

Class 1 Integrons in *Salmonella* Strains Causing Traveler's Diarrhea

Traveler's diarrhea (TD) is a frequent health problem among travelers abroad. Diarrheagenic *Escherichia coli*, *Shigella* spp., *Salmonella* spp., and *Campylobacter* spp. are among the most common causes of TD (3, 5). The antimicrobial resistance in *Salmonella* strains is an increasing problem (15). Genetic elements, such as plasmids, transposons, and integrons, carrying resistant genes have previously been reported for this microorganism (13, 14, 15). We previously studied the evolution of antimicrobial resistance and the mechanisms of resistance to several antimicrobial agents in *Salmonella* isolates causing TD and found different genes encoding resistant determinants (3). The aim of the present study was to determine the presence of class 1 integrons and identify the resistance genes located therein in different serotypes of TD-causing, resistant *Salmonella* strains obtained in the previous study.

Sixteen *Salmonella* strains that were isolated from the stool samples of patients with TD were analyzed (1) using the Kirby-Bauer method and chosen for their resistance to at least one of the following tested antimicrobial agents: ampicillin, amoxicillin-clavulanic acid, nalidixic acid, tetracycline, trimethoprim-sulfamethoxazole, chloramphenicol, gentamicin, ciprofloxacin, amikacin, imipenem, norfloxacin, and ceftazidime. The results were interpreted according to the Clinical and Laboratory Standards Institute (formerly NCCLS) guidelines (9). The strains belonged to the following *Salmonella enterica* serotypes: Enteritidis (seven strains), Typhimurium (two strains), Virchow (one strain), Haifa (one strain), Goldcoast (one strain), Risseu (one strain), Paratyphi A (one strain), Kiambu (one strain), and Hadar (one strain).

The presence of class 1 integrons was determined by PCR amplification (7, 16). The sequences obtained were compared to those in GenBank to identify the genes.

Class 1 integrons were present in 4/16 (25%) of the resistant strains analyzed (Table 1; Fig. 1). Three of the four strains presented one integron, whereas the fourth showed two integrons, with the integron sizes ranging from 1,050 to 1,700 bp. All integrons were sequenced to detect the gene cassettes located inside. The resistance genes located in the integrons encoded enzymes that were associated with resistance to aminoglycosides, β -lactams, trimethoprim, and chloramphenicol (Table 1). The prevalence of integrons among the *Salmonella* strains causing TD de-

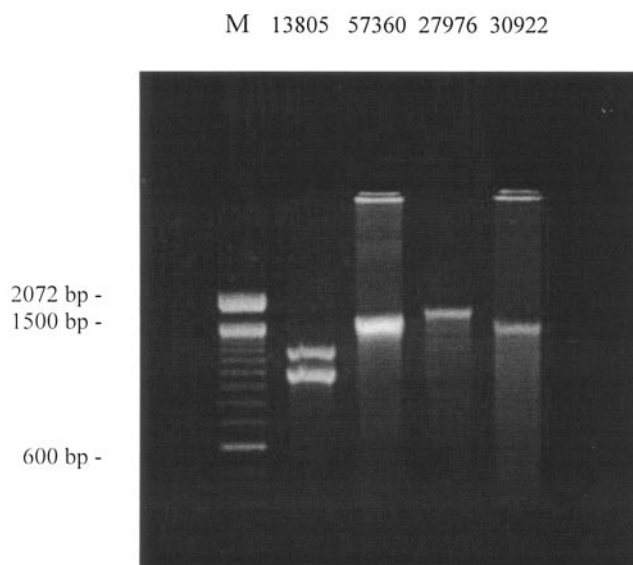


FIG. 1. Class 1 integrons of *Salmonella*-resistant strains. The designation numbers of the strains are reported above each lane. Lane M, the molecular weight marker.

scribed herein is similar to that described in other reports analyzing *Salmonella* strains not causing TD. Class 1 integrons were found in 20, 20, and 17% of the *Salmonella* strains that were isolated in Spain, the United Kingdom, and China (6, 12, 17), respectively. In these studies, serotype Virchow carried an integron containing the *aadA1a* and *dfrA1* genes and serotype Haifa carried an integron with the *tetA* gene (6, 12), which were different from those found in our study. We have not found any report in the scientific literature concerning the presence of integrons in *Salmonella* serotype Goldcoast. Moreover, the type of resistance genes that were found in the class 1 integrons agrees with previous studies that were undertaken with resistant *Shigella* strains causing TD (11). Serotype Kiambu had two integrons containing

TABLE 1. Characteristics of *Salmonella* strains with class 1 integrons

Strain	Serotype	Origin	Resistance ^a (MIC [μ g/ml])	Integron size (bp)	Resistance genes by type and location							
					Inside class 1 integrons				Outside class 1 integrons			
					Chl	Amp	Amg ^b	Sxt	Chl	Amp	Tet	Sxt
13805	Kiambu	Mali	Tet (64), Amp (\geq 256), Chl (\geq 256)	1,050/1,300 ^c		<i>carb-2</i>	<i>aadA2</i>			<i>floR</i>	<i>tem</i>	<i>tetG</i>
27976	Goldcoast	Senegal	Tet (128), Amp (\geq 256), Chl (32), Sxt (\geq 32)	1,700			<i>aadA5</i>	<i>dfrA17</i>		<i>tem</i>	<i>tetA</i>	
30922	Virchow	India	Nal (\geq 256), Sxt (\geq 32)	1,500	<i>catB3</i>		<i>aadB</i>					<i>dfrA14</i>
57360	Haifa	Egypt	Nal (\geq 256), Tet (\geq 256)	1,500			<i>aadA7</i> , <i>aac(3)I^d</i>			<i>tetA</i>		

^a Tet, tetracycline; Amp, ampicillin; Chl, chloramphenicol; Sxt, trimethoprim-sulfamethoxazole.

^b Amg, aminoglycosides.

^c The *carb-2* and *aadA2* genes are located in the integrons with sizes of 1,050 and 1,300 bp, respectively.

^d The *aadA7* and *aac(3)I* genes are located in the same integron.

the *aadA2* and *carb-2* genes, respectively, which have also been described in different serotypes of *Salmonella*, such as Typhimurium, Agona, Paratyphi B, and Albany. These two integrons have been located in a genomic resistance island (SGI1) (2, 4, 8), suggesting that our strain also carries this genomic island. The range in the geographic origins of our strains containing integrons demonstrates the wide dissemination of these genetic elements. Nowadays, widespread international travel has facilitated the dissemination of multiresistant pathogenic strains throughout the world, and this has become a great public health problem (10). In addition, if resistance is associated with genes that are located in genetic elements such as plasmids, transposons, or integrons, they can be transferred and disseminated to the local bacterial population.

This study was funded by grant FIS02/0353 from the Spanish Ministry of Health and by grant 2002 SGR 05/00444 from the Department d'Universitats, Recerca i Societat de la Informació de la Generalitat de Catalunya, Spain. R.C. has a fellowship from Fundació Carolina and BBVA, Spain, and J.R. has a fellowship from RICET.

We are grateful for the collaboration of the Institute Carlos III, Madrid, Spain.

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