



Review article

Extended-spectrum beta-lactamase (ESBL)-producing Enterobacteriaceae in cattle production – a threat around the world

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ABSTRACT

Food producing animal is a global challenge in terms of antimicrobial resistance spread. Extended-spectrum beta-lactamase (ESBL)-producing Enterobacteriaceae are relevant opportunistic pathogens that may spread in many ecological niches of the One Health approach as human, animal and environment due to intestinal selection of antimicrobial resistant commensals in food production animals. Cattle production is a relevant ecological niche for selection of commensal bacteria with antimicrobial resistance from microbiota. Enterobacteriaceae show importance in terms of circulation of resistant-bacteria and antimicrobial resistance genes via food chain creating a resistance reservoir, setting up a threat for colonization of humans and consequent health risk. ESBL-producing Enterobacteriaceae are a threat in terms of human health responsible for life threatening outbreaks and silent enteric colonization of community populations namely the elder population. Food associated colonization is a risk difficult to handle and control. In a time of globalization of food trading, population intestinal colonization is a mirror of food production and in that sense this work aims to make a picture of ESBL-producing Enterobacteriaceae in animal production for food over the world in order to make some light in this reality of selection of resistant threats in food producing animal.

1. Introduction

Extended-spectrum beta-lactamases (ESBL) are enzymes responsible for the hydrolysis of oxyimino-beta-lactam antibiotics, which are important therapeutic agents for the treatment of serious human and animal infections. ESBL were first described in 1983 in Enterobacteriaceae (new taxonomy *Enterobacterales*) and since then, with the research of the scientific community, it has been observed that ESBL-producing Enterobacteriaceae (E-ESBL) are a real threat to human health, being responsible for 1700 deaths in the USA due to therapeutic failure in severe infections in 2013 (Adeolu et al., 2016; CDC, 2013; Knothe et al., 1983). However, E-ESBL are not only limited to hospital environment, they are also present as human intestinal commensals (Gonçalves et al., 2016; Karanika et al., 2016). The presence of E-ESBL in several ecological niches, as commensals in humans and animals and as environmental contaminants, is reported worldwide, however, in the last decades a niche that has raised great concern, for being able to function as a reservoir and vehicle of transmission and dissemination of E-ESBL is the

production animals due to their direct connection with the food chain (Madec et al., 2017).

Cattle are one of the main sources of animal protein, becoming one of the most consumed meat around the world and milk, one of the main constituents of the human food chain (Alexandratos and Bruinsma, 2012). It is also one of the main sources of biological fertilizers, due to the high production of faecal mass of these animals (Smith and Williams, 2016). All this, highlights the importance of cattle production in the context of the food chain and the contaminated environment as reservoir and transmitting/disseminating vehicle of E-ESBL, thus configuring a threat to the world public health. This circulation of E-ESBL within our ecosystem creates a consensual concern of the scientific community and of the authority involved in the One health approach (Robinson et al., 2016).

The ESBL are enzymes that are classified in several types, being CTX-M, SHV and TEM the most prevalent around the world (Paterson and Bonomo, 2005). However, there are other ESBL such as OXA, PER, VEB, BES, GES, SFO, TLA, and IBC (Paterson and Bonomo, 2005). The CTX-M

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are enzymes with environmental origins which are currently the most widespread type of ESBL and are commonly associated with E-ESBL reports (Cantón et al., 2012). Variants such as CTX-M-15, responsible for infectious outbreaks around the world, are associated with a clone responsible for extraintestinal *E. coli* infections resistant to antibiotics, the ST131 (Price et al., 2013).

The objective of this study was to make an insight about the epidemiology of the spread of E-ESBL and the ESBL genes distribution in cattle around the world, in order to update the current scenario of E-ESBL dissemination through cattle production in all continents.

2. ESBL producing *Enterobacteriaceae* in cattle - a global view

The first description of an E-ESBL in cattle was in Japan, where a CTX-M-2 *E. coli* producer was detected in cattle faeces from an important region close to the centre of the country (Shiraki et al., 2004). From the first description to the present, E-ESBL has already been described in cattle production in 39 countries, with more concentration in Europe (n = 16) and Asia (n = 13) as shown in Figure 1. The origins of E-ESBL are diverse, being isolated from healthy animals (faecal samples) or from veterinary clinical origin (mastitis, diarrheal processes, infections or with any other pathological picture). The countries with the highest reports on E-ESBL in cattle, are the United Kingdom (n = 14), Germany (n = 11), France (n = 9) and the United States (n = 9), the last one being the world's largest cattle producer, and the 3 Europeans, 4th, 3rd and 1st, respectively, in number of cattle in Europe (Eurostat, 2016; USDA et al., 2017). Within the 5 world largest cattle producers (United States, Brazil, the European Union, China and India) there have been reports of animals harbouring commensal or clinical E-ESBL. The Table 1 shows all the descriptions of E-ESBL in cattle around the World, including the source, species and ESBL gene.

The most frequent ESBL types in E-ESBL in cattle, as expected, were the ones of CTX-M-1 group with higher prevalence for CTX-M-1, CTX-M-14 and CTX-M-15. CTX-M-1 was reported in 20 countries, most frequently in Europe (n = 14), being found in Germany, Denmark, Spain, Finland, France, Hungary, Portugal, Netherlands, United Kingdom, Czech Republic, Slovakia, Sweden, Switzerland and Turkey. CTX-M-1 was first described in human E-ESBL in 1989 in Germany, and it has

also been reported in other European countries such as Spain, France, Italy and United Kingdom as well as in Asia and North America (Cantón and Coque, 2006; Moosavian and Ahmadvhosravy, 2016; Wang et al., 2013).

CTX-M-15 and CTX-M-14 are the most important CTX-M enzymes due to their large diffusion and relation to outbreaks and severe extra-intestinal infections (Cantón et al., 2012; Matsumura et al., 2015; Price et al., 2013). CTX-M-14 was described in E-ESBL in cattle in 13 countries, mainly in Europe (Germany, Belgium, France, Netherlands, United Kingdom, and Switzerland) and in Asia (China, South Korea, Hong Kong, Japan, and Taiwan), as well as the United States and Oceania. CTX-M-14 was first described in 2002 in E-ESBL from a hospital in China (Chanawong et al., 2002; Ma et al., 2002). E-ESBL producers isolated from human of CTX-M-14 type are described in Europe, Asia, North and South America, Africa and Oceania, many times related to pandemic clones such as *E. coli* ST131 responsible for outbreaks in the last years (Cantón et al., 2008; Chen et al., 2014; Giedraitienė et al., 2017; Peirano et al., 2010, 2011; Pitout et al., 2005; Shin et al., 2011; Silva and Lincopan, 2012; Zong et al., 2008).

CTX-M-15 was first described in 2001 in E-ESBL isolate in a hospital in New Delhi, India, and today is the most widespread ESBL in the various niches and the most important of all, due to its high relation to important, for human health, E-ESBL clones (Cantón et al., 2012; Clermont et al., 2008; Karim et al., 2001; Kim et al., 2017; Price et al., 2013; Woodford et al., 2004). E-ESBL producing CTX-M-15 in cattle were described in 21 countries around the world, present in most of Europe, being reported in Germany, France, Italy, Netherlands, United Kingdom, Sweden, Switzerland and Turkey. In Asia they were described in China, South Korea, India, Israel, Japan, Lebanon and Taiwan and also reported in North and South America (Brazil, Canada and United States) and Africa (Egypt, Tanzania and Tunisia).

CTX-M-15 has been reported in all continents (Europe, North America, South America, Asia, Africa, Oceania and Antarctica with reports in all major ecological niches (humans, animals, and environment), these E-ESBL producers of CTX-M-15 are an excellent example of the public health threat that involves circulation of resistant *Enterobacteriaceae* and resistance genes among the different ecological niches that is currently evidenced under the prism of the "One Health" approach (Chen et al.,

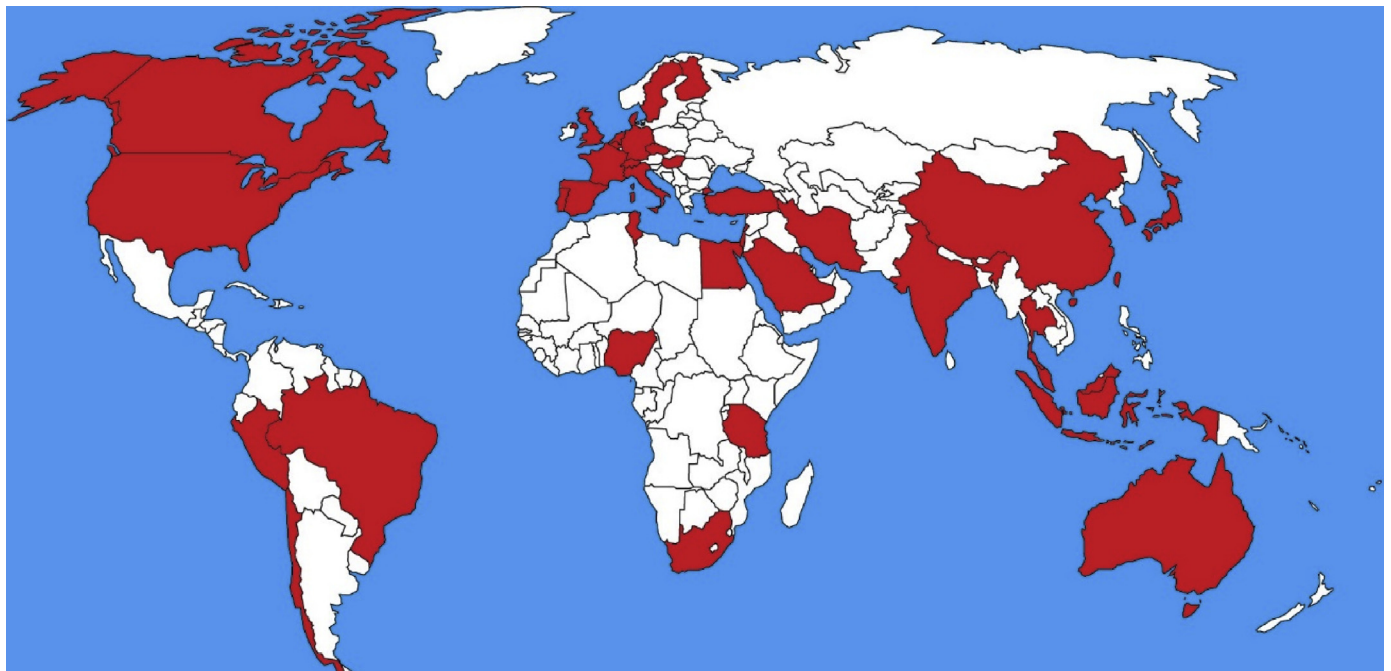


Figure 1. World map illustrating the countries with description of E-ESBL in cattle.

Table 1. Relation of ESBL described in cattle by type of ESBL, described species, country of report, origin of the isolate and bibliographic reference of the description.

Beta-lactamase	Enterobacteriaceae	Country	Source	Reference	
CTX-M-1	<i>Escherichia coli</i>	Europe			
		Germany	Faecal	(Wieler et al., 2011)	
			Mastitis	(Freitag et al., 2017; Michael et al., 2017)	
			Diarrheic	(Ewers et al., 2014)	
			Sick	(Michael et al., 2017)	
			Infection	(Brennan et al., 2016)	
		Denmark	Commensal	(Kjeldsen et al., 2015)	
			ND	(Garcia-Fernandez et al., 2011; Jakobsen et al., 2015)	
		Spain	Mastitis	(Brīnas et al., 2005)	
		Finland	Faecal	(Päivärinta et al., 2016)	
		France	Faecal	(Haenni et al., 2014; Hartmann et al., 2012; Madec et al., 2008; Meunier et al., 2006)	
				Mastitis	(Dahmen et al., 2013)
				Diarrheic	(Hartmann et al., 2012)
				Sick	(Madec et al., 2008; Valat et al., 2016)
				Infection	(Meunier et al., 2006)
		Hungary	Infection	(Toth et al., 2013)	
		Portugal	Faecal	(Ramos et al., 2013)	
		Mayotte	ND	(Gay et al., 2018)	
		Netherlands	Faecal	(Ceccarelli et al., 2019; Heuvelink et al., 2019; Hordijk et al., 2013a, b, c)	
		United Kingdom	Faecal	(Velasova et al., 2019)	
			Infection	(Hunter et al., 2010)	
			ND	(Stokes, 2014)	
		Czech Republic	Faecal	(Dolejska et al., 2011b)	
			Sick	(Dolejska et al., 2013)	
		Réunion	ND	(Gay et al., 2018)	
		Slovakia	Faecal	(Kmeť and Bujňáková, 2018)	
		Sweden	Faecal	(Duse et al., 2015)	
		Switzerland	Faecal	(Endimiani et al., 2012; Geser et al., 2012a; Zurfluh et al., 2015)	
		Turkey	Faecal	(Aslantaş et al., 2017; Pehlivanoglu et al., 2016)	
		North America			
		Canada	ND	(Cormier et al., 2019)	
		USA	Faecal	(Mir et al., 2016; Mollenkopf et al., 2012; Wittum et al., 2010)	
		Asia			
		China	Mastitis	(Ali et al., 2016, 2017)	
		South Korea	Mastitis	(Tark et al., 2017)	
		Indonesia	Faecal	(Sudarwanto et al., 2016)	
		Japan	Mastitis	(Ohnishi et al., 2013b)	
		<i>Klebsiella pneumoniae</i> Europe			
			Italy	Mastitis	(Locatelli et al., 2010)
		<i>Klebsiella ozaenae</i> Italy Faecal (Stefani et al., 2014)			
		<i>Salmonella enterica</i> Germany ND (Rodríguez et al., 2009)			
		CTX-M-1/61	<i>E. coli</i>	Europe	
	Germany	Faecal	(Dahms et al., 2015)		
CTX-M-2	<i>E. coli</i>	South America			
		Brazil	Faecal	(Palmeira et al., 2018)	
		Europe			
		Germany	Mastitis	(Eisenberger et al., 2017; Freitag et al., 2017; Michael et al., 2017)	
			Sick	(Michael et al., 2017)	
		Netherlands	Faecal	(Ceccarelli et al., 2019; Heuvelink et al., 2019)	
		North America			
		Canada	Faecal	(Cormier et al., 2016)	
		Asia			
		Japan	Faecal	(Shiraki et al., 2004)	
			Diarrheic	(Ohnishi et al., 2013a)	
			Infection	(Asai et al., 2011)	
<i>K. pneumoniae</i>	Japan	Mastitis	(Ohnishi et al., 2013a, b; Saishu et al., 2014)		
<i>Klebsiella oxytoca</i>	Japan	Mastitis	(Ohnishi et al., 2013b)		
<i>Citrobacter freundii</i>	Japan	Mastitis	(Ohnishi et al., 2013a)		

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Table 1 (continued)

Beta-lactamase	Enterobacteriaceae	Country	Source	Reference
	<i>Citrobacter koseri</i>	Japan	Mastitis	(Ohnishi et al., 2013b)
	<i>Enterobacter cloacae</i>	Japan	Mastitis	(Ohnishi et al., 2013a)
	<i>Enterobacter aerogenes</i>	Japan	Mastitis	(Ohnishi et al., 2013b)
CTX-M-2/97	<i>E. coli</i>	Europe		
		Netherlands	Faecal	(Hordijk et al., 2013a, b, c)
CTX-M-3	<i>E. coli</i>	Europe		
		Germany	Mastitis	(Michael et al., 2017)
		France	Faecal	(Haenni et al., 2014)
		Netherlands	Faecal	(Ceccarelli et al., 2019; Hordijk et al., 2013b)
		United Kingdom	Infection	(Hunter et al., 2010)
		Turkey	Faecal	(Aslantaş et al., 2017; Pehlivanoglu et al., 2016)
		Asia		
		China	Faecal	(Zheng et al., 2019)
			Mastitis	(Ali et al., 2016, 2017)
		South Korea	Mastitis	(Tark et al., 2017)
		Hong Kong	Faecal	(Ho et al., 2013)
CTX-M-8	<i>E. coli</i>	Europe		
		Netherlands	Faecal	(Ceccarelli et al., 2019)
CTX-M-9	<i>E. coli</i>	Europe		
		Netherlands	Faecal	(Ceccarelli et al., 2019)
		North America		
		USA	Faecal	(Poole et al., 2017)
		Asia		
		Indonesia	Faecal	(Sudarwanto et al., 2016)
		Africa		
		Egypt	Faecal	(Braun et al., 2016)
		Oceania		
		Australia	Sick	(Abraham et al., 2015)
	<i>S. enteric</i>	Australia	ND	(Sparham et al., 2017)
CTX-M-14	<i>E. coli</i>	Europe		
		Germany	Mastitis	(Eisenberger et al., 2017; Freitag et al., 2017; Michael et al., 2017)
			Sick	(Michael et al., 2017)
		Belgium	Faecal	(Pardon et al., 2017)
			Infection	(Pardon et al., 2017)
		France	Faecal	(Haenni et al., 2014; Madec et al., 2008)
			Mastitis	(Dahmen et al., 2013)
			Sick	(Madec et al., 2008)
		Wales	Sick	(Tyrrell et al., 2016)
		Netherlands	Faecal	(Ceccarelli et al., 2019; Heuvelink et al., 2019; Hordijk et al., 2013a, b, c)
		United Kingdom	Faecal	(Cottell et al., 2011; Horton et al., 2011; Randall et al., 2014; Snow et al., 2011)
			Infection	(Hunter et al., 2010)
			ND	(Stokes, 2014; Stokes et al., 2013)
		Switzerland	Faecal	(Geser et al., 2012a; Zurfluh et al., 2015)
			Mastitis	(Geser et al., 2012a)
		Asia		
		China	Faecal	(Zheng et al., 2012, 2019)
			Mastitis	(Ali et al., 2016, 2017)
		South Korea	Faecal	(Rayamajhi et al., 2011; Tamang et al., 2013a)
			Sick	(Lim et al., 2009)
		Hong Kong	Faecal	(Ho et al., 2011, 2013)
		Japan	Mastitis	(Ohnishi et al., 2013b)
			Diarrheic	(Ohnishi et al., 2013a)
		Taiwan	Mastitis	(Su et al., 2016)
		North America		
		Canada	ND	(Cormier et al., 2019)
		USA	Faecal	(Mollenkopf et al., 2012)
		Oceania		

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Table 1 (continued)

Beta-lactamase	Enterobacteriaceae	Country	Source	Reference
	<i>K. pneumoniae</i>	Australia	Sick	(Abraham et al., 2015)
		Europe		
		France	Mastitis	(Dahmen et al., 2013)
		Asia		
		Japan	Mastitis	(Ohnishi et al., 2013b)
CTX-M-15	<i>E. coli</i>	South America		
		Brazil	Faecal	(Sartori et al., 2017)
		Europe		
		Germany	Faecal	(Fischer et al., 2014; Wieler et al., 2011)
			Mastitis	(Eisenberger et al., 2017; Freitag et al., 2017; Michael et al., 2017)
			Sick	(Michael et al., 2017)
		France	Faecal	(Haenni et al., 2014)
			Sick	(Madec et al., 2008)
			Infection	(Madec et al., 2012; Meunier et al., 2006)
		Madagascar	ND	(Gay et al., 2018)
		Mayotte	ND	(Gay et al., 2018)
		Netherlands	Faecal	(Ceccarelli et al., 2019; Heuvelink et al., 2019; Hordijk et al., 2013a, b, c)
		United Kingdom	Faecal	(Horton et al., 2011; Randall et al., 2014; Watson et al., 2012)
			Mastitis	(Timofte et al., 2014)
			Infection	(Hunter et al., 2010)
		Sweden	Faecal	(Duse et al., 2015)
		Switzerland	Faecal	(Endimiani et al., 2012; Geser et al., 2012a; Zurfluh et al., 2015)
		Turkey	Faecal	(Aslantaş et al., 2017; Pehlivanoglu et al., 2016)
		Asia		
		China	Faecal	(Zheng et al., 2019)
			Mastitis	(Ali et al., 2016, 2017)
		Israel	ND	(Lifshitz et al., 2018)
		South Korea	Faecal	(Tamang et al., 2013a)
			Mastitis	(Tark et al., 2017)
		Japan	Faecal	(Usui et al., 2013)
			Mastitis	(Ohnishi et al., 2013b)
			Diarrheic	(Ohnishi et al., 2013a)
		Lebanon	Faecal	(Diab et al., 2016)
		Taiwan	Mastitis	(Su et al., 2016)
		North America		
		Canada	ND	(Cormier et al., 2019)
			Faecal	(Cormier et al., 2016)
USA	Faecal	(Mir et al., 2016; Mollenkopf et al., 2012)		
Africa				
Egypt	Faecal	(Braun et al., 2016)		
Tanzania	Faecal	(Seni et al., 2016)		
Tunisia	Faecal	(Grami et al., 2014)		
	Mastitis	(Saidani et al., 2018)		
	<i>K. pneumoniae</i>	Europe		
		France	Faecal	(Haenni et al., 2014)
		Asia		
		India	Mastitis	(Koovapra et al., 2016)
	<i>K. ozaenae</i>	Europe		
		Italy	Faecal	(Stefani et al., 2014)
	<i>K. oxytoca</i>	Asia		
		Egypt	Mastitis	(Ahmed and Shimamoto, 2011)
CTX-M-15/28	<i>E. coli</i>	Europe		
		United Kingdom	Faecal	(Snow et al., 2011)
CTX-M-17	<i>E. coli</i>	Asia		
		China	Faecal	(Zheng et al., 2019)
CTX-M-17/18	<i>E. coli</i>	Europe		
		United Kingdom	Faecal	(Liebana et al., 2006)

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Beta-lactamase	Enterobacteriaceae	Country	Source	Reference
CTX-M-20	<i>E. coli</i>	Europe		
		United Kingdom	Infection	(Hunter et al., 2010)
CTX-M-22	<i>E. coli</i>	Europe		
		Netherlands	Faecal	(Heuvelink et al., 2019)
CTX-M-24	<i>E. coli</i>	North America		
		Canada	Faecal	(Cormier et al., 2016)
CTX-M-27	<i>E. coli</i>	Europe		
		Netherlands	Faecal	(Ceccarelli et al., 2019)
		North America		
		USA	Faecal	(Tadesse et al., 2018)
			ND	(Afema et al., 2018)
		Canada	Faecal	(Cormier et al., 2016)
ND	(Cormier et al., 2019)			
CTX-M-28	<i>E. coli</i>	Asia		
		Hong Kong	Faecal	(Ho et al., 2011)
CTX-M-32	<i>E. coli</i>	Europe		
		France	Faecal	(Haenni et al., 2014)
		Germany	Mastitis	(Eisenberger et al., 2017)
		Mayotte	ND	(Gay et al., 2018)
		Netherlands	Faecal	(Ceccarelli et al., 2019; Heuvelink et al., 2019; Hordijk et al., 2013a, b, c)
		Portugal	Faecal	(Ramos et al., 2013)
		United Kingdom	Infection	(Hunter et al., 2010)
		North America		
		Canada	Faecal	(Cormier et al., 2016)
			ND	(Cormier et al., 2019)
		USA	Faecal	(Cottell et al., 2013; Poole et al., 2017)
		Asia		
		South Korea	Faecal	(Tamang et al., 2013a)
CTX-M-55	<i>E. coli</i>	Europe		
		France	Sick	(Haenni et al., 2018; Lupo et al., 2018)
		Netherlands	Faecal	(Ceccarelli et al., 2019; Heuvelink et al., 2019)
		Spain	Faecal	(Hernández et al., 2017)
		North America		
		Canada	Faecal	(Cormier et al., 2016)
			ND	(Cormier et al., 2019)
		Asia		
		China	Faecal	(Zheng et al., 2012, 2019)
			Mastitis	(Ali et al., 2016, 2017)
Hong Kong	Faecal	(Ho et al., 2011, 2013)		
Taiwan	Mastitis	(Su et al., 2016)		
CTX-M-57	<i>E. coli</i>	Europe		
		France	Faecal	(Haenni et al., 2014)
CTX-M-61	<i>E. coli</i>	North America		
		Canada	Faecal	(Cormier et al., 2016)
CTX-M-63	<i>K. pneumoniae</i>	Asia		
		India	Mastitis	(Koovapra et al., 2016)
CTX-M-65	<i>E. coli</i>	Europe		
		Netherlands	Faecal	(Ceccarelli et al., 2019; Heuvelink et al., 2019)
		North America		
		Canada	Faecal	(Cormier et al., 2016)
			ND	(Cormier et al., 2019)
USA	ND	(Tate et al., 2017)		
CTX-M-79	<i>E. coli</i>	Europe		
		Netherlands	Faecal	(Hordijk et al., 2013c)
		North America		
USA	Faecal	(Wittum et al., 2010)		
CTX-M-98	<i>E. coli</i>	Asia		
		Hong Kong	Faecal	(Ho et al., 2011)

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Beta-lactamase	Enterobacteriaceae	Country	Source	Reference	
CTX-M-115	<i>E. coli</i>	North America			
		Canada	Faecal	(Cormier et al., 2016)	
CTX-M-117	<i>E. coli</i>	Europe			
		Switzerland	Faecal	(Hächler et al., 2013; Zurfluh et al., 2015)	
CTX-M-123	<i>E. coli</i>	Asia			
		Hong Kong	Faecal	(Ho et al., 2015)	
CTX-M-132	<i>E. coli</i>	Asia			
		Hong Kong	Faecal	(Ho et al., 2015)	
CTX-M-172	<i>E. coli</i>	North America			
		Canada	Faecal	(Cormier et al., 2016)	
CTX-M – without variant description	<i>E. coli</i>	Europe			
		Germany	Faecal	(Wu et al., 2013)	
		France	Diarrheic	(Valat et al., 2012)	
		Netherlands	Faecal	(Wu et al., 2013)	
		United Kingdom	Faecal	(Wu et al., 2013)	
		Switzerland	Faecal	(Geser et al., 2011)	
		North America			
		Canada	Faecal	(Awosile et al., 2018)	
		USA	Faecal	(Davis et al., 2015)	
		Asia			
		China	Mastitis	(Yang et al., 2018)	
		Saudi Arabia	ND	(Hassan et al., 2015)	
		South Korea	Faecal	(Tamang et al., 2013b)	
		Hong Kong	Faecal	(Duan et al., 2006)	
		India	Faecal	(Borah et al., 2014)	
			Mastitis	(Bandyopadhyay et al., 2015; Ghatak et al., 2013; Kar et al., 2015)	
		Israel	Faecal	(Adler et al., 2015)	
		Malaysia	Faecal	(Kamaruzzaman, 2015)	
		Africa			
		South Africa	Faecal	(Iweriebor et al., 2015)	
		Nigeria	Faecal	(Olowe et al., 2015)	
		<i>K. pneumoniae</i>	South America		
			Brazil	Mastitis	(Nóbrega et al., 2013)
Asia					
India	Mastitis	(Das et al., 2017)			
<i>Salmonella sp</i>	North America				
	USA	Sick	(Frye and Fedorka-Cray, 2007)		
SHV-2	<i>E. coli</i>	North America			
		Canada	Faecal	(Cormier et al., 2016)	
SHV-5	<i>E. coli</i>	Europe			
		Turkey	Faecal	(Kucukbasmaci et al., 2008)	
		<i>C. freundii</i>	Turkey	Faecal	(Kucukbasmaci et al., 2008)
		<i>C. brakii</i>	Turkey	Faecal	(Kucukbasmaci et al., 2008)
SHV-11	<i>E. coli</i>	Asia			
		Japan	Diarrheic	(Ohnishi et al., 2013a)	
	<i>K. pneumoniae</i>	Japan	Diarrheic	(Ohnishi et al., 2013a)	
SHV-12	<i>E. coli</i>	Europe			
		Germany	Sick	(Michael et al., 2017)	
		France	Faecal	(Haenni et al., 2014; Madec et al., 2008)	
		Netherlands	Faecal	(Ceccarelli et al., 2019; Hordijk et al., 2013c)	
		Turkey	Faecal	(Kucukbasmaci et al., 2008; Pehlivanoglu et al., 2016)	
		Asia			
		China	Mastitis	(Ali et al., 2016, 2017)	
		<i>K. pneumoniae</i>	Europe		
			France	Faecal	(Haenni et al., 2014)
			United Kingdom	Mastitis	(Timofte et al., 2014)
			Africa		
		Egypt	Mastitis	(Ahmed and Shimamoto, 2011)	

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Table 1 (continued)

Beta-lactamase	Enterobacteriaceae	Country	Source	Reference
	<i>K. oxytoca</i>	Egypt	Mastitis	(Ahmed and Shimamoto, 2011)
	<i>E. cloacae</i>	Egypt	Mastitis	(Ahmed and Shimamoto, 2011)
SHV-28	<i>Serratia marcescens</i>	Africa		
		Egypt	Mastitis	(Ahmed and Shimamoto, 2011)
SHV-180	<i>K. pneumoniae</i>	Asia		
		India	Mastitis	(Koovapra et al., 2016)
SHV – without variant description	<i>E. coli</i>	Europe		
		Netherlands	Faecal	(Wu et al., 2013)
		Asia		
		India	Faecal	(Borah et al., 2014)
			Mastitis	(Kar et al., 2015)
		Israel	Faecal	(Adler et al., 2015)
	<i>K. pneumoniae</i>	South America		
		Brazil	Mastitis	(Nóbrega et al., 2013)
	<i>Salmonella</i> spp.	North America		
		USA	Sick	(Frye and Fedorka-Cray, 2007)
TEM-20	<i>E. coli</i>	Europe		
		Netherlands	Faecal	(Hordijk et al., 2013c)
TEM-24	<i>K. ozaenae</i>	Europe		
		Italy	Faecal	(Stefani et al., 2014)
TEM-52	<i>E. coli</i>	Europe		
		Germany	Faecal	(Wieler et al., 2011)
			Sick	(Michael et al., 2017)
		France	Diarrheic	(Haenni et al., 2012)
		Netherlands	Faecal	(Ceccarelli et al., 2019; Heuvelink et al., 2019; Hordijk et al., 2013a, b, c)
TEM-71	<i>E. coli</i>	Europe		
		France	Faecal	(Hartmann et al., 2012)
			Diarrheic	(Hartmann et al., 2012)
TEM-126	<i>E. coli</i>	Europe		
		France	Sick	(Madec et al., 2008)
TEM-186	<i>E. coli</i>	Europe		
		Switzerland	Faecal	(Geser et al., 2012a)
TEM-190	<i>E. coli</i>	Europe		
		Netherlands	Faecal	(Ceccarelli et al., 2019)
TEM – without variant description	<i>E. coli</i>	North America		
		USA	Faecal	(Donaldson et al., 2006; Mir et al., 2016)
		Asia		
		India	Faecal	(Borah et al., 2014)
		Thailand	Mastitis	(Hinthong et al., 2017)
		Africa		
		Egypt	Faecal	(Braun et al., 2016)
OXA-10	<i>E. coli</i>	Europe		
		Turkey	Faecal	(Kucukbasmaci et al., 2008)
	<i>C. freundii</i>	Turkey	Faecal	(Kucukbasmaci et al., 2008)
	<i>C. brakii</i>	Turkey	Faecal	(Kucukbasmaci et al., 2008)
OXA-30	<i>K. oxytoca</i>	Africa		
		Egypt	Mastitis	(Ahmed and Shimamoto, 2011)
	<i>E. cloacae</i>	Egypt	Mastitis	(Ahmed and Shimamoto, 2011)
ESBL producers - without beta-lactamase description (ND-ESBL)	<i>E. coli</i>	South America		
		Brazil	Mastitis	(Santos, 2006)
		Chile	Mastitis	(Gonzalez, 2006)
		Peru	Faecal	(Mendoza, 2017)
		Europe		
		Germany	Faecal	(Friese et al., 2013)
		Spain	Faecal	(Briñas et al., 2005)
		Pais de Gales	ND	(Teale et al., 2005)
		Netherlands	Faecal	(Gonggrijp et al., 2016)
		Switzerland	Faecal	(Reist et al., 2013)
		North America		

(continued on next page)

Table 1 (continued)

Beta-lactamase	Enterobacteriaceae	Country	Source	Reference
		Canada	Faecal	(Lussier, 2010)
		Asia		
		Iran	Faecal	(Barzan et al., 2017)
		Thailand	Mastitis	(Hinthong et al., 2017)
		Africa		
		Nigeria	Faecal	(Ogefere et al., 2017)
		Tanzania	Faecal	(Mkala and Azizi, 2017)
	<i>K. pneumoniae</i>	Asia		
		Israel	Faecal	(Adler et al., 2015)
	<i>Klebsiella</i> spp.	Africa		
		Nigeria	Faecal	(Ogefere et al., 2017)
	<i>Salmonella</i> spp.	Nigeria	Faecal	(Ogefere et al., 2017)
	<i>C. youngae</i>	Europe		
		Switzerland	Faecal	(Reist et al., 2013)
	<i>E. cloacae</i>	South America		
		Peru	Faecal	(Mendoza, 2017)
		Europe		
		Switzerland	Faecal	(Reist et al., 2013)
	<i>Proteus mirabilis</i>	Africa		
		Nigeria	Faecal	(Ogefere et al., 2017)
	<i>Proteus vulgaris</i>	Nigeria	Faecal	(Ogefere et al., 2017)
	<i>Providencia</i> spp.	Nigeria	Faecal	(Ogefere et al., 2017)
	<i>Shigella</i> spp.	Nigeria	Faecal	(Ogefere et al., 2017)

Source: ND – Not described isolate source.

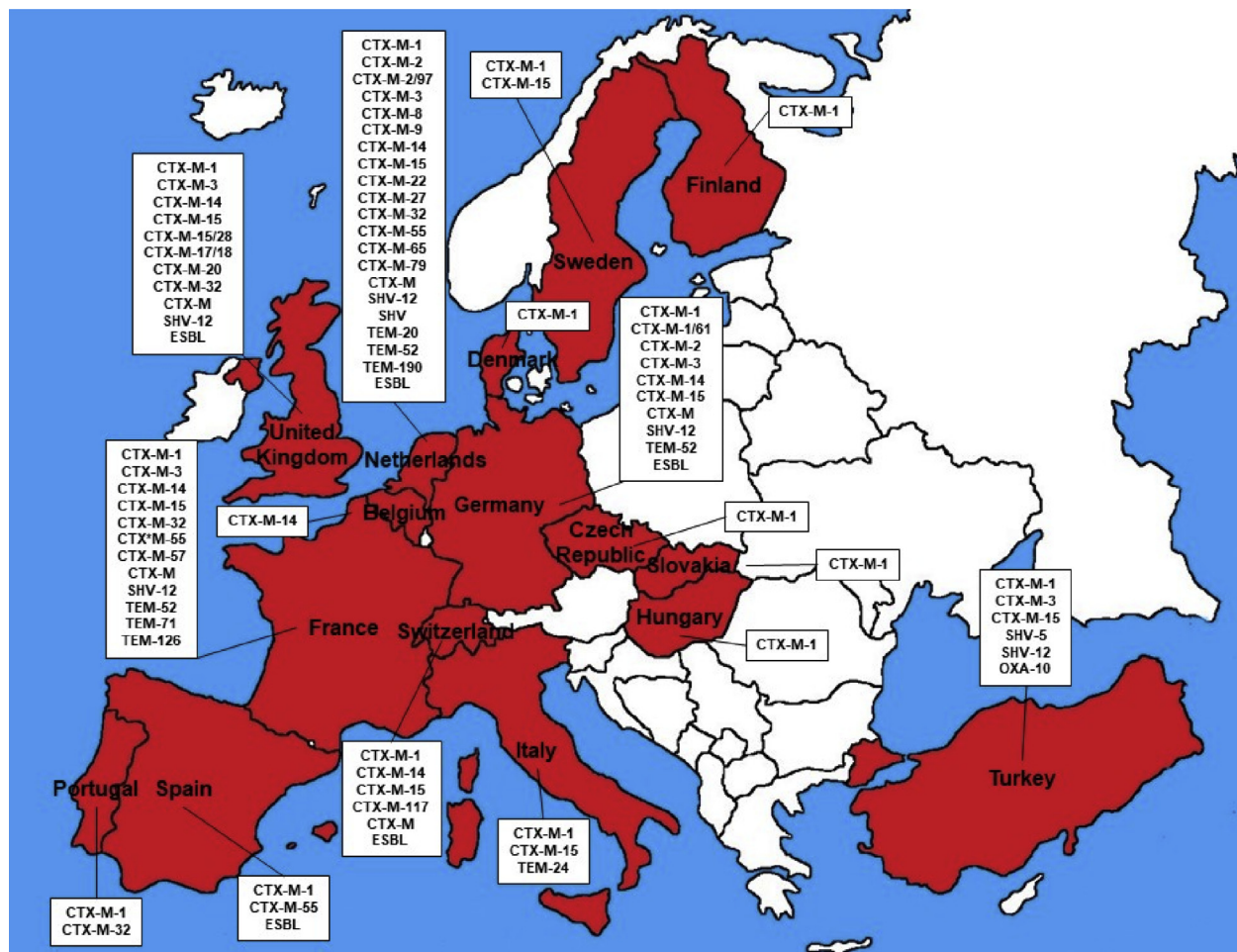


Figure 2. Illustrative map of Europe showing countries with description of E-ESBL in cattle and beta-lactamases type.

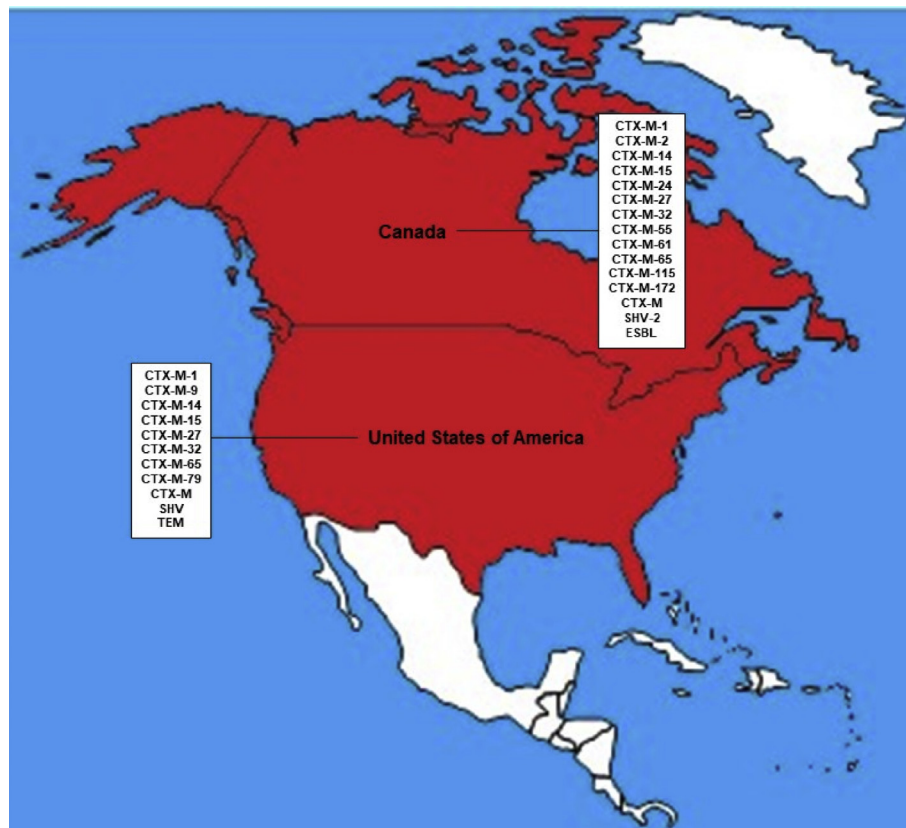


Figure 3. Illustrative map of North America with the countries with description of E-ESBL in cattle and the diversity of beta-lactamases presented.

2014; Dia et al., 2016; Fam et al., 2011; Hasan et al., 2016; Hernández et al., 2012; Liao et al., 2017; Poirel et al., 2013; Ruiz et al., 2011; Sidjabat et al., 2010).

The virulent and multi-resistant CTX-M-15-producing *E. coli* O25b-ST131 clone is certainly one of the most well adapted circulating clones among E-ESBL, which is responsible for outbreaks and deaths around the world and is not related only to infectious processes, but is also reported in human intestinal colonization (elderly, adults and children) and animals (terrestrial and aquatic) and environmental contamination (Badran et al., 2016; Brahmi et al., 2015; Dolejska et al., 2011a; Ewers et al., 2010; Gonçalves et al., 2016; Namaei et al., 2017; Naseer et al., 2007; Olesen et al., 2013; Oteo et al., 2009; Owens et al., 2011; Zhong et al., 2015).

3. Europe

Europe is the continent with more number of countries ($n = 16$) with description of E-ESBL in cattle, Figure 2 shows all countries. Belgium, Czech Republic, Denmark, Finland, France, Germany, Hungary, Italy, Netherlands, Portugal, Slovakia, Spain, Sweden, Switzerland, Turkey and United Kingdom, presented at least one report of E-ESBL in cattle (Aslantaş et al., 2017; Briñas et al., 2005; Dolejska et al., 2011b; Duse et al., 2015; Hordijk et al., 2013c; Hunter et al., 2010; Kjeldsen et al., 2015; Kmeř and Bujňáková, 2018; Michael et al., 2017; Päiväranta et al., 2016; Pardon et al., 2017; Ramos et al., 2013; Stefani et al., 2014; Toth et al., 2013; Valat et al., 2016; Zurfluh et al., 2015). CTX-M-1 was described in 14 of the 16 countries with E-ESBL in cattle, CTX-M-15 present in 7, CTX-M-14 in 6 and CTX-M-3 and SHV-12 in 5 (Aslantaş et al., 2017; Briñas et al., 2005; Dolejska et al., 2011b; Duse et al., 2015; Gay et al., 2018; Haenni et al., 2014; Hordijk et al., 2013b; Hordijk et al., 2013c; Hunter et al., 2010; Kjeldsen et al., 2015; Kmeř and Bujňáková, 2018; Michael et al., 2017; Päiväranta et al., 2016; Pardon et al., 2017; Pehlivanoglu et al., 2016; Ramos et al., 2013; Timofte et al., 2014; Toth et al., 2013; Valat et al., 2016; Zurfluh et al., 2015).

Germany presented the description of CTX-M-1, CTX-M-1/61, CTX-M-2, CTX-M-3, CTX-M-14, CTX-M-15, CTX-M without the variant description (CTX-M), SHV-12, TEM-52 and E-ESBL without the description or detection of beta-lactamase (ND-ESBL) described in *E. coli* and *Salmonella enterica* from faecal and clinical samples (Dahms et al., 2015; Friese et al., 2013; Michael et al., 2017; Wieler et al., 2011; Wu et al., 2013). CTX-M-1, CTX-M-3, CTX-M-14, CTX-M-15 and SHV-12 have already been reported in E-ESBL in humans in Germany associated with infections (Gerhold et al., 2016; Mshana et al., 2009; Schmitt et al., 2007).

The Netherlands, German neighbours, also presented high diversity and number of reports of E-ESBL in cattle. There were identified CTX-M-1, CTX-M-2, CTX-M-2/97, CTX-M-3, CTX-M-8, CTX-M-9, CTX-M-14, CTX-M-15, CTX-M-22, CTX-M-27, CTX-M-32, CTX-M-55, CTX-M-65, CTX-M-79, CTX-M, SHV-12, SHV without description of variant (SHV), TEM-20, TEM-52, TEM-190 and ND-ESBL, all of them described in faecal *E. coli*. CTX-M-1, CTX-M-2, CTX-M-14, CTX-M-15, SHV-12 and TEM-52 have already been described in E-ESBL of human (faecal and hospital) origin in the Netherlands (Naiemi et al., 2006; Overdeest et al., 2011).

The biggest European cattle producer, France, including 2 French departments in Africa (Mayotte and Réunion) has reported E-ESBL in cattle with CTX-M-1, CTX-M-3, CTX-M-14, CTX-M-15, CTX-M-32, CTX-M-55, CTX-M-57, CTX-M, SHV-12, TEM-52, TEM-71 and TEM-126 reported in *E. coli* and *K. pneumoniae* of faecal and clinical origin. All of the described beta-lactamases (CTX-M-1, CTX-M-3, CTX-M-14, CTX-M-15, CTX-M-32, CTX-M-57, SHV-12, TEM-52, TEM-71 and TEM-126) in cattle have been reported in E-ESBL from humans of hospital origin in France (De Champs et al., 2004; Robin et al., 2017).

The United Kingdom was the European country with the highest number of reported CTX-M variants. The CTX-M-1, CTX-M-3, CTX-M-14, CTX-M-15, CTX-M-15/28, CTX-M-17/18, CTX-M-20, CTX-M-32, CTX-M, SHV-12 and ND-ESBL were reported in E-ESBL in cattle. *E. coli* and *K. pneumoniae* were the species that harbour the genes and these are of



Figure 4. Map of South America illustrating the countries with description of E-ESBL in cattle and the diversity of beta-lactamases presented.

faecal and clinical origin. CTX-M-3, CTX-M-14, CTX-M-15, CTX-M-17/18 and SHV-12 have already been described in humans in E-ESBLs (Batchelor et al., 2005; Doumith et al., 2012).

Switzerland presented E-ESBL in cattle with CTX-M-1, CTX-M-14, CTX-M-15, CTX-M-117, CTX-M, TEM-186 and ND-ESBL (Geser et al., 2011, 2012a; Reist et al., 2013; Zurfluh et al., 2015). They were reported in 3 species: *E. coli*, *C. youngae* and *E. cloacae*. All reports were of faecal origin, with the exception of 1 case of mastitis (CTX-M-14) (Geser et al., 2012a). E-ESBL of human origin have been reported to harbour CTX-M-1, CTX-M-14 and CTX-M-15 in Switzerland (Geser et al., 2012b).

CTX-M-1, CTX-M-15 and TEM-24 were described in E-ESBL in cattle in Italy. Reported in *K. pneumoniae* (mastitis) and *K. ozaenae* (faecal carriage). The three types of ESBL described in cattle, CTX-M-1, CTX-M-15 and TEM-24, have also been described in human clinical isolates (Mugnaioli et al., 2006; Perilli et al., 2011).

Turkey is the second largest cattle producer in Europe and presented E-ESBL in cattle with CTX-M-1, CTX-M-3, CTX-M-15, SHV-5, SHV-12 and

OXA-10 in *E. coli*, *C. freundii* and *C. brakii* of faecal origin (Aslantaş et al., 2017; Kucukbasmaci et al., 2008; Pehlivanoglu et al., 2016). CTX-M-1, CTX-M-3, CTX-M-15, SHV-5 and SHV-12 were reported in human clinical isolates in Turkish hospitals (Gur et al., 2008; Tasli and Bahar, 2005).

The Nordic countries have few reports and diversity of beta-lactamases, with E-ESBL in cattle harbouring CTX-M-1 in Denmark and Finland and CTX-M-1 and CTX-M-15 in Sweden all in *E. coli* and of intestinal origin (Duse et al., 2015; Kjeldsen et al., 2015; Päivärinta et al., 2016). When analysed the description in E-ESBL of human origin, CTX-M-1 has been described in Denmark, Finland and Sweden and CTX-M-15 in Sweden (Brolund et al., 2014; Forssten et al., 2010; Jakobsen et al., 2015).

In the Iberian Peninsula, Spain and Portugal also presented E-ESBL in cattle, with descriptions on Spain of CTX-M-1, CTX-M-55 and ND-ESBL and in Portugal of CTX-M-1 and CTX-M-32 (Briñas et al., 2005; Hernández et al., 2017; Ramos et al., 2013). The descriptions in both countries were in *E. coli*, but in Spain they were of faecal and clinical

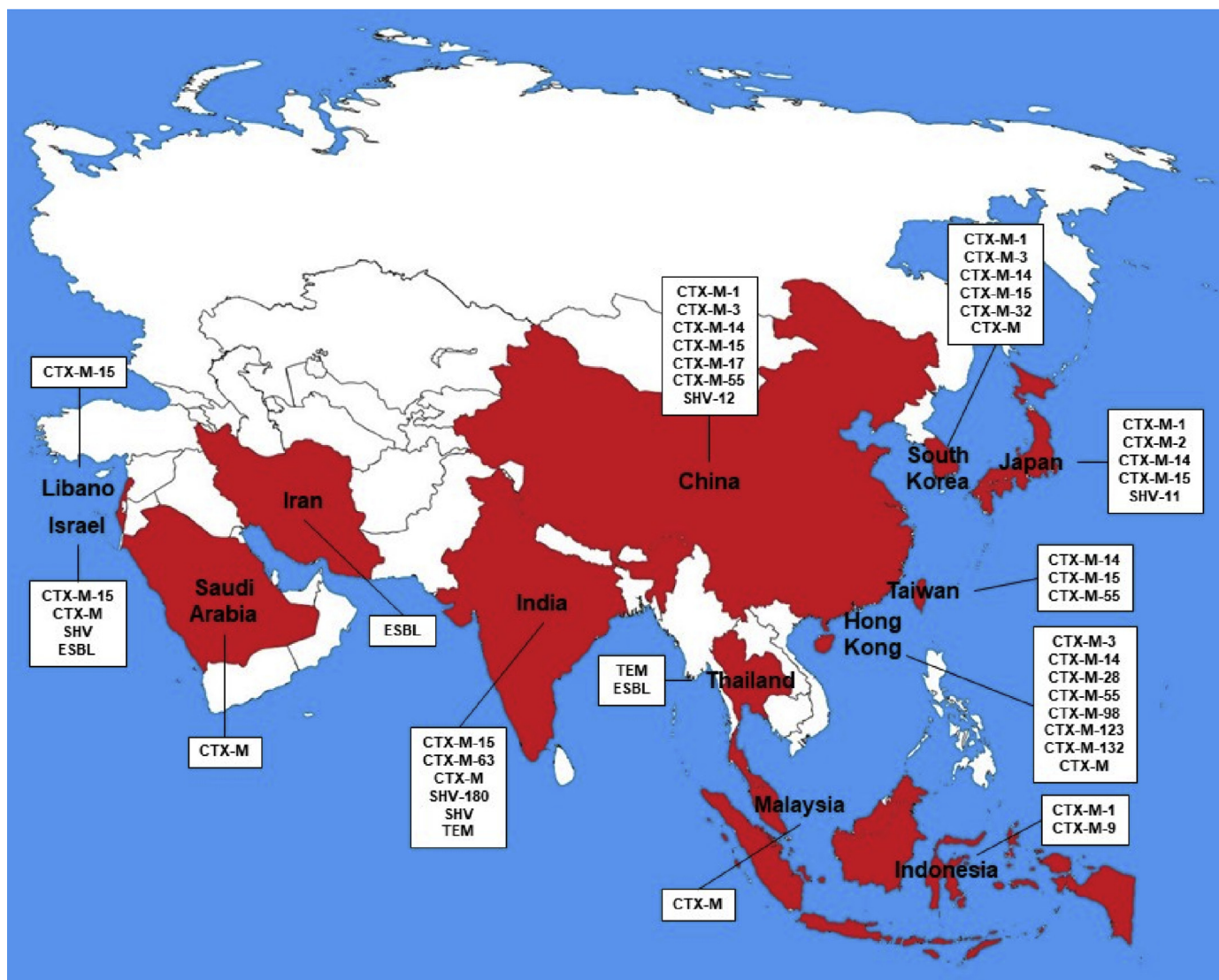


Figure 5. Asia illustrative map of countries with description of E-ESBL in cattle and the diversity of beta-lactamases presented.

origin and in Portugal only faecal. CTX-M-1 has already been described in E-ESBL in human in Spain and CTX-M-1 and CTX-M-32 in Portugal (Fernandes et al., 2014; Novais et al., 2007).

CTX-M-1 was described in Hungary, Czech Republic and Slovakia and CTX-M-14 in Belgium in E-ESBL in cattle. All in *E. coli* and with faecal and clinical origins (Dolejska et al., 2013; Kmet and Bujňáková, 2018; Pardon et al., 2017; Toth et al., 2013). In E-ESBL of human origin, CTX-M-1 has already been reported in Hungary, Czech Republic and CTX-M-14 in Belgium (Dolejska et al., 2013; Ebrahimi, 2016; Rodriguez-Villalobos et al., 2011).

4. North America

In North America only 2 countries registered E-ESBL description in cattle, Canada and the United States, the last one being the world's largest cattle producer (USDA et al., 2017). CTX-M-15, CTX-M-32 and CTX-M-65 were the only beta-lactamases described in both countries, the Figure 3 shows the complete described ESBL from cattle in the North America (Cormier et al., 2016; Mir et al., 2016; Poole et al., 2017; Tate et al., 2017).

In the United States there were described in E-ESBL in cattle the CTX-M-1, CTX-M-9, CTX-M-14, CTX-M-15, CTX-M-27, CTX-M-32, CTX-M-65, CTX-M-79, CTX-M, SHV and TEM. E-ESBL of clinical and faecal origin in

E. coli, *Salmonella* enteric and *Salmonella* spp (Afema et al., 2018; Davis et al., 2015; Frye and Fedorka-Cray, 2007; Mir et al., 2016; Mollenkopf et al., 2012; Poole et al., 2017; Tate et al., 2017; Wittum et al., 2010). CTX-M-1, CTX-M-14, CTX-M-15 and CTX-M-65 were reported in E-ESBL isolates from humans (Chen et al., 2014; Li et al., 2015; Tate et al., 2017; Wang et al., 2013).

CTX-M-1, CTX-M-2, CTX-M-14, CTX-M-15, CTX-M-24, CTX-M-27, CTX-M-32, CTX-M-55, CTX-M-61, CTX-M-65, CTX-M-115, CTX-M-172, CTX-M, SHV-2 and ND-ESBL were described in E-ESBL in cattle in Canada, which was the country where the largest variety of CTX-M's types were described (Awosile et al., 2018; Cormier et al., 2016; Lussier, 2010). All E-ESBLs were *E. coli* of faecal origin. In E-ESBL of human origin in Canada were detected similarly to cattle the CTX-M-2, CTX-M-15, CTX-M-24, CTX-M-27, CTX-M-55, CTX-M-65 and SHV-2 (Denisuik et al., 2013, 2015; Peirano et al., 2010; Pitout et al., 2008).

5. South America

In South America E-ESBL is still poorly described, being few and incomplete, from the molecular point of view, the reports of E-ESBL in cattle in the countries of this continent. Only Brazil, Chile and Peru present reports of E-ESBL in cattle. Figure 4 shows what E-ESBL has already been described in these countries.

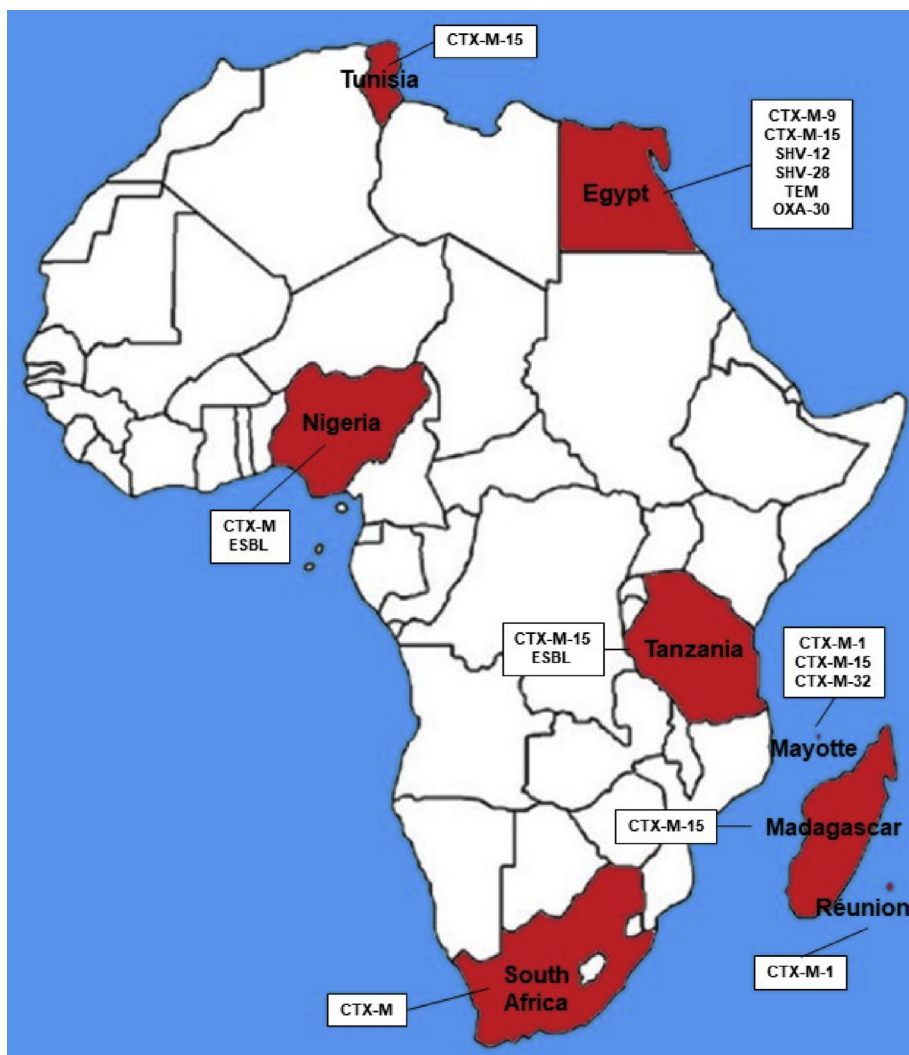


Figure 6. Map of Africa illustrating the countries with description of E-ESBL in cattle and the diversity of beta-lactamases presented.

Brazil is the world's second largest cattle producer and the world's second largest exporter of cattle (USDA et al., 2017). The presence of E-ESBL in cattle with CTX-M-2, CTX-M-15, CTX-M, SHV and ND-ESBL has already been described in the country (Nóbrega et al., 2013; Palmeira et al., 2018; Santos, 2006; Sartori et al., 2017). Originated from mastitis or with faecal origin in *E. coli* and *K. pneumoniae*. There are several reports in human clinical E-ESBL of CTX-M-2, CTX-M-15, CTX-M and SHV in Brazil (Sampaio and Gales, 2016).

Chile and Peru describe the presence of E-ESBL, but not described the enzymes responsible for ESBL phenotype. These reports were in *E. coli* in mastitis in Chile and in *E. coli* and *E. cloacae* of faecal origin in Peru (Gonzalez, 2006; Mendoza, 2017). Both countries have reports of E-ESBL in humans (Colquechagua Aliaga et al., 2015; Hernandez et al., 2013).

6. Asia

The second continent with the highest number of countries reporting E-ESBL in cattle is Asia, which shows description of E-ESBL in 13 countries (China, Hong Kong, India, Indonesia, Iran, Israel, Japan, Lebanon, Malaysia, Saudi Arabia, South Korea, Thailand and Taiwan), highlighting China and India which are the fourth and fifth largest cattle producers in the world (Adler et al., 2015; Ali et al., 2017; Barzan et al., 2017; Diab et al., 2016; Hassan et al., 2015; Hinthong et al., 2017; Ho et al., 2015; Kamaruzzaman, 2015; Koovapra et al., 2016; Ohnishi et al., 2013a; Su

et al., 2016; Sudarwanto et al., 2016; Tark et al., 2017). They have different roles in the import and export scenario, as India is the world's largest exporter of cattle and China the largest importer, since its internal production is not sufficient for internal consumption (USDA et al., 2017). Figure 5 shows the countries and the diversity of beta-lactamases found in each of them.

China presents a description of E-ESBL in cattle harbouring CTX-M-1, CTX-M-3, CTX-M-14, CTX-M-15, CTX-M-17, CTX-M-28, CTX-M-55, CTX-M-65, CTX-M-88, CTX-M-98, CTX-M-102, CTX-M-103, CTX-M-123, CTX-M and SHV-12. All descriptions were in *E. coli* and faecal origin and mastitis (Ali et al., 2017; Yang et al., 2018; Zheng et al., 2019). CTX-M-3, CTX-M-14, CTX-M-15, CTX-M-55 and SHV-12 were described isolated from E-ESBL of human origin in China (Hu et al., 2013; Tian et al., 2012).

In India CTX-M-15, CTX-M-63, CTX-M, SHV-180, SHV and TEM in E-ESBL from cattle have already been described. Faecal origin and mastitis, being detected in *E. coli* and *K. pneumoniae* (Borah et al., 2014; Das et al., 2017; Koovapra et al., 2016). The presence of CTX-M-15 and SHV in E-ESBL in India has been reported in humans (Hawkey, 2008).

Japan and South Korea, the 3rd and 4th largest world importers of cattle, presented E-ESBL in cattle, respectively, with CTX-M-1, CTX-M-2, CTX-M-14, CTX-M-15 and SHV-11 and CTX-M-1, CTX-M-3, CTX-M-14, CTX-M-15, CTX-M-32, and CTX-M. These were detected in faecal E-ESBL and clinical in the animals and in Japan in *E. coli*, *K. pneumoniae*, *K. oxytoca*, *C. freundii*, *C. koseri*, *E. cloacae* and *E. aerogenes* and in South

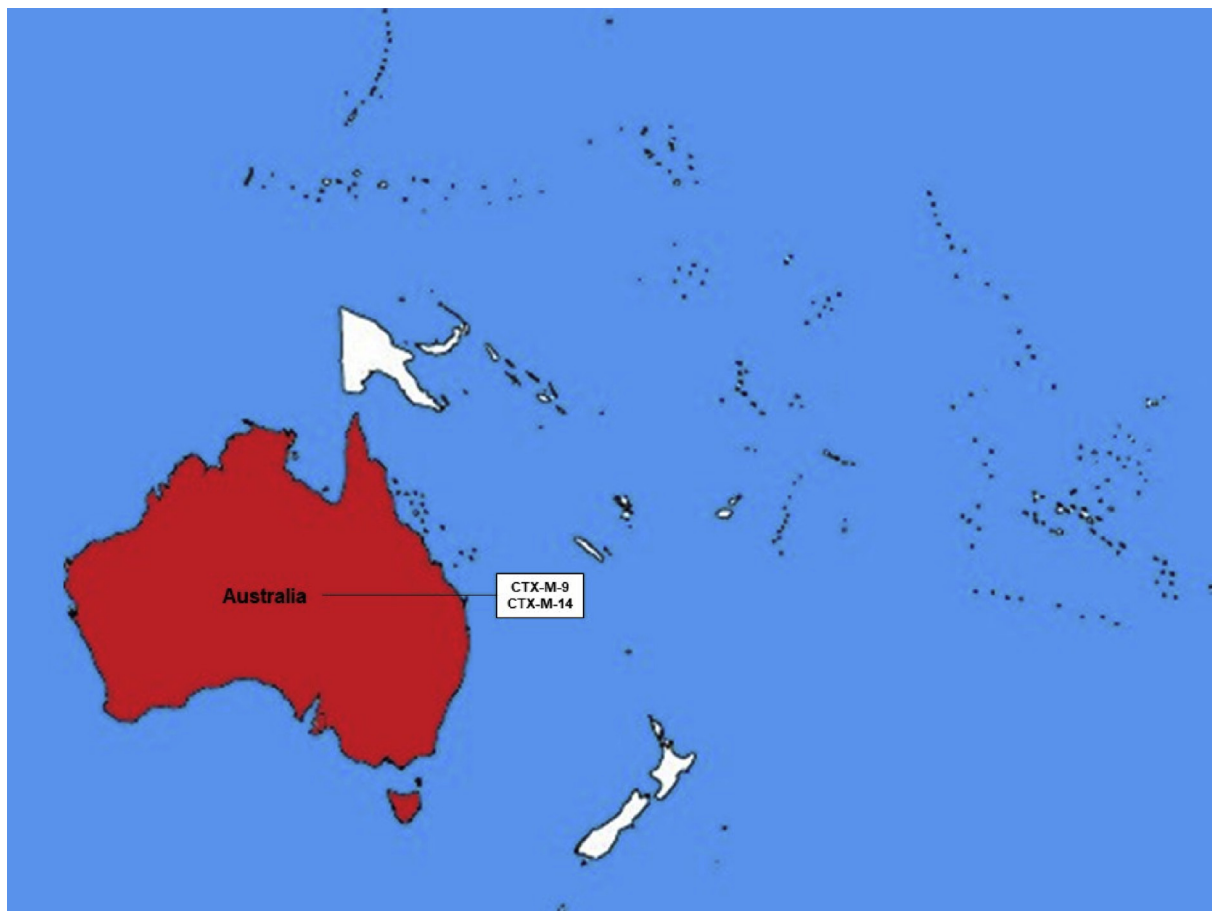


Figure 7. Map of Oceania illustrating countries with description of E-ESBL in cattle and the diversity of beta-lactamases presented.

Korea only in *E. coli* (Ohnishi et al., 2013a, b; Shiraki et al., 2004; Tamang et al., 2013a, b; Tark et al., 2017). In Japan CTX-M-14, CTX-M-15 and SHV-11 have been described in E-ESBL of human origin (Kuroda et al., 2012; Saito et al., 2014). The CTX-M-3, CTX-M-14, CTX-M-15 and CTX-M-32 beta-lactamases have already been described in E-ESBL of human origin in South Korea (Lee et al., 2009).

Hong Kong and Taiwan presented an E-ESBL profile in cattle only with reports of beta-lactamases of the CTX-M type. Hong Kong with CTX-M-3, CTX-M-14, CTX-M-28, CTX-M-55, CTX-M-98, CTX-M-123, CTX-M-132 and CTX-M (Duan et al., 2006; Ho et al., 2011, 2013, 2015). Taiwan already has CTX-M-14, CTX-M-15 and CTX-M-55 (Su et al., 2016). All in *E. coli* of faecal origin and mastitis. In Hong Kong the E-ESBL description of human origin has been reported well for CTX-M-14 and in Taiwan for CTX-M-14 and CTX-M-15 (Yan et al., 2006; Yeung, 2011).

Indonesia, Malaysia, and Thailand reported E-ESBL in cattle, respectively, for CTX-M-1 and CTX-M-9; CTX-M; and TEM and ND-ESBL. All in *E. coli* of origin in mastitis or faecal (Hinthonng et al., 2017; Kamaruzzaman, 2015; Sudarwanto et al., 2016). In humans, reports of E-ESBL have been described for CTX-M-1 in Indonesia, CTX-M in Malaysia and ND-ESBL in Thailand (Bagus Wasito et al., 2017; Ho et al., 2012; Kiratisin et al., 2008).

In the Middle East region there is a description of E-ESBL in cattle in Saudi Arabia (CTX-M), Iran (ND-ESBL), Israel (CTX-M-15, CTX-M, SHV and ND-ESBL) and in Lebanon (CTX-M-15). They were identified in *E. coli* and *K. pneumoniae* in faecal samples (Adler et al., 2015; Barzan et al., 2017; Diab et al., 2016; Hassan et al., 2015; Lifshitz et al., 2018). All E-ESBL profiles in cattle described above in these countries are also found described in humans (Bazzaz et al., 2009; Chmelnitsky et al., 2005; Hassan and Abdalhamid, 2014; Moubareck et al., 2005).

7. Africa

In Africa, only 6 countries presented reports of E-ESBL in cattle. They were Egypt, Madagascar, Nigeria, South Africa, Tanzania and Tunisia (Braun et al., 2016; Gay et al., 2018; Iweriebor et al., 2015; Mkala and Azizi, 2017; Olowe et al., 2015; Saidani et al., 2018; Seni et al., 2016). There are not numerous nor descriptive reports on this continent. They are also not very prominent countries within the world economic cattle cycle, highlighting only Egypt which is the 8th biggest importer of cattle in the world (USDA et al., 2017). Figure 6 shows the countries with E-ESBL reported in cattle and what beta-lactamase type has been described in them.

In Egypt E-ESBL was described in cattle harbouring CTX-M-9, CTX-M-15, SHV-12, SHV-28, TEM and OXA-30. Described in *E. coli*, *K. pneumoniae*, *K. oxytoca*, *E. cloacae* and *S. marcescens* of faecal origin and mastitis (Ahmed and Shimamoto, 2011; Braun et al., 2016). There are reports in human E-ESBL also with CTX-M-9, CTX-M-15 and SHV-12 (Fam et al., 2011; Hamdy Mohammed et al., 2016; Newire et al., 2013).

South Africa (CTX-M), Madagascar (CTX-M-15), Nigeria (CTX-M and ND-ESBL), Tanzania (CTX-M-15) and Tunisia (CTX-M-15) also presented reports of E-ESBL in cattle. The reports were *E. coli*, *Klebsiella* sp, *Salmonella* sp, *P. mirabilis*, *P. vulgaris*, *Providencia* sp e *Shigella* spp (Gay et al., 2018; Iweriebor et al., 2015; Ogefere et al., 2017; Olowe et al., 2015; Saidani et al., 2018; Seni et al., 2016). In all countries the origin was faecal (except Tunisia, with mastitis also). All types of descriptions presented in these 5 countries for E-ESBL in cattle also present reports in humans (Abbassi et al., 2008; Iroha et al., 2012; Manyahi et al., 2017; Ouedraogo et al., 2016).

8. Oceania

In Oceania as one might imagine, due to its size and number of countries, there exist few reports of E-ESBL in cattle production. The only country with reports is Australia, which is the 6th largest world producer country and the 3rd biggest exporter (USDA et al., 2017). Figure 7 shows the countries with E-ESBL description in cattle and what ESBL type has been described in them.

Australia presented a description of CTX-M-9 and CTX-M-14 in E-ESBL in cattle. The description was carried out in clinical isolated and in *E. coli* and in *S. enterica* (Abraham et al., 2015; Sparham et al., 2017). Both variants, CTX-M-9 and CTX-M-14, have already been described in human clinical isolates in Australia (Zong et al., 2008).

9. Conclusion

E-ESBL are a threat to human health and are now scattered around the world in intestinal colonization and clinical processes of cattle in Europe, the Americas, Asia, Africa and Oceania. These are described in 6 of the 7 major world cattle producers and certainly these E-ESBLs are contributing to the circulation of these and the ESBL genes through the ecosystems. A circulation that does not only concern the internal level of each country, since the circulation trade of cattle and their derivatives between countries is increasing, with E-ESBL being found in the animals of the world 5 largest meat exporters.

Further studies in the various areas of each country, as well as in other countries without data, are necessary for a better understanding of the presence and circulation of these E-ESBL through cattle and the food chain to assist in the implementation of measures to help in the surveillance and control of the E-ESBL dissemination and propagation.

Declarations

Author contribution statement

Josman Dantas Palmeira, Helena Maria Neto Ferreira: Analyzed and interpreted the data; Wrote the paper.

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Competing interest statement

The authors declare no conflict of interest.

Additional information

No additional information is available for this paper.

References

- Hächler, H., Kotsakis, S.D., Tzouveleakis, L.S., Geser, N., Lehner, A., Miriagou, V., Stephan, R., 2013. Characterisation of CTX-M-117, a Pro174Gln variant of CTX-M-15 extended-spectrum β -lactamase, from a bovine *Escherichia coli* isolate. *Int. J. Antimicrob. Agents* 41, 94–95.
- Jakobsen, L., Bortolaia, V., Bielik, E., Moodley, A., Olsen, S.S., Hansen, D.S., Frimodt-Møller, N., Guardabassi, L., Hasman, H., 2015. Limited similarity between plasmids encoding CTX-M-1 β -lactamase in *Escherichia coli* from humans, pigs, cattle, organic poultry layers and horses in Denmark. *J. Glob. Antimicrob. Resist.* 3, 132–136.
- Lee, S.-G., Jeong, S.H., Lee, H., Kim, C.K., Lee, Y., Koh, E., Chong, Y., Lee, K., 2009. Spread of CTX-M-type extended-spectrum β -lactamases among bloodstream isolates of *Escherichia coli* and *Klebsiella pneumoniae* from a Korean hospital. *Diagn. Microbiol. Infect. Dis.* 63, 76–80.
- Abbassi, M.S., Torres, C., Achour, W., Vinue, L., Saenz, Y., Costa, D., Bouchami, O., Ben Hassen, A., 2008. Genetic characterisation of CTX-M-15-producing *Klebsiella pneumoniae* and *Escherichia coli* strains isolated from stem cell transplant patients in Tunisia. *Int. J. Antimicrob. Agents* 32, 308–314.
- Abraham, S., Jordan, D., Wong, H.S., Johnson, J.R., Toleman, M.A., Wakeham, D.L., Gordon, D.M., Turnidge, J.D., Mollinger, J.L., Gibson, J.S., Trott, D.J., 2015. First detection of extended-spectrum cephalosporin- and fluoroquinolone-resistant *Escherichia coli* in Australian food-producing animals. *J. Glob. Antimicrob. Resist.* 3, 273–277.
- Adeolu, M., Alnajar, S., Naushad, S., R, S.G., 2016. Genome-based phylogeny and taxonomy of the 'Enterobacterales': proposal for Enterobacterales ord. nov. divided into the families Enterobacteriaceae, Erwiniaceae fam. nov., Pectobacteriaceae fam. nov., Yersiniaceae fam. nov., Hafniaceae fam. nov., Morganeliaceae fam. nov., and Budviciaceae fam. nov. *Int. J. Syst. Evol. Microbiol.* 66, 5575–5599.
- Adler, A., Sturlesi, N.a., Fallach, N., Zilberman-Barzilai, D., Hussein, O., Blum, S.E., Klement, E., Schwaber, M.J., Carmeli, Y., 2015. Prevalence, risk factors, and transmission dynamics of extended-spectrum- β -lactamase-producing enterobacteriaceae: a national survey of cattle farms in Israel in 2013. *J. Clin. Microbiol.* 53, 3515–3521.
- Afema, J.A., Ahmed, S., Besser, T.E., Jones, L.P., Sischo, W.M., Davis, M.A., 2018. Molecular epidemiology of dairy cattle-associated *Escherichia coli* carrying blaCTX-M genes in Washington state. *Appl. Environ. Microbiol.* 84.
- Ahmed, A.M., Shimamoto, T., 2011. Molecular characterization of antimicrobial resistance in Gram-negative bacteria isolated from bovine mastitis in Egypt. *Microbiol. Immunol.* 55, 318–327.
- Alexandratos, N., Bruinsma, J., 2012. World agriculture towards 2030/2050 - the 2012 revision. In: Global Perspective Studies Team. Food and Agriculture Organization of the United Nations.
- Ali, T., ur Rahman, S., Zhang, L., Shahid, M., Zhang, S., Liu, G., Gao, J., Han, B., 2016. ESBL-producing *Escherichia coli* from cows suffering mastitis in China contain clinical class 1 integrons with CTX-M linked to ISCR1. *Front. Microbiol.* 7.
- Ali, T., Rahman, S.U., Zhang, L., Shahid, M., Han, D., Gao, J., Zhang, S., Ruegg, P.L., Saddique, U., Han, B., 2017. Characteristics and genetic diversity of multi-drug resistant extended-spectrum beta-lactamase (ESBL)-producing *Escherichia coli* isolated from bovine mastitis. *Oncotarget* 8, 90144–90163.
- Asai, T., Masani, K., Sato, C., Hiki, M., Usui, M., Baba, K., Ozawa, M., Harada, K., Aoki, H., Sawada, T., 2011. Phylogenetic groups and cephalosporin resistance genes of *Escherichia coli* from diseased food-producing animals in Japan. *Acta Vet. Scand.* 53, 52.
- Aslantaş, Ö., Elmacioğlu, S., Yilmaz, E.Ş., 2017. Prevalence and characterization of ESBL- and AmpC-producing *Escherichia coli* from cattle. *Kafkas Universitesi Veteriner Fakültesi Dergisi* 23, 63–67.
- Awosile, B., McClure, J., Sanchez, J., Rodriguez-Lecompte, J.C., Keefe, G., Heider, L.C., 2018. *Salmonella enterica* and extended-spectrum cephalosporin-resistant *Escherichia coli* recovered from Holstein dairy calves from 8 farms in New Brunswick, Canada. *J. Dairy Sci.* 101, 3271–3284.
- Badran, E.F., Qamer Din, R.A., Shehabi, A.A., 2016. Low intestinal colonization of *Escherichia coli* clone ST131 producing CTX-M-15 in Jordanian infants. *J. Med. Microbiol.* 65, 137–141.
- Bagus Wasito, E., Shigemura, K., Osawa, K., Fardah, A., Kanaida, A., Raharjo, D., Kuntaman, K., Hadi, U., Harijono, S., Marto Sudarmo, S., Nakamura, T., Shibayama, K., Fujisawa, M., Shirakawa, T., 2017. Antibiotic susceptibilities and genetic characteristics of extended-spectrum beta-lactamase-producing *Escherichia coli* isolates from stools of pediatric diarrhea patients in Surabaya, Indonesia. *Jpn. J. Infect. Dis.* 70, 378–382.
- Bandyopadhyay, S., Samanta, I., Bhattacharyya, D., Nanda, P.K., Kar, D., Chowdhury, J., Dandapat, P., Das, A.K., Batul, N., Mondal, B., Dutta, T.K., Das, G., Das, B.C., Naskar, S., Bandyopadhyay, U.K., Das, S.C., Bandyopadhyay, S., 2015. Co-infection of methicillin-resistant *Staphylococcus epidermidis*, methicillin-resistant *Staphylococcus aureus* and extended spectrum β -lactamase producing *Escherichia coli* in bovine mastitis – three cases reported from India. *Vet. Q.* 35, 56–61.
- Barzan, M., Gharibi, D., Ghorbanpoor, M., Haji Hajikolaie, M., Pourmehdi-Boroujeni, M., 2017. Phylogenetic grouping and phenotypic detection of extended-spectrum β -lactamases among *Escherichia coli* from calves and dairy cows in Khuzestan, Iran. *Int. J. Enteric. Pathog.* 5, 24–29.
- Batchelor, M., Hopkins, K., Threlfall, E.J., Clifton-Hadley, F.A., Stallwood, A.D., Davies, R.H., Liebana, E., 2005. bla(CTX-M) genes in clinical *Salmonella* isolates recovered from humans in England and Wales from 1992 to 2003. *Antimicrob. Agents Chemother.* 49, 1319–1322.
- Bazzaz, B.S., Naderinasab, M., Mohamadpoor, A.H., Farshadzadeh, Z., Ahmadi, S., Yousefi, F., 2009. The prevalence of extended-spectrum beta-lactamase-producing *Escherichia coli* and *Klebsiella pneumoniae* among clinical isolates from a general hospital in Iran. *Acta Microbiol. Immunol. Hung.* 56, 89–99.
- Borah, V.V., Bora, P., Roy, M., Saikia, K.K., 2014. High prevalence of antibiotic resistance in *Escherichia coli* isolated from fecal sample of cows and assessment of antibacterial efficacy of indigenous medicinal plants from Assam, India. *Austin J. Biotechnol. Bioeng.* 1, 6.
- Brahmi, S., Dunyach-Remy, C., Touati, A., Lavigne, J.P., 2015. CTX-M-15-producing *Escherichia coli* and the pandemic clone O25b-ST131 isolated from wild fish in Mediterranean Sea. *Clin. Microbiol. Infect. : Off. Publ. Eur. Soc. Clin. Microbiol. Infect. Dis.* 21, e18–20.
- Braun, S.D., Ahmed, M.F.E., El-Adawy, H., Hotzel, H., Engelmann, I., Weiß, D., Monecke, S., Ehrlich, R., 2016. Surveillance of extended-spectrum beta-lactamase-producing *Escherichia coli* in dairy cattle farms in the Nile Delta, Egypt. *Front. Microbiol.* 7, 1020.
- Brennan, E., Martins, M., McCusker, M.P., Wang, J., Alves, B.M., Hurley, D., El Garch, F., Woehrlé, F., Miossec, C., McGrath, L., Srikumar, S., Wall, P., Fanning, S., 2016. Multidrug-resistant *Escherichia coli* in bovine animals, Europe. *Emerg. Infect. Dis.* 22, 1650–1652.
- Briñas, L., Moreno, M.A., Teshager, T., Sáenz, Y., Porrero, M.C., Domínguez, L., Torres, C., 2005. Monitoring and characterization of extended-spectrum β -lactamases in

- Escherichia coli strains from healthy and sick animals in Spain in 2003. *Antimicrob. Agents Chemother.* 49, 1262–1264.
- Brolund, A., Edquist, P.J., Mäkitalo, B., Olsson-Liljequist, B., Söderblom, T., Wisell, K.T., Giske, C.G., 2014. Epidemiology of extended-spectrum β -lactamase-producing Escherichia coli in Sweden 2007–2011. *Clin. Microbiol. Infect.* 20, O344–O352.
- Cantón, R., Novais, A., Valverde, A., Machado, E., Peixe, L., Baquero, F., Coque, T.M., 2008. Prevalence and spread of extended-spectrum β -lactamase-producing enterobacteriaceae in Europe. *Clin. Microbiol. Infect.* 14, 144–153.
- Cantón, R., González-Alba, J.M., Galán, J.C., 2012. CTX-M enzymes: origin and diffusion. *Front. Microbiol.* 3, 110.
- Cantón, R., Coque, T.M., 2006. The CTX-M β -lactamase pandemic. *Curr. Opin. Microbiol.* 9, 466–475.
- CDC, C.f.D.C.a.P., 2013. Antibiotic Resistance Threats in United States in 2013. U.S. Department of Health and Human Services.
- Ceccarelli, D., Kant, A., van Essen-Zandbergen, A., Dierikx, C., Hordijk, J., Wit, B., Mevius, D.J., Veldman, K.T., 2019. Diversity of plasmids and genes encoding resistance to extended spectrum cephalosporins in commensal Escherichia coli from Dutch livestock in 2007–2017. *Front. Microbiol.* 10.
- Chanawong, A., M'Zali, F.H., Heritage, J., Xiong, J.-H., Hawkey, P.M., 2002. Three cefotaximases, CTX-M-9, CTX-M-13, and CTX-M-14, among enterobacteriaceae in the People's Republic of China. *Antimicrob. Agents Chemother.* 46, 630–637.
- Chen, L.F., Freeman, J.T., Nicholson, B., Keiger, A., Lancaster, S., Joyce, M., Woods, C.W., Cook, E., Adcock, L., Louis, S., Cromer, A.L., Sexton, D.J., Anderson, D.J., 2014. Widespread dissemination of CTX-M-15 genotype extended-spectrum β -lactamase-producing enterobacteriaceae among patients presenting to community hospitals in the southeastern United States. *Antimicrob. Agents Chemother.* 58, 1200–1202.
- Chmelnitsky, I., Carmeli, Y., Leavitt, A., Schwaber, M.J., Navon-Venezia, S., 2005. CTX-M-2 and a new CTX-M-39 enzyme are the major extended-spectrum beta-lactamases in multiple Escherichia coli clones isolated in Tel Aviv, Israel. *Antimicrob. Agents Chemother.* 49, 4745–4750.
- Clermont, O., Lavollay, M., Vimont, S., Deschamps, C., Forestier, C., Branger, C., Denamur, E., Arlet, G., 2008. The CTX-M-15-producing Escherichia coli diffusing clone belongs to a highly virulent B2 phylogenetic subgroup. *J. Antimicrob. Chemother.* 61, 1024–1028.
- Colquechagua Aliaga, F., Sevilla Andrade, C., Gonzales Escalante, E., 2015. [Extended-spectrum beta-lactamase (esbl)-producing enterobacteriaceae in fecal samples at the National Institute of Child Health, Peru]. *Rev. Peru. Med. Exp. Salud Pública* 32, 26–32.
- Cormier, A.C., Chalmers, G., McAllister, T.A., Cook, S., Zaheer, R., Scott, H.M., Booker, C., Read, R., Boerlin, P., 2016. Extended-spectrum-Cephalosporin resistance genes in Escherichia coli from beef cattle. *Antimicrob. Agents Chemother.* 60, 1162–1163.
- Cormier, A., Zhang, P.L.C., Chalmers, G., Weese, J.S., Deckert, A., Mulvey, M., McAllister, T., Boerlin, P., 2019. Diversity of CTX-M-positive Escherichia coli recovered from animals in Canada. *Vet. Microbiol.* 231, 71–75.
- Cottell, J.L., Webber, M.A., Coldham, N.G., Taylor, D.L., Cerdeño-Tárraga, A.M., Hauser, H., Thomson, N.R., Woodward, M.J., Piddock, L.J.V., 2011. Complete sequence and molecular epidemiology of IncK epidemic plasmid encoding bla(CTX-M-14). *Emerg. Infect. Dis.* 17, 645–652.
- Cottell, J.L., Kanwar, N., Castillo-Courtade, L., Chalmers, G., Scott, H.M., Norby, B., Loneragan, G.H., Boerlin, P., 2013. blaCTX-M-32 on an IncN plasmid in Escherichia coli from beef cattle in the United States. *Antimicrob. Agents Chemother.* 57, 1096–1097.
- Dahmen, S., Métayer, V., Gay, E., Madec, J.-Y., Haenni, M., 2013. Characterization of extended-spectrum beta-lactamase (ESBL)-carrying plasmids and clones of Enterobacteriaceae causing cattle mastitis in France. *Vet. Microbiol.* 162, 793–799.
- Dahms, C., Hübner, N.-O., Kossov, A., Mellmann, A., Dittmann, K., Kramer, A., 2015. Occurrence of ESBL-producing Escherichia coli in livestock and farm workers in Mecklenburg-Western Pomerania, Germany. *PLoS One* 10, e0143326.
- Das, A., Guha, C., Biswas, U., Jana, P.S., Chatterjee, A., Samanta, I., 2017. Detection of emerging antibiotic resistance in bacteria isolated from subclinical mastitis in cattle in West Bengal. *Vet. World* 10, 517–520.
- Davis, M.A., Sischo, W.M., Jones, L.P., Moore, D.A., Ahmed, S., Short, D.M., Besser, T.E., 2015. Recent emergence of Escherichia coli with cephalosporin resistance conferred by blaCTX-M on Washington state dairy farms. *Appl. Environ. Microbiol.* 81, 4403–4410.
- De Champs, C., Chanal, C., Sirot, D., Baraduc, R., Romaszko, J.P., Bonnet, R., Plaidy, A., Boyer, M., Carroy, E., Gbadamassi, M.C., Laluque, S., Oules, O., Poupard, M.C., Villemain, M., Sirot, J., 2004. Frequency and diversity of Class A extended-spectrum beta-lactamases in hospitals of the Auvergne, France: a 2 year prospective study. *J. Antimicrob. Chemother.* 54, 634–639.
- Denisuik, A.J., Lagacé-Wiens, P.R.S., Pitout, J.D., Mulvey, M.R., Simmer, P.J., Taylor, F., Karlowsky, J.A., Hoban, D.J., Adam, H.J., Zhanel, G.G., Zhanel, G.G., Hoban, D.J., Adam, H.J., Karlowsky, J.A., Baxter, M.R., Nichol, K.A., Lagacé-Wiens, P.R.S., Walkty, A., 2013. Molecular epidemiology of extended-spectrum β -lactamase-, AmpC β -lactamase- and carbapenemase-producing Escherichia coli and Klebsiella pneumoniae isolated from Canadian hospitals over a 5 year period: CANWARD 2007–11. *J. Antimicrob. Chemother.* 68, i57–i65.
- Denisuik, A.J., Adam, H.J., Lagacé-Wiens, P., Simmer, P.J., Mulvey, M.R., Baxter, M., Gilmour, M., Karlowsky, J.A., Hoban, D.J., Zhanel, G.G., 2015. Rates of extended-spectrum β -lactamase-producing Escherichia coli quadruple in Canadian hospitals over an 8-year period: CANWARD 2007–2014. In: ICAAC/ICC 2015. San Diego, CA, USA.
- Dia, M.L., Ngom, B., Diagne, R., Ka, R., Lo, S., Cisse, M.F., Arlet, G., Sow, A.I., 2016. Molecular detection of CTX-M-15-type β -lactamases in Escherichia coli strains from Senegal. *New Microbes New Infections* 9, 45–46.
- Diab, M., Hamze, M., Madec, J.-Y., Haenni, M., 2016. High prevalence of non-ST131 CTX-M-15-producing Escherichia coli in healthy cattle in Lebanon. *Microb. Drug Resist.* 23, 261–266.
- Dolejska, M., Prolkova, P., Florek, M., Jamborova, I., Purgertova, M., Kutilova, I., Cizek, A., Guenther, S., Literak, I., 2011a. CTX-M-15-producing Escherichia coli clone B2-O25b-ST131 and Klebsiella spp. isolates in municipal wastewater treatment plant effluents. *J. Antimicrob. Chemother.* 66, 2784–2790.
- Dolejska, M., Jurcickova, Z., Literak, I., Pokludova, L., Bures, J., Hera, A., Kohoutova, L., Smola, J., Cizek, A., 2011b. IncN plasmids carrying blaCTX-M-1 in Escherichia coli isolates on a dairy farm. *Vet. Microbiol.* 149, 513–516.
- Dolejska, M., Villa, L., Hasman, H., Hansen, L., Carattoli, A., 2013. Characterization of IncN plasmids carrying blaCTX-M-1 and qnr genes in Escherichia coli and Salmonella from animals, the environment and humans. *J. Antimicrob. Chemother.* 68, 333–339.
- Donaldson, S.C., Straley, B.A., Hegde, N.V., Sawant, A.A., DebRoy, C., Jayarao, B.M., 2006. Molecular epidemiology of ceftiofur-resistant Escherichia coli isolates from dairy calves. *Appl. Environ. Microbiol.* 72, 3940–3948.
- Doumith, M., Dhanji, H., Ellington, M.J., Hawkey, P., Woodford, N., 2012. Characterization of plasmids encoding extended-spectrum β -lactamases and their addition systems circulating among Escherichia coli clinical isolates in the UK. *J. Antimicrob. Chemother.* 67, 878–885.
- Duan, R.S., Sit, T.H., Wong, S.S., Wong, R.C., Chow, K.H., Mak, G.C., Yam, W.C., Ng, L.T., Yuen, K.Y., Ho, P.L., 2006. Escherichia coli producing CTX-M beta-lactamases in food animals in Hong Kong. *Microb. Drug Resist.* 12, 145–148.
- Duse, A., Waller, K.P., Emanuelson, U., Unnerstad, H.E., Persson, Y., Bengtsson, B., 2015. Risk factors for antimicrobial resistance in fecal Escherichia coli from preweaned dairy calves. *J. Dairy Sci.* 98, 500–516.
- Ebrahim, F., 2016. Epidemiology of Faecal Carriage of Extended-Spectrum Beta-Lactamases in Healthy Individuals and in Different Patient Populations. PhD. University of Debrecen.
- Eisenberger, D., Carl, A., Balsliemke, J., Kampf, P., Nickel, S., Schulze, G., Valenza, G., 2017. Molecular characterization of extended-spectrum beta-lactamase-producing Escherichia coli isolates from milk samples of dairy cows with mastitis in Bavaria, Germany. *Microb. Drug Resist.*
- Endimiani, A., Rossano, A., Kunz, D., Overesch, G., Perreten, V., 2012. First countrywide survey of third-generation cephalosporin-resistant Escherichia coli from broilers, swine, and cattle in Switzerland. *Diagn. Microbiol. Infect. Dis.* 73, 31–38.
- Eurostat, 2016. *Livestock Population, 2015*. [http://ec.europa.eu/eurostat/statistics-explained/index.php/File:Livestock_population_2015_\(million_head\)_T1.png#file](http://ec.europa.eu/eurostat/statistics-explained/index.php/File:Livestock_population_2015_(million_head)_T1.png#file). (Accessed 21 October 2017).
- Ewers, C., Grobbel, M., Stamm, I., Kopp, P.A., Diehl, I., Semmler, T., Fruth, A., Beutlich, J., Guerra, B., Wieler, L.H., Guenther, S., 2010. Emergence of human pandemic O25:H4-ST131 CTX-M-15 extended-spectrum β -lactamase-producing Escherichia coli among companion animals. *J. Antimicrob. Chemother.* 65, 651–660.
- Ewers, C., Stamm, I., Stolle, I., Guenther, S., Kopp, P.A., Fruth, A., Wieler, L.H., Scheufen, S., Bauerfeind, R., Bethe, A., Prenger-Berninghoff, E., 2014. Detection of Shiga toxin- and extended-spectrum beta-lactamase-producing Escherichia coli O145:NM and Ont:NM from calves with diarrhoea. *J. Antimicrob. Chemother.* 69, 2005–2007.
- Fam, N., Leflon-Guibout, V., Fouad, S., Aboul-Fadl, L., Marcon, E., Desouky, D., El-Defrawy, I., Abou-Aitta, A., Klena, J., Nicolas-Chanoine, M.H., 2011. CTX-M-15-producing Escherichia coli clinical isolates in Cairo (Egypt), including isolates of clonal complex ST10 and clones ST131, ST73, and ST405 in both community and hospital settings. *Microb. Drug Resist.* 17, 67–73.
- Fernandes, R., Amador, P., Oliveira, C., Prudêncio, C., 2014. Molecular characterization of ESBL-producing enterobacteriaceae in northern Portugal. *Sci. World J.* 2014, 782897.
- Fischer, J., Rodríguez, I., Baumann, B., Guiral, E., Beutin, L., Schroeter, A., Kaesbohrer, A., Pfeifer, Y., Helmut, R., Guerra, B., 2014. blaCTX-M-15-carrying Escherichia coli and Salmonella isolates from livestock and food in Germany. *J. Antimicrob. Chemother.* 69, 2951–2958.
- Forssten, S.D., Kolho, E., Lauhio, A., Lehtola, L., Mero, S., Oksaharju, A., Jalava, J., Tarkka, E., Vaara, M., Vuopio-Varkila, J., 2010. Emergence of extended-spectrum β -lactamase-producing Escherichia coli and Klebsiella pneumoniae during the years 2000 and 2004 in Helsinki, Finland. *Clin. Microbiol. Infect.* 16, 1158–1161.
- Freitag, C., Michael, G.B., Kadlec, K., Hassel, M., Schwarz, S., 2017. Detection of plasmid-borne extended-spectrum β -lactamase (ESBL) genes in Escherichia coli isolates from bovine mastitis. *Vet. Microbiol.* 200, 151–156.
- Friese, A., Schulz, J., Laube, H., von Salviati, C., Hartung, J., Roesler, U., 2013. Faecal occurrence and emissions of livestock-associated methicillin-resistant Staphylococcus aureus (laMRSA) and Esbl/AmpC-producing E. coli from animal farms in Germany. *Berl. Münchener Tierärztliche Wochenschr.* 126, 175–180.
- Frye, J.G., Fedorka-Cray, P.J., 2007. Prevalence, distribution and characterisation of ceftiofur resistance in Salmonella enterica isolated from animals in the USA from 1999 to 2003. *Int. J. Antimicrob. Agents* 30, 134–142.
- García-Fernández, A., Villa, L., Moodley, A., Hasman, H., Miriagou, V., Guardabassi, L., Carattoli, A., 2011. Multilocus sequence typing of IncN plasmids. *J. Antimicrob. Chemother.* 66, 1987–1991.
- Gay, N., Leclaire, A., Laval, M., Miltgen, G., Jego, M., Stéphane, R., Jaubert, J., Belmonte, O., Cardinale, E., 2018. Risk factors of extended-spectrum beta-lactamase producing enterobacteriaceae occurrence in farms in Reunion, Madagascar and Mayotte Islands, 2016–2017. *Vet. Sci.* 5.
- Gerhold, G., Schulze, M.H., Gross, U., Bohne, W., 2016. Multilocus sequence typing and CTX-M characterization of ESBL-producing E. coli: a prospective single-centre study in Lower Saxony, Germany. *Epidemiol. Infect.* 144, 3300–3304.

- Geser, N., Stephan, R., Kuhnert, P., Zbinden, R., Kaeppli, U., Cernela, N., Haechler, H., 2011. Fecal carriage of extended-spectrum beta-lactamase-producing Enterobacteriaceae in swine and cattle at slaughter in Switzerland. *J. Food Prot.* 74, 446–449.
- Geser, N., Stephan, R., Hächler, H., 2012a. Occurrence and characteristics of extended-spectrum β -lactamase (ESBL) producing Enterobacteriaceae in food producing animals, minced meat and raw milk. *BMC Vet. Res.* 8, 21.
- Geser, N., Stephan, R., Korczak, B.M., Beutin, L., Hächler, H., 2012b. Molecular identification of extended-spectrum β -lactamase genes from enterobacteriaceae isolated from healthy human carriers in Switzerland. *Antimicrob. Agents Chemother.* 56, 1609–1612.
- Ghatak, S., Singha, A., Sen, A., Guha, C., Ahuja, A., Bhattacharjee, U., Das, S., Pradhan, N.R., Puro, K., Jana, C., Dey, T.K., Prashantkumar, K.L., Das, A., Shakuntala, I., Biswas, U., Jana, P.S., 2013. Detection of New Delhi metallo-beta-lactamase and extended-spectrum beta-lactamase genes in *Escherichia coli* isolated from mastitic milk samples. *Transbound. Emerg. Dis.* 60, 385–389.
- Giedraitienė, A., Vitkauskienė, A., Pavilionis, A., Patamsytė, V., Genel, N., Decre, D., Arlet, G., 2017. Prevalence of O25b-ST131 clone among *Escherichia coli* strains producing CTX-M-15, CTX-M-14 and CTX-M-92 β -lactamases. *Infect. Dis.* 49, 106–112.
- Gonggrijp, M.A., Santman-Berends, I.M.G.A., Heuvelink, A.E., Buter, G.J., van Schaik, G., Hage, J.J., Lam, T.J.G.M., 2016. Prevalence and risk factors for extended-spectrum β -lactamase- and AmpC-producing *Escherichia coli* in dairy farms. *J. Dairy Sci.* 99, 9001–9013.
- Gonzalez, C.M.A., 2006. Susceptibilidad microbiana: Un test rapido para el analisis de resistencia bacteriana en cepas aisladas de mastitis clinicas Bachelor. Universidad de Chile.
- Gonçalves, D., Cecílio, P., Ferreira, H., 2016. Nursing homes and long-term care facilities: reservoirs of CTX-M-15-producing *Escherichia coli* O25b-ST131 in Portugal. *J. Glob. Antimicrob. Resist.* 7, 69–71.
- Grami, R., Dahmen, S., Mansour, W., Mehri, W., Haenni, M., Aouni, M., Madec, J.Y., 2014. blaCTX-M-15-carrying F2A-B plasmid in *Escherichia coli* from cattle milk in Tunisia. *Microb. Drug Resist.* 20, 344–349.
- Gur, D., Gulay, Z., Akan, O.A., Aktas, Z., Kayacan, C.B., Cakici, O., Erac, B., Gultekin, M., Ogunc, D., Soyler, G., Unal, N., Uysal, S., 2008. [Resistance to newer beta-lactams and related ESBL types in gram-negative nosocomial isolates in Turkish hospitals: results of the multicentre HITIT study]. *Mikrobiyol. Bul.* 42, 537–544.
- Haenni, M., Saras, E., Métayer, V., Doublet, B., Cloeckaert, A., Madec, J.-Y., 2012. Spread of the blaTEM-52 gene is mainly ensured by IncII/ST36 plasmids in *Escherichia coli* isolated from cattle in France. *J. Antimicrob. Chemother.* 67, 2774–2776.
- Haenni, M., Châtre, P., Métayer, V., Bour, M., Signol, E., Madec, J.-Y., Gay, E., 2014. Comparative prevalence and characterization of ESBL-producing Enterobacteriaceae in dominant versus subdominant enteric flora in veal calves at slaughterhouse, France. *Vet. Microbiol.* 171, 321–327.
- Haenni, M., Beyrouthy, R., Lupo, A., Châtre, P., Madec, J.-Y., Bonnet, R., 2018. Epidemic spread of *Escherichia coli* ST744 isolates carrying mcr-3 and blaCTX-M-55 in cattle in France. *J. Antimicrob. Chemother.* 73, 533–536.
- Hamdy Mohammed, E.S., Elsadek Fakhr, A., Mohammed El sayed, H., Al Johery, S.a.e., Abdel Ghani Hassanein, W., 2016. Spread of TEM, VIM, SHV, and CTX-M β -lactamases in imipenem-resistant gram-negative bacilli isolated from Egyptian hospitals. *Int. J. Microbiol.* 2016, 8382605.
- Hartmann, A., Amoureux, L., Locatelli, A., Depret, G., Jolivet, C., Gueneau, E., Neuwirth, C., 2012. Occurrence of CTX-M producing *Escherichia coli* in soils, cattle, and farm environment in France (Burgundy region). *Front. Microbiol.* 3.
- Hasan, B., Laurell, K., Rakib, M.M., Ahlstedt, E., Hernandez, J., Caceres, M., Järhult, J.D., 2016. Fecal carriage of extended-spectrum β -lactamases in healthy humans, poultry, and wild birds in León, Nicaragua—a shared pool of blaCTX-M genes and possible interspecies clonal spread of extended-spectrum β -lactamases-producing *Escherichia coli*. *Microb. Drug Resist.* 22, 682–687.
- Hassan, H., Abdalhamid, B., 2014. Molecular characterization of extended-spectrum beta-lactamase producing Enterobacteriaceae in a Saudi Arabian tertiary hospital. *J. Infect. Dev. Ctries.* 8, 282–288.
- Hassan, S., Gherbawy, Y., Aitalhi, A.D., 2015. Genetic Heterogeneity of CTX-M Type Extended-Spectrum β -lactamase Producing *Escherichia coli* Strains from Diverse Sources in Saudi Arabia.
- Hawkey, P.M., 2008. Prevalence and clonality of extended-spectrum β -lactamases in Asia. *Clin. Microbiol. Infect.* 14, 159–165.
- Hernández, J., Stedt, J., Bonnedahl, J., Molin, Y., Drobni, M., Calisto-Ulloa, N., Gomez-Fuentes, C., Astorga-España, M.S., González-Acuña, D., Waldenström, J., Blomqvist, M., Olsen, B., 2012. Human-associated extended-spectrum β -lactamase in the Antarctic. *Appl. Environ. Microbiol.* 78, 2056–2058.
- Hernandez, J., Johansson, A., Stedt, J., Bengtsson, S., Porczak, A., Granholm, S., González-Acuña, D., Olsen, B., Bonnedahl, J., Drobni, M., 2013. Characterization and comparison of extended-spectrum β -lactamase (ESBL) resistance genotypes and population structure of *Escherichia coli* isolated from Franklin's Gulls (*Leucophaeus pipixcan*) and humans in Chile. *PLoS One* 8, e76150.
- Hernández, M., Iglesias, M.R., Rodríguez-Lázaro, D., Gallardo, A., Quijada, N., Miguela-Villoldo, P., Campos, M.J., Píriz, S., López-Orozco, G., de Frutos, C., Sáez, J.L., Ugarte-Ruiz, M., Domínguez, L., Quesada, A., 2017. Co-occurrence of colistin-resistance genes mcr-1 and mcr-3 among multidrug-resistant *Escherichia coli* isolated from cattle, Spain, September 2015. *Euro Surveill.* 22, 30586.
- Heuvelink, A.E., Gonggrijp, M.A., Buter, R.G.J., ter Bogt-Kappert, C.C., van Schaik, G., Velthuis, A.G.J., Lam, T.J.G.M., 2019. Prevalence of extended-spectrum and AmpC β -lactamase-producing *Escherichia coli* in Dutch dairy herds. *Vet. Microbiol.* 232, 58–64.
- Hinthong, W., Pumipuntu, N., Santajit, S., Kulpeanprasit, S., Buranasinsup, S., Sookrung, N., Chaicumpa, W., Aiumuray, P., Indrawattana, N., 2017. Detection and drug resistance profile of *Escherichia coli* from subclinical mastitis cows and water supply in dairy farms in Saraburi Province, Thailand. *PeerJ* 5, e3431.
- Ho, P.L., Chow, K.H., Lai, E.L., Lo, W.U., Yeung, M.K., Chan, J., Chan, P.Y., Yuen, K.Y., 2011. Extensive dissemination of CTX-M-producing *Escherichia coli* with multidrug resistance to 'critically important' antibiotics among food animals in Hong Kong, 2008–10. *J. Antimicrob. Chemother.* 66, 765–768.
- Ho, W.S., Balan, G., Puthuchery, S., Kong, B.H., Lim, K.T., Tan, L.K., Koh, X.P., Yeo, C.C., Thong, K.L., 2012. Prevalence and characterization of multidrug-resistant and extended-spectrum beta-lactamase-producing *Escherichia coli* from pediatric wards of a Malaysian hospital. *Microb. Drug Resist.* 18, 408–416.
- Ho, P.L., Chan, J., Lo, W.U., Law, P.Y., Li, Z., Lai, E.L., Chow, K.H., 2013. Dissemination of plasmid-mediated fosfomicin resistance fosA3 among multidrug-resistant *Escherichia coli* from livestock and other animals. *J. Appl. Microbiol.* 114, 695–702.
- Ho, P.-L., Liu, M.C.-J., Lo, W.-U., Lai, E.L.-Y., Lau, T.C.-K., Law, O.-K., Chow, K.-H., 2015. Prevalence and characterization of hybrid blaCTX-M among *Escherichia coli* isolates from livestock and other animals. *Diagn. Microbiol. Infect. Dis.* 82, 148–153.
- Hordijk, J., Mevius, D.J., Kant, A., Bos, M.E.H., Graveland, H., Bosman, A.B., Hartskeerl, C.M., Heederik, D.J.J., Wagenaar, J.A., 2013a. Within-farm dynamics of ESBL/AmpC-producing *Escherichia coli* in veal calves: a longitudinal approach. *J. Antimicrob. Chemother.* 68, 2468–2476.
- Hordijk, J., Wagenaar, J.A., Kant, A., van Essen-Zandbergen, A., Dierikx, C., Veldman, K., Wit, B., Mevius, D., 2013b. Cross-sectional study on prevalence and molecular characteristics of plasmid mediated ESBL/AmpC-Producing *Escherichia coli* isolated from veal calves at slaughter. *PLoS One* 8, e65681.
- Hordijk, J., Wagenaar, J.A., van de Giessen, A., Dierikx, C., van Essen-Zandbergen, A., Veldman, K., Kant, A., Mevius, D., 2013c. Increasing prevalence and diversity of ESBL/AmpC-type beta-lactamase genes in *Escherichia coli* isolated from veal calves from 1997 to 2010. *J. Antimicrob. Chemother.* 68, 1970–1973.
- Horton, R.A., Randall, L.P., Snary, E.L., Cockrem, H., Lotz, S., Wearing, H., Duncan, D., Rabie, A., McLaren, I., Watson, E., La Ragione, R.M., Coldham, N.G., 2011. Fecal carriage and shedding density of CTX-M extended-spectrum β -lactamase-producing *Escherichia coli* in cattle, chickens, and pigs: implications for environmental contamination and food production. *Appl. Environ. Microbiol.* 77, 3715–3719.
- Hu, Y.-Y., Cai, J.-C., Zhou, H.-W., Chi, D., Zhang, X.-F., Chen, W.-L., Zhang, R., Chen, G.-X., 2013. Molecular typing of CTX-M-producing *Escherichia coli* isolates from environmental water, swine feces, specimens from healthy humans, and human patients. *Appl. Environ. Microbiol.* 79, 5988–5996.
- Hunter, P.A., Dawson, S., French, G.L., Goossens, H., Hawkey, P.M., Kuijper, E.J., Nathwani, D., Taylor, D.J., Teale, C.J., Warren, R.E., Wilcox, M.H., Woodford, N., Wulf, M.W., Piddock, L.J.V., 2010. Antimicrobial-resistant pathogens in animals and man: prescribing, practices and policies. *J. Antimicrob. Chemother.* 65, i3–i17.
- Iroha, I.R., Esimone, C.O., Neumann, S., Marlinghaus, L., Korte, M., Szabados, F., Gatermann, S., Kaase, M., 2012. First description of *Escherichia coli* producing CTX-M-15 extended spectrum beta lactamase (ESBL) in out-patients from south eastern Nigeria. *Ann. Clin. Microbiol. Antimicrob.* 11, 19.
- Iweriebor, B.C., Iwu, C.J., Obi, L.C., Nwodo, U.U., Okoh, A.I., 2015. Multiple antibiotic resistances among Shiga toxin producing *Escherichia coli* O157 in feces of dairy cattle farms in Eastern Cape of South Africa. *BMC Microbiol.* 15, 213.
- Kamaruzzaman, E.A., 2015. Occurrence of Extended Spectrum Beta-Lactamase Producing *Escherichia coli* in Dairy Cattle, Farm Environment and Milk. Master. Universiti Putra, Malaysia.
- Kar, D., Bandyopadhyay, S., Bhattacharyya, D., Samanta, I., Mahanti, A., Nanda, P.K., Mondal, B., Dandapat, P., Das, A.K., Dutta, T.K., Bandyopadhyay, S., Singh, R.K., 2015. Molecular and phylogenetic characterization of multidrug resistant extended spectrum beta-lactamase producing *Escherichia coli* isolated from poultry and cattle in Odisha, India. *Infect. Genet. Evol.* 29, 82–90.
- Karanika, S., Karantanos, T., Arvanitis, M., Grigoras, C., Mylonakis, E., 2016. Fecal colonization with extended-spectrum beta-lactamase-producing enterobacteriaceae and risk factors among healthy individuals: a systematic review and metaanalysis. *Clin. Infect. Dis.* 63, 310–318.
- Karim, A., Poirer, L., Nagarajan, S., Nordmann, P., 2001. Plasmid-mediated extended-spectrum β -lactamase (CTX-M-3 like) from India and gene association with insertion sequence ISEcp1. *FEMS (Fed. Eur. Microbiol. Soc.) Microbiol. Lett.* 201, 237–241.
- Kim, J.S., Park, J., Shin, E., Kim, S., Oh, S.S., Yang, H.J., Kim, D.W., Oh, K.H., Kim, Y., Kim, M., Kwon, M.J., Na, K., Lee, J., Cho, E.H., Kang, B.H., Kwak, H.S., Seong, W.K., Kim, J., 2017. Outbreak of CTX-M-15-producing enterotoxigenic *Escherichia coli* O159:H20 in the Republic of Korea in 2016. *Antimicrob. Agents Chemother.* 61.
- Kiratisin, P., Apisarnthanarak, A., Laesripa, C., Saifon, P., 2008. Molecular characterization and epidemiology of extended-spectrum β -lactamase-producing *Escherichia coli* and *Klebsiella pneumoniae* isolates causing health care-associated infection in Thailand, where the CTX-M family is endemic. *Antimicrob. Agents Chemother.* 52, 2818–2824.
- Kjeldsen, T.S.B., Overgaard, M., Nielsen, S.S., Bortolaia, V., Jelsbak, L., Sommer, M., Guardabassi, L., Olsen, J.E., 2015. CTX-M-1 β -lactamase expression in *Escherichia coli* is dependent on cefotaxime concentration, growth phase and gene location. *J. Antimicrob. Chemother.* 70, 62–70.
- Kmeť, V., Bujňáková, D., 2018. Antimicrobial resistance *Escherichia coli* isolated from calves. *J. Microbiol. Biotechnol. Food Sci.* 7, 412–415.
- Knothe, H., Shah, P., Krcmery, V., Antal, M., Mitsuhashi, S., 1983. Transferable resistance to cefotaxime, cefoxitin, cefamandole and cefuroxime in clinical isolates of *Klebsiella pneumoniae* and *Serratia marcescens*. *Infection* 11, 315–317.
- Koovapra, S., Bandyopadhyay, S., Das, G., Bhattacharyya, D., Banerjee, J., Mahanti, A., Samanta, I., Nanda, P.K., Kumar, A., Mukherjee, R., Dimri, U., Singh, R.K., 2016. Molecular signature of extended spectrum β -lactamase producing *Klebsiella*

- pneumoniae isolated from bovine milk in eastern and north-eastern India. *Infect. Genet. Evol.* 44, 395–402.
- Kucukbasmaci, O., Ciftcioglu, G., Midilli, K., Issa, G., 2008. Detection of extended spectrum β -Lactamase producing Enterobacteriaceae from food animals in Turkey. *Rev. Méd. Vét.* 159, 586–592.
- Kuroda, H., Yano, H., Hirakata, Y., Arai, K., Endo, S., Kanamori, H., Yamamoto, H., Ichimura, S., Ogawa, M., Shimojima, M., Komatsu, M., Jonai, T., Itagaki, S., Nonomiya, Y., Suwabe, A., Kaku, M., 2012. Molecular characteristics of extended-spectrum β -lactamase-producing *Escherichia coli* in Japan: emergence of CTX-M-15-producing E. coli ST131. *Diagn. Microbiol. Infect. Dis.* 74, 201–203.
- Li, J.-J., Spychala, C.N., Hu, F., Sheng, J.-F., Doi, Y., 2015. Complete nucleotide sequences of blaCTX-M-harboring IncF plasmids from community-associated *Escherichia coli* strains in the United States. *Antimicrob. Agents Chemother.* 59, 3002–3007.
- Liao, K., Chen, Y., Wang, M., Guo, P., Yang, Q., Ni, Y., Yu, Y., Hu, B., Sun, Z., Huang, W., Wang, Y., Wu, A., Feng, X., Luo, Y., Hu, Z., Chu, Y., Chen, S., Cao, B., Su, J., Gui, B., Duan, Q., Zhang, S., Shao, H., Kong, H., Xu, Y., 2017. Molecular characteristics of extended-spectrum beta-lactamase-producing *Escherichia coli* and *Klebsiella pneumoniae* causing intra-abdominal infections from 9 tertiary hospitals in China. *Diagn. Microbiol. Infect. Dis.* 87, 45–48.
- Liebana, E., Batchelor, M., Hopkins, K.L., Clifton-Hadley, F.A., Teale, C.J., Foster, A., Barker, L., Threlfall, E.J., Davies, R.H., 2006. Longitudinal farm study of extended-spectrum β -lactamase-mediated resistance. *J. Clin. Microbiol.* 44, 1630–1634.
- Lifshitz, Z., Sturlesi, N., Parizade, M., Blum, S.E., Gordon, M., Taran, D., Adler, A., 2018. Distinctiveness and similarities between extended-spectrum beta-lactamase-producing *Escherichia coli* isolated from cattle and the community in Israel. *Microb. Drug Resist.*
- Lim, S.-K., Lee, H.-S., Nam, H.-M., Jung, S.-C., Bae, Y.-c., 2009. CTX-M-Type β -lactamase in *Escherichia coli* isolated from sick animals in Korea. *Microb. Drug Resist.* 15, 139–142.
- Locatelli, C., Scaccabarozzi, L., Pisoni, G., Moroni, P., 2010. CTX-M1 ESBP-producing *Klebsiella pneumoniae* subsp. *pneumoniae* isolated from cases of bovine mastitis. *J. Clin. Microbiol.* 48, 3822–3823.
- Lupo, A., Saras, E., Madec, J.-Y., Haenni, M., 2018. Emergence of blaCTX-M-55 associated with fosaA, rmtB and mcr gene variants in *Escherichia coli* from various animal species in France. *J. Antimicrob. Chemother.* dxk489.
- Lussier, P., 2010. Characterization of Putative Extended-Spectrum β -lactamases (ESBL) Producing *Escherichia coli* Isolated from Feedlot Cattle in Southern Alberta. Master. University of Lethbridge.
- Ma, L., Ishii, Y., Chang, F.-Y., Yamaguchi, K., Ho, M., Siu, L.K., 2002. CTX-M-14, a plasmid-mediated CTX-M type extended-spectrum β -lactamase isolated from *Escherichia coli*. *Antimicrob. Agents Chemother.* 46, 1985–1988.
- Madec, J.-Y., Lazizzera, C., Châtre, P., Meunier, D., Martin, S., Lepage, G., Ménard, M.-F., Lebreton, P., Rambaud, T., 2008. Prevalence of fecal carriage of acquired expanded-spectrum cephalosporin resistance in enterobacteriaceae strains from cattle in France. *J. Clin. Microbiol.* 46, 1566–1567.
- Madec, J.-Y., Poirer, L., Saras, E., Gourguechon, A., Girlich, D., Nordmann, P., Haenni, M., 2012. Non-ST131 *Escherichia coli* from cattle harbouring human-like blaCTX-M-15-carrying plasmids. *J. Antimicrob. Chemother.* 67, 578–581.
- Madec, J.-Y., Haenni, M., Nordmann, P., Poirer, L., 2017. Extended-spectrum beta-lactamase/AmpC- and carbapenemase-producing Enterobacteriaceae in animals: a threat for humans? *Clin. Microbiol. Infect. : Off. Publ. Eur. Soc. Clin. Microbiol. Infect. Dis.*
- Manyahi, J., Moyo, S.J., Tellevik, M.G., Ndugulile, F., Urassa, W., Blomberg, B., Langeland, N., 2017. Detection of CTX-M-15 beta-lactamases in Enterobacteriaceae causing hospital- and community-acquired urinary tract infections as early as 2004, in Dar es Salaam, Tanzania. *BMC Infect. Dis.* 17, 282.
- Matsumura, Y., Johnson, J.R., Yamamoto, M., Nagao, M., Tanaka, M., Takakura, S., Ichijima, S., 2015. CTX-M-27- and CTX-M-14-producing, ciprofloxacin-resistant *Escherichia coli* of the H30 subclonal group within ST131 drive a Japanese regional ESBP epidemic. *J. Antimicrob. Chemother.* 70, 1639–1649.
- Mendoza, M.V., 2017. Identificación de enterobacterias resistentes a antibióticos en el vampiro común (*Desmodus rotundus*) y en animales de traspatio en el departamento de Lima, Perú Bachelors. Universidad Peruana Cayetano Heredia.
- Meunier, D., Jouy, E., Lazizzera, C., Kobisch, M., Madec, J.-Y., 2006. CTX-M-1- and CTX-M-15-type β -lactamases in clinical *Escherichia coli* isolates recovered from food-producing animals in France. *Int. J. Antimicrob. Agents* 28, 402–407.
- Michael, G.B., Kaspar, H., Siqueira, A.K., de Freitas Costa, E., Corbellini, L.G., Kadlec, K., Schwarz, S., 2017. Extended-spectrum β -lactamase (ESBL)-producing *Escherichia coli* isolates collected from diseased food-producing animals in the GERM-Vet monitoring program 2008–2014. *Vet. Microbiol.* 200, 142–150.
- Mir, R.A., Weppelmann, T.A., Johnson, J.A., Archer, D., Morris Jr., J.G., Jeong, K.C., 2016. Identification and characterization of cefotaxime resistant bacteria in beef cattle. *PLoS One* 11, e0163279.
- Mkala, R.S., Azizi, K., 2017. Prevalence and Antimicrobial Resistance Patterns of Extended Spectrum Beta Lactamase Producing Enterohemorrhagic *Escherichia coli* Strain O157:H7 from Cattle and Humans in Moshi, Northern Tanzania.
- Mollenkopf, D.F., Weeman, M.F., Daniels, J.B., Abley, M.J., Mathews, J.L., Gebreyes, W.A., Wittum, T.E., 2012. Variable within- and between-herd diversity of CTX-M cephalosporinase-bearing *Escherichia coli* isolates from dairy cattle. *Appl. Environ. Microbiol.* 78, 4552–4560.
- Moosavian, M., Ahmadvhosravy, N., 2016. Survey of CTX-M gene frequency in extended-spectrum beta-lactamase-producing enterobacteriaceae isolates using the combination disk and PCR methods in Ahvaz, Iran. *Jundishapur J. Microbiol.* 9, e40423.
- Moubareck, C., Daoud, Z., Hakime, N.I., Hamze, M., Mangeney, N., Matta, H., Mokhbat, J.E., Rohban, R., Sarkis, D.K., Doucet-Populaire, F., 2005. Countrywide spread of community- and hospital-acquired extended-spectrum beta-lactamase (CTX-M-15)-producing Enterobacteriaceae in Lebanon. *J. Clin. Microbiol.* 43, 3309–3313.
- Mshana, S.E., Imirziloglu, C., Hossain, H., Hain, T., Domann, E., Chakraborty, T., 2009. Conjugative IncFI plasmids carrying CTX-M-15 among *Escherichia coli* ESBP-producing isolates at a University hospital in Germany. *BMC Infect. Dis.* 9, 97.
- Mugnaioli, C., Luzzaro, F., De Luca, F., Brigante, G., Perilli, M., Amicosante, G., Stefani, S., Toniolo, A., Rossolini, G.M., 2006. CTX-M-Type extended-spectrum β -lactamases in Italy: molecular epidemiology of an emerging countrywide problem. *Antimicrob. Agents Chemother.* 50, 2700–2706.
- Naiemi, N., Bart, A., de Jong, M.D., Vandenbroucke-Grauls, C.M., Rietra, P.J.G.M., Debets-Ossenkopp, Y.J., Wever, P.C., Spanjaard, L., Bos, A.J., Duim, B., 2006. Widely distributed and predominant CTX-M extended-spectrum β -lactamases in Amsterdam, The Netherlands. *J. Clin. Microbiol.* 44, 3012–3014.
- Namaei, M.H., Yousefi, M., Ziaee, M., Salehabadi, A., Ghannadkafi, M., Amini, E., Askari, P., 2017. First report of prevalence of CTX-M-15-producing *Escherichia coli* O25b/ST131 from Iran. *Microb. Drug Resist.* 23, 879–884.
- Naseer, U., Nat'AS, O.B., Haldorsen, B.C., Bue, B., Grundt, H., Walsh, T.R., Sundsfjord, A., 2007. Nosocomial outbreak of CTX-M-15-producing *E. coli* in Norway. *APMIS* 115, 120–126.
- Newire, E.A., Ahmed, S.F., House, B., Valiente, E., Pimentel, G., 2013. Detection of new SHV-12, SHV-5 and SHV-2a variants of extended spectrum beta-lactamase in *Klebsiella pneumoniae* in Egypt. *Ann. Clin. Microbiol. Antimicrob.* 12, 16.
- Nóbrega, D.B., Guiduce, M.V.S., Guimarães, F.F., Riboli, D.F., Cunha, M.L.R.S., Langoni, H.L., Pantoja, J.C.F., Lucheis, S.B., 2013. Molecular epidemiology and extended-spectrum β -lactamases production of *Klebsiella pneumoniae* isolated from three dairy herds. *Pesqui. Vet. Bras.* 33, 855–859.
- Novais, Á., Cantón, R., Moreira, R., Peixe, L., Baquero, F., 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. *Antimicrob. Agents Chemother.* 51, 796–799.
- Ogefere, H.O., Agbe, S.O., Ibadin, E.E., 2017. Detection of extended spectrum beta-lactamases among gram negative bacilli recovered from cattle feces in Benin city, Nigeria. *Not. Sci. Biol.* 9, 177.
- Ohnishi, M., Okatani, A.T., Esaki, H., Harada, K., Sawada, T., Murakami, M., Marumo, K., Kato, Y., Sato, R., Shimura, K., Hatanaka, N., Takahashi, T., 2013a. Herd prevalence of Enterobacteriaceae producing CTX-M-type and CMY-2 β -lactamases among Japanese dairy farms. *J. Appl. Microbiol.* 115, 282–289.
- Ohnishi, M., Okatani, A.T., Harada, K., Sawada, T., Marumo, K., Murakami, M., Sato, R., Esaki, H., Shimura, K., Kato, H., Uchida, N., Takahashi, T., 2013b. Genetic characteristics of CTX-M-type extended-spectrum- β -lactamase (ESBL)-Producing enterobacteriaceae involved in mastitis cases on Japanese dairy farms, 2007 to 2011. *J. Clin. Microbiol.* 51, 3117–3122.
- Olesen, B., Hansen, D.S., Nilsson, F., Frimodt-Møller, J., Leihof, R.F., Struve, C., Scheutz, F., Johnston, B., Krogfelt, K.A., Johnson, J.R., 2013. Prevalence and characteristics of the epidemic multi-resistant *Escherichia coli* ST131 clonal group among extended-spectrum beta-lactamase-producing *E. coli* isolates in Copenhagen, Denmark. *J. Clin. Microbiol.* 51, 1779–1785.
- Olowe, O.A., Adewumi, O., Odewale, G., Ojurongbe, O., Adefioye, O.J., 2015. Phenotypic and molecular characterisation of extended-spectrum beta-lactamase producing *Escherichia coli* obtained from animal fecal samples in Ado Ekiti, Nigeria. *J. Environ. Public Health* 2015, 7.
- Oteo, J., Orden, B., Bautista, V., Cuevas, O., Arroyo, M., Martínez-Ruiz, R., Pérez-Vazquez, M., Alcaraz, M., García-Cobos, S., Campos, J., 2009. CTX-M-15-producing urinary *Escherichia coli* O25b-ST131-phylogroup B2 has acquired resistance to fosfomicin. *J. Antimicrob. Chemother.* 64, 712–717.
- Ouedraogo, A.-S., Nagou, M., Kissou, A., Sanou, S., Solaré, H., Kaboré, F., Podá, A., Aberkane, S., Bouzinbi, N., Sano, I., Nacro, B., Sangaré, L., Carrière, C., Décré, D., Ouedraogo, R., Jean-Pierre, H., Godreuil, S., 2016. High prevalence of extended-spectrum β -lactamase producing enterobacteriaceae among clinical isolates in Burkina Faso. *BMC Infect. Dis.* 16, 326.
- Overdvest, I., Willemsen, I., Rijnsburger, M., Eustace, A., Xu, L., Hawkey, P., Heck, M., Savelkoul, P., Vandenbroucke-Grauls, C., van der Zwaluw, K., Huijsdens, X., Kluytmans, J., 2011. Extended-spectrum β -lactamase genes of *Escherichia coli* in chicken meat and humans, The Netherlands. *Emerg. Infect. Dis.* 17, 1216–1222.
- Owens, R.C., Johnson, J.R., Stogsdill, P., Yarmus, L., Lolans, K., Quinn, J., 2011. Community transmission in the United States of a CTX-M-15-producing sequence type ST131 *Escherichia coli* strain resulting in death. *J. Clin. Microbiol.* 49, 3406–3408.
- Päivärinta, M., Pohjola, L., Fredriksson-Ahomaa, M., Heikinheimo, A., 2016. Low occurrence of extended-spectrum β -lactamase-Producing *Escherichia coli* in Finnish food-producing animals. *Zoonoses and Public Hlth.* 63, 624–631.
- Palmeira, J.D., Ferreira, H., Madec, J.-Y., Haenni, M., 2018. Draft genome of an ST443 mcr-1- and blaCTX-M-2-carrying *Escherichia coli* from cattle in Brazil. *J. Glob. Antimicrob. Resist.*
- Pardon, B., Smet, A., Butaye, P., Argudín, M.A., Valgaeren, B., Catry, B., Haesebrouck, F., Deprez, P., 2017. Nosocomial intravascular catheter infections with extended-spectrum beta-lactamase-producing *Escherichia coli* in calves after strain introduction from a commercial herd. *Transbound. Emerg. Dis.* 64, 130–136.
- Paterson, D.L., Bonomo, R.A., 2005. Extended-spectrum β -lactamases: a clinical update. *Clin. Microbiol. Rev.* 18, 657–686.
- Pehlivanoglu, F., Turutoglu, H., Ozturk, D., Yardimci, H., 2016. Molecular characterization of ESBP-producing *Escherichia coli* isolated from healthy cattle and sheep. In: *Acta Veterinaria*, p. 520.
- Peirano, G., Richardson, D., Nigrin, J., McGeer, A., Loo, V., Toye, B., Alfa, M., Pienaar, C., Kibsey, P., Pitout, J.D.D., 2010. High prevalence of ST131 isolates producing CTX-M-

- 15 and CTX-M-14 among extended-spectrum- β -lactamase-producing *Escherichia coli* isolates from Canada. *Antimicrob. Agents Chemother.* 54, 1327–1330.
- Peirano, G., van Greune, C.H., Pitout, J.D., 2011. Characteristics of infections caused by extended-spectrum beta-lactamase-producing *Escherichia coli* from community hospitals in South Africa. *Diagn. Microbiol. Infect. Dis.* 69, 449–453.
- Perilli, M., Segatore, B., Mugnaioli, C., Celenza, G., Rossolini, G.M., Stefani, S., Luzzaro, F., Pini, B., Amicosante, G., 2011. Persistence of TEM-52/TEM-92 and SHV-12 extended-spectrum beta-lactamases in clinical isolates of Enterobacteriaceae in Italy. *Microb. Drug Resist.* 17, 521–524.
- Pitout, J.D.D., Gregson, D.B., Church, D.L., Elsayed, S., Laupland, K.B., 2005. Community-wide outbreaks of clonally related CTX-M-14 β -lactamase-producing *Escherichia coli* strains in the Calgary health region. *J. Clin. Microbiol.* 43, 2844–2849.
- Pitout, J.D.D., Le, P., Church, D.L., Gregson, D.B., Laupland, K.B., 2008. Antimicrobial susceptibility of well-characterised multidrug-resistant CTX-M-producing *Escherichia coli*: failure of automated systems to detect resistance to piperacillin/tazobactam. *Int. J. Antimicrob. Agents* 32, 333–338.
- Poirel, L., Nordmann, P., Ducroz, S., Boulouis, H.-J., Arné, P., Millemann, Y., 2013. Extended-spectrum β -lactamase CTX-M-15-producing *Klebsiella pneumoniae* of sequence type ST274 in companion animals. *Antimicrob. Agents Chemother.* 57, 2372–2375.
- Poole, T.L., Callaway, T.R., Norman, K.N., Scott, H.M., Loneragan, G.H., Ison, S.A., Beier, R.C., Harhay, D.M., Norby, B., Nisbet, D.J., 2017. Transferability of antimicrobial resistance from multidrug-resistant *Escherichia coli* isolated from cattle in the United States to *Escherichia coli* and *Salmonella* Newport recipients. *J. Glob. Antimicrob. Resist.*
- Price, L.B., Johnson, J.R., Aziz, M., Clabots, C., Johnston, B., Tchesnokova, V., Nordstrom, L., Billig, M., Chattopadhyay, S., Stegger, M., Andersen, P.S., Pearson, T., Riddell, K., Rogers, P., Scholes, D., Kahl, B., Keim, P., Sokurenko, E.V., 2013. The epidemic of extended-spectrum- β -lactamase-producing *Escherichia coli* ST131 is driven by a single highly pathogenic subclone, H30-Rx. *mBio* 4.
- Ramos, S., Igrejas, G., Silva, N., Jones-Dias, D., Capelo-Martinez, J.-L., Caniça, M., Poeta, P., 2013. First report of CTX-M producing *Escherichia coli*, including the new ST2526, isolated from beef cattle and sheep in Portugal. *Food Control* 31, 208–210.
- Randall, L., Heinrich, K., Horton, R., Brunton, L., Sharman, M., Bailey-Horne, V., Sharma, M., McLaren, I., Coldham, N., Teale, C., Jones, J., 2014. Detection of antibiotic residues and association of ceftinome residues with the occurrence of Extended-Spectrum β -Lactamase (ESBL)-producing bacteria in waste milk samples from dairy farms in England and Wales in 2011. *Res. Vet. Sci.* 96, 15–24.
- Rayamajhi, N., Cha, S.B., Shin, S.W., Jung, B.Y., Lim, S.-K., Yoo, H.S., 2011. Plasmid typing and resistance profiling of *Escherichia fergusonii* and other enterobacteriaceae isolates from south Korean farm animals. *Appl. Environ. Microbiol.* 77, 3163–3166.
- Reist, M., Geser, N., Hächler, H., Schärfer, S., Stephan, R., 2013. ESBL-producing enterobacteriaceae: occurrence, risk factors for fecal carriage and strain traits in the Swiss slaughter cattle population younger than 2 Years sampled at Abattoir level. *PLoS One* 8, e71725.
- Robin, F., Beyrouthy, R., Bonacorsi, S., Aissa, N., Bret, L., Brieu, N., Cattoir, V., Chapuis, A., Chardon, H., Degand, N., Doucet-Populaire, F., Dubois, V., Fortineau, N., Grillon, A., Lanotte, P., Leysse, D., Patry, I., Podglajen, I., Recule, C., Ros, A., Colomb-Cotinat, M., Ponties, V., Ploy, M.C., Bonnet, R., 2017. Inventory of extended-spectrum- β -lactamase-producing enterobacteriaceae in France as assessed by a multicenter study. *Antimicrob. Agents Chemother.* 61 e01911-01916.
- Robinson, T.P., Bu, D.P., Carrique-Mas, J., Fèvre, E.M., Gilbert, M., Grace, D., Hay, S.I., Jiwakanon, J., Kakkar, M., Kariuki, S., Laxminarayan, R., Lubroth, J., Magnusson, U., Thi Ngoc, P., Van Boeckel, T.P., Woolhouse, M.E.J., 2016. Antibiotic resistance is the quintessential One Health issue. *Trans. R. Soc. Trop. Med. Hyg.* 110, 377–380.
- Rodríguez, I., Barownik, W., Helmuth, R., Mendoza, M.C., Rodicio, M.R., Schroeter, A., Guerra, B., 2009. Extended-spectrum β -lactamases and AmpC β -lactamases in ceftiofur-resistant *Salmonella enterica* isolates from food and livestock obtained in Germany during 2003–07. *J. Antimicrob. Chemother.* 64, 301–309.
- Rodríguez-Villalobos, H., Bogaerts, P., Berhin, C., Bauraing, C., Deplano, A., Montesinos, I., de Mendonça, R., Jans, B., Glupezynski, Y., 2011. Trends in production of extended-spectrum β -lactamases among Enterobacteriaceae of clinical interest: results of a nationwide survey in Belgian hospitals. *J. Antimicrob. Chemother.* 66, 37–47.
- Ruiz, S.J., Montealegre, M.C., Ruiz-Garbayosa, P., Correa, A., Briceño, D.F., Martínez, E., Rosso, F., Muñoz, M., Quinn, J.P., Cantón, R., Villegas, M.V., 2011. First characterization of CTX-M-15-producing *Escherichia coli* ST131 and ST405 clones causing community-onset infections in South America. *J. Clin. Microbiol.* 49, 1993–1996.
- Saidani, M., Messadi, L., Soudani, A., Daaloul-Jedidi, M., Chatre, P., Ben Chehida, F., Mamlouk, A., Mahjoub, W., Madec, J.Y., Haenni, M., 2018. Epidemiology, antimicrobial resistance, and extended-spectrum beta-lactamase-producing enterobacteriaceae in clinical bovine mastitis in Tunisia. *Microb. Drug Resist.*
- Saishu, N., Ozaki, H., Murase, T., 2014. CTX-M-Type extended-spectrum β -lactamase-producing *Klebsiella pneumoniae* isolated from cases of bovine mastitis in Japan. *J. Vet. Med. Sci.* 76, 1153–1156.
- Saito, R., Takahashi, R., Sawabe, E., Koyano, S., Takahashi, Y., Shima, M., Ushizawa, H., Fujie, T., Tosaka, N., Kato, Y., Moriya, K., Tohda, S., Tojo, N., Koike, R., Kubota, T., 2014. First report of KPC-2 carbapenemase-producing *Klebsiella pneumoniae* in Japan. *Antimicrob. Agents Chemother.* 58, 2961–2963.
- Sampaio, J.L.M., Gales, A.C., 2016. Antimicrobial resistance in Enterobacteriaceae in Brazil: focus on β -lactams and polymyxins. *Braz. J. Microbiol.* 47, 31–37.
- Santos, C.D.M., 2006. *Staphylococcus sp* enterobactérias isoladas de mastite recorrente em oito rebanhos da região de Uberlândia-MG: perfil de suscetibilidade aos antimicrobianos. Master. Federal University of Uberlândia.
- Sartori, L., Fernandes, M.R., Ienne, S., de Souza, T.A., Gregory, L., Cerdeira, L., Lincopan, N., 2017. Draft genome sequences of two fluoroquinolone-resistant CTX-M-15-producing *Escherichia coli* ST90 (ST23 complex) isolated from a calf and a dairy cow in South America. *J. Glob. Antimicrob. Resist.* 11, 145–147.
- Schmitt, J., Jacobs, E., Schmidt, H., 2007. Molecular characterization of extended-spectrum beta-lactamases in Enterobacteriaceae from patients of two hospitals in Saxony, Germany. *J. Med. Microbiol.* 56, 241–249.
- Seni, J., Falgenhauer, L., Simeo, N., Mirambo, M.M., Imirzalioglu, C., Matee, M., Rweyemamu, M., Chakraborty, T., Mshana, S.E., 2016. Multiple ESBL-producing *Escherichia coli* sequence types carrying quinolone and aminoglycoside resistance genes circulating in companion and domestic farm animals in Mwanza, Tanzania, harbor commonly occurring plasmids. *Front. Microbiol.* 7, 142.
- Shin, J., Kim, D.H., Ko, K.S., 2011. Comparison of CTX-M-14 and CTX-M-15-producing *Escherichia coli* and *Klebsiella pneumoniae* isolates from patients with bacteremia. *J. Infect.* 63, 39–47.
- Shiraki, Y., Shibata, N., Doi, Y., Arakawa, Y., 2004. *Escherichia coli* Producing CTX-M-2 β -Lactamase in Cattle, Japan. *Emerg. Infect. Dis.* 10, 69.
- Sidjabat, H.E., Derrington, P., Nimmo, G.R., Paterson, D.L., 2010. *Escherichia coli* ST131 producing CTX-M-15 in Australia. *J. Antimicrob. Chemother.* 65, 1301–1303.
- Silva, K.C.d., Lincopan, N., 2012. Epidemiologia das betalactamases de espectro estendido no Brasil: impacto clínico e implicações para o agronegócio. *J. Bras. Patol. Med. Lab.* 48, 91–99.
- Smith, K.A., Williams, A.G., 2016. Production and management of cattle manure in the UK and implications for land application practice. *Soil Use Manag.* 32, 73–82.
- Snow, L.C., Wearing, H., Stephenson, B., Teale, C.J., Coldham, N.G., 2011. Investigation of the presence of ESBL-producing *Escherichia coli* in the North Wales and West Midlands areas of the UK in 2007 to 2008 using scanning surveillance. *Vet. Rec.* 169, 656.
- Sparham, S.J., Kwong, J.C., Valcanis, M., Easton, M., Trotter, D.J., Seemann, T., Steiner, T.P., Howden, B.P., 2017. Emergence of multidrug resistance in locally-acquired human infections with *Salmonella* Typhimurium in Australia owing to a new clade harbouring *bla*_{CTX-M-9}. *Int. J. Antimicrob. Agents* 50, 101–105.
- Stefani, S., Giovanelli, I., Anacarso, L., Condo, C., Messi, P., de Niederhausern, S., Bondi, M., Iseppi, R., Sabia, C., 2014. Prevalence and characterization of extended-spectrum beta-lactamase-producing Enterobacteriaceae in food-producing animals in Northern Italy. *New Microbiol.* 37, 551–555.
- Stokes, M.O., 2014. Comparative Genomics of blaCTX-M Plasmids from Veterinary and Human *Escherichia coli* and Methods for Their Identification and Differentiation. PhD. King's University.
- Stokes, M.O., AbuOun, M., Umur, S., Wu, G., Partridge, S.R., Mevius, D.J., Coldham, N.G., Fielder, M.D., 2013. Complete sequence of pSAM7, an IncX4 plasmid carrying a novel blaCTX-M-14b transposition unit isolated from *Escherichia coli* and *Enterobacter cloacae* from cattle. *Antimicrob. Agents Chemother.* 57, 4590–4594.
- Su, Y., Yu, C.-Y., Tsai, Y., Wang, S.-H., Lee, C., Chu, C., 2016. Fluoroquinolone-resistant and extended-spectrum β -lactamase-producing *Escherichia coli* from the milk of cows with clinical mastitis in Southern Taiwan. *J. Microbiol. Immunol. Infect.* 49, 892–901.
- Sudarwanto, M.B., Lukman, D.W., Latif, H., Pisestyani, H., Sukmawinata, E., Akineden, Ö., Usleber, E., 2016. CTX-M producing *Escherichia coli* isolated from cattle feces in Bogor slaughterhouse, Indonesia. *Asian Pac. J. Trop. Biomed.* 6, 605–608.
- Tadesse, D.A., Li, C., Mukherjee, S., Hsu, C.-H., Bodeis, J.S., Gaines, S.A., Kabera, C., Loneragan, G.H., Torrence, M., Harhay, D.M., McDermott, P.F., Zhao, S., 2018. Whole-Genome sequence analysis of CTX-M containing *Escherichia coli* isolates from retail meats and cattle in the United States. *Microb. Drug Resist.* 24, 939–948.
- Tamang, M.D., Nam, H.-M., Gurung, M., Jang, G.-C., Kim, S.-R., Jung, S.-C., Park, Y.H., Lim, S.-K., 2013a. Molecular characterization of CTX-M β -lactamase and associated addiction systems in *Escherichia coli* circulating among cattle, farm workers, and the farm environment. *Appl. Environ. Microbiol.* 79, 3898–3905.
- Tamang, M.D., Nam, H.M., Kim, S.R., Chae, M.H., Jang, G.-C., Jung, S.C., Lim, S.K., 2013b. Prevalence and molecular characterization of CTX-M beta-lactamase-producing *Escherichia coli* isolated from healthy swine and cattle. *Foodb. Pathog. Dis.* 10, 13–20.
- Tark, D.-S., Moon, D.C., Kang, H.Y., Kim, S.-R., Nam, H.-M., Lee, H.-S., Jung, S.-C., Lim, S.-K., 2017. Antimicrobial susceptibility and characterization of extended-spectrum β -lactamases in *Escherichia coli* isolated from bovine mastitic milk in South Korea from 2012 to 2015. *J. Dairy Sci.* 100, 3463–3469.
- Tasli, H., Bahar, I.H., 2005. Molecular characterization of TEM- and SHV-derived extended-spectrum beta-lactamases in hospital-based Enterobacteriaceae in Turkey. *Jpn. J. Infect. Dis.* 58, 162–167.
- Tate, H., Folster, J.P., Hsu, C.H., Chen, J., Hoffmann, M., Li, C., Morales, C., Tyson, G.H., Mukherjee, S., Brown, A.C., Green, A., Wilson, W., Dessai, U., Abbott, J., Joseph, L., Haro, J., Ayers, S., McDermott, P.F., Zhao, S., 2017. Comparative analysis of extended-spectrum-beta-lactamase CTX-M-65-producing *Salmonella enterica* serovar infantis isolates from humans, food animals, and retail chickens in the United States. *Antimicrob. Agents Chemother.* 61.
- Teale, C.J., Barker, L., Foster, A.P., Liebana, E., Batchelor, M., Livermore, D.M., Threlfall, E.J., 2005. Extended-spectrum beta-lactamase detected in *E. coli* recovered from calves in Wales. *Vet. Rec.* 156, 186–187.
- Tian, G.-B., Wang, H.-N., Zhang, A.-Y., Zhang, Y., Fan, W.-Q., Xu, C.-W., Zeng, B., Guan, Z.-B., Zou, L.-K., 2012. Detection of clinically important β -lactamases in commensal *Escherichia coli* of human and swine origin in western China. *J. Med. Microbiol.* 61, 233–238.
- Timofte, D., Maciucă, L.E., Evans, N.J., Williams, H., Wattret, A., Fick, J.C., Williams, N.J., 2014. Detection and molecular characterization of *Escherichia coli* CTX-M-15 and

- Klebsiella pneumoniae SHV-12 β -lactamases from bovine mastitis isolates in the United Kingdom. *Antimicrob. Agents Chemother.* 58, 789–794.
- Toth, A., Juhász-Kaszanyitzky, E., Mag, T., Hajbel-Vekony, G., Paszti, J., Damjanova, L., 2013. Characterization of extended-spectrum beta-lactamase (ESBL) producing *Escherichia coli* strains isolated from animal and human clinical samples in Hungary in 2006–2007. *Acta Microbiol. Immunol. Hung.* 60, 175–185.
- Tyrrell, J.M., Wootton, M., Toleman, M.A., Howe, R.A., Woodward, M., Walsh, T.R., 2016. Genetic & virulence profiling of ESBL-positive *E. coli* from nosocomial & veterinary sources. *Vet. Microbiol.* 186, 37–43.
- USDA, United, State, Department, Agriculture, o., 2017. *Livestock and Poultry: World Markets and Trade*.
- Usui, M., Iwasa, T., Fukuda, A., Sato, T., Okubo, T., Tamura, Y., 2013. The role of flies in spreading the extended-spectrum beta-lactamase gene from cattle. *Microb. Drug Resist.* 19, 415–420.
- Valat, C., Auvray, F., Forest, K., Métayer, V., Gay, E., Peytavin de Garam, C., Madec, J.-Y., Haenni, M., 2012. Phylogenetic grouping and virulence potential of extended-spectrum- β -lactamase-producing *Escherichia coli* strains in cattle. *Appl. Environ. Microbiol.* 78, 4677–4682.
- Valat, C., Goldstone, R.J., Hirschfeld, E., Haenni, M., Smith, D.G.E., Madec, J.-Y., 2016. Draft genome sequences of enterohemorrhagic *Escherichia coli* encoding extended-spectrum beta-lactamases. *Genome Announc.* 4.
- Velasova, M., Smith, R.P., Lemma, F., Horton, R.A., Duggett, N.A., Evans, J., Tongue, S.C., Anjum, M.F., Randall, L.P., 2019. Detection of extended-spectrum β -lactam, AmpC and carbapenem resistance in Enterobacteriaceae in beef cattle in Great Britain in 2015. *J. Appl. Microbiol.* 126, 1081–1095.
- Wang, G., Huang, T., Surendraiah, P.K.M., Wang, K., Komal, R., Zhuge, J., Chern, C.-R., Kryszuk, A.A., King, C., Wormser, G.P., 2013. CTX-M β -lactamase-producing *Klebsiella pneumoniae* in Suburban New York city, New York, USA. *Emerg. Infect. Dis.* 19, 1803–1810.
- Watson, E., Jeckel, S., Snow, L., Stubbs, R., Teale, C., Wearing, H., Horton, R., Toszeghy, M., Tearne, O., Ellis-Iversen, J., Coldham, N., 2012. Epidemiology of extended spectrum beta-lactamase *E. coli* (CTX-M-15) on a commercial dairy farm. *Vet. Microbiol.* 154, 339–346.
- Wieler, L.H., Semmler, T., Eichhorn, I., Antao, E.M., Kinnemann, B., Geue, L., Karch, H., Guenther, S., Bethe, A., 2011. No evidence of the Shiga toxin-producing *E. coli* O104:H4 outbreak strain or enteroaggregative *E. coli* (EAEC) found in cattle faeces in northern Germany, the hotspot of the 2011 HUS outbreak area. *Gut Pathog.* 3, 17.
- Wittum, T.E., Mollenkopf, D.F., Daniels, J.B., Parkinson, A.E., Mathews, J.L., Fry, P.R., Abley, M.J., Gebreyes, W.A., 2010. CTX-M-type extended-spectrum beta-lactamases present in *Escherichia coli* from the feces of cattle in Ohio, United States. *Foodb. Pathog. Dis.* 7, 1575–1579.
- 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., Livermore, D.M., 2004. Community and hospital spread of *Escherichia coli* producing CTX-M extended-spectrum beta-lactamases in the UK. *J. Antimicrob. Chemother.* 54, 735–743.
- Wu, G., Day, M.J., Mafura, M.T., Nunez-Garcia, J., Fenner, J.J., Sharma, M., van Essen-Zandbergen, A., Rodríguez, I., Dierikx, C., Kadlec, K., Schink, A.-K., Wain, J., Helmuth, R., Guerra, B., Schwarz, S., Threlfall, J., Woodward, M.J., Woodford, N., Coldham, N., Mevius, D., 2013. Comparative analysis of ESBL-positive *Escherichia coli* isolates from animals and humans from the UK, The Netherlands and Germany. *PLoS One* 8, e75392.
- Yan, J.-J., Hsueh, P.-R., Lu, J.-J., Chang, F.-Y., Shyr, J.-M., Wan, J.-H., Liu, Y.-C., Chuang, Y.-C., Yang, Y.-C., Tsao, S.-M., Wu, H.-H., Wang, L.-S., Lin, T.-P., Wu, H.-M., Chen, H.-M., Wu, J.-J., 2006. Extended-spectrum β -lactamases and plasmid-mediated AmpC enzymes among clinical isolates of *Escherichia coli* and *Klebsiella pneumoniae* from seven medical centers in Taiwan. *Antimicrob. Agents Chemother.* 50, 1861–1864.
- Yang, F., Zhang, S., Shang, X., Wang, L., Li, H., Wang, X., 2018. Characteristics of quinolone-resistant *Escherichia coli* isolated from bovine mastitis in China. *J. Dairy Sci.*
- Yeung, M.-k., 2011. *Epidemiology of CTX-M Type Extended-Spectrum Beta-Lactamase-producing Escherichia Coli Among Blood Culture Isolates in Hong Kong*. Master. University of Hong Kong.
- Zheng, H., Zeng, Z., Chen, S., Liu, Y., Yao, Q., Deng, Y., Chen, X., Lv, L., Zhuo, C., Chen, Z., Liu, J.-H., 2012. Prevalence and characterisation of CTX-M β -lactamases amongst *Escherichia coli* isolates from healthy food animals in China. *Int. J. Antimicrob. Agents* 39, 305–310.
- Zheng, B., Feng, C., Xu, H., Yu, X., Guo, L., Jiang, X., Song, X., 2019. Detection and characterization of ESBL-producing *Escherichia coli* expressing mcr-1 from dairy cows in China. *J. Antimicrob. Chemother.* 74, 321–325.
- Zhong, Y.-M., Liu, W.-E., Liang, X.-H., Li, Y.-M., Jian, Z.-J., Hawkey, P.M., 2015. Emergence and spread of O16-ST131 and O25b-ST131 clones among faecal CTX-M-producing *Escherichia coli* in healthy individuals in Hunan Province, China. *J. Antimicrob. Chemother.* 70, 2223–2227.
- Zong, Z., Partridge, S.R., Thomas, L., Iredell, J.R., 2008. Dominance of bla(CTX-M) within an Australian extended-spectrum β -lactamase gene pool. *Antimicrob. Agents Chemother.* 52, 4198–4202.
- Zurfluh, K., Cernela, N., Stephan, R., 2015. Quinolone resistance mechanisms among extended-spectrum beta-lactamase (ESBL)-producing *Escherichia coli* isolated from farm animals in Switzerland. *Schweizer Archiv für Tierheilkunde* 157, 59–62.