ORIGINAL ARTICLE

CONTENTS

Exploring the Association of *Campylobacter jejuni* with inflammatory bowel diseases: insight from a clinical study

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ABSTRACT

Aim: To demonstrate a possible association between *Campylobacter jejuni* and inflammatory bowel disease Iraqi patients.

Materials and methods: The study involved two groups. The inflammatory bowel disease patient group consisted of 90 participants. This group was further classified into two subgroups: Crohn's disease (n) and Ulcerative colitis (n). The control group consisted of 90 healthy participants who had no history of inflammatory bowel disease. Age and gender distributions in inflammatory bowel disease patient and control groups were computed. The association between inflammatory bowel disease and *C. jejuni* was determined by identifying the bacterial infection using various detection methods, including culturing, biochemical tests and real-time PCR (Polymerase chain reaction). The association was further assessed by comparing the symptoms of IBD patients and *C. jejuni* positive samples.

Results: Finding of the conventional identification showed 5% prevalence of *C. jejuni* among inflammatory bowel disease patients whereas the real-time Polymerase chain reaction. Results showed significantly higher prevalence. Based on real-time Polymerase chain reaction. Results, a significant association was found between *C. jejuni* infection with inflammatory bowel disease and Crohn's disease patients (P-value=<0.001).

Conclusions: No significant differences observed in detection of inflammatory bowel disease and Crohn's disease using conventional and molecular methods. The study provides valuable insights into a possible association between *C. jejuni* and inflammatory bowel disease.

KEY WORDS: *C. jejuni,* inflammatory bowel disease, culturing, biochemical test

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ABBREVIATIONS

IBD - Inflammatory Bowel Disease
CD - Crohn's Disease
UC - Ulcerative Colitis
PCR - Polymerase Chain Reaction

INTRODUCTION

Inflammatory Bowel Disease (IBD) is a recurring inflammatory disorder that affects the gastrointestinal system. It comprises two main types: Crohn's disease (CD) and ulcerative colitis (UC). IBD is most prevalent in North America and Western Europe, with a rate of 0.3%. However, in recent year, there has been an increase in its occurrence in other regions globally, making it a significant healthcare concern worldwide [1], while IBD can affect individuals of all age groups, it tends to be more commonly diagnosed in late adolescents and young adults [2]. This particular age bracket seems to be more susceptible to developing IBD, although it can still occur at any age. Furthermore, there is a notable gender-based variation in the distribution of IBD within this demographic. Studies have shown that IBD can affect both males and females, but the prevalence and disease patterns may differ between the genders. For instance, males tend to have a higher incidence of Crohn's disease, while females have a higher incidence of ulcerative colitis. The reasons for these gender-based differences are not yet fully understood and require further research [2-6]. Though the specific cause of IBD is still unknown, it is believed to be a consequence of a patient's genetics, microbiome, immunological response, and environment, which generate an excessive and inappropriate immune reaction to commensal flora in genetically predisposed individuals [7-9]. Previous studies have indicated a connection between IBD and microbes in patients with IBD [1, 7]. *C. jejuni* is one of the reported causes of gastroenteritis in humans [7]. The disruptive nature of *C. jejuni* infections on normal gut homeostasis have been unveiled, which, in turn, is believed to contribute to the development of IBD [8]. Despite efforts to implement treatment measures, the prevalence of

C. jejuni infections continues to escalate globally. In Iraq, as in numerous other nations, IBD constitutes a prevailing health concern, posing significant challenges to human well-being [9-10], however, despite its substantial impact, the research landscape concerning the relationship between IBD and the bacterium *C. jejuni* remains notably underexplored. Addressing this research gap in the etiology of IBD is imperative not only for expanding our scientific understanding of its etiology in a specific region but also for potentially developing improved diagnostic and therapeutic strategies that are specifically tailored to the unique healthcare landscape of the country in question. The identification and confirmation of *C. jejuni* in clinical samples involve a multifaceted strategy encompassing several techniques. The process usually initiates with the isolation and culture of the bacteria on selective media. Subsequently, a combination of biochemical and molecular tests is used to confirm the existence of the pathogen [11]. The clinical presentation of IBD is known to appear differently among affected person, with symptoms ranging from abdominal pain and diarrhea to more serious indication, such as weight loss and rectal bleeding [12]. Contrasting the symptom profiles of IBD patients to those individuals carrying positive *C. jejuni* samples can contributes to a more nuanced understanding of the potential effects of bacterial presence on symptomatology. This clinical study aimed to provide insights in to the possible association of *C. jejuni* with IBD through the detection of the bacteria in stool samples of local patients with IBD diseases. Strain typing of *Campylobacter conscious* has previously been done using a variety of typing techniques, including multi-locus sequence typing (MLST) and amplified fragment length polymorphisms (AFLP) 23 S rRNA PCR [13]. Multilocus sequence typing (MLST) is a commonly used typing technique that may identify population patterns and lineages in microorganisms [14]. Research has demonstrated that MLST has a good discriminatory power for *Campylobacter jejun*i, *Campylobacter coli*, and developing *Campylobacter* species. The ease with which sequence data can be shared across laboratories for use in international epidemiological research is one of the benefits of MLST [15]. This includes the identification of the bacteria within the studied groups through conventional and real time PCR techniques, also examined the clinical symptoms of IBD patients in comparison to individuals who had positive *C. jejuni* samples.

MATERIALS AND METHODS

SAMPLES PREPARATION

The study included a total of 180 participants, 90 diagnosed with IBD by specialist in gastroenterology comprising the patient group. The remaining 90 participants were apparently healthy individuals and formed control group. The samples for the study had been collected during a period ranging from December 2022 to the end of March 2023, from Al-Imamain Al-Kadhimain Medical City. The study was conducted in the laboratories of Microbiology Department in the College of Medicine-Al-Nahrain University.

INCLUSION CRITERIA

Inclusion criteria were taking samples from patients with IBD over than 18 years old, while exclusion criteria were avoiding patients have or had previously any type of malignancy, or have other disease such as muscular dystrophy (MD), thyroid disorder, congenital adrenal disease, and renal disorder, any congenital or inherited metabolic disorder. Also, pregnant or lactating women and patient on antibacterial drugs with the last three days were avoided. Small quantities of diarrheal stool samples were collected from all participants by plastic spoon and transferred to pre-labeled clean dry plastic container with locked cup under sterile condition. Samples were then transported to the laboratory in cool box within three hours of collection [16].

ETHICAL APPROVAL

This study was approved by the Institutional Review Board of the College of Medicine; Al-Nahrain University under the number 239 and date 30/7/2019.

BACTERIAL IDENTIFICATION

CONVENTIONAL METHOD

Totally, 5 g of freshly collected faucal sample was pre-enriched by suspending the faeces in 45 ml buffered nutrient broth and incubating the suspension at 42°C for 18 hours in a 50-ml closed culture tube were immediately inoculated onto the chromogenic medium CASA (AES Chemunex, France) proved highly efficient for *C. jejuni* and incubated to 48 hours at 42°C under conditions that were microaerophilic .Gram staining, microscopy examination, and Oxidase, catalase, and indoxyl hydrolysis biochemical tests were used to confirm the identity of the suspected colony. The same colonies were tested for cytochrome oxidase enzyme production by placing a portion of the test colony onto oxidase paper impregnated with NNN'N' tetramethyl-p-phenylene-diamine dihydrochloride (Oxoid, Basingstoke, UK). Purple color change was recorded as positive reaction. Reactive colonies were processed for DNA and a portion stored in skimmed milk at -80°C for further characterization [17]. Following this, a series of biochemical assessments were performed, encompassing glucose fermentation, nitrate reduction, oxidase and catalase tests, as well as hippurate hydrolysis tests [18-20].

DNA PREPARATION

Strains isolated from our hospital were cultured in brain-heart infusion (BHI) broth medium and shaken in an oscil-

Table 1. Primer sequence and PCR product

Gene	Primer	Amplified DNA fragment
CAMP-JEJUNI	F: 5′-TAAAAGCGGTGGATTTGGAC-3› R: 5′-CTTTTTCCTTTTTGCCACCA-3′	167 bp

Source: compiled by the authors of this study

Table 2. PCR reaction solution for detection of CAMP-JEJUNI

Component	Volume [µL]
GoTaq® qPCR Master Mix	10
Forward Primer	0.5
Reverse Primer	0.5
Supplemental CXR Reference Dye	0.2
DNA template	4
Nuclease-Free Water	4.8
Total volume	20

Source: compiled by the authors of this study

Table 3. Real-time PCR protocol

No.	Steps	Temperature	Time	Cycle No.
1	Initial denaturation	94˚C	6 min	1
2	Denaturation	94˚C	40 sec	35 cycles
3	Annealing	56 ˚C	45 sec	
4	Extension	72 ˚C	1 min	
5	Final extra extension	72 ˚C	10 min	1

Source: compiled by the authors of this study

Table 4. Account of IBD patient group and control group based on sex and age

Demographic Data			Study groups		P value
			IBD Patient	Control	
Age	(Mean ±SD) years		34.21±10.16	33.47±11.06	0.778
	(Min-Max)		(19-57)	(18-70)	
Sex	Female	n	36	42	0.215*
		[%]	45.0	52.5	
	Male	n	44	38	
		[%]	55.0	47.5	

*P value less than 0.05 was considered as statistically significant

Source: compiled by the authors of this study

Table 5. Growth of *C. Jejuni* in Skirrow's medium

lator at full temperature of 37°C for 20–24 h. DNA was then extracted using a bacterial genomic DNA extraction kit to prepare for subsequent experiments. DNA extraction .The bacterial genomic DNA extraction kit used in this paper was purchased from Alpha DNA Ltd. (Canada).

REAL TIME PCR METHOD

Extraction of DNA from the entirety of stool samples was executed meticulously, adhering to the comprehensive guidelines provided by the Geneaid Presto Stool DNA Extraction Kit. Using a LAMBDA Bio PLUS, the concentrations and purities of the extracted DNA were calculated from the absorbance at 260 nm (A260) and the A260/A280 ratio. Spectrophotometer (Perkin-Elmer, Norwalk, CT, USA), and sterile deionized water was used to dilute the DNA to the proper quantities. Assessment of DNA concentration and subsequent purification steps were meticulously conducted through employment of the Nano-drop system. Designing of primers was performed using the robust Primer 3plus software. These primers, specifically designed for the V4 region, underwent a meticulous validation process, inclusive

Bacteria culture	n	[%]
No growth	76	95.0
Growth	4	5.0
Total	80	100

Source: compiled by the authors of this study

Table 6. Occurrence of *C. jejuni* in IBD patients according to disease type

C. jejuni		IBD		P value
		Crohn's disease	Ulcerative colitis	
		[%]	[%]	
Bacteria culture	No growth	97.4	92.9	0.347*
	Growth	2.6	7.1	

*P value less than 0.05 was considered as statistically significant
Source: compiled by the authors of this study

Table 7. PCR detection of *C. jejuni* in studied groups

Bacteria		Study Groups		P value
		IBD	Controls	
C. jejuni [copy/m]	Median	796.68	370.34	<0.001*
	Percentile 05	193.22	32.5	
	Percentile 95	5685.9	2340.02	

* P value less than 0.05 was considered as statistically significant
Source: compiled by the authors of this study

of scrutiny under the University Code of Student Conduct (UCSC) programs, alongside alignment with corresponding reference sequences housed within the National Center for Biotechnology Information (NCBI) database. The synthesis and lyophilization of these primers were entrusted to the expertise of Alpha DNA Ltd. (Canada), (Table 1).

A total of 40 µL of the PCR mixture were spun down with a minicentrifuge. PCR protocol (Table 3).

COMPARING CLINICAL SYMPTOMS IN INDIVIDUALS WITH IBD AND C. JEJUNI POSITIVE SAMPLES

The symptom data from the IBD patients were collected and compare with signs exhibited in samples that indicate a positive presence of *C. jejuni* [19].

RESULTS

AVERAGE AGE AND GENDER DISTRIBUTION IN IBD PATIENTS

The average age of individuals in both studied groups was computed, the mean age among individuals diagnosed with IBD is 34.21±10.16 years and among healthy individuals is 33.47 ± 11.06. Examining the gender distribution within this cohort, males accounted for a predominant 55% representation, while females constituted 45%. Statistical analysis indicated that no statistically significant disparities, bearing a P-value of less than 0.05, emerged between the patient cohort and the control group in relation to both age and gender (Table 4).

BACTERIAL DETECTION

CONVENTIONAL IDENTIFICATION OF C. JEJUNI

The outcomes arising from the cultivation of *C. jejuni* showed that the bacterial growth rate stood at approximately 5% within the studied samples. In contrast, the control group presented an entirely negative outcome, with no occurrences of *C. jejuni* (Table 5).

Notably, the prevalence of *C. jejuni* growth exhibited distinct patterns based on the subcategories of the disease. For example, among individuals diagnosed with Crohn's disease, the presence of *C. jejuni* was observed in approximately 2.6% of cases. While the occurrence of *C. jejuni* growth within the subset of individuals afflicted by ulcerative colitis, registered at a relatively higher rate of 7.1%. However, these observed differences were not found to be statistically significant (P-value <0.05) (Table 6).

The dark field or phase contrast preparations showed that all bacterial isolates have a distinctive darting motility. Gram stain preparations revealed Gram negative, curved or spiral rods. All isolates were positive for reduced nitrate, oxidase and catalase, indoxyl acetate and hippurate-tests, while were

Table 8. Molecular detection of *C. jejuni* in IBD types

		IBD		P Value
		Crohn's disease	Ulcerative colitis	
C. jejuni (copy/mL)	Median	834.14	758.52	0.583
	Percentile 05	177.4	198.35	
	Percentile 95	5478.3	5893.5	

Source: compiled by the authors of this study

Table 9. Signs and symptoms of IBD patients in association with C. *jejuni*

Signs and symptoms	Bacteria culture								P value
	No Growth				Growth				
Bloody diarrhea	Present		Absent		Present		Absent		0.408*
	n	[%]	n	%	n	[%]	n	[%]	
	34	97.1	42	93.3	1	2.9	3	6.7	
Smoking	Yes		No		Yes		No		0.647
	n	[%]	n	[%]	n	[%]	n	[%]	
	17	94.4	59	95.2	1	5.6	3	4.8	
Abdominal pain	Present		Absent		Present		Absent		0.608
	n	[%]	n	[%]	n	[%]	n	%	
	25	96.2	51	94.4	1	3.8	3	5.6	
Biology Therapy	Yes		No		Yes		No		0.728
	n	%	n	%	n	%	n	%	
	6	100.0	70	94.6	0	0.0	4	5.4	
Behavior	B1		B2		B1		B2		0.136*
	n	[%]	n	[%]	n	[%]	n	[%]	
	26	100.0	11	91.7	0	0.0	1	8.3	
UC extent	No Growth						Growth						0.280*
	E1: Ulcerative proctitis		E2: Left sided UC		E3: Extensive UC		E1: Ulcerative proctitis		E2: Left sided UC		E3: Extensive UC		
	n	[%]	n	[%]	n	[%]	n	[%]	n	[%]	n	[%]	
	28	93.3	3	75.0	8	100.	2	6.7	1	25.0	0	0.0	
CD location	L1: Ileal		L2: Colonic		L3: Ileocolonic		L1: Ileal		L2: Colonic		L3:Ileocolonic		0.630
	n	[%]	n	[%]	n	[%]	n	[%]	n	[%]	n	[%]	
	8	100.0	10	100.0	19	95.0	0	0.0	0	0.0	1	5.0	

*P value less than 0.05 was considered as statistically significant
Source: compiled by the authors of this study

negative for glucose fermentation. This preliminary diagnosis therefore further designated the bacteria as *C. jejuni,* according [20]. This distribution of *Campylobacter* species is consistent with findings from earlier studies conducted in industrialized and developing nations, including Out of the 580 stool samples that were gathered from 11 Kibera schools, 294(51%) of them fit the suspicious Campylobacter spp. phenotype. Upon subjecting these isolates to PCR Campylobacter spp. were identified in 106(18%) of the isolates by means of genus- and species-specific primers. Of the 106 isolates, 28(4.8%) and 44(7.6%) were of the type *C. jejuni* [21].

QUANTITATIVE PCR ANALYSIS OF C. JEJUNI

The utilization of a quantitative PCR approach in this study provided a precise assessment of the presence of *C. jejuni*. The results revealed a noteworthy disparity between the cohort of individuals diagnosed with IBD and the control group. Upon conducting in-depth analysis, a statistically significant difference in the occurrence of *C. jejuni* between these two groups was observed (P-value <0.05) (Table 7).

Conversely, the statistical analysis of the tabulated data revealed a lack of statistically significant differ-

Table 10. Signs and Symptoms of IBD Patients in association with C. *jejuni*

Signs and symptoms		C. jejuni (copy/mL)		
		Median		Percentile 05-95
Abdominal pain	Absent	809.81	177.40	5893.50
	Present	796.68	198.35	4298.66
	P value		0.906	
Smoking	No	851.00	239.60	5893.50
	Yes	607.33	188.09	4298.66
	P value		0.345*	
Bloody diarrhea	Absent	794.33	198.35	5478.30
	Present	813.31	188.09	5893.50
	P value		0.996	
Biology therapy	No	796.68	188.09	5478.30
	Yes	1199.53	198.35	19372.22
	P value		0.465*	
Behavior	B2: stricturing	857.17	124.36	36987.00
	B1: nonstricturing, nonpenetrating	831.79	277.30	4396.32
	P value		0.792	
UC extent	E1: Ulcerative proctitis	843.97	323.78	14852.30
	E2: Left sided UC	793.19	569.30	1642.04
	E3: Extensive UC	420.99	152.07	960.35
	P value		0.048*	
CD location	L1: Ileal	787.32	319.98	5478.30
	L2: Colonic	696.91	124.36	36987.00
	L3: Ileocolonic	892.28	251.20	3595.20
	P value		0.815	

*P value less than 0.05 was considered as statistically significant
Source: compiled by the authors of this study

ence between the two subgroups, Crohn's Disease (CD) and Ulcerative Colitis (UC) within IBD patients (P-value > 0.05), as shown in Table 8.

A COMPARATIVE ANALYSIS OF CLINICAL MANIFESTATIONS BETWEEN IBD PATIENTS AND *C. JEJUNI* POSITIVE SAMPLES

Based on the conventional method results and the statistical analysis conducted, it was found that there was no significant association between signs and symptoms of IBD with and smoking, ulcerative colitis (UC) extent, bloody diarrhea, abdominal pain, use of biological therapy, behavior, CD (Crohn's disease) location (P-value > 0.05), (Table 9).

However, according to the Real time PCR results, signs and symptoms of IBD with *C jejuni* were not correlated with abdominal pain, smoking, bloody diarrhea, behavior, CD location, while were significantly correlated in UC extent (P-value <0.05), (Table 10).

DISCUSSION

AVERAGE AGE AND GENDER DISTRIBUTION ANALYSIS IN IBD PATIENTS

The exact cause of IBD is not well understood, but it is believed to involve a combination of genetic, environmental, and immune system factors. IBD can affect individuals of any age but often presents itself between the ages of 15-30 years [22]. This is consistent with the findings of our study as the mean age of patient group was 34 years. One of the potential factors could indeed contribute to the increased diagnosis of IBD at older ages is the increased awareness among both patients and healthcare providers. As medical technology and awareness have advanced, more individuals might be seeking medical attention for their gastrointestinal symptoms, which in turn leads to more diagnoses being made across a broader age range [23]. Regarding the distribution between males and females, no statistically significant difference in the number of affected males and females, observed little increase in number of affected males over

females. This was consistent with previous studies, which adds credibility to the present study's findings [24-26]. The fact that there is a an increase in the number of males affected with IBD compared to females raises interesting questions about the potential underlying mechanisms and the factors contributing to this gender distribution. While the reasons for this observation might not be fully understood at this point, several hypotheses can be considered. One of them can be the immune response differences between genders which lead to differences in susceptibility to IBD [27]. Exploring the reasons behind such patterns can be crucial for understanding the disease, developing targeted treatments, and improving overall healthcare outcomes.

INTERPRETING THE CLINICAL SIGNIFICANCE OF CONVENTIONAL AND PCR FINDINGS IN IBD PATIENTS WITH *C. JEJUNI*

The results demonstrated the presence of *C. jejuni* in a subset of participants, with a notably higher prevalence observed using the real-time PCR method compared to conventional culturing methods. This underscores the importance of employing advanced molecular tools for accurate detection, which might otherwise be missed using traditional approaches [28]. According to the real time PCR results, there was a significant difference in the prevalence of *C. jejuni* between IBD patients and controls. Several studies also reported an increase in the distribution of *C. jejuni* in IBD patients comparing with the general healthy population. For example, Kaakoush and colleagues found a substantial correlation between *C. jejuni* infection and Crohn's disease compared to healthy controls in their meta-analysis study [29]. Similarly, the work of Barker *et al.* further supports the argument on a relationship between *C. jejuni* and IBD [30]. Their study demonstrated a higher prevalence of this bacterium in individuals with UC compared to healthy controls. The consistency in results across different studies reinforces the reliability of the observed association between *C. jejuni* and IBD. Several hypotheses in literature have been provided in how *C. jejuni* may contribute to the development or exacerbation of IBD, which reinforce the reliability of the observed association between *C. jejuni* and IBD. For instance, *C. jejuni* infection has been found to break an exaggerated immune response, represented by pro-inflammatory cytokines and activation of different immune cells. This may disrupt the balance of the gut microbiota and lead to chronic inflammation in infected individuals [31]. Additionally, *C. jejuni* exhibits surface structures that resemble some host antigens. This mimicry may trigger an autoimmune response, where the immune system attacks both the bacterium and the host's self-tissues, leading to inflammation and disease [32]. Furthermore, *C. jejuni* possesses the ability to adhere and invade intestinal epithelial cells, compromising the integrity of the intestinal barrier. This defect in the barrier can help bacterial translocation and trigger an immune response, hence chronic inflammation [33]. Interestingly, the study did not show significant variations in the detection of *C. jejuni* bacteria between the two types of IBD, UC and CD. This means that the potential contribution of *C. jejuni* may go beyond specific IBD subtypes, suggesting a wider impact on the disease process itself. According to our study, there is a significant correlation between female sex, shorter exclusive breastfeeding length, lower maternal age, lower maternal education, untreated drinking water, and inadequate sanitation and Campylobacter infections [34]. Although the presence of *Campylobacter* species is linked to growth deficiencies, birth weight for age is just a marginal predictor for these species.1. The prevalence of *Campylobacter* was higher in malnourished children from a case control study in Dhaka (6–23 months old) with weight-for-age z score (WAZ) <−2 than in healthy (control) children [weight-for-age z score (WAZ)>−1], but the adjusted effect size was not statistically significant [35]. Using the well-characterized human clinical *C. jejuni* isolate 81–176, another investigation showed that translocation of noninvasive bacteria is increased in C. jejuni-infected human intestinal epithelium [36]. In [37], we have found campylobacter in 5(5%) of our samples overall, additionally, campylobacter was found throughout Iraq, including in the city of Duhok. *Campylobacter* is one of four individuals with diarrhea who are segregated [38]. In the city of Mosul, an incidence of 6.3% of patients with diarrhea had *Campylobacter*. In the western Iraqi city of Ramadi, secluded *Campylobacter* at an 8.92% rate [39]. It is comparable to the findings of a study where the two researchers isolated Campylobacter from the city of Al-Duwaniyah. Using the technique of direct DNA isolation from feces, 100 infected patients had diarrhea, and the percentage of Campylobacter infection was (5.8%) [40] Conversely, a study conducted in India discovered that just 3.40 percent of the 88 participants had diarrhea, which is similar to our findings [41]. Compared to our investigation, current research in New Zealand discovered a negligible amount of *Campylobacter*, finding only 2.9% of all of her samples (1604) [42]. Our study's findings are different from those of Liang et al., who discovered that the lowest percentage of females (36.31%) and the highest percentage of males 63.69% [43], however, Karikari et al. indicate that 32.4% of men and 67.6% of women experienced diarrhea [44-45].

RELATIONSHIP BETWEEN C. JEJUNI INFECTION AND IBD SYMPTOMS

Current study also reveals a lack of significant correlations between certain signs and symptoms of IBD with *C. jejuni* infection and several features defined by the Montreal classification. This may indicate that *C. jejuni's* effect on IBD is not mainly determined by these particular clinical and categorization parameters. This highlights the multifactorial nature of IBD and the numerous complicated interactions that affect the disease development, progression, and symptoms.

CONCLUSIONS

This study clearly shows how crucial *Campylobacter jejuni* is to gastrointestinal health, especially when it comes to the emergence of post-infectious irritable bowel syndrome (IBS). It draws attention to the bacterium's rising prevalence worldwide, its significant effects on the gut microbiota, and the ensuing medical difficulties. It emphasizes the necessity of better epidemiological surveillance, the creation of targeted therapeutic approaches, and a more thorough comprehension of the host-pathogen relationship's dynamics. Examine how *Campylobacter jejuni* contributes to post-infectious IBS.

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CONFLICT OF INTEREST
The Authors declare no conflict of interest

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