

Presence of Extended-Spectrum β -lactamase, CTX-M-65 in *Salmonella enterica* serovar Infantis Isolated from Children with Diarrhea in Lima, Peru

Ana Granda¹ Maribel Riveros¹ Sandra Martínez-Puchol² Karen Ocampo¹ Laura Laureano-Adame³
Alfredo Corujo³ Isabel Reyes⁴ Joaquim Ruiz²  Theresa J. Ochoa^{1,5}

¹ Department of Pediatrics, Instituto de Medicina Tropical "Alexander von Humboldt," Universidad Peruana Cayetano Heredia, Lima, Perú

² ISGlobal, Hospital Clinic, Universitat de Barcelona, Barcelona, Spain

³ Food Research Center, Nutreco, Toledo, Spain

⁴ Unidad de investigación pediátrica, Hospital de Emergencias Pediátricas, Lima, Perú

⁵ Center for Infectious Diseases, University of Texas Health Science Center at Houston, Houston, TX, United States

Address for correspondence Theresa J. Ochoa, MD, Department of Pediatrics, Instituto de Medicina Tropical "Alexander von Humboldt," Universidad Peruana Cayetano Heredia, Av. Honorio Delgado 430, San Martín de Porras, Lima 33, Perú

(e-mail: Theresa.J.Ochoa@uth.tmc.edu; Theresa.Ochoa@upch.pe).

J Pediatr Infect Dis 2019;14:194–200.

Abstract

Gastroenteritis in children is a serious condition in many parts of the world. *Salmonella enterica* is one of the causes of the disease. In this study, 280 fecal samples from children with diarrhea in four hospitals in Lima, Peru, were collected between September 2012 and March 2013. *Salmonella* was detected in 26 of the samples. Serotyping demonstrated that 25 of the isolates were *S. enterica* Infantis, and one isolate was *S. enterica* Typhimurium. Repetitive extragenic palindromic–polymerase chain reaction analysis suggests that all *S. Infantis* belong to the same clone. All but one of the *S. Infantis* isolates exhibited an extended-spectrum β -lactamase phenotype as they harbored *bla*_{CTX-M 65}. Two strains also carried *bla*_{TEM-1}. Nine of the isolates were resistant to azithromycin and two to ciprofloxacin. This study demonstrates that a multidrug-resistant *S. Infantis* clone carrying *bla*_{CTX-M 65} was circulating among children in Lima, Peru. The development of molecular epidemiology studies in *Salmonella*-causing diarrhea or other pathologies in Lima and in other areas will be useful to determine the permanence, geographical spread, and clinical implications of this clone.

Keywords

- ▶ extended-spectrum β -lactamases
- ▶ *Salmonella enterica* serovar Infantis
- ▶ diarrhea

Introduction

Worldwide, gastroenteritis is one of the major causes of morbidity and mortality in children under 5 years of age; it was estimated that the annual incidence of diarrhea is 2.8 million cases,¹ leading to around 500,000 deaths each year.²

Salmonella is a common cause of gastroenteritis.¹ This bacterium has more than 2500 serovars, but *Salmonella enterica* serovar Typhimurium and *S. enterica* serovar Enteritidis are isolated most frequently worldwide.³ *Salmonella enterica* serovar Infantis has increasingly been detected in

several parts of the world.⁴ In the recent years, it has been associated with outbreaks in Latin American countries like Brazil, Ecuador,^{5,6} and Peru, where it has been reported as the third most common serotype.⁷

In Peru, *Salmonella sp.* resistant to β -lactam antibiotics is a problem, and extended-spectrum β -lactamases (ESBLs) are frequently present. In 2010, Lima and its vicinity reported a considerable increase in the number of isolates resistant to ceftriaxone (CRO), with the presence of β -lactamases belonging to the CTX-M family.⁸ Previously, in 2006, a nosocomial outbreak of *S. Typhimurium* harboring a *bla*_{SHV-5} gene was also reported.⁹ These findings are relevant because although antibiotic treatment is not usually indicated in acute diarrhea,

 Joaquim Ruiz's ORCID is <https://orcid.org/0000-0002-4431-2036>.

received

July 17, 2018

accepted after revision

March 7, 2019

published online

April 20, 2019

Copyright © 2019 by Georg Thieme
Verlag KG, Stuttgart · New York

DOI <https://doi.org/10.1055/s-0039-1685502>.
ISSN 1305-7707.

third-generation cephalosporins, together with azithromycin (AZM) and ciprofloxacin (CIP), can be used as a treatment in high-risk groups such as infants, the elderly, and immunocompromised patients.¹⁰

The main genes encoding ESBLs are *bla*_{TEM}, *bla*_{SHV}, *bla*_{OXA}, and *bla*_{CTX-M}. The latter, which confers high levels of resistance to cefotaxime (CTX), encodes enzymes that are subdivided into five subclasses (CTX-M-1, CTX-M-2, CTX-M-8, CTX-M-9, and CTX-M-25).¹¹ Currently, the CTX-M family is the most commonly disseminated in the world and different microbial species.¹²

The objectives of this study were to determine the presence of *Salmonella* in fecal samples of children admitted to four hospitals in Lima, Peru, and to determine whether the *Salmonella* isolates were related and expressed an ESBL phenotype. The genetic basis of the ESBL phenotype was also determined.

Methods

Bacterial Isolates

A total of 280 stool specimens from children under 6 years of age hospitalized with gastroenteritis and persistent diarrhea were collected from September 2012 to April 2013 from four hospitals in Lima: Hospital de Emergencias Pediátricas (HEP)

(*n* = 212), Hospital Nacional Cayetano Heredia (HNCH) (*n* = 17), Hospital Nacional Docente Madre Niño San Bartolomé (HSB) (*n* = 2), and Centro de Salud Materno Infantil Tahuantinsuyo Bajo (CST) (*n* = 49) (►Fig. 1). *Salmonella* sp. were isolated on differential culture media such as xylose lysine deoxycholate agar and Salmonella–Shigella agar. Presumptive *Salmonella* colonies were identified through biochemical¹³ and serological (detection of somatic antigen O, [Probac do Brasil, Sao Paulo, SP, Brazil]) tests and then confirmed by polymerase chain reaction (PCR)¹⁴ in the Laboratory of Enteric Diseases and Nutrition (LEEN), Tropical Medicine Institute Alexander von Humboldt from Universidad Peruana Cayetano Heredia (UPCH). *Salmonella* isolates were sent to the Nutreco Food Research Center (Toledo, Spain), where serotyping was performed using a commercial DNA microarray system, Check & Trace Salmonella (Check-Points, the Netherlands, Holland).

Antibiotic Susceptibility

The antibiotic susceptibility was determined by Kirby–Bauer tests according to the Clinical & Laboratory Standards Institute (CLSI) guidelines.^{15,16} Antibiotics included in this study were chloramphenicol (C), aztreonam (ATM), trimethoprim-sulfamethoxazole (TMP/SMX), cefotaxime (CTX), ampicillin (AMP), furazolidone (F), nalidixic acid (NA), CRO, CIP,



Fig. 1 Geographical distribution of point locations of four hospitals in Lima: Hospital de Emergencias Pediátricas (HEP), Hospital Nacional Cayetano Heredia (HNCH), Hospital Nacional Docente Madre Niño San Bartolomé (HSB), and Centro de Salud Materno Infantil Tahuantinsuyo Bajo (CST).

tetracycline (TE), AZM, erythromycin (E), amoxicillin plus clavulanic acid (AMC) and ceftazidime (CAZ). In the case of AZM, an isolate was considered resistant if the halo was <12 mm as proposed for other enterobacteria.¹⁵

Phenotypic Methods for Detection of ESBL

The presence of ESBLs was verified by two tests: double-disc synergy test with AMC (30 µg), CAZ (30 µg), CTX (30 µg), CRO (30 µg), and ATM (30 µg)¹⁷; and the CLSI confirmatory test using both CTX (30 mg) and CAZ (30 mg) disks alone and in combination with clavulanic acid (10 mg). The second test was considered positive when an increase in the growth inhibitory zone diameter around a disk containing CTX or CAZ with the addition of clavulanic acid was 5 mm or greater than the diameter around the disk containing CTX or CAZ alone.¹⁵

Molecular Detection of ESBL Genes

The presence of *bla*_{TEM},¹⁸ *bla*_{SHV},¹⁹ and *bla*_{CTX-M}²⁰ was determined by PCR in isolates presenting an ESBL phenotype. The CTX-M variants, CTX-M 1, CTX-M 2, CTX-M 8, and CTX-M 9,^{21,22} were also confirmed by PCR (► **Table 1**). The amplification products were purified (Gel Extraction Kit from Omega Bio-tek, Norcross, Georgia, United States) and sequenced (Beckman Coulter; Takeley, Great Britain).

Repetitive Extragenic Palindromic–Polymerase Chain Reaction

Clonal relationships between strains were determined by repetitive extragenic palindromic–PCR (REP-PCR) using the primer GCG CCG ICA TGC GGC ATT²³ with the following amplification conditions: 95°C for 5 minutes followed by 30 cycles of 95°C for 1 minute, 40°C for 1 minute, and 65°C for 1 minute, and final extension at 65°C for 16 minutes. A

phylogenetic tree was constructed by the unweighted pair group method with arithmetic mean analysis using the Phoretix 1D Pro software.

Results

Bacterial Isolates

Of 280 clinical fecal samples from children with diarrhea, 26 (9%) were identified as *Salmonella* sp., 25 were serotyped as *S. Infantis*, and 1 as *S. Typhimurium*. When analyzed for Hospital settings, it was observed that *Salmonella* sp. isolates were only recovered from HEP (21/212; 10%) and HNCH (5/17; 29%).

Antibiotic Susceptibility

All *S. Infantis* were resistant to AMP, E, F, NA, SXT, and TE, 24/25 isolates were also resistant to ATM, CRO, CTX, and C, and 10/25 (40%) were resistant to AZM. Two out of the 25 isolates were resistant to CIP, and the remaining 92% (23/25) exhibited intermediate resistance. Four isolates were resistant to CAZ and 18 presented intermediate resistance. *Salmonella* Typhimurium only presented resistance to E and AZM. The CLSI confirmatory test results were concordant with the result of the double-disc synergy test.

Molecular Detection of Extended-Spectrum β-Lactamase

All strains with an ESBL phenotype harbored *bla*_{CTX-M}. Two isolates, E-25 (from HNCH) and 2-094 (from HEP), also presented with *bla*_{TEM} (► **Table 2**). Subsequent analysis showed the presence of a *bla*_{CTX-M 65} gene belonging to CTX-M group 9. The *bla*_{TEM} gene was identified as encoding TEM-1 and therefore not classified as ESBL. No *bla*_{SHV} gene was detected.

Table 1 Primers used for the molecular detection of ESBL and variants

Primer	Nucleotide sequence 5'–3'	Amplicon size (bp)	Annealing temperature used for PCR (°C)	Reference
TEM-F	ATTCTTGAAGACGAAAGGGC	1,150	60	18
TEM-R	ACGCTCAGTGGAACGAAAAC			
SHV-F	CACTCAAGGATGTATTGTG	885	52	19
SHV-R	TTAGCGTTGCCAGTTATTGTG			
CTXM- Univ- F	CGATGTGCAGTACCAGTAA	585	52	20
CTXM- Univ- R	TTAGTGACCAGAATCAGCGG			
CTXM-3G (group 1)-F	GTTACAATGTGTGAGAAGCAG	1,017	60	21
CTXM-3G (group 1)-R	CCGTTTCCGCTATTACAAAC			
CTXM-9 (group 9)-F	TGACCGTATTGGGAGTTTCAG	917	55	22
CTXM-9 (group 9)-R	GATTTATTCAACAAAACCAG			
CTXM-8 (group 8)-F	TGATGAGACATCGCGTTAAG	873	60	21
CTXM-8 (group 8)-R	TAACCGTCGGTGACGATTTT			
CTXM-10-F	CCGCGCTACACTTTGTGGC	944	60	21
CTXM-10-R	TTACAAACCGTTGGTGACG			

Abbreviation: ESBL, extended-spectrum β-lactamase.

Table 2 Characteristics of *Salmonella* Infantis strains

Isolate	Date	Hospital	Specie/Serovar	ESBL type
E-25	September 12, 2012	HNCH	<i>Salmonella</i> Infantis	<i>bla</i> _{CTX-M 65} , <i>bla</i> _{TEM-1}
E-28	November 12, 2012	HNCH	<i>Salmonella</i> Infantis	<i>bla</i> _{CTX-M 65}
2-015	January 7, 2013	EP	<i>Salmonella</i> Infantis	<i>bla</i> _{CTX-M 65}
2-016	January 7, 2013	EP	<i>Salmonella</i> Infantis	<i>bla</i> _{CTX-M 65}
2-017	January 8, 2013	EP	<i>Salmonella</i> Infantis	<i>bla</i> _{CTX-M 65}
2-023	January 14, 2013	EP	<i>Salmonella</i> Infantis	<i>bla</i> _{CTX-M 65}
2-024	January 14, 2013	EP	<i>Salmonella</i> Infantis	<i>bla</i> _{CTX-M 65}
2-026	January 15, 2013	EP	<i>Salmonella</i> Infantis	<i>bla</i> _{CTX-M 65}
2-029	January 17, 2013	EP	<i>Salmonella</i> Infantis	<i>bla</i> _{CTX-M 65}
2a-002	January 18, 2013	HNCH	<i>Salmonella</i> Infantis	<i>bla</i> _{CTX-M 65}
2-031	January 21, 2013	EP	<i>Salmonella</i> Infantis	<i>bla</i> _{CTX-M 65}
2-032	January 22, 2013	EP	<i>Salmonella</i> Infantis	<i>bla</i> _{CTX-M 65}
2-040	January 24, 2013	EP	<i>Salmonella</i> Infantis	<i>bla</i> _{CTX-M 65}
2-047	January 28, 2013	EP	<i>Salmonella</i> Infantis	<i>bla</i> _{CTX-M 65}
2-050	29 January, 2013	EP	<i>Salmonella</i> Infantis	<i>bla</i> _{CTX-M 65}
2-065	February 1, 2013	EP	<i>Salmonella</i> Infantis	<i>bla</i> _{CTX-M 65}
2-068	February 4, 2013	EP	<i>Salmonella</i> Infantis	<i>bla</i> _{CTX-M 65}
2-094	February 14, 2013	EP	<i>Salmonella</i> Infantis	<i>bla</i> _{CTX-M 65} , <i>bla</i> _{TEM-1}
2-125	February 27, 2013	EP	<i>Salmonella</i> Infantis	<i>bla</i> _{CTX-M 65}
2-144	March 14, 2013	EP	<i>Salmonella</i> Infantis	<i>bla</i> _{CTX-M 65}
2-161	March 20, 2013	EP	<i>Salmonella</i> Infantis	<i>bla</i> _{CTX-M 65}
DEC 1-009	March 25, 2013	HNCH	<i>Salmonella</i> Infantis	<i>bla</i> _{CTX-M 65}
1-013	April 4, 2013	HNCH	<i>Salmonella</i> Infantis	<i>bla</i> _{CTX-M 65}
2-204	April 17, 2013	EP	<i>Salmonella</i> Infantis	<i>bla</i> _{CTX-M 65}
2-013	January 3, 2013	EP	<i>Salmonella</i> Infantis	–
2-145	March 18, 2013	EP	<i>Salmonella</i> Typhimurium	–

Abbreviations: EP, Hospital de Emergencias Pediátricas; ESBL, extended-spectrum β -lactamase; HNCN, Hospital Nacional Cayetano Heredia.

Molecular Typing by Repetitive Extragenic Palindromic-Polymerase Chain Reaction

REP-PCR data suggested a clonal relationship among 24 of the 25 isolates of *S. Infantis*. All ESBL-producing strains have identical REP-PCR profiles. The isolate, *S. infantis* 2-013, that did not have the ESBL phenotype showed a different REP-PCR profile (► Fig. 2).

Discussion

In this study, 92% of 25 *S. Infantis* strains were ESBL. Since 2010, an unusual increase in *Salmonella* cases has been reported in pediatric patients from various hospitals in Lima, including the National Institute for Child Health,⁸ and in food samples.²⁴ *S. Infantis* is the third most frequent serovar identified in Peru and is associated with the consumption of contaminated eggs and meat products.²³ Some findings show that this serotype can persist and proliferate in the environment, as well as in hospitals, for a long period of time,^{7,25,26} as observed in studies conducted in Brazil,⁵ Ecuador,⁶ and Argentina.²⁷

Most cases of gastroenteritis caused by *Salmonella* do not require treatment with antibiotics unless patients are young infants, are malnourished, have systemic disease, or are immunocompromised. In these cases, cephalosporins or quinolones are commonly used.²⁸ Nonetheless, severe cases related to multidrug-resistant *S. Infantis* have been described in Peru, including cases of bacteremia.²⁹

A previous report analyzing quinolone resistance in *Salmonella* sp. from the area of Lima, Peru, showed that 33 and 14% of *Salmonella* Typhi and non-Typhi, respectively, were resistant to NA, whereas 24% and 13% presented diminished susceptibility to CIP.³⁰ In our study, 100% of the isolates were NA resistant and 8% were resistant to CIP.

Usually, a single mutation in *gyrA* leads to resistance to NA but only decreased susceptibility to fluoroquinolones.³¹ In fact, this is the most common scenario in *Salmonella* sp.^{32,33} as the presence of additional mutations in quinolone-targets leading to high levels of CIP resistance seems to have a deleterious effect on bacterial fitness.³⁴ Despite this impaired fitness, isolates exhibiting resistance to CIP likely

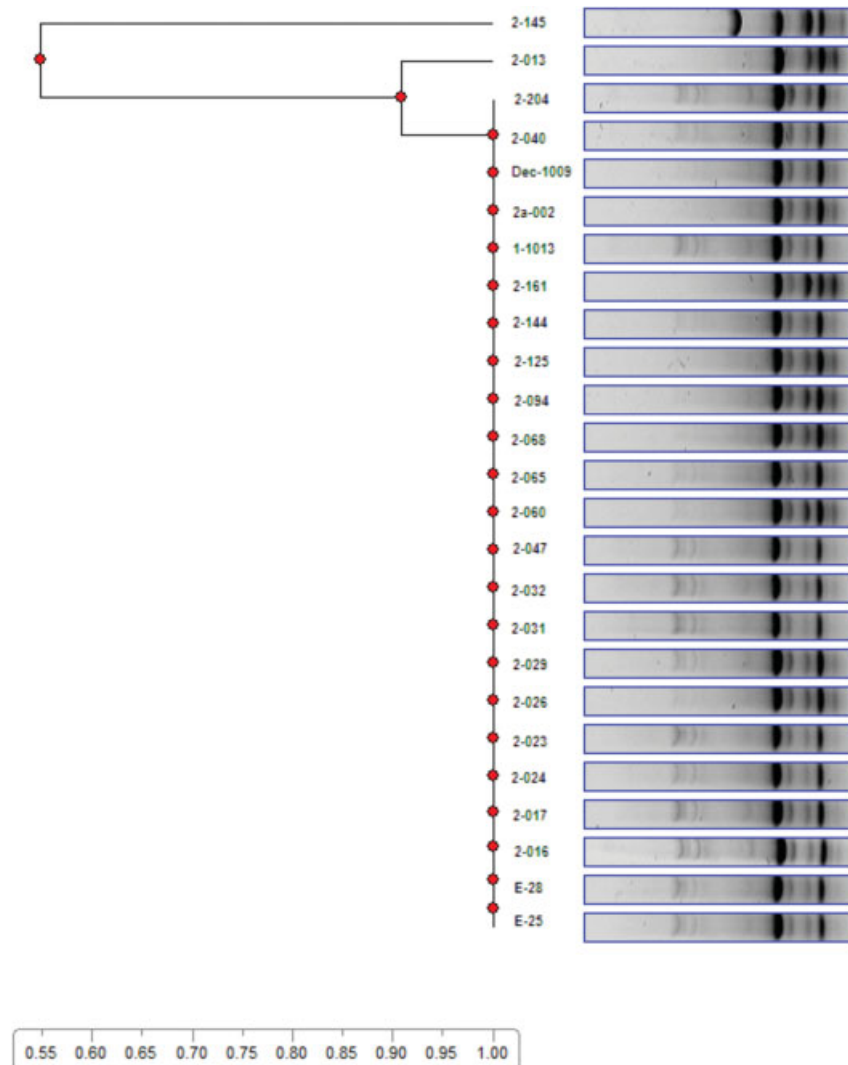


Fig. 2 *Salmonella* sp. similarity dendrogram: analysis of repetitive extragenic palindromic-polymerase chain reaction profiles using the unweighted pair group method with arithmetic mean analysis method shows that all *S. Infantis* carrying the $bla_{CTX-M 65}$ belong to the same clone, whereas isolate 2-103 does not possess the $bla_{CTX-M 65}$ presented an identity level of >90%. The *S. Typhimurium* 2-145 showed a fully unrelated pattern.

harbor additional target mutation, as was observed for highly fluoroquinolone-resistant *S. Kentucky* ST198-X1-SGI1 that has been disseminated worldwide.³⁵ Regarding other antimicrobial agents, studies in our geographical area have shown the presence of *S. Typhimurium* exhibiting resistance to CRO, CAZ, and amikacin, producing the bla_{SHV-5} .⁹

CTX-M group 9 ($bla_{CTX-M 65}$) was found in 24 of our *S. infantis* isolates with resistance to CTX and CRO and 4 out of 24 (17%) with decreased susceptibility to CAZ, characteristic of an isolate carrying the bla_{CTX-M} gene.³⁶ Although $bla_{CTX-M 65}$ has been frequently found in neighboring countries³⁷ and has been observed in strains of *Escherichia coli* causing bacteremia in children²² in Peru, to our knowledge, this is the first report in Peru of the $bla_{CTX-M 65}$ gene in *Salmonella* strains.

In Peru, the prevalence of $bla_{CTX-M 14}$, $bla_{CTX-M 24}$, $bla_{CTX-M 15}$, and $bla_{CTX-M 2}$ in *E. coli* has been reported as 45, 22, 22, and 11%, respectively.³⁸ Between July 2012 and January 2013, bla_{CTX-M} was detected in four strains of *Salmonella* at the National Institute of Child Health in Lima, Peru.³⁹ These strains are contemporaneous with *Salmonella* ESBL strains

found in this study, which suggests the presence of an outbreak in the city of Lima. This hypothesis is supported by the REP-PCR results, which showed the presence of an *S. Infantis* clone disseminated between two of the Hospitals included in the study. Furthermore, it is necessary to consider the distance of around 6 km between HEP and HNCH, which likely precludes the presence of common environments such as schools.

Between 2014 and 2015, 5 of 28 *Salmonella* strains isolated in Ecuador were clonally related to *S. Infantis* harboring a $bla_{CTX-M 65}$ gene.⁶ Also, in 2005, strains of *S. Infantis* with an ESBL phenotype belonging to an outbreak were found in Argentina.²⁷ All these findings suggest that an epidemic clone of *S. Infantis* has spread to different countries in Latin America. Riccobono et al⁴⁰ studied the spread of the $bla_{CTX-M 65}$ gene, and the authors concluded it was because of a polyclonal spread of the Inc11 ST71 epidemic plasmid transferable to other enterobacteria by conjugation. Therefore, the presence of this epidemic plasmid in *S. Infantis* clone is highly probable.

The *S. Infantis* 2-013 isolate, the only *S. Infantis* without ESBL pattern, showed a different REP-PCR profile. Nonetheless, the pattern was closely similar to exhibiting more than 90% identity and therefore could possibly be an “ancestral” non-ESBL isolate or it could have lost the resistance gene at some point.

In conclusion, this is the first report of an epidemic strain of *S. enterica* serovar *Infantis* carrying *bla*_{CTX-M 65} in Peru. The data suggest that this strain is widely distributed in the area of Lima. Furthermore, indirect evidence (e.g. similarity of antibiotic resistance patterns or the presence of CTX-M 65) suggests the presence of multidrug-resistant ESBL carrying *S. Infantis* spreading in Latin America. Further studies on *S. Infantis* from nonhuman origin are needed in order to determine the possible acquisition of this pathogen. Moreover, new research should include samples from different Latin American countries to determine cross-border dissemination of a multidrug-resistant *S. Infantis*.

Funding

J. R. was supported by the I3 program of the Ministerio de Economía y Competitividad, Spain (grant number: CES11/012). ISGlobal is a member of the CERCA Programme, Generalitat de Catalunya.

Conflict of Interest

None declared.

References

- Majowicz SE, Musto J, Scallan E, et al; International Collaboration on Enteric Disease ‘Burden of Illness’ Studies. The global burden of nontyphoidal *Salmonella* gastroenteritis. *Clin Infect Dis* 2010;50(06):882–889
- Liu L, Oza S, Hogan D, et al. Global, regional, and national causes of under-5 mortality in 2000–15: an updated systematic analysis with implications for the Sustainable Development Goals. *Lancet* 2016;388(10063):3027–3035
- Tapalski D, Hendriksen RS, Hasman H, Ahrens P, Aarestrup FM. Molecular characterisation of multidrug-resistant *Salmonella enterica* serovar Typhimurium isolates from Gomel region, Belarus. *Clin Microbiol Infect* 2007;13(10):1030–1033
- Aviv G, Rahav G, Gal-Mor O. Horizontal transfer of the *Salmonella enterica* Serovar *Infantis* resistance and virulence plasmid pESI to the gut microbiota of warm-blooded hosts. *MBio* 2016;7(05):e01395–e01416
- Almeida F, Pitondo-Silva A, Oliveira MA, Falcão JP. Molecular epidemiology and virulence markers of *Salmonella* *Infantis* isolated over 25 years in São Paulo State, Brazil. *Infect Genet Evol* 2013;19:145–151
- Cartelle Gestal M, Zurita J, Paz Y, Mino A, Ortega-Paredes D, Alcocer I. Characterization of a small outbreak of *Salmonella enterica* serovar *Infantis* that harbour CTX-M-65 in Ecuador. *Braz J Infect Dis* 2016;20(04):406–407
- Hendriksen RS, Vieira AR, Karlsmose S, et al. Global monitoring of *Salmonella* Serovar distribution from the world health organization global foodborne infections network country data bank: results of quality assured laboratories from 2001 to 2007. *Foodborne Pathog Dis* 2011;8(08):887–900
- Gonzales Escalante E. Incremento de aislamientos de *Salmonella* spp. productora de β-lactamasas de espectro extendido en pacientes pediátricos del Instituto Nacional de Salud del Niño. *Rev Peru Med Exp Salud Publica* 2015;32(03):605–607
- Del Pozo L, Silva N, Valencia A, et al. Estudio de un brote intrahospitalario por *Salmonella* Typhimurium productora de beta-lactamasa de espectro extendido SHV-5. *An Fac Med Lima* 2006;67(04):318–326
- World Health Organization (WHO) Drug-resistant *Salmonella*. 2005 Fact sheet No 139. Available at: <http://www.who.int/mediacentre/factsheets/fs139/en/>
- Tipper DJ, Strominger JL. Mechanism of action of penicillins: a proposal based on their structural similarity to acyl-D-alanyl-D-alanine. *Proc Natl Acad Sci U S A* 1965;54(04):1133–1141
- Cantón R, González-Alba JM, Galán JC. CTX-M enzymes: origin and diffusion. *Front Microbiol* 2012;3:110
- Mikoleit M. Biochemical identification of *Salmonella* and *Shigella* using an abbreviated panel of tests. WHO Global Foodborne Infections Network. (Protocol Number: 2010GFNLAB001) Enteric Diseases Laboratory Branch Centers for Disease Control and Prevention Atlanta, GA USA; 2015
- Pusterla N, Byrne BA, Hodzic E, Mapes S, Jang SS, Magdesian KG. Use of quantitative real-time PCR for the detection of *Salmonella* spp. in fecal samples from horses at a veterinary teaching hospital. *Vet J* 2010;186(02):252–255
- Clinical and Laboratory Standards Institute (CLSI) Performance Standards for Antimicrobial Susceptibility Testing; Twenty-seven Informational Supplement. 2017 CLSI Document M100-S27Wayne PA: Clinical and Laboratory Standards Institute. Available at: <http://file.qums.ac.ir/repository/mmrc/clsi%202017.pdf>
- Bauer AW, Kirby WM, Sherris JC, Turck M. Antibiotic susceptibility testing by a standardized single disk method. *Am J Clin Pathol* 1966;45(04):493–496
- Jarlier V, Nicolas MH, Fournier G, Philippon A. Extended broad-spectrum β-lactamases conferring transferable resistance to newer β-lactam agents in Enterobacteriaceae: hospital prevalence and susceptibility patterns. *Rev Infect Dis* 1988;10(04):867–878
- Belaouaj A, Lapoumeroulie C, Caniça MM, et al. Nucleotide sequences of the genes coding for the TEM-like β-lactamases IRT-1 and IRT-2 (formerly called TRI-1 and TRI-2). *FEMS Microbiol* 1994;120(1–2):75–80
- Pitout JD, Thomson KS, Hanson ND, Ehrhardt AF, Moland ES, Sanders CC. β-Lactamases responsible for resistance to expanded-spectrum cephalosporins in *Klebsiella pneumoniae*, *Escherichia coli*, and *Proteus mirabilis* isolates recovered in South Africa. *Antimicrob Agents Chemother* 1998;42(06):1350–1354
- Batchelor M, Hopkins KL, Threlfall EJ, et al. Characterization of AmpC-mediated resistance in clinical *Salmonella* isolates recovered from humans during the period 1992 to 2003 in England and Wales. *J Clin Microbiol* 2005;43(05):2261–2265
- Jouini A, Vinué L, Slama KB, et al. Characterization of CTX-M and SHV extended-spectrum beta-lactamases and associated resistance genes in *Escherichia coli* strains of food samples in Tunisia. *J Antimicrob Chemother* 2007;60(05):1137–1141
- Palma N, Pons MJ, Gomes C, et al. Resistance to quinolones, cephalosporins and macrolides in *Escherichia coli* causing bacteraemia in Peruvian children. *J Glob Antimicrob Resist* 2017; 11:28–33
- Vila J, Marcos MA, Jimenez de Anta MT. A comparative study of different PCR-based DNA fingerprinting techniques for typing of the *Acinetobacter calcoaceticus*-*A. baumannii* complex. *J Med Microbiol* 1996;44(06):482–489
- Zamudio ML, Meza A, Bailón H, Martínez-Urtaza J, Campos J. Experiencias en la vigilancia epidemiológica de agentes patógenos transmitidos por alimentos a través de electroforesis en campo pulsado (PFGE) en el Perú. *Rev Peru Med Exp Salud Publica* 2011;28(01):128–135
- Miller T, Prager R, Rabsch W, Fehlhaber K, Voss M. Epidemiological relationship between *Salmonella* *Infantis* isolates of human and broiler origin. *Lohmann Inf* 2010;45(02):27–31

- 26 Di Conza JA, Mollerach ME, Gutkind GO, Ayala JA. Dos aislamientos de *Salmonella infantis* multirresistentes se comportan como hipoinvasivos pero con elevada proliferación intracelular. *Rev Argent Microbiol* 2012;44(02):69–74
- 27 Merino L, Ruiz J, Alonso J, Via J. Resistencia antimicrobiana y epidemiología molecular en cepas de *Salmonella enterica* serovar Enteritidis aisladas en las provincias de Chaco y Corrientes (Argentina). *Comunicaciones científicas y tecnológicas. Universidad Nacional del Nordeste Resumen*; 2005:M-020
- 28 Hohmann EL. Nontyphoidal salmonellosis. *Clin Infect Dis* 2001;32(02):263–269
- 29 Silva C, Betancor L, García C, et al; Salmolber CYTED Network. Characterization of *Salmonella enterica* isolates causing bacteremia in Lima, Peru, using multiple typing methods. *PLoS One* 2017;12(12):e0189946
- 30 García C. Resistencia antibiótica en el Perú y América Latina. *Acta Méd Peruana* 2012;29(02):99–103
- 31 Ruiz J. Mechanisms of resistance to quinolones: target alterations, decreased accumulation and DNA gyrase protection. *J Antimicrob Chemother* 2003;51(05):1109–1117
- 32 Ruiz J, Castro D, Goñi P, Santamaria JA, Borrego JJ, Vila J. Analysis of the mechanism of quinolone resistance in nalidixic acid-resistant clinical isolates of *Salmonella* serotype Typhimurium. *J Med Microbiol* 1997;46(07):623–628
- 33 Malorny B, Schroeter A, Guerra B, Helmuth R. Incidence of quinolone resistance in strains of *Salmonella* isolated from poultry, cattle and pigs in Germany between 1998 and 2001. *Vet Rec* 2003;153(21):643–648
- 34 Fàbrega A, Soto SM, Ballesté-Delpierre C, Fernández-Orth D, Jiménez de Anta MT, Vila J. Impact of quinolone-resistance acquisition on biofilm production and fitness in *Salmonella enterica*. *J Antimicrob Chemother* 2014;69(07):1815–1824
- 35 Le Hello S, Bekhit A, Granier SA, et al. The global establishment of a highly-fluoroquinolone resistant *Salmonella enterica* serotype Kentucky ST198 strain. *Front Microbiol* 2013;4:395
- 36 Rossolini GM, D'Andrea MM, Mugnaioli C. The spread of CTX-M-type extended-spectrum beta-lactamases. *Clin Microbiol Infect* 2008;14(Suppl 1):33–41
- 37 Pallecchi L, Malossi M, Mantella A, et al. Detection of CTX-M-type beta-lactamase genes in fecal *Escherichia coli* isolates from healthy children in Bolivia and Peru. *Antimicrob Agents Chemother* 2004;48(12):4556–4561
- 38 Pallecchi L, Bartoloni A, Fiorelli C, et al. Rapid dissemination and diversity of CTX-M extended-spectrum β -lactamase genes in commensal *Escherichia coli* isolates from healthy children from low-resource settings in Latin America. *Antimicrob Agents Chemother* 2007;51(08):2720–2725
- 39 Colquechagua Aliaga F, Sevilla Andrade C, Gonzales Escalante E. Enterobacterias productoras de betalactamasas de espectro extendido en muestras fecales en el Instituto Nacional de Salud del Niño, Perú. *Rev Peru Med Exp Salud Publica* 2015;32(01):26–32
- 40 Riccobono E, Di Pilato V, Di Maggio T, et al. Characterization of IncI1 sequence type 71 epidemic plasmid lineage responsible for the recent dissemination of CTX-M-65 extended-spectrum β -lactamase in the Bolivian Chaco region. *Antimicrob Agents Chemother* 2015;59(09):5340–5347