



### Keywords

Integron,  
*Shigella*,  
Costa Rica

Received: March 21, 2014

Revised: April 11, 2014

Accepted: April 12, 2014

## Class 1 integrase and genetic cassettes *bla<sub>oxa</sub>* and *bla<sub>tem</sub>* among multi-drug resistant *Shigella* isolates in Costa Rica

Kenia Barrantes<sup>\*</sup>, Luz Chacón, Melissa Solano, Rosario Achí

Nutrition and Infection Section, Instituto de Investigaciones en Salud (INISA), University of Costa Rica, San José, Costa Rica

### Email address

kenia.barrantes@ucr.ac.cr (K. Barrantes)

### Citation

Kenia Barrantes, Luz Chacón, Melissa Solano, Rosario Achí. Class 1 Integrase and Genetic Cassettes *bla<sub>oxa</sub>* and *bla<sub>tem</sub>* among Multi-Drug Resistant *Shigella* Isolates in Costa Rica. *International Journal of Biological Sciences and Applications*.

Vol. 1, No. 1, 2014, pp. 24-27

### Abstract

*Shigella* is an important enteropathogen and the major cause of dysentery and diarrheal disease around the world. There are no studies related to the molecular detection of integrons among *Shigella spp.* isolates in Costa Rica. Here we are reporting for the first time the presence of class 1 integrase (*intI-1*) and extended spectrum  $\beta$ -lactamases genetic cassettes, *bla<sub>oxa</sub>*, and *bla<sub>TEM</sub>* among multidrug resistant *Shigella* isolates in Costa Rica. The antibiotic resistance pattern and presence of integrase class 1 (*intI-1*) and genetic cassettes *bla<sub>oxa</sub>* and *bla<sub>TEM</sub>* were analyzed in 30 *Shigella* isolates (*S. flexneri* (83%) and *S. sonnei* (17%). Bacteria were collected at hospitals and clinics in Costa Rica and exclusively from stools of individuals with diarrhea, from Costa Rica. Twenty nine out of 30 isolates were resistant to at least, one antibiotic. Multidrug resistance was observed in 26 out of 30 isolates (87%), and found to carry integrase class 1 (93%), and genetic cassettes *bla<sub>oxa</sub>* (76%) and *bla<sub>TEM</sub>* (7%).

### 1. Introduction

*Shigella spp.* is a virulent bacterium and a major cause of dysentery throughout the world. This pathogen is associated with 5% to 15% of cases of diarrhea and 30% to 50% of cases of dysentery, particularly in developing countries (1).

In Costa Rica, *Shigella spp.* has been isolated from fecal, water and food samples (2-6). It is considered an endemic pathogen in Central American countries, causing severe diarrheal diseases that require hospitalization in young children (2).

The emergence of antibiotic resistance among the bacterial enteropathogens, such as *Shigella*, is considered a global problem that requires urgent actions (1).

Antimicrobial resistance is not a new phenomenon and it is considered as a major threat to effective treatment outcome (1,7).

Multidrug resistance is associated with mobile genetic elements including transmissible plasmids, transposons and insertion sequences (i.e. integrons). The importance of integrons in the acquisition of resistance genes, and therefore to emergence of multidrug resistant strains, was only recognized late the 1980's

decade (7,8). Mobile genetic elements may facilitate the dissemination of multidrug resistance genes among species and even genera (8,9).

Integrans are assembly platforms that incorporate genetic determinants or cassettes by site-specific recombination and convert them to functional genes (8,10).

They are composed of three key elements: a tyrosine-recombinase gene or integrase (*intI*), a recombination site (*attI*) and a promoter site ( $P_c$ ) (7,9, 10). All integrans analyzed today are composed by an *intI* gene encoding an integrase. This enzyme belongs to the tyrosine-recombinase family, which can recombine discrete units of circularized DNA known as genetic cassettes (8,10). The other integran component is the primary recombination site (*attI*). A wide variety of genetic cassettes that confers resistance to antibiotics, are found to insert this region (8). And the third important component is a strong promoter ( $P_c$ ,  $P_{ant}$ ) that directs transcription of the captured genes or genetic cassettes (11).

Recent studies have detected class 1 and class 2 integrans among multidrug-resistant *Shigella spp.* (12-14). However, there are no studies related to the molecular detection of integrans among *Shigella spp.* isolates in Costa Rica.

In this study, we report for the first time the presence of class 1 integrase and the extended spectrum  $\beta$ -lactamase genetic cassette, *bla<sub>OXA</sub>*, and *bla<sub>TEM</sub>* among multidrug resistant isolates in Costa Rica.

## 2. Methodology

Bacterial strains:

Thirty isolates were obtained from INISA bacterial collection. Bacteria were collected at hospitals and clinics in Costa Rica and exclusively from stools of individuals with diarrhea. All of the strains were *S. flexneri* (83%) and *S. sonnei* (17%).

Antibiotic susceptibility testing:

Antibiotic susceptibility testing was determined by disc diffusion assay, according to Clinical and Laboratory Standards Institute 2012 Guide (CLSI).

The isolates were tested for susceptibility to: amoxicillin (AML), ampicillin (AMP), ceftazidime (CAZ), cephalotin (KF), chloramphenicol (C), co-trimoxazole (SXT), gentamicin (CN), nalidixic acid (NA), tetracycline (TE) and norfloxacin (NOR).

DNA extraction and PCR analysis:

Preparation of the bacterial DNA samples and PCR conditions have been described previously (Barrantes et al. 2010).

Class 1 integrase (*intI1*), *bla<sub>OXA</sub>* and *bla<sub>TEM</sub>* genetic cassettes were detected by PCR. The sequences of *intI1* 899 bp product primer pair (fw 5'-ATGGCCGAGCAGATCCTGCACG -3' and rv 5'-GCCACTGCGCCGTTACCACCGC -3') (12), *bla<sub>OXA</sub>* 820 bp product primer pair (fw 5'-

ATGAAAAACACAATACATATCAACTTCGC-3' and rv 5'-GG GTGTGTTTAGAATGGTGATCGCATT -3'), *bla<sub>TEM</sub>* 859 bp product primer pair (fw 5'-ATGAGTATTCAACATTTCCG- 3' and rv 5'-ACCAATGCTTAATCAGTGAG- 3') (14), and amplification control 16S 585 bp product primer pair (fw 5'-GGGAGTAAAGTTAATACCTTTGCTC-3' and rv 5'-TTCCCGAAGGCACATTCT-3') were prepared by Invitrogen (USA).

The PCR products were detected by 2% agarose gel electrophoresis (140V, at 45 min) in 1X TBE Buffer at pH 8.3 and stained with GelRed (Biotium). Gen Ruler 50 bp DNA ladder ( Thermo Scientific) was used as DNA size marker. Strains E705 and EIEC were used as *intI-1* and *bla<sub>TEM</sub>* positive controls, respectively.

The products were visualized as 899 bp (*intI-1*), 820 bp (*bla<sub>OXA</sub>*), 859 (*bla<sub>TEM</sub>*) and 585 bp (*16S*) bands using an UVITEC transilluminator (Cambridge, UK).

DNA sequences of these products were determined (310 ABI Genetic Analyzer, Applied Biosystems) to confirm amplification of the correct genes.

Statistical analysis:

Statistical calculations were performed with SPSS software v. 17.0 (SPSS, Chicago, IL. USA). Student T-Test was used for statistical comparisons.

## 3. Results and Conclusions

Twenty nine out of 30 isolates were resistant to at least, one antibiotic. Multidrug resistance was observed in 26 out of 30 isolates (87%) (Table 1).

Most of the isolates were resistant to  $\beta$ -lactamic antibiotics, amoxicillin (24/30, 80%) and ampicillin (23/30, 77%), followed by tetracycline (22/30, 73%), cotrimoxazole (19/30, 63%), chloramphenicol (13/30, 43%), cephalotin (9/30, 30%) and gentamicin (2/30, 7%). No resistant phenotypes to ceftazidime, nalidixic acid and norfloxacin were observed.

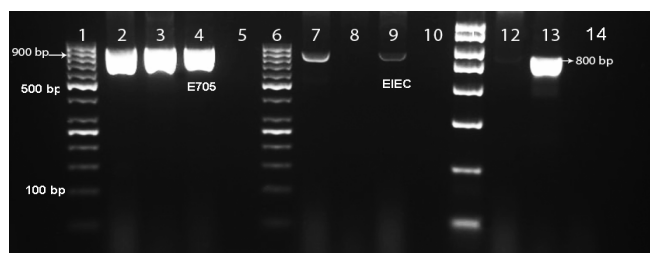
It is well recognized that *Shigella* have progressively become resistant to most of the widely used antibiotics, resulting in treatment failure and increased mortality (7).

Ampicillin and trimethoprim-sulfamethoxazole have been recommended for treating shigellosis, but according to this study, the observed resistance profile of almost all *Shigella* isolates confirmed the recommendation that these antibiotics are considered ineffective for empirical therapy (7, 15).

Multidrug resistance dissemination in Gram negative pathogens by mobile elements such as integrans and gene cassettes is a well known and frequently reported phenomenon (8,11-15). Those resistance determinants are frequently carry within R plasmids, transposons and genomic islands, which facilitate the dissemination of resistance genes among bacteria (7). Horizontal transfer of these resistance determinants is possible between species in *Shigella* and also in other enteropathogens (10, 11).

In this study, Class I integrase (*intl-1*) was detected in 28 (93%) isolates and extended spectrum  $\beta$ -lactamases, *bla<sub>OXA</sub>*, in 23 (76%) and *bla<sub>TEM</sub>* in one isolate (7%). (Figure 1).

Presence of *intl-1* correlates with the zone inhibition diameter in amoxicillin and ampicillin (Table 2). *Shigella* isolates which were positive for *intl-1*, showed shorter diameters comparing to *intl-1* negative isolates ( $p < 0.05$ ). This situation was also observed for *bla<sub>OXA</sub>* positive and negative isolates and the antibiotics chloramphenicol, cotrimaxole and tetracycline ( $p < 0.05$ ).



**Figure 1.** PCR results of *intl-1*, *bla<sub>OXA</sub>* and *bla<sub>TEM</sub>* detection in *Shigella* isolates: Lane 1: molecular marker; lane 2: INISA-02; lane 3: INISA-07; lane 4: E705(*intl-1* positive control); lane 5: negative control; PCR *bla<sub>TEM</sub>* lane 6: molecular marker; lane 7: INISA-02; lane 8: INISA-07; lane 9: EIEC(*bla<sub>TEM</sub>* positive control); lane 10: negative control; PCR *bla<sub>OXA</sub>* lane 11: molecular marker; lane 12: INISA-02; lane 13: INISA-07; lane 14: negative control.

On the other hand, *intl-1* and genetic cassettes *bla<sub>OXA</sub>* and *bla<sub>TEM</sub>* were not detected in one *Shigella* isolate susceptible to antibiotics.

In *S. flexneri* and *S. dysenteriae*, resistance to some antibiotics, such as ampicillin, streptomycin and/or trimethoprim is mostly associated with the presence of class 1 integrons, meanwhile, class 2 integrons are detected more frequently in *S. sonnei* and *S. boydii* (8,11).

**Table 1.** Antibiotic resistant phenotype and number of resistant isolates of *Shigella* spp.

Phenotype	Number of isolates
SXT	2
TE	1
SXT-TE	2
AML-KF	1
AML-AMP-TE	1
AML-AMP-KF	1
AML-AMP-SXT	1
AML-AMP-KF-SXT	2
AML-AMP-SXT-TE	1
AML-AMP-C-TE	6
AML-AMP-KF-SXT-TE	3
AML-AMP-C-SXT-TE	6
AML-AMP-KF-SXT-CN-TE	1
AML-AMP-C-KF-SXT-CN-TE	1
Total	29

AML=amoxicillin; AMP=ampicillin; C=chloramphenicol; CN=gentamicin; KF=cephalotin; SXT=co-trimaxole; TE=tetracycline

In Latin America, classes 1 and 2 integrons has been detected more frequently in *S. flexneri*, resistant to trimethoprim, sulfamethoxazole, streptomycin, ampicillin, chloramphenicol and tetracyclin (8, 13, 14). Class 2

integrons were mainly tested in *S. sonnei* strains in earlier reports. This observation is consistent with results of class 1 and class 2 integrases detection mainly in *S. flexneri* isolates in this study (data not shown).

**Table 2.** Antibiotic zone diameter (ZD) means (disk diffusion method) and presence of *intl-1* and *bla<sub>OXA</sub>* in *Shigella* spp isolates.

Antibiotic*	<i>intl-1</i>		<i>bla<sub>OXA</sub></i>	
	Positive isolates ZD mean (SD)	Negative isolates ZD mean (SD)	Positive isolates ZD mean (SD)	Negative isolates ZD mean (SD)
AML	6.4(9.7)**	23.5(2.1)**	6.0(10.2)	12.4(9.7)
AMP	6.6(8.5)**	22.0(0.0)**	6.5(9.2)	11.3(8.5)
CAZ	29.7(3.0)	34.0(5.6)	29.6(2.9)	31.6(4.1)
KF	19.0(3.7)	21.0(2.1)	19.5(3.2)	18.7(4.9)
C	19.0(13.1)	37.0(7.0)	16.2(12.7)**	33.6(5.1)**
CN	20.0(3.2)	21.0(6.3)	20.4(3.2)	22.6(3.7)
SXT	10.1(14.1)	31.0(11.3)	7.8(12.2)**	23.6(16.8)**
TE	6.7(11.0)	13.0(18.3)	4.2(9.6)**	16.7(11.6)**
NA	26.6(2.3)	32.0(9.9)	26.3(2.3)	29.0(4.9)
NOR	32.3(4.4)	36.0(8.5)	31.9(3.9)	34.9(6.3)

\* AML= amoxicillin; AMP=ampicillin; CAZ=ceftazidime; KF=cephalotin; C=chloramphenicol; CN= gentamicin; SXT= cotrimaxole; TE= tetracycline; NA= nalidixic acid; NOR= norfloxacin.

\*\*  $p < 0.05$

Gene cassettes that encoded resistance to  $\beta$ -lactamic antibiotics are more related to integrons class 1, and they are detected in the bacterial chromosome and plasmids (8). The *bla<sub>OXA</sub>* gene has often been identified in ampicillin resistant enterobacterial strains such as isolates of *Escherichia coli*, *Shigella flexneri*, and *Salmonella* spp. This gene encoded for a class D  $\beta$ -lactamase, is also known as oxacillinase or OXA type  $\beta$ -lactamase (11). Antimicrobial susceptibility of *Shigella* strains is related to general use of antimicrobials in population. This study provided evidence that in Costa Rica,  $\beta$ -lactams antibiotics such as ampicillin, amoxicillin and cephalotin are not effective against shigellosis and it seems that this is the situation worldwide (16). Also, tetracycline, cotrimaxole (trimetoprim-sulphametoxazole), chloramphenicol and gentamicin showed important resistance rates among *Shigella* isolates. Nevertheless, third generation cephalosporin (i.e. ceftazidime) and quinolons, such as nalidixic acid and norfloxacin, could be considered still helpful tools in the management of shigellosis, at least, in Costa Rica.

We are reporting for the first time the presence of class 1 integrase and extended spectrum  $\beta$ -lactamase genetic cassettes, *bla<sub>OXA</sub>* and *bla<sub>TEM</sub>* among multidrug resistant *Shigella* spp. isolates in Costa Rica. The importance of integrons in the acquisition of resistance genes, and therefore the emergence of multidrug resistant strains, is a major public health problem. Information about epidemiology and molecular mechanisms of multidrug resistance determinants in *Shigella* spp. and other enteropathogens is important to develop intervention strategies. Regional and local antimicrobial resistance

pattern in *Shigella* should be considered as a part of control strategies. (7)

## Acknowledgments

We are grateful to Dra. Daniela Centrón, from University of Buenos Aires, Argentina, for providing PCR positive controls

This study was supported by Consejo Nacional para Investigaciones Científicas y Tecnológicas-Costa Rica (CONICIT-MICITT), Vicerrectoría de Investigación, Universidad de Costa Rica and FUNDEVI 1210 Project.

## References

- [1] World Health Organization. 2001. Global strategy for containment of Antimicrobial Resistance. Available: [http://whqlibdoc.who.int/hq/2001/WHO\\_CDS\\_CSR\\_DRS2\\_001.1.pdf](http://whqlibdoc.who.int/hq/2001/WHO_CDS_CSR_DRS2_001.1.pdf). Accessed 01 November 2012.
- [2] Achi, R.; Siles, X.; Mata, L.; Lindberg, A.A. (1996). Shigellae assays based on immunomagnetic separation in children from urban marginal communities of Costa Rica. *J. Infect.* 32, 211-218.
- [3] Barrantes, K.; Achi R.; Bolaños, S.; Cerdas, M.; Cortés, X. (2006). Calidad microbiológica y aislamiento de *Shigella flexneri* en vegetales frescos del Área Metropolitana de Costa Rica, 2001-2002. *Avances de Investigación en Seguridad Alimentaria y Nutricional (SAN)*. NCAP, ME/11. 42-48.
- [4] Barrantes, K; McCoy C; Achi R. (2010). Detection of *Shigella* in lettuce by the use of a rapid molecular assay with increased sensitivity. *Braz. J. Microbiol.* 41(4), 993-1000.
- [5] Barrantes, K.; Veko, P.; Achi, R. (2004). Brote de diarrea asociado a *Shigella sonnei* debido a contaminación hídrica. San José, Costa Rica, 2001. *Rev. Costarric. Cienc. Méd.* 25, 15-22.
- [6] Valiente, C.; Mora, D. (2005). Estudio bacteriológico del agua asociado a brotes de diarrea en Costa Rica, 1999-2005. *Rev. Colegio Microb. Quim. Clin. Costa Rica.* 11(suppl), 11-14.
- [7] Niyogi S.K. (2005). Shigellosis. *J Microbiol.* 43(2), 133-143.
- [8] Ke X.; Gu B.; Pan S; Tong M. (2011). Epidemiology and molecular mechanism of integron-mediated antibiotic resistance in *Shigella*. *Arch Microbiol.* 193, 767-774.
- [9] Stokes, HW; Gillings MR. (2011). Gene flow, mobile genetic elements and the recruitment of antibiotic resistance genes into Gram-negative pathogens. *FEMS Microbiol. Rev.* 35, 790-819.
- [10] Mazel, D. (2006). Integrons: agents of bacterial evolution. *Nature.* 4, 608-620.
- [11] Poirel L.; Naas T.; Nordmann P. (2010). Diversity, Epidemiology, and Genetics of Class D (beta)-Lactamases. *Antimicrob. Agents Chemother.* 54(1), 24-38.
- [12] Frank T.; Gautier V.; Talarmin A.; Bercion R.; Arlet G.(2007). Characterization of sulphonamide resistance genes and Class 1 integron gene cassettes in Enterobacteriaceae, Central African Republic (CAR). *Antimicrob. Agents. Chemother.* 59,742-745.
- [13] Muñoz J.; Bello H.; Domínguez M.; Mella S.; Zemelman R.;González G. (2003). Integrones y cassettes genéticos de resistencia a antimicrobianos en cepas de *Shigella flexneri*. *Rev. Med.Chile.* 131-137.
- [14] Peirano G.; Agerso Y.; Aarestrup F.M.;dos Prazeres Rodríguez D. (2005). Ocurrance of integrons and resistance genes among sulphonamide-resistant *Shigella* spp. from Brazil. *J. Antimicrob. Chem.* 55, 301-305.
- [15] Chang CY; Lu PL; Lin CC; Lee TM; Tsai MY and Chang L.(2011). Integron types, gene cassettes, antimicrobial resistance genes and plasmids of *Shigella sonnei* isolates from outbreaks and sporadic cases in Taiwan. *J. Med. Microbiol.* 60, 197-204.
- [16] DuPont. Chapter 57: Antimicrobial resistance of *Shigella* spp, typhoid *Salmonella* and nontyphoid *Salmonella*. In: D.L. Mayer (ed).Antimicrobial Drug Resistance. Humana Press, as part of Springer Science + Business Media. LLc 2009.825:831.