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MOLECULAR DETECTION OF *CAMPYLOBACTER JEJUNI* IN BROILERS WITH REGARDS TO BIOFILM AND VIRULENCE GENES

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ABSTRACT

Campylobacter is one of the most frequent bacterial foodborne pathogens worldwide. Poultry is the disease's most clinically significant host species. Despite their importance to public health, the virulence factors and mechanisms that drive *C. jejuni* pathogenicity are poorly understood, and the relationships between these genes and strain origins remain unclear. In this study, we intended to examine the prevalence, virulence and biofilm formation genes, and antibiotic resistance of *C. jejuni* isolated from cloacal swab samples of commercial chicken in Aswan Governorate, Egypt. Random samples of fresh chickens (n = 103) were collected from different retail markets. To identify the virulence genes (*flaA*, *cdtB*, and *cadF* genes), polymerase chain reaction was employed in conjunction with the 23S rRNA and mapA genes unique to *Campylobacter* and *C. jejuni*, respectively. 17 (16.5%) of the 103 samples had positive *Campylobacter* spp. tests. *C. jejuni* was present in nine (8.7%) of the positive isolates. In 77%, 100%, and 88.8% of *C. jejuni* strains, the genes *flaA*, *cdtB*, and *cadF* were detected, respectively. The antibiotic resistance of the *C. jejuni* isolates was determined via the disc diffusion method and was observed most frequently to ceftazidime (88.9%), ceftriaxone (77.8%), cephalexin (77.8%), erythromycin (66.6%), while low resistance to levofloxacin (11.1%), and chloramphenicol (11.1%) was detected. These findings highlight the high prevalence of *Campylobacter* in fresh chickens, which is thought to be the main risk factor for domestically obtained campylobacteriosis in Aswan Governorate, Egypt.

Keywords: *C. Jejuni; broilers; 23S rRNA; virulence genes; antibiotic resistance*

INTRODUCTION

In outbreaks of foodborne illnesses involving chicken meat, *campylobacter* spp. is the most frequently found pathogen (Gourley *et al.,* 2017). The deadly zoonotic illness known as campylobacteriosis, or infection with *Campylobacter* spp., induces gastroenteritis in humans. Eating undercooked poultry meat is one of the biggest risk factors for infection (Freitas and Noronha, 2007).

In accordance with the European Food and Safety Authority (EFSA) and the European Center for Disease Control (ECDC, 2006). The Community Overview Report on Zoonoses, campylobacteriosis continues to

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be the most commonly reported zoonotic disease that affects individuals in the European Union (EU). In addition to the long-term consequences of arthritis, hemolytic uremic disorder, bowel inflammation, functional gastrointestinal abnormalities, and, in extreme cases, Guillain-Barre syndrome, this infection usually presents as acute gastroenteritis.

As reported on http://www.bacterio.net/, the genus *Campylobacter* currently has 66 species and 16 subspecies identified. (Man, 2011; Kaakoush *et al.*, 2015 and Van *et al.*, 2015).

At about 80% of all *Campylobacter* infections, *Campylobacter jejuni* is the species with the largest clinical impact (Whitehouse *et al.*, 2018 and WHO, 2020). *C. jejuni* is susceptible to acidity, freezing, warmth, and normal oxygen concentrations (Nayak, 2012). Relatively common *campylobacter* infections lead to significant medical and financial costs (O'Brien SJ, 2017).

Because of the helical, curved, or S-shaped appearance of these bacteria, the family *Campylobacter* was given its name after the Greek word "curved rod" (Jordan *et al.*, 2001).

According to Gharst, Oyarzabal, and Hussain (2013), *Campylobacter* is a microaerobe that grows best in a temperature range of 35 to 42°C and requires from 2% to 10% oxygen levels (microaerophilic).

During the rearing phase, *C. jejuni* can appear in broiler chicks as early as 14 days of age. By the end of the grow-out period, a low percentage of the birds will have been highly contaminated (EFSA, 2010). A significant amount of *Campylobacter* species are known to be present in the gastrointestinal tract of chickens during processing, especially in the caecum and colon. This is especially the case if the gastrointestinal tract breaks down and the contents are transferred to the skin, further contaminating the meat (Vinueza-Burgos *et al.*, 2017).

Intestinal colonization, the invasion of bacteria into intestinal cells, cytotoxin production, and extra intestinal translocation mechanisms are all examples of *Campylobacter* infection (Dasti *et al.*, 2010; Tresse *et al.*, 2017). Some virulence-associated genes have been identified as being responsible for these mechanisms, such as *flaA* and *cadF*, which are responsible for adhesion and colonization, *ciaB* and virB11, which are involved in host cell invasion, and *cdtA*, *cdtB*, and *cdtC* which are responsible for cytotoxin production (Bolton, 2015).

According to research by Bronnec *et al.* (2016), *C. jejuni* has been shown to form biofilm on a variety of surfaces, including plastic, glass, and steel, at varying oxygen concentrations. As a result, biofilms containing *C. jejuni* pose a serious risk to food safety.

Until now, it is unclear how *C. jejuni's* biofilm formation is regulated at the molecular level. Some of the involved genes include those responsible for cell motility (*flaA*) (Reuter *et al.*, 2010), cell adhesion (*cadF*), quorum-sensing (*luxS*) (Plummer, 2012).

Antibiotic-resistant *Campylobacteria* develop into multidrug resistance bacteria (MDR) (Mansouri *et al.*, 2012). The MDR *Campylobacter* has been and raised worries due to its resistance to quinolones and erythromycin (Ge *et al.*, 2013). These concerns could have a major impact on public health (Iovine, 2013). According to Chai *et al.* (2008), there was a belief that the resistant strain of *Campylobacter* was inherently harder than the sensitive strain.

This study aimed to determine the prevalence of *C. jejuni* species, their virulence and biofilm formation genes, and

their sensitivity to various antimicrobial drugs in the broiler chickens and birds sold in markets in Aswan governorate of Egypt.

MATERIALS AND METHOD

1. Sample collection

Cloacal swabs (n=103) were taken from broilers in Aswan governorate, Egypt, of 35–40 days old in retail markets. For microbiological analysis, all samples were gathered in sterilized containers and sent to the lab under frigid temperatures.

2. Isolation and identification

2.1 Isolation step:

Samples were cultured on modified *Campylobacter* chosen blood-free agar, mCCDA (Oxoid, CM0739B, England) (Bolton *et al.,* 1984) at 42 °C for 48 hours in the microaerophilic environment, after having been enriched in Bolton selectively enriched broth (Oxoid) (FDA *et al.,* 1998) for 24 hours at 10% CO2 at 42°C. Following incubation, staining with Gram's (Gram negative, S-shaped, curved rod) and biochemical testing (catalase, oxidase, and hippurate hydrolysis tests) were used to identify suspicious colonies.

2.2 DNA extraction

Fresh cultures of a likely *Campylobacter* species that were cultivated in a microaerophilic environment for 48 hours at 42°C yielded bacterial DNA. Genomic DNA was extracted using the QIAamp DNA Mini Kit (Qiagen, GmbH, Germany), following the manufacturer's instructions.

2.3 Molecular confirmation of *C. jejuni* isolates and virulence genes:

PCR is used to identify *Campylobacter* and other bacteria focused on the 23S rRNA gene (Wang *et al.,* 2002). The *mapA* was the intended target gene of a PCR that was used to identify *C. jejuni*, according to Eunju & Lee (2009). Table (1) lists the primers acquired from Metabion (Germany) for this project. Using 250-µL PCR reaction tubes, 12.5 µL of EmeraldAmp GT PCR master mixes (2x premix), 2 µL of 20× the primer mix (1 µM for every primer), 5.5 µL of PCR graded water, and 5 µL of DNA fragments were used for the PCR amplifications. Table (2) contains the cycling parameters for every gene. After staining with ethidium bromide, the generated PCR products were electrophoresed with 1.5% (w/v) agarose in 1× TBE buffer and examined by UV transillumination.

3. Antimicrobial susceptibility testing

Following the manufacturer's instructions, according to Finegold and Martin (1982), the conventional disc diffusion method was used on Mueller-Hinton agar mixed with 5% defibrinated sheep blood to assess *C. jejuni* susceptibility to antibiotics. Azithromycin (15µg/mL), erythromycin (15µg/mL), levofloxacin (5µg/mL), norfloxacin (10µg/mL), ceftazidime (30µg/mL), ceftriaxone (30µg/mL), cephalexin (30µg/mL), and chloramphenicol (30µg/mL) where the eight antimicrobials from four classes were employed.

The plates have been incubated for forty-eight hours at 37 °C in a microaerobic environment. The diameter of the zone of inhibition encircling each disc was used to measure the sensitivity of each isolate. The findings were analyzed using Enterobacteriaceae family standards developed by the European Centre for Prevention and Control of Disease (2014) and the Clinical and Lab Standards Institute (CLSI, 2016).

RESULT

In this investigation, twenty-five (24.3%) suspected *Campylobacter* isolates out of 103 samples gathered from different sources in Aswan governorate, Egypt. The colonies had a smooth, transparent appearance with a regular border. When the colonies were examined under a microscope while still fresh, bacteria with the distinctive motility of *Campylobacter* were found in the midge's

flight. Gram staining, or microscopic immersion observation, verified the presence of spiral or S-curved or Gram-negative bacilli.

A conventional biochemical method was employed to identify 25 isolates of *Campylobacter* that were similar. These isolates also showed positive results for hippurate hydrolysis, oxidase, and catalase. Then, using PCR, the similar 25 isolates of *C. jejuni* were genotypically identified. The isolates were sent for genetic verification *Campylobacter* and *C. jejuni* species using amplification with PCR of the 23S rRNA and *mapA* genes, respectively. Of the examined isolates, 8 (7.8%) tested negative and 17 (16.5%) were recognized as *Campylobacter*. Table (3) shows that 9 isolates (8.7%) were confirmed to be *C. jejuni*.

Three critical virulence genes (*flaA*, *cdtB*, and *cadF*) implicated in *C. jejuni* pathogenicity were screened for in all nine molecularly verified *C. jejuni* isolates. Of the nine examined isolates, Table (4) showed that 7 (77.7%), 9 (100%) and 8 (88.8%) tested positive for the *flaA*, *cdtB*, and *cadF* genes, respectively.

As shown in Table (5), the sensitivity of each of the nine *C. jejuni* isolates to different antimicrobial medications from different groups was examined. A significant number of C. jejuni were resistant to the cephalosporins group (Ceftazidime, Ceftriaxone, Cephalexin) (81.4%), Erythromycin (66.6%) and Norfloxacin (55.6%). Conversely, the results showed a noteworthy frequency of levofloxacin susceptibility (88.9%), followed by chloramphenicol (66.6%).

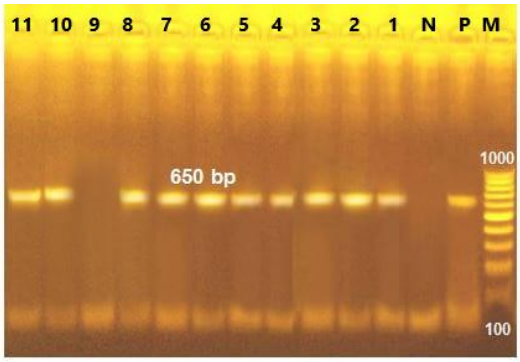

Figure 1: Agarose gel electrophoresis of 23S rRNA gene showing bands at 650 bp. Lane M: Marker (DNA ladder 100 bp), Lane P: positive control, Lane N: negative control, Lane (1, 2, 3, 4, 5, 6, 7, 8, 10): positive 23S rRNA gene and Lane (9): negative isolate.

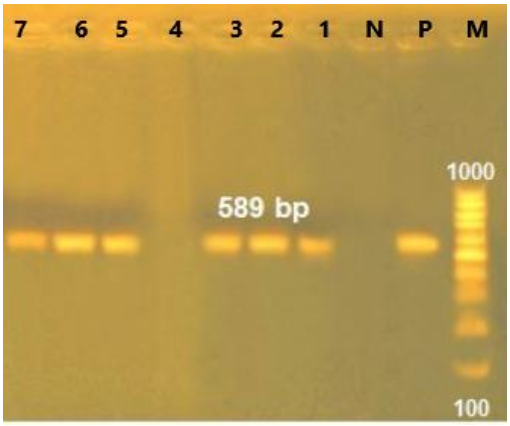

Figure 2: Agarose gel electrophoresis of mapA gene showing bands at 589 bp. Lane M: Marker (DNA ladder 100 bp), Lane P: positive control, Lane N: negative control, Lane (1, 2, 3, 5, 6, 7,): positive mapA gene and Lane 4: negative isolate

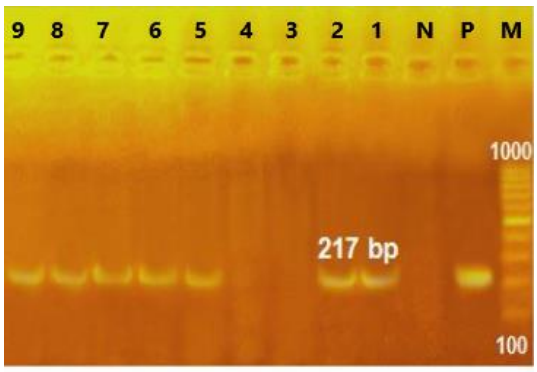

Figure 3: Agarose gel electrophoresis of flaA gene showing bands at 217 bp. Lane M: Marker (DNA ladder 100 bp), Lane P: positive control, and Lane N: negative control, Lane (1, 2, 5, 6, 7, 8, 9): positive *flaA* gene, Lane (3,4): negative isolate,

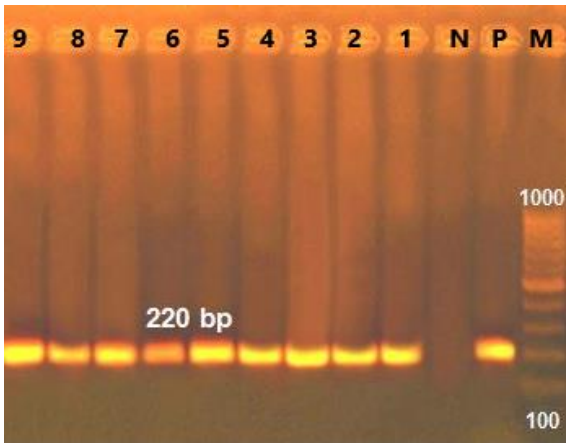

Figure 4: Agarose gel electrophoresis of cdtB gene showing bands at 220 bp. Lane M: Marker (DNA ladder 100 bp), Lane P: positive control, and lane N: negative control, Lane (1, 2, 3, 4, 5, 6, 7, 8, 9): positive cdtB gene.

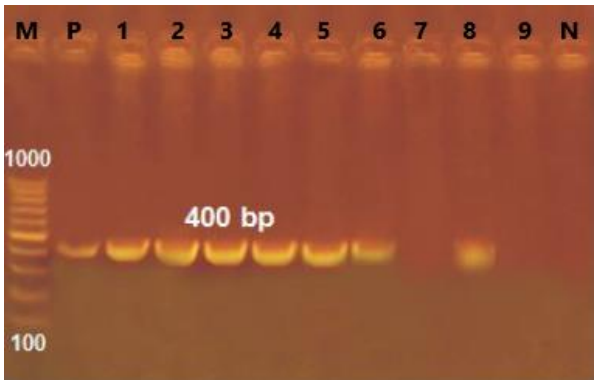

Figure 5: Agarose gel electrophoresis of cadF gene showing bands at 400 bp. Lane M: Marker (DNA ladder 100 bp), Lane P: positive control, Lane (1, 2, 3, 4, 5, 6, 8): positive *cadF* gene, Lane (7, 9): negative isolate, and Lane N: negative control

Table 1: Oligonucleotide primers sequences.

Target gene	Primer sequence (5'-3')	Length of amplified product	Reference
C. jejuni mapA	CTA TTT TAT TTT TGA GTG CTT GTG	589 bp	Eunju and Lee, 2009
	GCT TTA TTT GCC ATT TGT TTT ATT A		
Campylobacter 23S Rrna	TATACCGGTAAGGAGTGCTGGAG	650 bp	Wang *et al*., 2002
	ATCAATTAACCTTCGAGCACCG		
FlaA	TCCAAATCGGCGCAAGTTCA	217 bp	Zheng *et al*., 2006
	TCAGCCAAAGCTCCAAGTCC		
cdtB	CAGAAAGCAAATGGAGTGTT	220 bp	Nahar and Bin Rashid, 2018
	AGCTAAAAGCGGTGGAGTAT		
CadF	TTG AAG GTA ATT TAG ATA TG	400 bp	Al Amri *et al*., 2007
	CTA ATA CCT AAA GTT GAA AC		

Table 2: Cycling conditions of the primers during cPCR.

Gene	Primary denaturation	Secondary denaturation	Annealing	Extension	No. of cycles	Final extension
C. jejuni	94˚C 5 min.	94˚C 30 sec.	55˚C 45 sec.	72˚C 45 sec.	35	72˚C 10 min.
Campylobacter 23S rRNA	94˚C 5 min.	94˚C 30 sec.	55˚C 40 sec.	72˚C 45 sec.	35	72˚C 10 min.
FlaA	94˚C 5 min.	94˚C 30 sec.	55˚C 30 sec.	72˚C 30 sec.	35	72˚C 7 min.
CdtB	94˚C 5 min.	94˚C 30 sec.	51˚C 40 sec.	72˚C 45 sec.	35	72˚C 10 min.
CadF	94˚C 5 min.	94˚C 30 sec.	49˚C 40 sec.	72˚C 40 sec.	35	72˚C 10 min.

Table 3: Occurrence of *Campylobacter* in the examined samples using PCR:

No. of examined samples	+Ve *Campylobacter* spp.		+Ve *C. Jejuni*		Other Spp.	
	No.	%	No.	%	No.	%
103	17	16.5%	9	8.7%	8	7.8%

Table 4: Occurrence of some virulence genes in *Campylobacter* isolates obtained from the examined samples

No. of C. Jejuni isolates	flaA gene		cdtB gene		cadF gene	
	No.	%	No.	%	No	%
9	7	77.7%	9	100%	8	88.8%

Table 5: Antimicrobial susceptibility patterns of *C. jejuni* isolates.

Classes of antibiotics	Antimicrobial agents	Resistant strains S	I	R	% of resistant strains to all antibiotic classes
Macrolides	Erythromycin(15µg/mL)	3(33.4%)	0(0%)	6(66.6%)	
	Azithromycin(15µg/mL)	5(55.6%)	1 (11.1%)	3(33.3%)	50%
Fluoroquinolones	Levofloxacin (5µg/mL)	7(77.8%)	1 (11.1%)	1(11.1%)	
	Norfloxacin (10µg/mL)	3(33.3%)	2(22.2%)	4(44.5%)	33.3%
Cephalosporins	Ceftazidime (30µg/mL)	0(%)	1(11.1%)	8(88.9%)	
	Ceftriaxone (30µg/mL)	1(11.1%)	1(11.1%)	7(77.8%)	81.4%
	Cephalexin (30µg/mL)	2(22.2%)	0(0%)	7(77.8%)	
Quinolones	Chloramphenicol (30µg/mL)	6(66.6%)	2(22.3%)	1(11.1%)	11.1%

Zone diameter of Erythromycin, Azithromycin, levofloxacin, Norfloxacin, Ceftazidime, Ceftrixone, Cephalexine and Chloramphenicol were recommended by the (CLSI-2016) for Enterobacteriaceae and European Centre for Disease Prevention and Control (2014). S, susceptible; I, intermediate; R, resistant

DISCUSSION

Even in wealthy countries, *C. jejuni* is considered one of the most common and dangerous foodborne pathogens. It induces serious gastroenteritis with bacteria in humans who consume contaminated food, especially poultry and related products (Eurosurveillance Editorial Team, 2012). Using both conventional and polymerase chain reaction approaches, we were able to determine the overall prevalence of *campylobacter* species in the analyzed samples. These results came out to be 24.3% and 8.7%, respectively.

This prevalence may be related to the intestinal tract of the chicken, specifically the colon and caecum, which are thought to be regions of tropism for a variety of species of *Campylobacter* (Jokinen *et al.*, 2011).

As to Hansson *et al.* (2018), the prevalence of *campylobacter* differs depending on the nation. One cause of these changes is *C. jejuni* mutations, because of intragenomic processes as well as strain-specific genetic exchange, *C. jejuni* possesses a high level of genetic diversity. Through *C. jejuni* genome sequencing, homopolymeric tract-based hypervariable transcripts have been found, most of the hypervariable sequences that have been described are located in regions that encode proteins that are involved in the synthesis or modification of surface-accessible carbohydrate structures such the capsule, lipooligosaccharide (LOS), or flagellum. Change in these structures is caused by a variety of causes, including frame shifts, points of mutation, duplication of genes and suppression, and phase variation.

The plasmids of *Campylobacter* species play a major role in determining their capacity to adapt and turn harmful. Research has identified many plasmid families, including pVir-like and pTet-like; these families each contain distinct relaxases or replicon types, and their effects

may have an impact on the virulence and survival of bacteria (van Vliet *et al.,* 2021; Hull *et al.,* 2023). Additionally, plasmids aid in the horizontal transfer of genes, which transmits genetic material and traits quickly and increases the adaptability of populations of *Campylobacter* spp. The presence of plasmids containing virulence factors emphasizes their importance in the potential for infections of these bacteria.

According to Ica *et al.* (2012), *Campylobacter* may be able to live in biofilms outside of stress response mechanisms in natural environmental settings. *Campylobacter* biofilms can develop in the plumbing and water supply systems of poultry husbandry establishments and food processing factories, in addition to the gastrointestinal tracts of poultry. Poultry can then either directly or indirectly introduce these biofilms into the human food chain (Siringan *et al.,* 2011).

Molecular understanding of *C. jejuni* biofilm formation is still in its infancy although there is evidence for the role of flagella and gene regulation in biofilm formation (Reeser *et al.,* 2007 and Svensson *et al.,* 2009), For instance, genes involved in stress response and flagella synthesis (*flaA*) can control the development of *C. jejuni* biofilms (Kalmokoff *et al.,* 2006; Reeser *et al.,* 2007 and Svensson *et al.,* 2014). Reeser *et al.* (2007) discovered that a *C. jejuni* flagella knockout mutant (ΔflaAB) produced a notably decreased level of biofilm in contrast to its wild-type counterpart.

Of virulence genes identified in isolates of *Campylobacter jejuni* found in poultry, the *flaA* genes, which are necessary for flagellar motility, were present in 77.7% of *C. jejuni* isolates. Our results are entirely in line with earlier research conducted in Egypt. As it affects the mobility, adhesion, and invasion of host intestinal epithelial cells and biofilm formation, the *flaA* gene is a virulent marker in *C. jejuni* strains.

CadF is one of the reference virulence genes that encode proteins involved in the attack and attachment of *C. jejuni* (Elmali & Can, 2019), and this gene is present at a high prevalence in *C. jejuni* isolates (Andrzejewska *et al.,* 2015). According to Melo *et al.* (2017), the presence of the genes *flaA* and *cadF* in *Campylobacter* strains indicated a high potential for biofilm formation.

CadF gene was detected in 8 (88.8%) of *Campylobacter* isolates. These results are similar to data previously reported by other authors Datta *et al*. (2003); Rozynek *et al*. (2005); Krutkiewicz and Klimuszko (2010). A higher result (100%) was obtained by da Silva *et al.* (2021), while Ghoneim *et al*. (2020) and Abbas *et al.* (2021) recorded a lower result (20.58%) and (20.5%), respectively.

Another significant component of *Campylobacter* is the *CDT* complex, which codes for cytolethal distending toxin, with *cdtB* serving as the catalytic site. *CDT* is composed of three subunits (*CdtA, CdtB* and *CdtC*), the catalytic subunit *CdtB*, which triggers cell cycle arrest and causes the intestinal epithelium and immune cells to undergo apoptosis, whereas *CdtA*, and *CdtC* are binding proteins for delivering *CdtB* into target cells (Jain *et al.,* 2008). 100% of the isolates examined in this investigation had the *cdtB* identified, which is in line with earlier findings by Asakura *et al*. (2010) and Jribi *et al*. (2017).

Antibiotics are profusely administered for therapeutic and prophylaxis purposes in the veterinary field (Dandachi *et al.,* 2018). In recent years, disinfectants have been used with carelessness leading to the adaptation of bacteria and augmenting the spread of resistant bacteria.

Nowadays, Antimicrobial resistance, especially to fluoroquinolone (ciprofloxacin) and macrolides (erythromycin), has emerged in *Campylobacter* (Lehtopolku *et al*., 2011). The use of tetracycline while rearing farm animals has been reviewed in recent years because of its growth-promoting properties**,** The addition of a subtherapeutic dose of chlortetracycline in livestock rations positively affects the rate of growth and feed utilization of young chickens. Therefore, a significant increase in antibiotic resistance has been observed in *Campylobacter* isolates recovered from chickens (EFSA, 2012).

In the present study, very high resistance rates (81.4%) to cephalosporins were detected. Similar results have been found by varela *et al.* (2007), Griggs *et al.* (2009) and Giacomelli *et al.* (2014). On the contrary, Raeisi *et al.* (2017) and Ghoneim *et al.* (2020) reported high susceptibility of *C.jejuni* to cephalosporins.

Meanwhile, the isolates were susceptible to fluoroquinolones (Levofloxacin) and chloramphenicol, similar to other studies Barco *et al.* (2010), De Cesare *et al.* (2008), Parisi *et al*. (2007), Pezzotti *et al*. (2003). However, our results contrast those of Mackiw *et al*. (2012) Zhu *et al*. (2006).

The strategies adopted to limit antimicrobial resistance (AMR) will vary globally, particularly across countries with different degrees of wealth and development. The most effective intervention will likely depend on prevailing conditions. For example, high-income countries and low-income countries can differ in antimicrobial resistance patterns, antimicrobial use practices, access to healthcare services (human and animal), sanitation and infrastructures regulation (Collignon *et al.*, 2018 and Caudell *et al.*, 2017).

CONCLUSION

This study provided sufficient information on the presence of *Campylobacter* in chickens, with the assumption that fresh birds are the main source of campylobacteriosis.

In addition, customers run the risk of contracting *Campylobacter* infections due to the virulent features present in *C. jejuni* isolates and the bacteria's strong resistance to both cephalosporins and macrolides.

The aforementioned results underscore the significance of instituting hygienic protocols on the farm and controlling the number of *Campylobacter* during the processing of carcasses. Additionally, it is imperative to establish a proficient system for managing *Campylobacter* infections in chickens and curtailing the usage of antibiotics in the poultry industry.

Our research leads us to the conclusion that PCR is essential for the identification of numerous bacteria. PCR is a significant and widely utilized technology that has many uses in medical and biological research labs today.

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الكشف الجزيئي لميكروب الكامبيلوباكتر جيجناي المعزول من دواجن التسمين فيما يتعلق بالجينات الخاصة بالضراوة وتكوين الأغشية الحيوية

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يعد ميكروب الكامبيلوباكتر من أكثر الميكروبات المسببة للامراض البكتيرية الغذائية شيوعا في جميع أنحاء العالم، والدواجن هي أكثر الأنواع المضيفة. وعلى الرغم من أهمية ميكروب الكامبيلوباكتر جيجناي في المرض من الناحية السريرية ، إلا أن عوامل الضراوة والآليات التي تدفع مرضية وأصول السلالات لا تزال غير واضحة.

ولذلك قمنا في هذه الدراسة بفحص انتشار جينات الضراوة ومقاومة المضادات الحيوية للكامبيلوباكتر جيجناي والتي تم عزلها من عينات تم أخذها من منافذ الدواجن التجارية في محافظة أسوان بمصر.

تم جمع عينات عشوائية من الدواجن الحية من محلات التجزئة للحوم الداجنة وعددها ١٠٣ عينة بهدف تحديد جينات الضراوة (الجينات *flaA* و *cdtB* و *cadF*)، تم استخدام تفاعل البلمرة المتسلسل بالإضافة إلى جيناتrRNA 23S و mapA الخاصة لكامبيلوباكتر وكامبيلوباكتر جيجناي، على التوالي. كانت ١٧ عينة (١٦,٥٪) من العينات الـ ١٠٣ إيجابية لفحص سلالات الكامبيلوباكتر وكانت سلالة الكامبيلوباكتر جيجناي موجودة في تسع عينات (٨,٧٪) من السلالات الإيجابية. تم الكشف عن الجينات *flaA* و *cdtB* و *cadF* في ٧٧٪ و١٠٠٪ و٨٨,٨٪ من سلالات كامبيلوباكتر جيجناي، على التوالي.

كذلك قمنا بإجراء اختبار حساسية لثمانية أنواع من المضادات الحيوية لتسع سلالات كامبيلوباكتر جيجناي، أظهرت السلالات مقاومة للسيفتازيديم بنسبة(٨٨,٩٪) والسيفترياكسون بنسبة (٧٧,٨٪) والسيفاليكسين بنسبة (٧٧,٨%) والإريثرومايسين بنسبة(٦٦,٦٪) والنورفلوكساسين بنسبة (٤٤,٤٪) والأزيثرومايسين بنسبة(٣٣,٣٪) والليو فلوكساسين بنسبة (١١,١٪) والكلورامفينيكول بنسبة (١١,١%)

كانت أغلب سلالات C. jejuni التي تم العثور عليها مقاومة للسيفالوسبورين والمكروليدات، وكان هناك انتشار مرتفع للحساسية للكلورامفينيكول. تدعم هذه النتائج الحاجة الملحة لرقابة سلامة الغذاء وتبرز الانتشار العالي لكامبيلوباكتر في الدواجن الطازجة، والتي يُعتقد أنها العامل الرئيسي في الإصابة بمرض كامبيلوباكتر في المنازل في محافظة أسوان، مصر.