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Research Article

Molecular Characterization and Virulence of *Campylobacter jejuni* Isolated from Broiler Chickens

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Abstract

Background and objective: *Campylobacter jejuni* (*C. jejuni*) is a commensal microorganism in birds that causes diarrhea due to intestinal inflammation, which leads to feet damage from standing on wet litter. This study aimed to investigate the prevalence and virulence of *C. jejuni* in broiler chickens, as well as determine histopathological changes in the chicken gut following infection. **Materials and Methods:** A total of 200 infected broiler chicken samples (100 cecal contents, 50 livers and 50 spleens) were collected from different farms at Dakahlia Governorate in Egypt. Broilers samples were subjected to *Campylobacter* isolation procedures. *Campylobacter jejuni* isolates were distinguished from other *Campylobacter* spp. using the uniplex PCR-targeting *mapA* gene. *Campylobacter jejuni* isolates were also evaluated for the presence of *cdtA* and *flaA* genes. Evaluation of gut histopathological changes after *C. jejuni* infection was carried out in twenty day-old broiler chicks. **Results:** In total, sixty-eight *C. jejuni* isolates (18 isolates from the liver samples, 12 from spleen samples and 38 from cecal contents) were recovered with an overall prevalence rate of 34%. The *flaA* gene was successfully identified in all *Campylobacter* isolates, while *cdtA*, was identified in only 62 (91.17%) isolates. Several pathological changes and inflammatory responses were found in the chicken gut as a result of *C. jejuni* infection. **Conclusion:** The prevalence of *flaA* and *cdtA* revealed a high rate of adherence and cytotoxicity-associated genes. In addition, several histopathological changes were found in the chicken gut. These findings confirmed that *C. jejuni* infection has a significant impact on poultry health and welfare and *C. jejuni* is a harmful gut commensal microorganism.

Key words: *Campylobacter jejuni*, broiler chickens, virulence genes, colonization, histomorphological changes

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Competing Interest: The author has declared that no competing interest exists.

Data Availability: All relevant data are within the paper and its supporting information files.

INTRODUCTION

Campylobacter is one of the most important bacterial sources of human enteritis worldwide and it has been isolated from a variety of animal species, including, poultry, cattle, pigs, sheep, pets, wild birds and rodents¹⁻³. Chicken is considered the main source of *Campylobacter* and may responsible for approximately 70.9% of human cases, as contaminated chicken meat and meat by-products often cause human infections^{4,5}. It is difficult to control the spread of *Campylobacter* in the slaughterhouse and in kitchens; however, controlling *Campylobacter* on the farm may help reduce the number of bacteria in food processing plants^{6,7}.

The mechanisms of disease of *C. jejuni* starts with colonization in the chicken gut and adhesion and invasion of the gut epithelial cells followed by cytotoxin production⁸. Once colonization is established, *Campylobacter* can multiply rapidly in the cecal contents⁹. While *C. jejuni* colonizes chicken ceca and small intestines, it may also be isolated from different places in the chicken gut, as well as from internal organs such as spleen and liver¹⁰. *Campylobacter* may present in poultry internal organs tissues via bacterial translocation by which it can cross the intestinal barrier of humans and animals and invade internal organs; the lymphatic path is thought to be the primary route of translocation¹¹.

Detection of virulence in *C. jejuni* can be used to evaluate the potential risk of poultry as a source of *Campylobacter* infection¹². Motility is one of the main factors of *Campylobacter* pathogenicity and it can be identified by its spiral form and flagella bundles on cell tips. Due to these features, *Campylobacter* can move against peristaltic movements and colonize intestinal cells. The flagellum is built from a protein known as flagellum which is encoded by the *flaA* and *flaB* genes. The *flaA* gene is expressed at higher rates than *flaB* and thus is essential to *Campylobacter* motility¹³. Most *C. jejuni* strains have relatively higher cytolethal distending toxin (CDT) activity comparing to *C. coli* strains; the *C. jejuni* CDT is encoded by a three-gene operon (*cdtABC*)¹⁴⁻¹⁶.

The aims of this study were to characterize *C. jejuni* isolated from chicken cecal contents, determine whether *Campylobacter* can be isolated from the liver and spleen and

determine the prevalence of virulence genes. In addition, we examined intestinal epithelial changes caused by *C. jejuni* infection.

MATERIALS AND METHODS

Sample collection: A total of 200 infected broiler chicken samples (100 cecal contents, 50 livers and 50 spleens) were collected from different broiler farms at Dakahlia Governorate, Egypt from October 2016 to February 2017. Cecal contents and internal organs from each chicken were individually packed into sterile plastic bags. All samples were immediately transported to the laboratory in an ice box to isolate *C. jejuni*.

Isolation and identification of *C. jejuni* isolates:

Campylobacter isolation procedures were performed according to ISO 10272-1:2006¹⁷. Samples from cloaca swabs were dissolved into Bolton broth (CM0983, Oxoid) with *Campylobacter* growth supplement (SR0183, Oxoid) and incubated at 42°C for 24 h under microaerobic conditions followed by streaking into mCCDA agar plates (CM0739; Oxoid/UK) with a selective supplement (SR0155, Oxoid) according to the manufacturer's instructions. For internal organs (liver and spleen), 25 g of each sample were homogenized for 1min in stomacher (Stomacher 400 Lab Blender) with Bolton broth; then, the homogenate was transferred to screw-capped sterile bottle. The bottles were then incubated aerobically at 37°C for 4 h followed by 42°C for 48 h. Approximately 0.1-0.2 mL of each samples' enrichment broth was streaked into mCCDA agar plates and then incubated at 42°C for 48 h under microaerobic conditions using Oxoid Campy Gen (CN035A, Oxoid). Presumptive *Campylobacter* colonies were tested biochemically by catalase and oxidase and subjected to Gram staining¹⁸.

PCR-based confirmation of *C. jejuni*: Genomic DNA were obtained using a conventional boiling method according to De Lamballerie *et al.*¹⁹. *Campylobacter jejuni* was distinguished from other *Campylobacter* spp. by the uniplex PCR-targeting *mapA* gene (Table1). PCR reactions consisted

Table 1: Oligonucleotide primers used in the study

Target gene	Primer sequence (5'-3')	Length of amplified product	Reference
<i>mapA</i>	F-CTA TTT TAT TTT TGA GTG CTT GTG R-GCT TTA TTT GCC ATT TGT TTT ATT A	589 bp	Shin and Lee ²⁰
<i>flaA</i>	F-AATAAAAATGCTGATAAAACAGGTG R-TACCGAACCAATGTCTGCTCTGATT	855 bp	Datta <i>et al.</i> ²¹
<i>cdtA</i>	F-GGAAATTGGATTGGGGCTATACT R-ATCAACAAGGATAATGGACAAT	165 bp	Wieczorek <i>et al.</i> ²²

of 12.5 µL of 2×PCR master mix (Takara RR310A), 6 µL DNA template and 1 µL of each primer; the volume was completed to 25 µL with nuclease-free water. PCR conditions were followed according to the referenced study (Table 2).

Molecular characterization of *cdtA* and *flaA* genes:

Campylobacter jejuni isolates were examined for the presence of *cdtA* and *flaA* genes (Table 1). The PCR reaction mixture for both genes consisted of 12.5 µL of 2×PCR master mix (Takara RR310A), 6 µL DNA template and 1 µL of 20 pmol of forward and reverse primer, the mixture was completed to 25 µL with DNA/RNA-free water (Table 2).

Poultry infections: Twenty one-day-old broiler chicks were used in this study. At one and 14 days of age, cloacal swabs were taken from all chickens and directly plated on mCCDA for *Campylobacter* determination to ensure absence of *C. jejuni*. At 14 days of age, each chicken was orally dosed with 1×10⁸ *C. jejuni* in 0.5 mL of phosphate buffer saline²³. Chicks were reared under strict biosecure conditions. At 7 days post-infection, the chicks were killed by cervical dislocation. One gram of cecal content was collected for *C. jejuni* analysis. Cecal contents were streaked on the surface of mCCDA and incubated under microaerobic condition at 42 °C for 48 h²⁴.

Histopathology: For histomorphological analysis, tissue samples were taken from the jejunum, liver and spleen and

fixed in 4% buffered formalin for 48 h. The formalin fixed tissue was processed and stained using hematoxylin and eosin according to Lynch *et al.*²⁵.

RESULTS

A total of 200 samples were collected from 100 chickens as follows: 50 samples from the liver, 50 samples from the spleen and 100 cecal swab samples. Each sample was tested for the presence of *C. jejuni* by isolation on mCCDA followed by the confirmatory PCR-targeting *mapA* gene (Fig. 1). Sixty eight *C. jejuni* isolates were recovered (18 from the liver samples, 12 from spleen samples and 38 from cecal swab samples), with an overall prevalence frequency of 34% (68/200).

Virulence genes were determined by uniplex PCR-targeting *flaA* and *cdtA* genes. The *flaA* gene was identified in all *Campylobacter* isolates used in this study, while *cdtA* was identified in only 62 (91.17%) *Campylobacter* isolates (Table 3, Fig. 2-3).

Campylobacter were successfully isolated from chicken ceca after infection in 2-week-old chicks. We identified several histopathological changes in the chicken gut from infection. There were alterations in the small intestinal architecture including, loss of tips, thickening and shortening of villi, inflammatory cell infiltration, sub-epithelial edema and edema and hemorrhage in serosal blood vessels (Fig. 4-6). However, no pathological changes were found in the liver and spleen.

Table 2: Cycling conditions of the primers during PCR

Genes	Primary denaturation		Secondary denaturation		Annealing		Extension		Final extension		
	°C	Min	°C	Sec	°C	Sec	°C	Sec	No. of cycles	°C	Min
<i>mapA</i>	94	5	94	30	55	45	72	45	35	72	10
<i>flaA</i>	94	5	94	30	53	45	72	50	35	72	10
<i>cdtA</i>	94	5	94	30	55	30	72	30	35	72	7

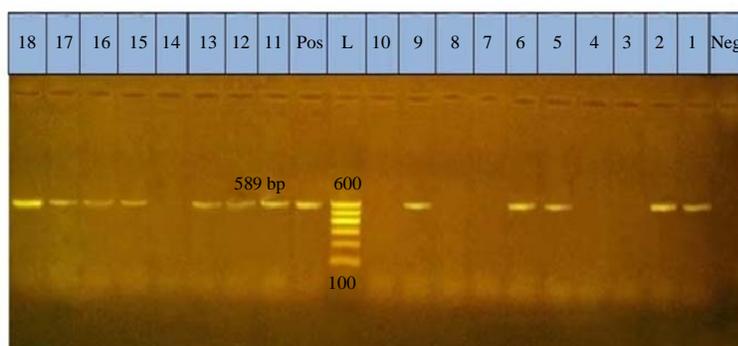


Fig. 1: Agarose gel electrophoresis showing amplification of 589 bp fragment *mapA* gene

L: Ladder, Lane: 1, 2, 5, 6, 9, 11, 12, 13, 15, 16, 17 and 18 positive for *mapA* gene, Neg: Negative control, Pos: Positive control

Table 3: Prevalence of *Campylobacter jejuni* in chicken samples

Type of samples	No. of samples	Positive samples		<i>flaA</i>		<i>cdtA</i>	
		No.	Percentage	No.	Percentage	No.	Percentage
Cloaca swabs	100	38	38	38	100	37	97.36
Liver	50	18	36	18	100	16	88.88
Spleen	50	12	24	12	100	9	75
Total	200	68	34	68	100	62	91.17

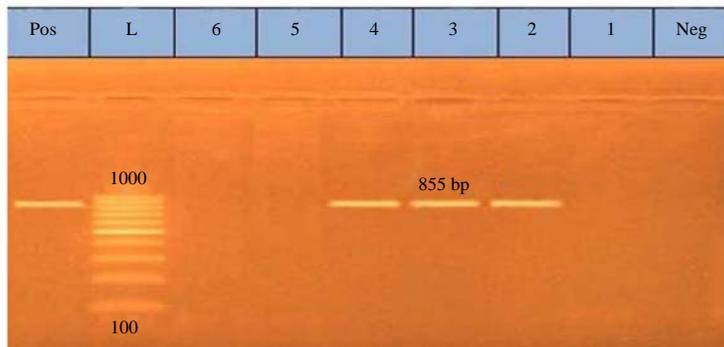


Fig. 2: Agarose gel electrophoresis showing amplification of 855 bp fragment *flaA* primer
L: Ladder, Lane: 2, 3 and 4 positive for *flaA* gene, Neg: Negative control, Pos: Positive control

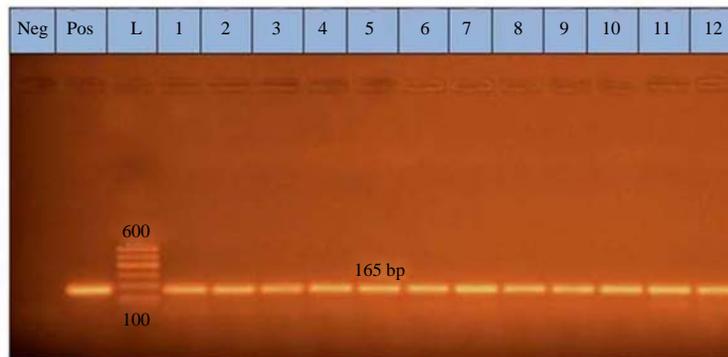


Fig. 3: Agarose gel electrophoresis showing amplification of 165 bp fragment of *cdtA* gene
L: Ladder, Lane: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 and 12 positive for *cdtA* gene, Neg: Negative control, Pos: Positive control

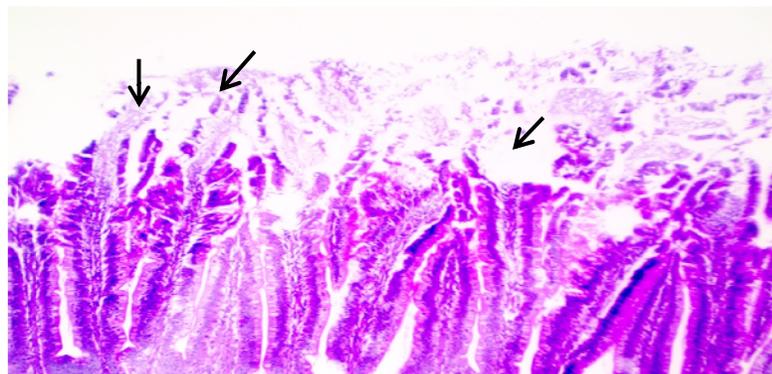


Fig. 4: Small intestine shows loss of tips of villi HE, \times : 100 arrows

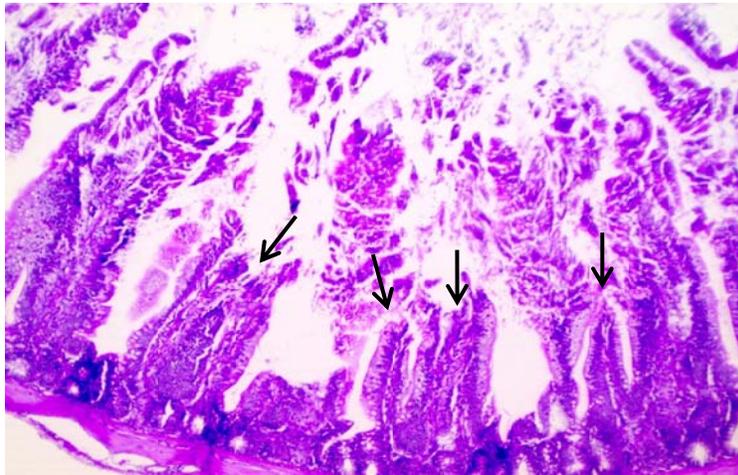


Fig. 5: Small intestine in broiler showing thickening and shortening of some villi HE, \times : 200

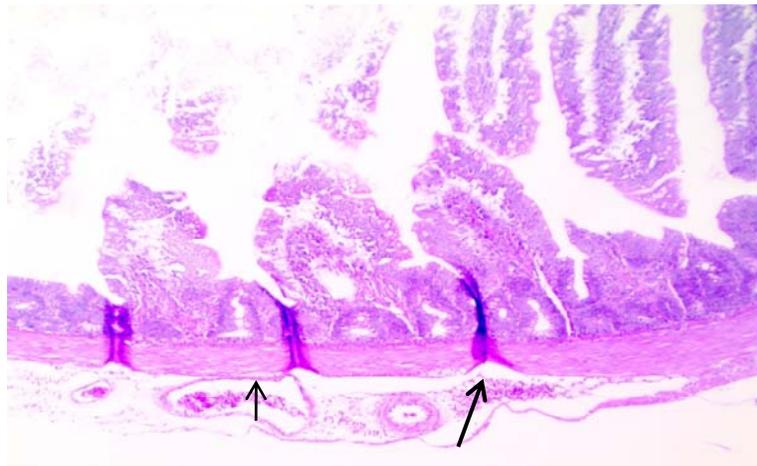


Fig. 6: Small intestine showing: Congestion and edema asterisk and hemorrhage in serosal blood vessels. HE, \times : 100

DISCUSSION

The presence of *C. jejuni* in internal organs indicates that *Campylobacter* can cross the intestinal barrier of animals and humans through bacterial translocation, which may occur via the lymphatic path or venous system¹¹. In this study, the isolation rate of *C. jejuni* (34%) was relatively high, which indicates that this may be a significant avian pathogen; these results are consistent with previous studies²⁶⁻²⁹. *Campylobacter jejuni* was isolated from cloacal swabs, as well as the liver and spleen, which is also consistent with previous studies³⁰⁻³². *Campylobacter* frequency may vary from one country to the other depending on many factors, such as hygienic measures and seasonal variations.

The *flaA* gene is involved in the invasion of the intestinal mucosa³³. Therefore, its absence indicates severe reduction in motility and colonization of the human and chicken gut³⁴. In this study, PCR showed that the *flaA* gene was present in all isolated *C. jejuni* strains, which is consistent with previous studies³⁵⁻³⁷.

Cytolethal distending toxin is conserved among *Campylobacter* strains and causes direct DNA damage, which leads to induction of DNA damage checkpoint pathways^{38,39}. Three genes, (*cdtA*, *cdtB* and *cdtC*), are required to produce CDT and complete cellular toxicity⁴⁰. In this study, 62 (91.17%) *C. jejuni* isolates carried the *cdtA* gene, which is in agreement with Bang *et al.*³⁷, who found that the frequency of these genes exceeds 90% in *Campylobacter* isolates from

different sources³⁷. In addition, Hanning *et al.*³⁶ reported that all *Campylobacter* isolates test were positive for the presence of *cdtA* and *flaA*³⁶.

The role of CDT in pathogenesis is undistinguishable; however, there are many studies on its toxic effect on cultured mammalian cells^{16,41,42}. According to a study conducted in Bangladesh by Talukder *et al.*⁴³, CDT was identified as a virulence determinant which lead to increase fluid secretion in the intestine that causes diarrhea.

In the current study, experimental infection of commercial chickens with *C. jejuni* was associated with intestinal inflammation and pathological changes which is a harmful pathogen. Histopathological examination revealed many pathological changes including villi atrophy, which could explained by production of cytolethal distending toxin⁴⁴. However, the role of other bacteria in the intestinal microbiota cannot be excluded^{45,46}.

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SIGNIFICANCE STATEMENT

This study shows that *Campylobacter* infection is associated with intestinal inflammation and other pathological changes. This study revealed significant effects of *C. jejuni* infection on commercial chickens. These findings confirm that *C. jejuni* can have a significant effect on poultry health and welfare and is a harmful gut commensal microorganism. Thus, strict control measures are required to reduce its colonization.

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