beta-lactamase-containing *Escherichia coli* isolates from birds of prey from Serra da Estrela Natural Reserve in Portugal. *Applied Environmental Microbiology*76: 4118 – 4120.

[47] Pitout, J. D. D., Kenneth, S. T, Hanson, N. D., Ehrhardt, A. F., Moland, E. S. and Sanders, C. C. (1998) Beta-lactamases responsible for resistance to expanded-spectrum cephalosporins in *Klebsiellapneumoniae*, *Escherichia coli,* and *Proteus mirabilis* isolates recovered in South Africa. *Antimicrobial Agents and Chemotherapy*42: 1350 – 1354.

[48] Poirel, L., T. Naas, and P. Nordman (2010). Diversity, Epidemiology, and genetics of class D {beta-lactamses}. *Antimicrobial Agents and Chemotherapy*, 54: 24 – 38.

[49] Ritu, A., Uma, C. and Aparna,Y. (2006)Prevalence and antimicrobial susceptibility of extended-spectrum beta-lactamase-producing Gram-negative bacilli in blood stream infection. *Journal of Infectious Diseases and Antimicrobial Agents* 23, 111-114.

[50] Saeed, A. K., Mohammed, S. N., Ashraf, A. K. and Carl, E. C. (2000) Transfer of erythromycin resistance from poultry to human clinical strains of *Staphylococcus aureus*. *Journal of clinical Microbiology*38: 1832-1838.

[51] Seguin, J. C., Walker, R. D., Caron, J. P., Kloos, W. E., George, C. G., Hollis, R. J., Jones, R. N. and Pfaller, M. A. (1999) Methicillin–Resistant *Staphylococcus aureus* outbreaks in a Veterinary Teaching Hospital; Potential human to human transmission. *Journal of Clinical Microbiology* 37: 1459 – 1463.

[52] Sidjabat, H. E., Hanson, N. D., Smith-Moland, E., Bell, J. M., Gibson, J. S., Philippich, L. J. and Trott, D. J. (2007) Identification of plasmid-mediated extended-spectrum and AmpC beta-lactamase in *Enterobacterspp* isolated from dogs. *Journal of Medical Microbiology*56: 436 – 434.

[53] Song, W., Kim, J-S., Kim, H-S., Park, M-J. and Lee, K. M. (2005) Appearance of *Salmonella enteric*a isolates producing plasmid-mediated AmpCbeta-lactamase CMY-2, in South Korea. *Diagnostic Microbiology and Infectious Diseases*52: 281 – 284.

[54] Stevenson, K., M-Samore, B., Barbera, J., Moore, J.W., Hannaah, E., Houck, P., Tenover, F. C. and Gerberding, J. L. (2003) Detection of Antimicrobial resistance by small rural hospital microbiology laboratories: comparison of survey responses with current NCCLS laboratory standards. *Diagnostic Microbiology and Infectious Diseases*47: 301–311.

[55] Teresa, C., Novais, A., aratolli, A., Poirel, L., Pitout, J., Peixe, L., Baquero, F., Canton,R. and Nordman, P. (2008) Dissemination of clonally related *Escherichia coli* strains expressing extended-spectrum beta-lactamase CTX–M–15.*Emeging Infectious Diseases*14: 196 – 200.

[56] Thomson, K. S. (2001) Controversies about extended-spectrum and AmpC beta–lactamases. *Emerging Infectious Diseases*7: 333 – 336.

[57] Thomson, K. S., and Moland, E. S.(2000) Version 2000: the new beta-lactamases of gram-negative bacteria at the dawn of the new millennium. *Microbes Infections*, 2: 1225 – 1235.

[58] Van Duijkeren, E., Box, A. T. A., Heck, M. E. O. C., Wannet, W. J. B. and Fluit, A. C. (2004) Methicillin-Resistant Staphylococci isolated from animals. *Veterinary Microbiology*103: 91 – 97.

[59] Vo, A. T. T., van Duijkeren, E., Fluit, A. C. and Gaastra, W. (2007) Characteristics of extended cephalosporin-resistant *Escherichia coli* and *Klebsiellapneumonia*e isolates from *horses. Veterinary Microbiology*124: 248 – 255.

[60] Woodford, N., Ward, M. E., Kaufmann, M. E., Turton, J., Fagan, E. J., James, D., Johnson, A. P., Pike, R., Warner, M., Cheasty, T., Pearson, A., Harry, S., Leach, J. B., Loughrey, A, Lowes, J. A., Warren, R. E. and Livermore, D. M. (2004) Community and hospital spread of *Escherichia coli* producing CTX-M extended-spectrum ß–lactamases in the UK. *Journal of Antimicrobial Chemotherapy* 54: 735 – 743.

[61] Yu, C., Karr, T., Tunner, D., Towns, V. and Sinha, J. (1999) Rapid detection of ß–lactamase production in penicillin-sensitive Staphylococci by the phoenix automated ID/AST system. Presented at the 19th *European Congress of Clinical Microbiology and Infectious Diseases*, March, 1999.

[62] Zhao, S., White, D. G., Ge, B., Ayers, S., Friedman, S., English, L., Wagner, D., Gaines, S. and Meng, J. (2001) Identification and characterization of integron-mediated antibiotics resistance amo ng Shiga toxin-producing *Escherichia coli* isolates. *Appllied Environmental Microbiology*67: 1558 – 1564.