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Short Communication

Antimicrobial resistance genotypes and phenotypes of *Campylobacter coli* isolated from different sources over a 16-year period in Brazil

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ABSTRACT

Objectives: This study aimed to identify antimicrobial resistance genotypes in 63 *Campylobacter coli* strains isolated from humans (12), animals (21), the environment (20), and food (10) in Brazil using whole genome sequencing (WGS) tools, comparing them with results obtained by antimicrobial susceptibility testing (AST) against some important antimicrobials in clinical use.

Methods: Phenotypic resistance profiles were determined by minimal inhibitory concentrations and the disk diffusion technique. The prediction of the resistance genes was performed using ABRicate v.0.8 and the Resistance Gene Identifier software of the CARD.

Results: The percentage of *C. coli* strains phenotypically resistant to antimicrobials were: ampicillin, 44.4%; doxycycline, 20.6%; tetracycline, 20.6%; ciprofloxacin, 12.7%; nalidixic acid, 12.7%; streptomycin, 6.3%; erythromycin, 4.8%; and gentamicin, 1.6%. The genes $bla_{OXA-605}$ / bla_{OXA-61}, *tet*(O), *cme*B, *aadE*-Cc, *aph* (3 ') – IIIa, *sat*4 and *aad*9 were detected in 54%, 22.2%, 9.5%,6.3%, 1.6%, 1.6%, and 1.6% strains, respectively. Mutations T86I in the QRDR region of *gyr*A were detected in 8 (12.7%) strains. The agreement between AST and WGS was 100%, 92.9%, 82.4%, and 80% for quinolones, tetracycline, β-lactam, and aminoglycoside classes, respectively.

Conclusions: The rates of *C. coli* strains resistant to β- lactams and quinolones may represent a public health concern. The partial agreement between AST and WGS shows that improvement in antibiotic resistance databases may be required to minimize this discrepancy observed in some antimicrobial classes and to become an acceptable tool to both clinical microbiologists and regulatory agencies.

1. Introduction

One of the biggest public health challenges of our time is antimicrobial resistance (AMR). According to the Centers for Disease Control and Prevention, at least 2.8 million people in the US acquire an antibiotic-resistant infection each year, from which more than 35 000 people die [1]. High rates of resistance have enhanced the morbidity and economic burden associated with infections. Therefore, accurate detection of AMR is necessary to guide treatment decisions and thereby improve the management of infections in both the clinic and community [2].

Culture-based antimicrobial susceptibility testing (AST) has been the most commonly employed method by the majority of clinical laboratories [2]. However, traditional methods of AST are time consuming and laborious. In this context, whole genome sequencing (WGS) technology has become an important tool for public health surveillance and tracking of microorganisms by being able to define resistance genotypes and predict resistance phenotypes in several bacterial species [3].

Campylobacter Spp., especially *Campylobacter jejuni* and *Campylobacter coli*, have been reported as one of the most frequent causes of acute gastroenteritis in humans worldwide [4]. The disease caused by these species is usually self-limiting and typically

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does not require antimicrobial therapy. However, prompt antimicrobial treatment is recommended in severe and prolonged cases of enteritis or extra-intestinal infections. In these cases, fluoroquinolones, tetracyclines, macrolides, and selected β-lactams are the drugs of choice. Alternatively, aminoglycosides have been used in cases of systemic infections caused by multiresistant strains [5].

Regarding AMR in *Campylobacter*, the percentage of strains resistant to fluoroquinolones or macrolides has increased considerably in recent years [1]. AMR trends have shown that the increased antibiotic resistance of *Campylobacter* strains isolated from humans is related to use of antimicrobial agents in animal production as a growth promoter and for the treatment of diseases [3].

In light of the importance of monitoring antimicrobial resistance in *Campylobacter,* this study aimed to identify AMR genotypes in *C. coli* strains isolated from humans, animals, the environment, and food in Brazil using WGS tools, comparing findings with results obtained by AST testing of some important antimicrobials in clinical use.

2. Material and Methods

2.1. Bacterial strains

In a previous study [6] the whole genomes of 63 *C. coli* strains isolated in Brazil from human faeces (12 strains), animals (21 strains), the environment (20 strains), and food (10 strains) were sequenced between 1995–2011, and their accession numbers reported. Table 1 lists the year, sources, and states of origin of the 63 *C. coli* strains studied.

2.2. AMR prediction

The prediction of the resistance genes present in the *C. coli* strains studied was performed using ABRicate v.0.8 (available at https://github.com/tseemann/abricate/), which performs a mass screening for antimicrobial resistance genes in assemblies submitted based on multiple databases: ResFinder, National Center for Biotechnology Information (NCBI), Antibiotic Resistance Gene-ANNOTation (ARG-ANNOT), Comprehensive Antibiotic Resistance Database (CARD) and MEGARes [7–11]. In addition, the assemblies were also analysed using the Resistance Gene Identifier software of the Comprehensive Antibiotic Resistance Database (CARD) database [10].

2.3. Antimicrobial susceptibility testing

Minimal inhibitory concentrations (MICs) were determined for the 63 *C. coli* strains listed in Table 1, of which 39 strains (highlighted with asterisks) were studied in previous work by our research group [12] using E-test® (bioMérieux, Marcy-l'Étoile, France) as recommended by the Clinical Laboratory and Standards Institute (CLSI) M45Ed3 for the antimicrobials ciprofloxacin, doxycycline, tetracycline, and erythromycin [13].

Furthermore, the phenotypic resistance of the 63 strains bearing AMR genes identified by WGS analyses was also determined by the disk diffusion technique for the antimicrobials ampicillin (10µg), azithromycin (15µg), streptomycin (10 µg), gentamicin (10 µg), and nalidixic acid (30 µg) provided by Oxoid (Hampshire, United Kingdom). The antimicrobials were selected according to the predicted genotypic resistance profiles of the strains studied, and as the CLSI does not recommend these antimicrobials for *Campylobacter,* we used the protocol for *Enterobacterales* [14].

The *C. coli* strains were grown as described by Gomes et al. [12]. After antimicrobial application, the plates were incubated at 42°C under microaerophilic atmosphere for 24 h and then screened. The *C. jejuni* strain ATCC 33291 was included as quality control for antimicrobial susceptibility experiments.

2.4. Statistical analysis

The results of AST and AMR prediction were expressed as percentages of strains that were susceptible or resistant, respectively. The statistical significance of the agreement between AMR phenotype and genotype was calculated by the χ^2 test, which analyses the association between two categorical variables, using GraphPad Prism 5 (GraphPad Software, San Diego, CA). We considered *P* values ≤ 0.05 to be significant.

3. Results

3.1. AMR Prediction

According to the ABRicate v. 0.8 software, the $bla_{\text{OXA-605}}$, OXA-61 family class D β-lactamase, was found in 34 (54%) of the *C. coli* strains studied. The *tet*(O) gene related to tetracycline resistance was detected in 14 (22.2%) strains, and the *aadE*-Cc, *aph* (3') - IIIa, *sat*4, *aad*9 genes that confer resistance to aminoglycosides were detected in 4 (6.3%), 1 (1.6%), 1 (1.6%), and 1 (1.6%) strain, respectively (Table 1).

In predictions performed by the Resistance Gene Identifier software, the $bla_{\text{OXA-61}}$ gene was detected in 34 (54%) of the *C. coli* strains studied. The *tet*(O) was detected in 14 (22.2%) strains, and the *cme*B gene that encodes an antimicrobial efflux pump was detected in six (9.5%) strains. The *aph* (3′) - IIIa, *sat*4 genes were detected in 1 (1.6%) strain, and mutations in the QRDR region of *gyr*A, which is related to fluoroquinolone resistance, were detected in 8 (12.7%) strains. Seventeen (27%) strains did not show any antimicrobial resistance genes or mutations associated with resistance (Table 1).

3.2. Antimicrobial susceptibility testing

The MICs and disk diffusion results are demonstrated in Table S1, and the phenotypic AMR patterns of the 63 *C. coli* strains are presented in Table 1. Forty-three (68.3%) strains were phenotypically resistant to at least one of the antimicrobials tested. The number of *C. coli* strains resistant to ampicillin, doxycycline, tetracycline, ciprofloxacin, nalidixic acid, streptomycin, erythromycin, and gentamicin was 28 (44.4%), 13 (20.6%), 13 (20.6%), 8 (12.7%), 8 (12.7%), 4 (6.3%), 3 (4.8%), and 1 (1.6%), respectively (Table 1 and Table S1). Of note, three strains isolated from animals [2] and the environment [1] were considered multidrug resistant because they were phenotypically resistant to three different antimicrobial agents class (Table 1).

3.3. Agreement between AMR phenotype and genotype

The phenotypic and genotypic resistance profiles did not match with 100% concordance for the 63 *C. coli* strains studied (Table 2). Thirty-four of the 63 strains studied carried the $bla_{\text{OXA-605}}$ / $bla_{\text{OXA-61}}$ gene. However, only 28 strains were phenotypically resistant to β-lactam antibiotics, which represents agreement of 82.4%. Thirteen of 14 strains were phenotypically resistant to tetracycline and carried the *tet*(O) gene, showing agreement of 92.9%. All ciprofloxacin-resistant strains in the AST had a *gyr*A T86I point mutation, with 100% agreement among the strains. Four out of 5 strains that were AST aminoglycoside resistant carried the genes related to this resistance showing 80% agreement. Macrolide resistance was phenotypically present in three strains; however, no genotypic resistance was found. No statistical significance in agreement between AMR phenotype and genotype was observed (Table 2).

Table 1
Phenotypic and genotypic resistance profiles of the 63 *Campylobacter coli* strains studied.

Strains	Year	Source	State	Phenotypic Resistance Profile	Antimicrobial Resistance Genes		Mutations QRDR *gyrA*	Antimicrobial class
					ABRicate v. 0.8	RGI	RGI	
CCAMP 771[a]	1995	Sewage	RJ	Amp	*bla*$_{OXA-605}$	*bla*$_{OXA-61}$	ND	Beta-lactam
CCAMP 773[a]	1995	Sewage	RJ	Amp	*bla*$_{OXA-605}$	*bla*$_{OXA-61}$	ND	Beta-lactam
CCAMP 820[a]	1995	Monkey	RJ	ND	*bla*$_{OXA-605}$	*bla*$_{OXA-61}$	ND	Beta-lactam
CCAMP 821	1995	Monkey	RJ	Amp	*bla*$_{OXA-605}$	*bla*$_{OXA-61}$	ND	Beta-lactam
CCAMP 840	1995	Sewage	RJ	ND	ND	ND	ND	
CCAMP 625	1996	Monkey	RJ	ND	*bla*$_{OXA-605}$	*bla*$_{OXA-61}$, *cme*B	ND	Beta-lactam, efflux pump membrane transporter
CCAMP 761[a]	1996	Sewage	RJ	Amp, Ery,	*bla*$_{OXA-605}$	*bla*$_{OXA-61}$	ND	Beta-lactam
CCAMP 764	1996	Sewage	RJ	Amp	*bla*$_{OXA-605}$	*bla*$_{OXA-61}$	ND	Beta-lactam
CCAMP 765	1996	Sewage	RJ	Amp	*bla*$_{OXA-605}$	*bla*$_{OXA-61}$	ND	Beta-lactam
CCAMP 767[a]	1996	Sewage	RJ	ND	ND	ND	ND	
CCAMP 768[a]	1996	Monkey	RJ	ND	*bla*$_{OXA-605}$	*bla*$_{OXA-61}$, *cmeB*	ND	Beta-lactam, efflux pump membrane transporter
CCAMP 774	1996	Sewage	RJ	Amp	*bla*$_{OXA-605}$	*bla*$_{OXA-61}$	ND	Beta-lactam
CCAMP 787	1996	Sewage	RJ	Amp	*bla*$_{OXA-605}$	*bla*$_{OXA-61}$	ND	Beta-lactam
CCAMP 819[a]	1996	Sewage	RJ	Amp	*bla*$_{OXA-605}$	*bla*$_{OXA-61}$	ND	Beta-lactam
CCAMP 825	1996	Monkey	RJ	Amp	*bla*$_{OXA-605}$	*bla*$_{OXA-61}$	ND	Beta-lactam
CCAMP 775	1997	Sewage	RJ	ND	ND	ND	ND	
CCAMP 791[a]	1997	Monkey	RJ	Amp	*bla*$_{OXA-605}$	*bla*$_{OXA-61}$	ND	Beta-lactam
CCAMP 818[a]	1997	Sewage	RJ	Amp, Dox, S, Tet,	*bla*$_{OXA-605}$, *tet*(O), *aad*E-Cc	*bla*$_{OXA-61}$, *tet*(O)	ND	Beta-lactam, tetracycline, aminoglycoside
CCAMP 490[a]	1998	Human	RJ	Amp	*bla*$_{OXA-605}$	*bla*$_{OXA-61}$	ND	Beta-lactam
CCAMP 494[a]	1998	Human	RJ	Amp	*bla*$_{OXA-605}$, *aad*E-Cc	*bla*$_{OXA-61}$	ND	Beta-lactam, aminoglycoside
CCAMP 495[a]	1998	Human	RJ	Amp, Cip, Na	*bla*$_{OXA-605}$	*bla*$_{OXA-61}$	T86I	Beta-lactam, quinolones
CCAMP 841	1998	Monkey	RJ	ND	ND	ND	ND	
CCAMP 498[a]	1999	Human	RJ	Cip, Na	*bla*$_{OXA-605}$	*bla*$_{OXA-61}$	T86I	Beta-lactam, quinolones
CCAMP 502	1999	Human	RJ	Cip, Na, S	*tet*(O), *aad*E-Cc	*tet*(O)	T86I	Tetracycline, aminoglycoside, quinolones
CCAMP 975[a]	1999	Monkey	RJ	ND	ND	ND	ND	
CCAMP 988	1999	Monkey	RJ	Amp	*bla*$_{OXA-605}$	*bla*$_{OXA-61}$	ND	Beta-lactam
CCAMP 503[a]	2000	Human	RJ	ND	ND	ND	ND	
CCAMP 726	2000	Monkey	RJ	Amp	*bla*$_{OXA-605}$	*bla*$_{OXA-61}$	ND	Beta-lactam
CCAMP 834	2000	Water	RJ	Dox,Tet,	*tet*(O)	*tet*(O)	ND	Tetracycline
CCAMP 595[a]	2001	Human	RJ	Amp, Cip, Na	*bla*$_{OXA-605}$	*bla*$_{OXA-61}$	T86I	Beta-lactam, quinolones
Cc 01[a]	2002	Human	SP	Dox, Tet	*bla*$_{OXA-605}$	*bla*$_{OXA-61}$	ND	Beta-lactam
CCAMP 667	2002	Monkey	RJ	Amp, Cip, Gen, Na	*bla*$_{OXA-605}$, *aph(3')-IIIa, sat*4, *aad*9	*bla*$_{OXA-61}$, *aph(3')-IIIa, sat*4	T86I	Beta-lactam, aminoglycoside, quinolones
Cc 03[a]	2003	Human	SP	Dox, Ery, Tet	*tet*(O)	*tet*(O)	ND	Tetracycline
Cc 04[a]	2003	Human	SP	Amp	*bla*$_{OXA-605}$	*bla*$_{OXA-61}$	ND	Beta-lactam
Cc 05	2003	Human	SP	ND	*tet*(O)	*tet*(O)	ND	Tetracycline
Cc 10	2003	Human	SP	Amp	*bla*$_{OXA-605}$	*bla*$_{OXA-61}$	ND	Beta-lactam
CCAMP 73	2003	Monkey	RJ	Amp, Dox, Tet	*bla*$_{OXA-605}$, *tet*(O)	*bla*$_{OXA-61}$, *tet*(O)	ND	Beta-lactam, tetracycline
CCAMP 165[a]	2003	Monkey	RJ	Amp	*bla*$_{OXA-605}$	*bla*$_{OXA-61}$	ND	Beta-lactam
CCAMP 170	2003	Monkey	RJ	ND	ND	ND	ND	
CCAMP 182[a]	2003	Monkey	RJ	Amp	*bla*$_{OXA-605}$	*bla*$_{OXA-61}$	ND	Beta-lactam
CCAMP 394[a]	2004	Monkey	RJ	ND	*bla*$_{OXA-605}$	*bla*$_{OXA-61}$	ND	Beta-lactam
CCAMP 446[a]	2004	Monkey	RJ	Amp	*bla*$_{OXA-605}$	*bla*$_{OXA-61}$	ND	Beta-lactam
CCAMP 463[a]	2004	Potable Water	MG	Dox, Tet	*tet*(O)	*tet*(O)	ND	Tetracycline
CCAMP 464	2004	Potable Water	MG	Dox, Tet	*tet*(O)	*tet*(O), *cmeB*	ND	Tetracycline, efflux pump membrane transporter
CCAMP 465[a]	2004	Water	MG	Dox, Tet	*tet*(O)	*tet*(O)	ND	Tetracycline
CCAMP 466	2004	Potable Water	MG	Dox, Tet	*tet*(O)	*tet*(O)	ND	Tetracycline
CCAMP 467	2004	Water	MG	Dox, Tet	*tet*(O)	*tet*(O)	ND	Tetracycline
CCAMP 469[a]	2004	Potable Water	MG	Dox, Tet	*tet*(O)	*tet*(O), *cmeB*	ND	Tetracycline, efflux pump membrane transporter
CCAMP 769	2004	Sewage	MG	Amp	*bla*$_{OXA-605}$	*bla*$_{OXA-61}$	ND	Beta-lactam
CCAMP 392[a]	2007	Monkey	RJ	ND	ND	ND	ND	
CCAMP 1000[a]	2007	Monkey	RJ	Amp	*bla*$_{OXA-605}$	*bla*$_{OXA-61}$, *cmeB*	ND	Beta-lactam, efflux pump membrane transporter
CCAMP 1010[a]	2007	Monkey	RJ	Cip, Dox, Na, S, Tet	*tet*(O), *aad*E-Cc	*tet*(O)	T86I	Tetracycline, aminoglycoside, quinolones
CCAMP 1117	2009	Monkey	RJ	ND	ND	ND	ND	
CCAMP 1062[a]	2010	Chicken wing	RJ	Cip, Dox, Na, Tet	*tet*(O)	*tet*(O), *cmeB*	T86I	Tetracycline, efflux pump membrane transporter, quinolones
CCAMP 1063[a]	2010	Chicken gizzard	RJ	ND	ND	ND	ND	
CCAMP 1064[a]	2010	Chicken wing	RJ	ND	ND	ND	ND	

(*continued on next page*)

Table 1 (*continued*)

Strains	Year	Source	State	Phenotypic Resistance Profile	Antimicrobial Resistance Genes		Mutations QRDR *gyrA*	Antimicrobial class
					ABRicate v. 0.8	RGI	RGI	
CCAMP 1066[a]	2010	Chicken liver	RJ	ND	ND	ND	ND	
CCAMP 1067[a]	2010	Chicken liver	RJ	Amp, Cip, Na	$bla_{OXA-605}$	bla_{OXA-61}	T86I	Beta-lactam, quinolones
CCAMP 1068[a]	2010	Chicken wing	RJ	ND	ND	ND	ND	
CCAMP 1071[a]	2011	Chicken wing	RJ	S	ND	ND	ND	Aminoglycoside
CCAMP 1073	2011	Chicken wing	RJ	ND	ND	ND	ND	
CCAMP 1074[a]	2011	Chicken gizzard	RJ	Ery	ND	ND	ND	Macrolides
CCAMP 1075[a]	2011	Chicken liver	RJ	ND	ND	ND	ND	

[a] Results published in Gomes *et al.*, 2019.
Chicken, non diarrheal faeces; Cip, ciprofloxacin; Dox, doxycycline; Ery, erythromycin; Human, diarrheal faeces; MG, Minas Gerais; Monkey, non-diarrheal faeces; ND, not detected; R, resistance; RJ, Rio de Janeiro; RS, Rio Grande do Sul; SP, São Paulo; Tet, tetracycline;.

Table 2
Analysis of the phenotypic and genotypic antimicrobial resistance agreement among the 63 *Campylobacter coli* strains studied.

Antibiotic class	Number of isolates with phenotypic resistance	Number of isolates with genotypic resistance	Number of discordant isolates between genotypic and phenotypic resistance	Agreement between AMR phenotype and genotype (%)	*P* value*
Aminoglycoside	4	5	1	80	0.284989 (NS)
Beta-lactam	28	34	6	82.4	0.729406 (NS)
Quinolones	8	8	0	100	1 (NS)
Tetracycline	13	14	1	92.9	0.82812 (NS)
Macrolide	3	0	3	0	0.30023 (NS)

[a] $P < 0.05$ indicates significance, calculated by χ^2 test.
NS, not significant.

4. Discussion

Antibiotic resistance is one of the world's most challenging and urgent health problems; it has the potential to affect healthcare systems and the veterinary and agriculture fields [1]. Detecting antimicrobial resistance is necessary to guide treatment decisions for managing bacterial infections in both clinical and community settings. AST based on bacterial culture is still the most widely used method in clinical laboratories. However, WGS has been described as a rapid, consistent, and accurate tool for prediction of every known resistance phenotype of a strain [2].

This study assessed the AMR phenotypes and genotypes of *C. coli* strains isolated from different sources over 16 years in Brazil, using WGS tools and comparing findings with results obtained by AST, by testing eight clinically important antimicrobials.

According to published data, resistance to ampicillin and other antimicrobial agents belonging to a β-lactams class has been widely reported among *Campylobacter* species. In this work, 44.4% of the *C. coli* studied was resistant to ampicillin. Similarly, Corcoran and colleagues reported 48.5% ampicillin resistance among *Campylobacter* isolates in Ireland [15].

Regarding genotypic resistance, in a study carried out by Griggs and collaborators, 380 isolates were studied, of which 347 (91.3%) had the bla_{OXA-61} gene [16]. In the study carried out by our group, the presence of the $bla_{OXA-605}$ and bla_{OXA-61} gene was found in 54% (n = 34) of the studied strains, corroborating literature in which this gene was reported in a large number of strains (Table 1).

In a study performed by Wozniak-Biel and collaborators, 78.6% of *Campylobacter* strains isolated from broiler and 58.1% from turkey isolates were resistant to tetracycline [17]. Ferro and colleagues reported a similarly high prevalence of tetracycline resistance of *C. jejuni* and *C. coli* isolated from broiler carcasses in Brazil [18].

In contrast to studies observing that *C. coli* strains isolated from diverse countries have high rates of tetracycline resistance, in the present work, only 13 (20.6%) strains showed phenotypic resistance to this antimicrobial class, and the *tet*(O) gene was detected in 14 (22.2%). Our findings might be attributable to the fact that most of our strains were isolated from healthy monkeys and the environment, and they were probably not indiscriminately exposed to this antimicrobial class.

Fluoroquinolones are often used in veterinary and human medicine, especially for enteric infections. Thus, a high prevalence of resistance to this antimicrobial class has been reported in several studies. Wozniak-Biel and collaborators, for example, found fluoroquinolone resistance in all (n = 45) strains studied [17]. Likewise, *Campylobacter* isolates presenting high levels of resistance to fluoroquinolones have also been found in Spain [19].

Mutations in the QRDR region of the *gyrA* gene are related to fluoroquinolone resistance and were detected in 8 (12.7%) of the 63 *C. coli* strains studied, showing a 100% agreement between AMR phenotype and genotype.

Despite a relatively low proportion observed in this study, resistance of *Campylobacter* to fluoroquinolones is extremely important and has been monitored by public health agencies in several countries worldwide [1,4].

The results obtained in this study showed a low prevalence of resistance to antibiotics of the aminoglycosides class, which corroborates studies performed in different countries [3,17,19].

The CmeABC and CmeDEF efflux pumps have been frequently described as the main drug efflux mechanism for *Campylobacter*, and they confer resistance to several antimicrobial agents [3]. The *cme*B gene was detected in 6 (9.5%) of strains studied, differing substantially from previous work by our research group, where this gene was identified by polymerase chain reaction in 38 of the 39 (97.4%) *C. coli* strains studied [12]. Likewise, a study performed by Marotta and colleagues evaluated the presence of *cme*B gene in 644 *C. jejuni* strains from the collection at the National Reference Laboratory for *Campylobacter,* and this gene was detected in 100% of strains [3].

Comparing results obtained in the present work by AST and by *in silico* search of AMR genetic profiles, agreement was observed between phenotype and genotype profiles of 100%, 92.9%, 82.4%, 80%, for quinolones, tetracycline, β-lactam, and aminoglycoside classes, respectively (Table 2). Specifically in relation to macrolide resistance, CCAMP 761, Cc03, and CCAMP 1074 strains

were phenotypically erythromycin-resistant with no mutation in the 23S rRNA gene, suggesting that another mechanism, such as other points of mutation and/or efflux pumps, may be responsible for such resistance. Although the results obtained in the agreement between AMR phenotype and genotype were not statistically significant, they are clinically relevant.

The prediction of resistance genes by WGS may estimate the resistance phenotype that is usually verified according to the guidelines of the CLSI [14] and/or the European Committee on Antimicrobial Susceptibility Testing. For this, it is necessary to use a database containing the gene sequences linked to antibiotic resistance phenotypes, and software to perform the query between the unknown sequence and the gene sequences deposited in the databases [20]. Because of a scarcity of genomic studies involving the species *C. coli*, few genomic annotations are available, which may have contributed to the relatively low proportion of resistance genes found. Furthermore, the research literature demonstrates that genome fragmentation generated by next-generation sequencing can affect the prediction of resistance genes and make it difficult to determine whether the resistance genes are located on a chromosome or mobile element due to gaps between the contigs [2].

5. Conclusion

In conclusion, the rates of *C. coli* strains resistant to antimicrobials, especially to β-lactams and quinolones, and the prediction of genes related to resistance in these strains may represent a public health concern for *Campylobacter* infections in humans when treatment is needed. In addition, this is the first study performed in Brazil that used next generation sequencing technology to assess AMR genotypes in *C. coli* isolated from humans, animals, the environment, and food, comparing them with results obtained by AST testing in some important antimicrobials of clinical use.

The present results improve the characterization of *C. coli* strains from different sources circulating in Brazil over a span of 16 years. WGS is an important tool in genomic analysis and offers potential for accurate predictions of phenotype resistance for *C. coli.* However, the partial agreement between the phenotypic and genotypic profiles of antimicrobial resistance using WGS shows that improvement in antibiotic resistance databases may be required to minimize the discrepancy observed in some antimicrobial classes and to become an acceptable tool to both clinical microbiologists and regulatory agencies.

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Competing Interests: None to declare.

Ethical approval: The authors declare that ethical approval was not required. The study was conducted using isolates belonging to the culture collection of the Oswaldo Cruz Institute (FIOCRUZ-RJ).

Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.jgar.2023.03.004.

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