




Plasmid-Mediated Antibiotic Resistance and Class 1 Integron in *Salmonella* Heidelberg Isolated from Poultry Farms in Santander - Colombia

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■ Keywords

Antibiotic resistance, integrons, *Salmonella*, poultry.



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ABSTRACT

Salmonella enterica is a zoonotic pathogen transmitted to humans by the consumption of contaminated poultry products. *Salmonella* causes around 93 million cases of gastroenteritis and 155,000 deaths worldwide. A high number of multidrug-resistant *Salmonella* isolates has been found from different segments of poultry production, and it is often associated with horizontal antibiotic resistance gene transfer through mobile elements such as plasmids, integrons, and transposons. The emergence of antibiotic-resistant *Salmonella* has been associated with the misuse of antibiotics in animal production and it is classified as a highly important pathogen from public health due to its zoonotic character and its high dissemination ability. This study aimed to determine the antibiotic resistance associated with plasmids, and class 1 and 2 integrons from *Salmonella* Heidelberg isolates from healthy chickens in poultry farms from Santander, Colombia. 15 *Salmonella* Heidelberg isolates obtained from cloacal samples, were evaluated through endpoint PCR to determine the presence of plasmid-encoded resistance genes, and class 1 and 2 integrons. The *bla*_{CMY2}, *strA* and *strB*, *sul1* and *sul2*, and *tetB* genes were found in all 15 *Salmonella* Heidelberg. The class 1 integron was present in 11 out of 15 isolates, harbored the gene cassette *dfra7*. The results indicate the presence of a high number of antibiotic resistance genes associated with plasmids and class 1 integrons in *Salmonella* Heidelberg strains isolated from poultry farms, resulting in a public health concern, both in humans and poultry production in Colombia.

INTRODUCTION

Salmonella enterica is a zoonotic pathogen, considered as one of the main causes of foodborne disease, associated with the consumption of poultry products (Donado-Godoy *et al.*, 2012; McMillan *et al.*, 2019). In humans, the infectious dose is generally 10⁶ to 10⁸ organisms and the disease manifestations include acute abdominal pain, diarrhea, and fever (Cosby *et al.*, 2015; Antunes *et al.*, 2016). The indiscriminate use of antibiotics in animal production as prophylactic or as growth promoters has participated in the selection of multidrug-resistant strains, hindering treatment in humans (Barreto *et al.*, 2016; Zhu *et al.*, 2017).

The antibiotic resistance can be shared between bacteria of different or same genus by horizontal gene transfer via mobile genetic elements such as integrons associated to transposons and plasmids (Zhou *et al.*, 2018). Plasmids are extra-chromosomal DNA containing an origin of replication and genes that can be transferred by conjugation, transformation, and transduction into a new bacterial host (Smillie *et al.*, 2010). In *Salmonella*, plasmids that carry quinolone and beta-



lactam resistance genes have been reported (Chen *et al.*, 2010). Integrons are composed by an integrase gene (*intI*), the attachment site (*attI*), and the promoter (*Pant*) are classified based on the variation in the amino acid sequence of integrase, some of the most common classes in the clinical context are *intI1* that is classified as class 1 integron, followed by *intI2* as class 2 integron, and *intI3* as class 3 integron (Carattoli, 2001; Severino & Magalhães, 2004; Gillings, 2014).

The present study aims to characterize the genotypic resistance associated to plasmids in *Salmonella* Heidelberg strains, and characterize class 1 and 2 integrons from the strains isolated from broiler farms of Santander, Colombia.

MATERIALS AND METHODS

Sample collection

15 isolates were obtained from 8 poultry farms with a capacity of 70,000 broilers, located in the region of Santander, Colombia (Table 1). Samples were taken by cloacal swabbing from healthy Ross 308 broiler chickens on the 35th day of production. All strains were processed according to the international guidelines ISO 6579-1 (ISO, 2017) and identified as *Salmonella* Heidelberg by microbiological, serological, and molecular methods.

Table 1 – Distribution of 15 *S. Heidelberg* isolates from healthy broiler chickens in 8 farms in Santander, Colombia.

Farm number	Number of isolates
Farm 1	1
Farm 2	1
Farm 3	2
Farm 4	5
Farm 5	3
Farm 6	3
Farm 7	None
Farm 8	None

Resistance genes in plasmids

The DNA was extracted from fresh colonies using the Easy-DNA kit (Invitrogen, USA) and stored at -20°C until its use. Bacterial DNA was used as a template in a PCR reaction to determine the presence of resistance genes for antibiotics, using specific primer sets (Table 2). A total volume of 25 µL was prepared for each sample containing 1 µL of the DNA template, 1 µL of each primer (forward and reverse) (Invitrogen, USA), 1 µL of Taq DNA polymerase (Invitrogen, USA), 2.5 µL of dNTPs (Invitrogen, USA) and buffer, 2 µL of MgCl₂ and 14 µL of nuclease-free water for PCR. The PCR was run in a T100 thermal cycler (BIO-RAD, USA) with

an initial denaturation step of 3 minutes at 95°C, followed by 35 cycles as follows: 30 seconds at 95°C for denaturation, 30 seconds at 55°C for annealing, 30 seconds at 72°C for extension and a final extension step of 7 minutes at 72°C. Amplification products were revealed by horizontal electrophoresis on 2% agarose gel stained with GelGreen® (Biotium, Russia) using the PowerPac HC (BIO-RAD, USA). The gel was visualized and documented using the gel documentation system ENDURO GDS (Labnet International, USA).

Class 1 and 2 integrons

Genomic DNA (gDNA) was extracted from bacterial colonies using the Invisorb® Spin Universal Kit (Stratec, Berlin, Germany). PCR was performed for amplification of the gene cassettes inserted in the variable regions of class 1 using primers Forward (5'-GGCATCCAAGCAGCAAG-3') and Reverse (5'-AAGCAGACTTGACCTGA-3') (Levesque *et al.*, 1995) and class 2 integrons using primers Forward (5'-CGGGATCCCGGACGGCATGCACGATTTGTA-3') and Reverse (5'-GATGCCATCGCAAGTACGAG-3') (White *et al.*, 2001). PCR conditions were the same as described above and the annealing at 55°C. The PCR products were sequenced by the Sanger method (Macrogen Inc., Korea). The DNA sequences were assembled using the software Geneious version 8 (Kearse *et al.*, 2012) and analyzed using the online software BLASTN of the National Center for Biotechnology Information.

RESULTS

Antibiotic resistance genes in plasmids

Resistance genes such as *bla*_{CMY2} (ceftriaxone) (n=15/15; 100%), *strA* and *strB* (streptomycin) (n=15/15; 100%), *sul1* and *sul2* (sulfamethoxazole) (n=15/15; 100%), *tetB* (tetracycline) (n=15/15; 100%) were detected in *S. Heidelberg* isolates (Table 3). Low prevalence was determined for *bla*_{PSE-1} (n=6/15; 40%) related with ampicillin resistance. In contrast, none of the isolates were positive to *qnrA*, *bla*_{TEM}, *bla*_{CTX-M}, *catA*, *catB*, *cmlA*, *aadA1*, *aadA2*, *aadB*, *oqxA*, *sul3*, *tetA*, *dfrA1*, *dfrA10*, and *dfrA12* genes.

Class 1 and 2 integrons

11 out of 15 strains showed the class 1 integron with a cassette structure size of 741 bp (Figure 1). None of the strains showed class 2 integron. Resistance gene mapping showed 100% of identity in all 11 sequences with the *dfrA7* gene of *Escherichia coli* (accession number MF465028.1) and 99.8% identity with the



Table 2 – Primer sequences used to detect resistance genes in *S. Heidelberg* isolates*.

Antibiotic	Gene	Primer sequence	Annealing temperature (°C)	Amplicon size (bp)
Ampicillin	<i>bla_{PSE-1}</i>	F-GCAAGTAGGGCAGGCAATCA R-GAGCTAGATAGATGCTCACAA	55	422
	<i>bla_{TEM}</i>	F-ATCAGTTGGGTGCACGAGTG R-ACGCTCACCGGCTCCAGA	55	608
Chloramphenicol	<i>catA</i>	F-CCAGACCGTTCAGCTGGATA R-CATCAGCACCTTGTCGCCT	55	454
	<i>catB</i>	F-CGGATTACAGCCTGACCACC R-ATACGCGGTACACCTTCTG	55	461
	<i>cmIA</i>	F-TGGACCGCTATCGGACCG R-CGCAAGACACTGGGCTGC	55	641
Gentamicin	<i>aadB</i>	F-CTAGCTGCGGACAGATGAGC R-CTCAGCCGCCTCTGGGCA	55	300
Spectinomycin	<i>aadA1</i>	F-CTCCGCAGTGGATGGCGG R-GATCTGCGCGGAGGCCA	55	631
	<i>aadA2</i>	F-CATTGAGCGCCATCTGGAAT R-ACATTTGCTCATCGCCGGC	55	500
Tetracycline	<i>tetA</i>	F-GCTGTGGATCGTTTCGG R-CATTCCGAGCATGAGTGCC	55	658
	<i>tetB</i>	F-CTGTGCGGCATCGGTCAT R-CAGGTAAGCGATCCACC	55	615
Piperacillin/tazobactam	<i>dfrA1</i>	F-CAATGGCTGTTGTTGGAC R-CCGGCTCGATGTCTATTGT	55	254
	<i>dfrA10</i>	F-TCAAGGCAAATTACCTTGGC R-ATCTATTGGATCACCTACCC	55	432
	<i>dfrA12</i>	F-TTCGCAGACTCACTGAGGG R-CGGTTGAGACAAGCTCGAAT	55	330
Streptomycin	<i>strA</i>	F-TGGCAGGAGGAACAGGAGG R-AGGTCGATCAGACCCGTGC	55	405
	<i>strB</i>	F-GCGGACACTTTTCCAGCCT R-TCCGCCATCTGTGCAATGCC	55	621
Ceftriaxone	<i>bla_{CMY2}</i>	F-AAATCGTTATGCTGCGCTCT R-CCGATCCTAGCTCAAACAGC	55	224
	<i>bla_{CTX-M}</i>	F-TTCGCTAAATACCGCCATTC R-TATCGTTGGTTGTGCCGTAA	55	236
Trimethoprim/sulfamethoxazole	<i>sul1</i>	F-CGGACGCGAGGCCTGTATC R-GGGTGC GGACGTAGTCAGC	55	591
	<i>sul2</i>	F-GCGCAGGCGCGTAAGCTGAT R-CGAAGCGCAGCCGCAATTC	55	514
	<i>sul3</i>	F-GGGAGCCGCTTCCAGTAAT R-TCCGTGACTGCAATCATT	55	500
Quinolones and fluoroquinolones	<i>oqxA</i>	F-GGTGAAGTCGATCAGTCAGT R-ATCTATCGTGAACAGCACCT	55	154
Nalidixic acid	<i>qnrA</i>	F-CCGCTTTTATCAGTGTGACT R-ACTCTATGCCAAGCAGTTG	55	188

*Based in Chuanchuen & Padungtod (2009).

cassette containing the *dfrA7* gene of *Salmonella* Typhi (accession number AY245101.1) (Figure 2). The *dfrA7* gene codes for a Dihydrofolate reductase that confers resistance to trimethoprim.

DISCUSSION

In recent years, the role of antimicrobial resistance in livestock has been suggested as a potential source of bacterial infections and antibiotic resistance, representing a risk at the clinical level with great challenges for clinical treatment (Berg *et al.*, 2017; Ewers *et al.*, 2012).

The antibiotic resistance genotypes as *bla_{CMY2}* have been found in poultry farms in Brazil (Biffi *et al.*, 2014) and in Colombia, where 168 isolates from different poultry production levels (farms, slaughter, and retail) were positive to *bla_{CMY2}* gene (Castellanos *et al.*, 2018). The presence of Extended Spectrum β -lactamase (ESBL) codified by *bla_{CMY2}* and other genes from this group reduce the effectiveness of antibiotics such as ceftriaxone, ceftazidime, and cefotaxime by the hydrolyzing of the β -lactam ring preventing the union with the penicillin-binding protein (PBP) (De Souza *et al.*, 2019; Kong *et al.*, 2010).



Table 3 – Genotypic profiles of resistance in *S. Heidelberg* isolates associated with plasmids and class I and II integrons.

Isolate code	Antimicrobial resistance profile in plasmid DNA	Class 1 integron*	Class 2 integron
1	<i>bla</i> _{CMY2} <i>strA</i> , <i>strB</i> , <i>sul1</i> , <i>sul2</i> , <i>tetB</i>	-	-
2	<i>bla</i> _{CMY2} <i>bla</i> _{PSE-1} <i>strA</i> , <i>strB</i> , <i>sul1</i> , <i>sul2</i> , <i>tetB</i>	+	-
3	<i>bla</i> _{CMY2} <i>bla</i> _{PSE-1} <i>strA</i> , <i>strB</i> , <i>sul1</i> , <i>sul2</i> , <i>tetB</i>	+	-
4	<i>bla</i> _{CMY2} <i>bla</i> _{PSE-1} <i>strA</i> , <i>strB</i> , <i>sul1</i> , <i>sul2</i> , <i>tetB</i>	+	-
5	<i>bla</i> _{CMY2} <i>bla</i> _{PSE-1} <i>strA</i> , <i>strB</i> , <i>sul1</i> , <i>sul2</i> , <i>tetB</i>	-	-
6	<i>bla</i> _{CMY2} <i>bla</i> _{PSE-1} <i>strA</i> , <i>strB</i> , <i>sul1</i> , <i>sul2</i> , <i>tetB</i>	+	-
7	<i>bla</i> _{CMY2} <i>strA</i> , <i>strB</i> , <i>sul1</i> , <i>sul2</i> , <i>tetB</i>	-	-
8	<i>bla</i> _{CMY2} <i>bla</i> _{PSE-1} <i>strA</i> , <i>strB</i> , <i>sul1</i> , <i>sul2</i> , <i>tetB</i>	+	-
9	<i>bla</i> _{CMY2} <i>strA</i> , <i>strB</i> , <i>sul1</i> , <i>sul2</i> , <i>tetB</i>	+	-
10	<i>bla</i> _{CMY2} <i>strA</i> , <i>strB</i> , <i>sul1</i> , <i>sul2</i> , <i>tetB</i>	+	-
11	<i>bla</i> _{CMY2} <i>strA</i> , <i>strB</i> , <i>sul1</i> , <i>sul2</i> , <i>tetB</i>	+	-
12	<i>bla</i> _{CMY2} <i>strA</i> , <i>strB</i> , <i>sul1</i> , <i>sul2</i> , <i>tetB</i>	+	-
13	<i>bla</i> _{CMY2} <i>strA</i> , <i>strB</i> , <i>sul1</i> , <i>sul2</i> , <i>tetB</i>	+	-
14	<i>bla</i> _{CMY2} <i>strA</i> , <i>strB</i> , <i>sul1</i> , <i>sul2</i> , <i>tetB</i>	+	-
15	<i>bla</i> _{CMY2} <i>strA</i> , <i>strB</i> , <i>sul1</i> , <i>sul2</i> , <i>tetB</i>	-	-

*+: presence of the mobile element.

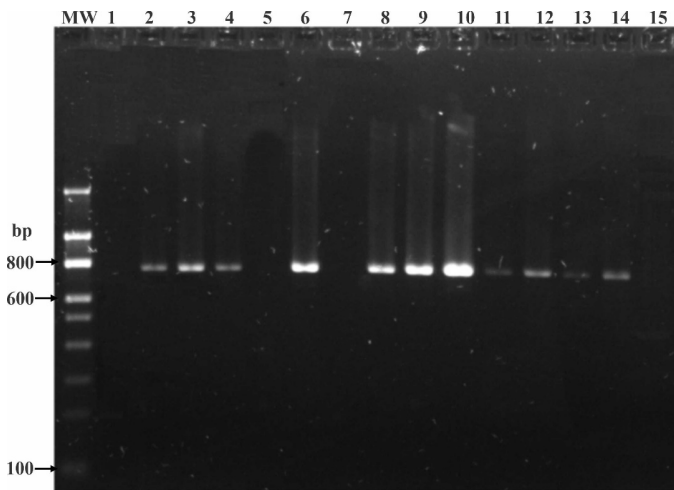


Figure 1 – PCR product of the variable region of class 1 integron from *Salmonella* Heidelberg strains. MW: 100 bp DNA ladder (Corpogen, Colombia).

The *strA* and *strB* genes confer resistance to streptomycin by encoding a phosphotransferase that catalyzes the ATP-dependent phosphorylation of hydroxyl groups in streptomycin (Ashenafi *et al.*, 2014). The presence of these genes was also found in isolates of *S. Typhimurium* from poultry farms from Pakistan (20.5% and 41.1%) (Wajid *et al.*, 2019) and poultry carcasses in Iran, with values of 37.6% and 22.4%, respectively (Doosti *et al.*, 2016). In the case of *sul1*, it is normally found in the conserved region of class 1 integrons, while *sul2* is located on small plasmids such as IncQ family (RSF1010) and pBP1 and both encode a variant of sulfonamide resistant dihydropteroate synthase protein that has no affinity with the antibiotic (Van Treeck *et al.*, 1981; Sköld, 2000; Chen *et al.*, 2015; Deng *et al.*, 2015). These genes were found in poultry farms from Egypt with values of 97.3% and 5.3%, respectively (Abdel-Maksoud *et al.*, 2015) and

sul2 gene in isolates from chickens sold at retail in Colombia (57.4%) (Cortés *et al.*, 2017). The *tetB* gene was found in broiler chickens from Portugal (45.4%) (De Souza *et al.*, 2019) and in chicken carcasses retailed in Colombia (42.5%) (Cortés *et al.*, 2017). This gene codes for a tetracycline resistance protein, which promotes the elimination of tetracycline from the inside of cells by an energy-dependent efflux pump (Grossman, 2016).

Castro *et al.* (2019) reported the phenotypic resistance of these strains, and all 15 isolates showed resistance to nalidixic acid, ciprofloxacin, levofloxacin, cefotaxime, ceftazidime, cefazolin and ceftriaxone, ampicillin, ampicillin/sulbactam, streptomycin, and tetracyclines as well as high resistance to trimethoprim/sulfamethoxazole (n=14/15; 93%), aztreonam and cefepime (n=7/15; 46%). In our study, phenotypic resistance to trimethoprim/sulfamethoxazole may be mediated mainly by the *sul1* and *sul2* genes and by the *dfrA7* gene found in class 1 integron. In addition, the presence of non-endemic serotypes in Colombia, such as *S. Heidelberg* has been supported by a high number of resistance genes as well as class 1 integrons in the first part of the poultry production segment causing a major public health impact.

Class 1 integrons are adapted to capture, integrate, and express around 130 different gene cassettes that encoding proteins with resistance to cationic surfactants and main antibiotic families such as quaternary ammonium-compound family, erythromycin, aminoglycosides, sulfonamides, quinolones, chloramphenicol, fosfomicin, trimethoprim, and β -lactamases (Stokes & Hall, 1989; Partridge *et al.*, 2009; Cambray *et al.*, 2010; Kung *et al.*, 2010). This



allows the appearance of multi-drug resistance (MDR) strains in different bacteria species (Firoozeh *et al.*, 2012). In addition, other pathogenic bacteria such as nosocomial methicillin-resistant *Staphylococcus aureus* (MRSA) 42.5% (n=76/179), *Escherichia coli* 31% (n=340/1098), *Aeromonas* spp. 39.02% (n=16/41), *Stenotrophomonas maltophilia* 22% (n=20/93), *Salmonella* spp. 42% (n=77/183), and *Shigella* spp. 3.85% (n=1/26) have reported class 1 integrons (Ahmed *et al.*, 2006; Chang *et al.*, 2004; Odetoyin *et al.*, 2017; Pérez-Valdespino *et al.*, 2009; S. Rao *et al.*, 2020; Xu *et al.*, 2011).

isolates from humans, food products, and pork 13% (n=154/1183) (Antunes *et al.*, 2006). In addition, in Brazilian strains isolated from broiler chicken and pork, 45% (n=9/20) had the class 1 integron, lower than the values obtained in this study (Ribeiro *et al.*, 2011). In our study, only class 1 integron was found, which is a common finding in *Salmonella* and other members of *Enterobacteriaceae*, contributing to the dissemination of gene cassettes (White *et al.*, 2001; Rao *et al.*, 2006).

The class 1 integron from the present study contains a cassette with the *dfrA7* gene that confers resistance to trimethoprim by the expression of a modified dihydrofolate reductase enzyme that catalyzes the reduction of dihydrofolic acid to tetrahydrofolate, which is necessary for the synthesis of purines and pyrimidines (Brolund *et al.*, 2010; Joyner *et al.*, 1984). The importance of this finding is because antibiotic treatment is based on the use of trimethoprim/sulfamethoxazole, fluoroquinolones, and oximinocephalosporins, even in children, elderly, and immunocompromised people (Guerrant *et al.*, 2001; Mthembu *et al.*, 2019). In agreement with authors such Argüello *et al.* (2018), *dfrA7* gene is one of the classic genes carried by class 1 integrons and this was first reported by Wain *et al.* (2003) in isolates from Vietnam in 1994. Additionally, the gene has been found in isolates from livestock production in South Africa (Mthembu *et al.*, 2019), isolates of *Salmonella* Heidelberg from poultry in Colombia (Donado-Godoy *et al.*, 2015), and in class 1 integrons from *S. Typhi* isolates from clinical patients in Pakistan (Afzal *et al.*, 2013).

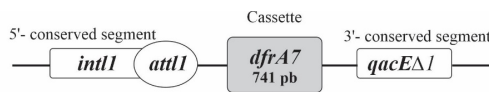
In conclusion, this study found a high presence of resistance genes associated with commonly used antibiotics in both human and animal medicine, as well as class 1 integron with the gene cassette *dfrA7* in *Salmonella* Heidelberg strains isolated from farms in Santander that belong to the first part of the Colombian poultry segment.

COMPETING OF INTERESTS

The authors declare no competing of interest.

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AGCGCGTTACGCCGTGGGGTCGATGTTGATGTTATGGAGCAGCAACGATGTTACGCAGCAGGGCAGTC
GCCCTAAAACAAAGTTAGCCATTACGGGGGTTGAATGAAAATTTTCATTGATTTCTGCAACGTCAGAA
AATGGCGTAATCGGTAATGGCCCTGATATCCATGGTCAGCAAAAAGGTGAGCAGTTACTITTTAAAGC
GTCACATATAATCAGTGGCTCCTGTTGGAAGGAAAACATTTGACTCTATGGGTGTTCTTCCAAATCG
AAAATATGCAGTAGTGTGCGAGGAAAGGAATTTCAAGCTCAAATGAAAATGTAATTAGTCTTTCCTCAA
TAGAAATCGCTTGAAGAATATCGAAAATTACAGATCAITTTATATGCTCTCGTGGCGGTCAAATCT
ACAATAGTCTTATTGAAAAGCAGATATAATTCATTTGCTACTGTTACAGTTGAGGTTGAAGGTGATA
TCAATTTTCTAAAATTCAGAGAATTTCAATTTGGTTTTTGAGCAGTTTTTTTTGCTCAATATAAATTA
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TTTTAAGTCGCGGTTTTATGGTTTTGCTGCGCAAAAGTATTCCATAAAAACCAACATTAATAAACTGCC
CTGAACCTCGCGTTAGATGCACTAAGCACATAATTGCTCACAGCCAAACTATCAG
    
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Figure 2 – Graphical representation of the class 1 integron found in *Salmonella* Heidelberg strains isolated from broiler farms located in Santander. *intI1*: integrase class 1; *attI1*: recombination and integration site; *dfrA7*: Dihydrofolate reductase gene; *qacEΔ1*: quaternary ammonium resistance gene.

In the case of *Salmonella*, class 1 integron has been reported from different sources in the food chain. In animal farms from China class 1 integron was identified in chicken, ducks, and pigs that carried resistance genes cassettes against β -lactams and aminoglycosides (Zhao *et al.*, 2017). Other sources have presented *Salmonella* as in broiler samples (n=20/26; 76.9%), poultry (n=4/5; 80%), human (n=1/2; 50%) and calves (n=5/5; 100%) in Egypt (Abdel Aziz *et al.*, 2018; Elkenany *et al.*, 2018). In addition, *Salmonella* strains were isolated from dead-in-shell chicken embryos (n=24/86; 27.9%), raw chicken meat (n=1/7; 14.2%), beef meat (n=1/8; 12.5%), and seafood (n=3/40; 7.5%) (Deekshit *et al.*, 2012; Moawad *et al.*, 2017; Zhao *et al.*, 2021).

In Colombia, few data on molecular resistance to antibiotics in different segments of the poultry chain is available and to date, this is the first report of class 1 integrons characterized in poultry production in Colombia. In this study, 73.33% (n=11/15) of *S. Heidelberg* isolates contained class 1 integron which is higher than reported in *S. Typhi* from human isolates 30% (n=24/80) (Afzal *et al.*, 2013), in *Salmonella* spp. isolates from lettuce samples 40% (n=40/100) in Burkina Faso (Somda *et al.*, 2018), and



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