Letter to the Editor

Plasmid-mediated quinolone resistance by genes *qnrA1* and *qnrB19* in *Salmonella* strains isolated in Brazil

Rafaela Ferrari[1], Antonio Galiana[2], Rosa Cremades[2], Juan Carlos Rodríguez[2], Marciane Magnani[1], Maria Cristina B. Tognim[3], Tereza C.R.M. Oliveira[1], Gloria Royo[2]

[1]*Centro de Ciências Agrárias, Departamento de Ciência e Tecnologia de Alimentos, Universidade Estadual de Londrina, Londrina, Paraná, Brazil*
[2]*Servicio de Microbiología. Hospital General Universitario de Elche, Universidad Miguel Hernández. Camí de l'almàssera, 11, 03203 Elche, Spain*
[3]*Centro de Ciências da Saúde, Departamento de Análises Clínicas, Universidade Estadual de Maringá, Paraná, Brazil*

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Resistance to fluoroquinolones (FQs) is relatively uncommon in *Salmonella* spp. when compared to other genera of the *Enterobacteriaceae*. However, the number of clinical isolates with reduced susceptibility to FQs has increased in recent years [1]. These isolates with reduced susceptibility to FQs are linked to chromosomal mutations and other mechanisms, such as efflux pump, change in permeability of the membrane, or plasmid-mediated quinolone resistance (PMQR) [2].

To date, at least four types of PMQR genes are known, including the *qnr* genes (*A, B, C, D, S, VC*), the *aac(6')-Ib-cr* gene, *oqxAB* gene, and the *qepA* gene [2,3]. Quinolones are used in poultry production, and poultry products are frequently related to salmonellosis outbreaks in Brazil. Nonetheless, it was unknown whether PMQR determinants were present in *Salmonella* strains isolated in outbreaks. The aim of this study was to investigate the presence of PMQR by *qnr* and *aac(6')-Ib* genes in 126 *Salmonella enterica* strains isolated from poultry origin (n = 12), from patients (n = 46), and foods (n = 68) related to outbreaks that occurred between 1999 and 2007 in Parana state, Brazil.

The strains were obtained from the Central Laboratory of Parana (LACEN) Curitiba, Parana State, Brazil, and the serotyping and phagotyping were conducted at the Foundation Oswaldo Cruz (FIOCRUZ), Rio de Janeiro State, Brazil. The resistance to nalidixic acid (NAL) by disk diffusion tests, and minimum inhibitory concentration (MIC) by broth dilution for ciprofloxacin (CipMIC), were previously evaluated according to CLSI guidelines [4].

A total of 112 (88.8%) isolates were resistant to nalidixic acid, and 29 (23.01%) showed reduced susceptibility to ciprofloxacin (MIC 0.125µg/ml or 0.5µg/ml) [1]. All the isolates were screened by PCR for PMQR determinants *qnr* (*qnrA, qnrB1, qnrB5, qnrB19, qnrS1, qnrC*, *qnrD* alleles and *aac*(*6')-Ib-cr* gene) as described previously [5,6]. The PCR products positive for *qnr* were sequenced and compared with the NCBI sequences.

The *qnrA1* gene was detected in one epidemic strain of *S.* Enteritidis with CipMIC 0.062 ug/ml (GenBank accession number GU731067). The *qnrB19* gene was detected in *S.* Corvallis of poultry origin with CipMIC of 0.5 ug/ml (GenBank accession number GU731069) (Table 1). There are several reports of *qnr* genes detection in *Salmonella* strains susceptible to or with reduced susceptibility to ciprofloxacin [2,5]. In Brazil, despite previous detection of *qnrA1*, *qnrB2*, *qnrB8*, *qnrVC1*, *qnrVC2* genes in other bacterial species, as described by Minarini *et al*. [7], this is the first report of the *qnr* gene in *Salmonella*, and also the first detection of the *qnrB19* gene in this country.

Table 1. Distribution of *Salmonella* strains analyzed in the present study according serovar, resistance to nalidixic acid (NAL), minimum inhibitory concentration to ciprofloxacin (CipMIC) and presence of genes *qnr*.

Serovar	Number of strains	NAL[a]	CipMIC[b] range (mg/L)	Gene
Enteritidis	13	S	0.078 - 0.625	-
	100	R	0.625 - 0.5	*qnrA1*
Johannesburg	1	S	0.0625	-
	3	R	0.0625	-
Typhimurium	1	S	0.078	-
	2	R	0.125	-
Heidelberg	2	R	0.0625 - 0.75	-
Infantis	1	R	0.078	-
Newport	1	R	0.0625	-
Corvallis	1	R	0.5	*qnrB19*
Bredeney	1	R	0.125	-
Total	**126**			**2**

Nalidixic acid[a] (NAL); minimum inhibitory concentration (MIC) for Ciprofloxacin (Cip)[b]

The *qnrB19* gene was recently detected in the Netherlands by Garcia-Fernandez *et al*. [8] in two strains of *S.* Typhimurium with reduced susceptibility to ciprofloxacin. Similarly, Dionisi *et al*. [9] detected, in Italy, a *qnrB19* in *S.* Typhimurium with reduced susceptibility to ciprofloxacin. The *S*. Corvallis with a *qnrB19* gene isolated in this study also had reduced susceptibility to ciprofloxacin. These results are significant because, as described in previous studies, the presence of PMQR genes may facilitate the development of mutations in the *gyrA* QRDR region, as well as increase the resistance to FQs and, consequently, reduce their clinical use [2,3].

Salmonellosis is one of the major foodborne illnesses in Brazil, and antibiotic therapy is required for treatment of systemic infections and/or for immunocompromised patients. The detection of *qnr* genes in *Salmonella* spp., and the identification in Brazil of the *qnrB19* variant in a strain of poultry origin, alert for the control of quinolone use that is essential to avoid pressure for mutant selection of resistant strains and clinical limitation use of FQs. It is necessary to monitor and minimize the spread of such resistance determinants among these bacteria.

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Corresponding author

Rafaela Gomes Ferrari
Centro de Ciências Agrárias
Departamento de Ciência e Tecnologia de Alimentos
Universidade Estadual de Londrina
Londrina, Paraná, Brazil
Av. Celso Garcia Cid s/n
Phone: 55 43 33714080
Fax: 55 43 33714080
Email: rafaelaferrari@yahoo.com.br

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