Strain-specific virulence signatures of *Campylobacter jejuni* associated with watery versus

bloody diarrhea in the neonatal piglet model

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Abstract

Campylobacter jejuni is the leading cause of bacterial gastroenteritis globally, presenting with either watery or bloody/inflammatory diarrhea. Despite this clinical variability, the underlying mechanisms driving these distinct diarrheal manifestations remain unclear. The neonatal piglet model provides a unique opportunity to investigate these differences using strains with defined disease manifestations. We evaluated ten *C. jejuni* strains previously shown to cause consistent diarrheal manifestations in neonatal piglets: five strains associated with watery diarrhea and five associated with bloody/inflammatory diarrhea. The study found significant strain to strain variation among most assays, but overall strains associated with bloody/inflammatory diarrhea exhibited significantly higher levels of epithelial cell invasion, intracellular survival, macrophage survivability, and disruption of intestinal barrier integrity compared to watery diarrhea strains. Notably, both groups had similar levels of adherence, produced similar levels of cytolethal distending toxin (CDT) and elicited comparable IL-8 responses. While both groups facilitated translocation of commensal *E. coli*, only bloody/inflammatory strains caused increased paracellular permeability, as shown by TEER and FITC-dextran assays. This study reveals that there is significant variation in the virulence phenotype of *C. jejuni* strains and identifies several characteristics consistently associated with a specific diarrheal manifestation group. These findings provide new insights into the strain-specific pathogenic mechanisms of *C. jejuni*, with implications for understanding host-pathogen interactions and informing targeted diagnostic and therapeutic strategies.

Author Summary

Campylobacter jejuni is one of the most common bacterial causes of diarrhea worldwide, affecting millions each year. Infected individuals may experience either watery or bloody/inflammatory diarrhea, but the reasons why different strains cause different types of illness have remained a mystery. In this study, we used a neonatal piglet model, which accurately mimics human diarrheal disease, to investigate why certain *C. jejuni* strains cause more severe symptoms than others. We compared strains known to cause either watery or bloody diarrhea and found key differences in their ability to invade intestinal cells, survive inside immune cells, and damage the intestinal barrier. While both groups of strains could trigger inflammation and translocate *E. coli* through the intestinal lining, only the strains linked to bloody diarrhea caused significant barrier disruption and had increased intracellular survival. These findings reveal that different *C. jejuni* strains follow distinct paths during infection, which helps explain why they produce different symptoms. Unraveling these differences improves our overall understanding of *Campylobacter* pathogenesis that could lead to improved diagnostics and/or treatments to reduce the burden of campylobacteriosis around the world.

Introduction

Campylobacter jejuni is the leading cause of bacterial gastroenteritis worldwide, responsible for over 550 million cases annually[1]. In the United States alone, it affects more than 1.9 million people per year, imposing significant economic and public health burdens[2]. While typically self-limiting, C. jejuni infection can lead to long-term sequelae such as post-infectious irritable bowel syndrome (PI-IBS), reactive arthritis, and Guillain-Barré syndrome[3-5]. Increasing evidence also links Campylobacter to growth stunting in children from low- and middle-income countries due to chronic enteric infections[6-8].

Clinically, C. jejuni infection presents as watery or bloody/inflammatory diarrhea, with up to 27% of U.S. cases involving visible blood in stools[9]. Bloody/inflammatory diarrhea suggests deeper intestinal invasion and inflammation, often associated with more severe outcomes[10]. Despite decades of reporting this clinical distinction, the mechanisms driving these divergent diarrheal manifestations remain poorly understood. Several virulence factors have been proposed to influence disease severity, including enterotoxin production, cytotoxins like cytolethal distending toxin (CDT), and bacterial invasiveness[11-13]. However, no studies have definitively linked these traits to specific diarrheal outcomes. Clinical data are often confounded by subjective patient reporting and variable strain backgrounds, complicating direct comparisons. Additionally, many Campylobacter studies rely heavily on just a few clinical C. jejuni strains, most commonly NCTC11168, 81-176, or 81116[14, 15], which may unintentionally bias findings, given the well-documented heterogeneity in virulence factors across C. jejuni strains virulence factors[16-18].

The neonatal piglet model provides a robust platform for studying C. jejuni-induced diarrhea[19]. Unlike murine models, piglets exhibit human-like disease and can consistently replicate both watery and bloody/inflammatory diarrheal manifestations following infection with

specific *C. jejuni* strains[20, 21]. Additionally, piglets are recognized as strong alternatives to both

canines or non-human primates for non-rodent evaluations that are required by regulatory

agencies[22, 23], and also have intestinal functions physiologically similar to humans[24-26].

Utilization of this model allows for controlled, strain-specific comparisons with minimized host

variation. Healthy piglets typically do not develop disease when exposed to *C. jejuni*[27].

However, colostrum-deprived neonatal piglets consistently develop clinical symptoms such as

large intestinal lesions, inflammation, and diarrhea lasting up to six days depending on the *C. jejuni*

strain used for infection[28]. Similarly, gnotobiotic piglets infected with *C. jejuni* also display

symptoms of diarrhea and sloughing of epithelial cells from the mucosa in the cecum and colon

closely resembling human campylobacteriosis pathologies[20, 29]. Despite these advantages, the

use of piglets in *C. jejuni* research remains limited due to the high costs and specialized housing

requirements, leading many researchers to favor more accessible models such as mice, ferrets,

guinea pigs, or rats.

In this study, we leveraged the neonatal piglet model to investigate phenotypic differences between

C. jejuni strains that cause watery diarrhea compared to those that cause bloody/inflammatory

diarrhea. Using ten strains classified by the resultant diarrheal manifestation, we assessed virulence

traits including invasion, intracellular survival, epithelial barrier disruption, and

immunostimulation. Our goal was to evaluate these virulence and pathogenicity traits that may

relate to the differences in diarrheal presentation, advancing our understanding of *C. jejuni*

pathogenesis and informing new approaches to diagnosis or intervention.

Materials and Methods

Bacterial Culturing and Growth

C. jejuni strains used in this study are listed in **Table 1**. All strains were grown and maintained on Mueller-Hinton agar plates supplemented with 5% defibrinated bovine blood (MHB; Becton, Dickinson and Company Difco) for 48 hours at 37°C with 10% CO_2. Strains for assays that required liquid culture were grown in Mueller-Hinton broth (MH; Becton, Dickinson and Company Difco) with constant shaking (100 rpm) for 16-18 hours at 37°C with 10% CO_2. Assay control strains *Escherichia coli* DH5α and *Salmonella enterica* subspecies *enterica* serovar Typhimurium str. RM6835 were both grown aerobically either on Luria-Bertani (LB) agar (Fisher Bioreagents) at 37°C for 24 hours or in LB broth (Fisher Bioreagents) with constant shaking (100 rpm) at 37°C for 24 hours. For selective isolation of *Campylobacter* in select assays, *C. jejuni* strains were cultured on *Campylobacter* CEFEX agar, a modified MH agar with the addition of vancomycin (20 mg/L), polymyxin B (0.35 mg/L), trimethoprim (26.4 mg/L), sodium cefoperazone (20 mg/L) and amphotericin B (10 mg/L).

Cytolethal Distending Toxin (CDT) Assay

CDT activity was measured using a modified protocol from Abuoun et al[30]. Briefly, *C. jejuni* strains were grown overnight on MHB plates at either 37°C or 42°C under microaerobic conditions (10% CO_2). Bacterial growth was harvested by resuspending the entire plate in 5 ml of *Brucella* broth (Becton, Dickinson and Company, BBL). The suspension was centrifuged at $10,000 \times g$ for 20 minutes at 4°C. The supernatant was discarded, and the bacterial pellet was resuspended in 3 ml of Eagle's Minimum Essential Medium (EMEM; Corning) supplemented with 10% fetal bovine serum (FBS; Corning). The OD_{600} of the suspension was adjusted to 1.0 using EMEM +

10% FBS. Lysates were prepared by sonicating the suspension on ice using a QSonica sonicator

(20-second pulses, 20-second rests, five cycles total). The lysate was centrifuged at $10,000 \times g$ for

20 minutes at 4°C, and the supernatant was filter-sterilized using a 0.22 μm syringe filter (Fisher

Scientific) to remove viable bacteria. Sterile lysates were serially diluted two-fold (1:1 to 1:128)

in EMEM + 10% FBS. HeLa cells (ATCC CCL-2) were seeded into 96-well plates at 2×10^4

cells/ml in 100 μl of EMEM + 10% FBS and incubated for 3 hours at 37°C with 5% CO_2.

Subsequently, 100 μl of each dilution of filtered cell lysate was added to the HeLa cells. Plates

were incubated at 37°C with 5% CO_2 for five days. Following incubation, cells were fixed with

10% formalin and stained with 0.8% crystal violet. The CDT titer was defined as the reciprocal of

the highest dilution showing >50% cell distension. *E. coli* DH5α was used as a negative control.

Each strain was tested in three biologically independent assays (n = 3).

Attachment Assays

Attachment was assessed using three epithelial cell lines: non-polarized INT407 (ATCC CCL-6),

and polarized Caco-2 BBE (ATCC HTB-37) and T84 (ATCC CCL-248) cells. Cell lines were

seeded in 24-well tissue culture-treated plates (1 ml per well at 1×10^6 cells/ml) and incubated for

18 hours at 37°C with 5% CO_2. *Campylobacter* cultures were grown overnight in MH broth with

shaking (100 rpm) at 37°C in 10% CO_2. The OD_{600} was adjusted to 0.1 in the appropriate medium

for each cell line: EMEM + 10% FBS for INT407, EMEM + 20% FBS for Caco-2 BBE, and

DMEM/F-12 + 5% FBS for T84. Each well was washed twice with sterile PBS, then inoculated

with 1 ml of *C. jejuni* inoculum (approximately 1×10^8 CFU, multiplicity of infection (MOI) 100).

To enhance bacterial contact with host cells, plates were centrifuged at $600 \times g$ for 5 minutes then

incubated for 1 hour at 37°C with 5% CO_2. Wells were then washed twice with PBS to remove

non-adherent bacteria. Host cells were lysed by adding 1 ml of 0.1% Triton X-100 in PBS and

incubating for 10 minutes at room temperature. Lysates were serially diluted and plated on MHB

agar for CFU enumeration after incubation at 37°C in 10% CO_2 for 48 hours. Attachment

percentage was calculated as: (CFU recovered / CFU inoculated) × 100. Each strain was tested in

technical duplicates in three independent experiments (n = 3). Negative controls included two

wells inoculated with only sterile PBS. *E. coli* DH5α was used as a positive control. Due to

insufficient T84 cell growth, *C. jejuni* strain 81-176 was unable to be included in attachment assays

using this line.

Invasion assays

Enterocyte invasion was assessed using INT407, Caco-2 BBE, and T84 cells, following the same

seeding and infection conditions described for attachment assays. After overnight growth of *C.*

jejuni in MH broth at 37°C with 10% CO_2 and shaking (100 rpm), cultures were diluted to OD_{600}

= 0.1 in the appropriate medium for each cell line to achieve a MOI of 100. Each well of the 24-

well plates was washed twice with PBS and then inoculated with 1 ml of the bacterial suspension.

Plates were centrifuged at 600 × g for 5 minutes and incubated for 3 hours at 37°C with 5% CO_2

to allow for bacterial invasion. Following incubation, wells were washed twice with PBS, and 1

ml of cell line-specific medium containing gentamicin (250 µg/ml; Acros Organics) was added to

each well. Plates were incubated for an additional hour to eliminate extracellular bacteria. After

gentamicin treatment, wells were washed twice with PBS and then lysed with 1 ml of 0.1% Triton

X-100 in PBS. The lysates were serially diluted and plated on MHB agar, which was incubated at

37°C with 10% CO_2 for 48 hours. The percent invasion was calculated as: (CFU recovered after

gentamicin / CFU in initial inoculum) × 100. Each strain was assessed in technical duplicates in

three biologically independent experiments (n = 3). *Salmonella* Typhimurium strain RM6835 was

used as a positive control, and *E. coli* DH5α as a negative control. Every assay included two

uninoculated wells and were processed exactly as the positive and negative controls. Due to

insufficient T84 cell growth, *C. jejuni* strain 81-176 was unable to be included in invasion assays

using this cell line.

Macrophage Survivability

The ability of the different *C. jejuni* strains to survive intracellularly in macrophages was assessed

using J774A.1 mouse macrophages (ATCC TIB-67). Cells were seeded into 24-well plates at $1 \times$

10^6 cells/ml in 1 ml per well and incubated for 18 hours at 37°C with 5% CO_2 to establish

monolayers. Overnight MH broth cultures of each *C. jejuni* strain were prepared, adjusted to OD_{600}

$= 0.1$ (~1×10^8 CFU/ml) in DMEM + 10% FBS (J7774A.1 culture media), and added to each well

at an MOI of 100. Two wells were left uninoculated as negative controls. Plates were incubated at

37°C with 5% CO_2 for 24, 48, or 72 hours. At each time point, wells were washed twice with PBS

and then treated with 1 ml of gentamicin (250 μg/ml in DMEM + 10% FBS) for 1 hour to eliminate

extracellular bacteria. After treatment, wells were washed again, and macrophages were lysed by

adding 1 ml of 0.1% Triton X-100 in PBS. Lysates were serially diluted and plated on MHB agar,

incubated at 37°C with 10% CO_2 for 48 hours, and colonies enumerated. Each strain was tested in

two technical replicates across three independent biological assays (n=3). *C. jejuni* strain 81-176

was included as a positive control due to its known interaction with macrophages[31].

IL-8 ELISA and 24-hour Intracellular Survivability

T84 cells were seeded into 24-well plates at 5.5×10^5 cells/well and cultured for approximately 7

days until reaching 100% confluence. *C. jejuni* strains were grown overnight in MH broth and

diluted to $OD_{600} = 0.1$ in DMEM/F-12 with 5% FBS (T84 medium). Each well was infected with

1 ml of bacterial suspension ($\sim 1 \times 10^8$ CFU, MOI 100) and incubated at 37°C with 5% CO_2 for 3

hours. Following infection, wells were washed with PBS and treated with 1 ml of gentamicin (250

µg/ml in T84 medium) for 1 hour. Wells were then washed again, fresh medium was added, and

plates were incubated for 24 hours at 37°C with 5% CO_2. After 24 hours, media from each well

was collected, centrifuged at $12,000 \times g$ for 1 minute, and the supernatant stored at –80°C for

cytokine analysis. Human IL-8 levels were measured using the BD OptEIA™ ELISA kit (BD

Biosciences) per the manufacturer's instructions. To assess intracellular bacterial survival,

epithelial cells were lysed after supernatant removal by adding 1 ml of 0.1% Triton X-100 in PBS.

Lysates were serially diluted and plated on MHB agar. Plates were incubated at 37°C in 10% CO_2

for 48 hours, and colonies were counted. Each strain was evaluated in two technical replicates per

assay, with three independent biological replicates (n = 3). Due to insufficient T84 cell growth, *C.*

jejuni strain 81-176 was unable to be included in IL-8 and intracellular assays using this cell line.

Transepithelial Electrical Resistance (TEER)

To evaluate epithelial barrier integrity, transepithelial electrical resistance (TEER) was measured

using Caco-2 BBE cells. Cells were seeded at 2×10^5 cells per well into 0.4 µm pore-size Transwell

inserts (Falcon, Corning) placed in 24-well tissue culture-treated plates. Cells were cultured in

EMEM with 20% FBS at 37°C with 5% CO_2 until a confluent monolayer formed (TEER > 250

$\Omega \cdot cm^2$), typically by day 14. Monolayer integrity was assessed microscopically and with an

EVOM2 volt/ohm meter (World Precision Instruments). Following confluence, cells were

maintained for an additional 120 hours to promote tight junction maturation. Prior to infection,

TEER was recorded, and a cell count was performed using a hemocytometer to calculate the

bacterial concentration needed for MOI 100. *C. jejuni* cultures were prepared by growing strains

overnight in MH broth, adjusting to $OD_{600} = 0.1$, and diluting in Caco-2 BBE medium. From each

Transwell, 50 µl of media was removed from the apical compartment and replaced with 50 µl of

the corresponding *C. jejuni* inoculum ($\sim 5 \times 10^6$ CFU; MOI 100). Each strain was tested in duplicate

Transwells, with two uninoculated wells serving as negative controls (sterile medium only).

Infected plates were incubated at 37°C with 5% CO_2 for 72 hours. TEER measurements were taken

at 24, 48, and 72 hours using Millicell ERS-2 electrodes (Millipore). Electrodes were disinfected

and rinsed between each well using the following sequence: 10% bleach, sterile water (×2), 70%

ethanol, sterile water (×2), and pre-warmed media. Each *C. jejuni* strain was tested in duplicates

during three independent biological experiments (n = 3).

FITC-Dextran Translocation

To assess paracellular permeability to small molecules, a 4-kDa fluorescein isothiocyanate (FITC)-

dextran probe (Millipore Sigma) was applied to mature Caco-2 BBE monolayers grown on 0.4 µm

Transwell inserts in phenol red-free MEM (Gibco). Cells were seeded at 2×10^5 cells per insert

and cultured to confluence (TEER > 250 Ω·cm²), then maintained for an additional 120 hours to

allow tight junction maturation. Overnight *C. jejuni* cultures were adjusted to $OD_{600} = 0.1$ ($\sim 5 \times$

10^6 CFU) and used to inoculate the apical compartments (50 µl per insert, MOI 100). Two wells

were left as negative controls (sterile medium only). After 72 hours of incubation at 37°C with 5%

CO_2, 100 µl of media was removed from the apical compartment and replaced with 100 µl of 4-

kDa FITC-dextran solution (10 mg/ml in PBS). Plates were incubated for 3 hours, then 100 µl was

collected from the basolateral compartment and transferred to a black walled 96-well plate for fluorescence measurement. Fluorescence was measured using a SpectraMax M2 plate reader (Molecular Devices) with excitation at 490 nm and emission at 530 nm. Relative fluorescence units (RFUs) were blanked against sterile Caco-2 BBE medium. Each *C. jejuni* strain was tested in three biological experiments with two technical replicates each (n = 3).

Commensal Bacteria Translocation

The ability of *C. jejuni* to disrupt the epithelial barrier and promote translocation of non-invasive commensal bacteria was assessed using *E. coli* DH5α as a model commensal. Two experimental approaches were performed: (1) a 6-hour co-inoculation and (2) a 72-hour pre-infection with *C. jejuni* followed by 3-hour *E. coli* exposure. For both approaches, Caco-2 BBE cells were seeded at 1.5×10^5 cells/ml into 3 μm pore-size Transwell inserts and cultured to confluence (TEER > 250 Ω·cm²), with daily monitoring of TEER.

6-hour co-culture: Overnight cultures of *C. jejuni* and *E. coli* DH5α were grown and adjusted to $OD_{600} = 0.1$ (~5×10^6 CFU). The apical compartment was inoculated with 50 μl of each strain (MOI 100 per organism). After 6 hours of incubation, media from the basal compartment was collected and plated on MacConkey agar for *E. coli* and CEFEX agar for *C. jejuni*. CEFEX agar was incubated at 37°C with 10% CO_2 for 48 hours; MacConkey plates were incubated aerobically at 37°C for 24 hours. Each strain was tested in three independent biological experiments with two technical replicates each (n = 3).

72-hour pre-infection + 3-hour E. coli exposure: Caco-2 BBE cells were infected with *C. jejuni* as described for the TEER assay. After 72 hours, 50 μl of *E. coli* DH5α (MOI 100) was added to the apical compartment and incubated for an additional 3 hours. Basolateral media was collected

and plated as described above. Each strain was tested in three independent biological experiments

with two technical replicates per experiment (n = 3). To assess intracellular *C. jejuni* and *E. coli*,

the apical compartment was treated with gentamicin (250 µg/ml) for 1 hour, washed, and lysed

with 0.1% Triton X-100. Lysates were plated on CEFEX and MacConkey agar for quantification.

Translocation efficiency was calculated as: (CFU in basal compartment / CFU inoculated) × 100.

Statistical Analysis

Statistical analyses were performed using GraphPad Prism (v10.4.1) for comparisons between

diarrheal manifestations or RStudio (v2022.07.1) for comparisons between strains. All data were

tested for normality (Shapiro–Wilk test) and equal variance (Levene's test). For comparisons

between strains associated with watery and bloody/inflammatory diarrhea (n = 15 per group), the

non-parametric Mann–Whitney U test was applied. For comparisons across multiple strains or

conditions, non-parametric Kruskal–Wallis tests with Dunn's post hoc test were used. Compact

Letter Display (CLD) notation was used to visualize the results of the pairwise comparisons.

Strains that do not share a letter are significantly different from each other (p < 0.05), while strains

sharing the same letter are not significantly different. Letters were assigned using the

multcompView package in R, based on adjusted p-values. Statistical significance was defined as

p ≤ 0.05. Each assay included a minimum of three independent biological replicates per strain (n

= 3 per group), with technical replicates as noted. Data are presented as mean ± SEM unless

otherwise stated.

Results

***C. jejuni* strains associated with bloody/inflammatory diarrhea exhibit increased invasion and intracellular survival in epithelial cells.** To assess whether *C. jejuni* strains associated with distinct diarrheal phenotypes exhibit differences in virulence potential both on a strain-to-strain level and between groups, we compared five strains associated with watery diarrhea and five associated with bloody/inflammatory diarrhea (**Table 1**). All ten strains have previously been investigated in the neonatal piglet model to confirm their diarrheal manifestations *in vivo* (**Fig 1A-B**). Invasion assays were conducted using INT407, Caco-2 BBE and T84 cells. Significant differences were observed between several strains, notably, A9a was a significantly better invader of Caco-2 BBE and T84 cells than most other strains, particularly the watery diarrhea associated strains (Note: 81-176 was not tested with T84 cells), whereas all five of the watery diarrhea associated strains were poor invaders regardless of the cell line tested (**Fig 2A, Supplementary Fig S1A, Supplementary Fig S2A**). Interestingly, no significant differences were observed on a strain to strain level using INT407 cells. Invasion assays conducted in polarized Caco-2 BBE cell revealed significantly greater invasion by bloody/inflammatory associated strains compared to watery diarrhea strains (p = 0.0014; **Fig 2B**) Similar trends were observed using non-polarized INT407 cells (p = 0.0006; **Supplementary Fig S1B**) and T84 cells (p = 0.0063; **Supplementary Fig S2B**).

To evaluate whether increased invasion correlated with improved intracellular persistence, we measured viable intracellular bacteria at 24 hours post-infection in T84 cells. Strain to strain variation was observed among bloody/inflammatory strains M129 and A9a, where they displayed significantly higher intracellular survival than most other strains (**Fig 3A**). As a group,

bloody/inflammatory diarrhea associated strains exhibited significantly higher intracellular survival than watery diarrhea associated strains (p = 0.0007; **Fig 3B**).

Similar attachment of C. jejuni strains across intestinal cell lines. To determine whether differences in invasion were due to upstream differences in adherence, we assessed attachment efficiency after a 1-hour infection of epithelial cell lines INT407, Caco-2 BBE and T84. Few significant differences were observed between strains across INT407 (**Fig 4A**), Caco-2 BBE cells (**Fig 4C**) and T84 cells (**Supplementary Fig S3A**). There were no significant differences in attachment between watery and bloody/inflammatory diarrhea associated strains, regardless of the cell line used: INT407 cells (p = 0.20; **Fig 4B**), Caco-2 BBE (p = 0.14; **Fig 4D**), T84 cells (p = 0.90; **Supplementary Fig S3B**).

CDT production does not distinguish between watery and bloody/inflammatory strains. All *C. jejuni* strains in this study produced detectable CDT activity, as measured by the HeLa cell distension assay. We did not observe any strain variation in CDT production between watery and bloody/inflammatory diarrhea associated strains at either 37°C or 42°C (**Supplementary Fig S4A**). When compared as groups at 37°C, mean CDT titers were comparable between watery (geometric mean = 0.094) and bloody/inflammatory diarrhea associated strains (geometric mean = 0.086; p = 0.74; **Supplementary Fig S4B**). Due to the commensal relationship between poultry and *C. jejuni*, CDT production was also measured at the poultry internal body temperature of 42°C and here mean CDT titers were different between watery (geometric mean = 0.10) and bloody/inflammatory strains but not statistically significant (geometric mean = 0.041; p = 0.086; **Supplementary Fig S4B**).

Bloody/inflammatory strains exhibit greater 24-hour intracellular survival in T84 cells but
induce similar IL-8 responses. To evaluate whether differences in intracellular persistence
affected epithelial inflammatory signaling, we quantified human IL-8 production in T84 cell
supernatants at 24 hours post-infection and measured viable intracellular *C. jejuni* following
gentamicin treatment and lysis. IL-8 production was not significantly different between strains but
did show variability (**Supplementary Fig S5A**). Strain A9a induced the highest mean IL-8 levels
(1202.04 pg/ml), whereas D33a produced the lowest (437.03 pg/ml), highlighting strain-level
variability. Strains associated with bloody/inflammatory diarrhea demonstrated significantly
greater intracellular survival at 24 hours than watery diarrhea strains ($p = 0.0007$; **Fig 3B**). Despite
this, IL-8 secretion was not significantly different between groups: mean concentrations were
809.10 pg/ml for watery strains and 702.60 pg/ml for bloody/inflammatory strains ($p = 0.61$;
Supplementary Fig S5B).

Bloody/inflammatory strains more profoundly disrupt epithelial barrier function over time. To
assess whether *C. jejuni* strains differ in their capacity to disrupt epithelial barrier integrity, we
measured TEER in polarized Caco-2 BBE monolayers at 24-, 48-, and 72-hours post-infection.
Across 24-, 48- and 72-hours, strains A14a, A13a and S3 had the lowest changes in TEER while
strains A9a, M129 and 81-176 had the highest changes in TEER (**Fig 5A**). When grouped by
diarrheal manifestation, bloody/inflammatory diarrhea associated strains caused a significantly
greater reduction in TEER at all time points. At 24 hours, TEER decreased by an average 15.9%
compared to 4.03% in watery diarrhea associated strains ($p < 0.0001$; **Fig 5B**). Differences
remained significant at 48 hours (27.1% verses 10.7%; $p < 0.0001$) and 72 hours (43.4% verses
18.3%; $p < 0.0001$).

Bloody/inflammatory strains increase paracellular permeability to small molecules. To directly measure functional barrier permeability, we quantified apical-to-basolateral flux of 4-kDa FITC-dextran across polarized Caco-2 BBE monolayers following 72-hour infection. Strain-specific permeability values were observed to be highest among strain A9a (a bloody/inflammatory strain) while the lowest was observed among strain A13a (a watery diarrhea associated strain; **Fig 6A**). Infection with bloody/inflammatory strains resulted in a 2-fold higher FITC-dextran translocation compared to watery strains (p = 0.0027; **Fig 6B**).

C. jejuni promotes translocation of commensal E. coli across the epithelial barrier. We next assessed whether barrier disruption by *C. jejuni* strains altered host susceptibility to microbial translocation. Using polarized Caco-2 BBE monolayers in Transwell inserts, we evaluated whether a non-invasive commensal strain of *E. coli* (DH5α) could cross the epithelial barrier during or after infection with *C. jejuni* strains. Two experimental approaches were tested: (i) co-inoculation of *C. jejuni* and *E. coli* for 6 hours, and (ii) pre-infection with *C. jejuni* for 72 hours followed by 3-hour exposure to *E. coli*. In both models, *E. coli* translocation was observed among all strains and there were no significant differences between strains (**Supplementary Fig S6A, S6C**). During co-inoculation, the mean *E. coli* CFU recovered from the basal chamber was not significantly different between bloody/inflammatory and watery diarrhea associated strains (p = 0.66; **Supplementary Fig S6B**). In the sequential infection model, basal recovery of *E. coli* was more pronounced, but no significant difference was observed between bloody/inflammatory and watery diarrhea associated strains (p = 0.30; **Supplementary Fig S6D**).

Strains associated with bloody/inflammatory diarrhea demonstrate enhanced intracellular survival in macrophages. To investigate whether there was strain variation in the interactions with innate immune cells, we measured intracellular survival of the *C. jejuni* strains in J774A.1 murine macrophages at 24-, 48-, and 72-hours post-infection. There were significant differences between strains at all time points. Notably, strain A9a had the highest percent survivability across all time points while 81-176 had the lowest (**Fig 7A, 7C, 7E**). At 24 hours, viable intracellular *C. jejuni* was 2.6-fold higher among bloody/inflammatory diarrhea associated strains but there was no significant difference compared to watery diarrhea associated strains ($p = 0.23$; **Fig 7B**). At 48 hours post infection, bloody/inflammatory diarrhea associated strains showed significantly greater intracellular survivability ($p = 0.011$; **Fig 7D**). However, by 72-hours post infection, there was again no significant difference between bloody/inflammatory and watery diarrhea associated strains ($p = 0.43$; **Fig 7F**).

Discussion

Clinical outcomes associated with different *C. jejuni* strains vary widely, from mild, self-

limiting watery diarrhea to more severe presentations involving bloody and/or inflammatory

diarrhea, abdominal cramping, and fever[10]. While host factors such as immune status and

microbiota composition influence disease severity, accumulating evidence suggests that bacterial

strain differences also contribute significantly to clinical heterogeneity[6, 32]. However,

identifying phenotypic or molecular markers that distinguish high- and low-virulence *C. jejuni*

strains has proven challenging[33]. While group-level differences were clear, we observed notable

variation within each group, consistent with strain-to-strain variations from studies mentioned

previously. Some watery strains exhibited moderate invasion or barrier disruption, and not all

bloody/inflammatory strains displayed the most extreme phenotypes. A study by Law et al

performed invasion, attachment and macrophage survivability assays using six out of the 10 *C.*

jejuni strains used in this study[21]. In contrast to our study which used human intestinal epithelial

cells (Caco-2 BBE, INT-407 and T84), the previous study used non-polarized human epithelial

cells (HEp-2) that don't form tight junctions for attachment and invasion assays. Our study has

shown that different cell lines can provide very different results among *C. jejuni* strains.

Furthermore, macrophage survivability was only performed at 72 hours post infection, missing

significant differences at 48 hours that exist between watery and bloody/inflammatory diarrhea

associated strains. This study dramatically expands from the Law et al study by examining a more

detailed phenotypic analysis between *C. jejuni* strains, in addition to approaching the strains as

two groups with distinct diarrheal manifestations confirmed in neonatal piglets.

Using a neonatal piglet model, which closely recapitulates human *C. jejuni* associated

diarrheal disease[21, 29, 34], *C. jejuni* strains can be classified into two groups that consistently

induce a particular diarrheal manifestation of either watery diarrhea or bloody/inflammatory in the

neonatal piglet model[21, 34, 35]. The strains used in this study were chosen for their known

diarrheal manifestation as well as their varied source background of either clinical or poultry

sources. Given that poultry are the primary reservoirs of *C. jejuni*, our strains represent both mild

and severe infections that can arise from poultry. Individuals experiencing milder, self-limiting

symptoms such as watery diarrhea may be less likely to seek medical attention, leading to a lack

of clinical isolates. By comparing *in vitro* virulence traits, we found significant strain to strain

variation both within and between diarrheal manifestation groups, particularly among strains

associated with bloody/inflammatory diarrhea which consistently exhibited enhanced invasion,

intracellular persistence, epithelial barrier disruption and macrophage survivability, each a

hallmark of a more invasive and inflammatory disease mechanism.

Adherence to intestinal epithelial cells is one of the primary steps to initiating *C. jejuni*

infection[36, 37]. Here we found no significant differences in adherence levels between watery

and bloody/inflammatory diarrhea associated strains to small intestinal INT407 cells or polarized

large intestinal cells Caco-2 BBE and T84. Non-polarized cells such as INT407 cells lack a defined

brush border and other features such as tight junctions that are more representative of the epithelial

cells of the intestinal tract[38]. While as a group adherence levels were not significantly different,

there was strain to strain variation observed, particularly with strain M129 having higher adherence

levels than strains D33a, A9a, NCTC11168, and RM1221. Other studies have observed higher

INT407 adherence among *C. jejuni* strains associated with febrile diarrhea or those from clinical

sources compared to strains from patients without diarrhea/fever or from environmental

sources[39, 40]. Similarly, adherence levels were not significantly different between groups when

using Caco-2 BBE cells, a differentiated epithelial cell line originating from the human colon[41].

Using this cell line, there was lower strain to strain variation, where only 81-176 had significantly

lower levels of adherence than strain A9a. Polarized cells such as Caco-2 BBE cells are able to

form polarized monolayers with microvilli, and tight junctions, in addition to displaying brush

border proteins that, despite being of colonic origin, are characteristic of small intestinal villus

cells, including villin, fimbrin and the terminal web proteins fodrin and myosin II[42-45].

Adherence to T84 cells was similar across all *C. jejuni* strains and no significant differences were

observed between diarrheal manifestation groups or between strains. T84 cells are derived from a

human colonic carcinoma and are highly polarized with short microvilli, tight junctions and

desmosomes between cells[46]. T84 cells offer a more accurate model of colonocytes due to their

retention of key colonic features, including high expression of colonic markers and the presence

of short microvilli characteristic of colonocytes[47]. Variation in the adherence of *C. jejuni* strains

among polarized and non-polarized tissue culture cell lines requires more investigations into the

mechanisms driving this individual strain variation. However, our findings support that both

watery and bloody/inflammatory diarrhea associated strains are able to attach at similar levels to

intestinal epithelial cells from the small and large intestine, however their invasiveness once at that

epithelial surface is where they really differ.

Invasion has long been regarded as a hallmark of *C. jejuni* pathogenesis and has been

studied extensively in tissue culture models[37, 48-51]. In the present study we found that

bloody/inflammatory diarrhea associated strains demonstrated significantly higher invasiveness of

both non-polarized and polarized intestinal epithelial cells. While the individual invasiveness of

bloody/inflammatory diarrhea strains varied, there were few significant differences between

strains from the same diarrheal manifestation, as all bloody/inflammatory diarrhea associated

strains were invasive and all watery diarrhea associated strains were poor to non-invasive. Several

groups have also observed variation in the invasiveness of *C. jejuni* strains. Everest et al (1992)

found that *C. jejuni* clinical isolates from patients with colitis were more invasive than isolates

from patients with non-inflammatory diarrhea[52]. Strain dependent invasiveness has also been

observed using environmental strains compared to clinical strains, where clinical strains were

found to be significantly more invasive[40]. Even intra-strain invasiveness has been found,

particularly among continuously passed laboratory strains. For example, the clinical strain 81-176

has been reported to range in its invasiveness from 0.8 to 1.8%[53-55], while the genome

sequenced clinical strain NCTC11168 (NCTC11168-GS) had diminished invasiveness and

translocation abilities compared to the original isolate (NCTC11168-O), highlighting the potential

effects of high laboratory passage on strain pathogenicity and colonization[56]. Furthermore,

Cooper et al (2013) found that NCTC11168-GS had decreased disease production in the neonatal

piglet model compared to NCTC11168-O[35]. Taken together, the consistent invasiveness

observed among bloody/inflammatory diarrhea associated strains in our study, regardless of cell

line used, supports invasion as a defining characteristic of the bloody/inflammatory diarrheal

manifestation. The lack of invasiveness among watery diarrhea-associated strains may reflect

alternative pathogenic strategies, such as growth capabilities and metabolic adaptability, that do

not rely on epithelial invasion. These differences in invasive capacity likely contribute to the

distinct clinical presentations observed between strain groups and reinforce the need for broader

strain inclusion in *C. jejuni* pathogenesis research.

Bloody/inflammatory strains not only exhibit greater invasion of both polarized and non-

polarized epithelial cells but also demonstrate enhanced intracellular persistence. Intracellular

survival of *C. jejuni* has been linked to proinflammatory signaling and immune evasion in both *in*

vitro and *in vivo* models [31, 57], but this is the first study to demonstrate that such phenotypes are

heightened in strains associated with a consistent bloody/inflammatory diarrheal manifestation *in*

vivo. Through macrophage survivability assays, we observed a connection to immune evasion by

bloody/inflammatory diarrhea associated strains where these strains exhibited prolonged

persistence within macrophages up to 48 hours post-infection. This suggests that not only are

bloody/inflammatory diarrhea associated strains able to survive for at least 24 hours within

intestinal epithelial cells, but they also have an ability to evade phagocytic killing for several days.

Strain variation in macrophage survivability was most pronounced between bloody/inflammatory

diarrhea strains, particularly among strain A9a at 24 hours where it had higher levels of

survivability, although not statistically significant, compared to all other strains. Consistent with

our study, Day et al (2000) and Law et al (2009) found that M129 was able to be recovered from

J774A.1 macrophages after 72-hours, while the later study also observed survivability among A9a,

A13a, A14a and D42a[21, 58]. Survivability differences between watery and bloody/inflammatory

diarrhea associated strains at 48 hours, but not at 24 or 72 hours, suggests a transient but critical

window during which certain *C. jejuni* strains, particularly those associated with

bloody/inflammatory diarrhea, are better equipped or contain alternative mechanisms to persist

slightly longer within host immune cells. *C. jejuni* contains one catalase enzyme, encoded by the

katA gene, which aids in protection from reactive oxygen species generated during the oxidative

burst once the bacterium is phagocytosed within macrophages[59, 60]. The *katA* gene has been

found to be critical for *C. jejuni* macrophage survivability, where wildtype strain M129 was shown

to be able to persist at levels significantly higher than a M129 *katA* mutant at 24, 48 and 72 hours

within J774A.1 macrophages[58]. Another study found that the downregulation of *katA* in *C. jejuni*

strain NCTC11168 through a mutation in a MarR-type transcriptional regulator (Cj1556) was also

reduced in J774A.1 macrophage survivability[61, 62]. Future studies should investigate catalase

expression or activity contributes to the prolonged intracellular persistence observed in

bloody/inflammatory diarrhea-associated strains.

Disruption of epithelial barrier function further differentiated the two diarrheal

manifestation groups. Bloody/inflammatory strains induced greater reductions in TEER and

increased paracellular flux of FITC-dextran across polarized monolayers - both indicators of tight

junction impairment[63, 64]. Other studies evaluating the changes to the TEER *in vitro* utilizing

invasive *C. jejuni* strains, particularly 81-176 and NCTC11168, did find a significant drop in the

TEER. However, none of these studies utilized strains with defined diarrheal manifestations or

compared them to watery diarrhea associated strains[65-68]. This disruption in barrier integrity

was significantly more pronounced in bloody/inflammatory strains and our study is the first to

directly link this phenotype with reproducible diarrheal manifestations across multiple isolates.

The effects we observed on the integrity of the Caco-2 BBE monolayers, regardless of defined

diarrheal manifestation, translated into increased translocation of a non-invasive commensal *E.*

coli strain, providing evidence that the barrier compromise facilitated microbial movement across

the epithelium. The translocation of noninvasive bacteria such as *E. coli* during *C. jejuni* infection

has been previously investigated *in vitro* with varying results. Konkel et al (1992) observed no

change in the TEER or translocation of *E. coli* DH5α up to 6 hours following inoculation of Caco-

2 cell monolayers using bloody/inflammatory strain M129 and strains of unknown diarrheal

manifestations; F38011, 81116 and 78-27[69]. In our study, despite watery diarrhea associated

strains being poorly invasive or non-invasive, we observed *E. coli* translocation at similar levels

to bloody/inflammatory strains, suggesting alternate means for *E. coli* translocation other than

invasion. Translocation of *E. coli* was found to not correspond with *C. jejuni* invasiveness in one

study that used invasion-defective *C. jejuni* flagella mutant strains, with lipid raft-mediated

endocytosis suggested to induce this effect[70]. The use of M cells to promote transcytosis of non-

invasive bacteria was also observed using bloody/inflammatory diarrhea associated strain 81-176

but was not investigated using any other strains[71]. Both lipid rafts and M cells should be further

investigated as potential mechanisms behind *E. coli* translocation by invasive and non-invasive *C.*

jejuni strains.

Not all measured pathogenicity phenotypes differed between the two manifestation groups.

Our study found that CDT production levels were not altered both between strains and across

diarrheal manifestation groups at either temperature, suggesting CDT is not a discriminating factor

for diarrheal severity. CDT is widespread among *C. jejuni* isolates and contributes to host cell

cycle arrest, DNA damage, and epithelial disruption[72], however the specific contributions of

CDT in *C. jejuni* pathogenesis remains unclear[73, 74]. There is limited evidence that CDT

expression is critical to disease but it was found that CDT contributes to greater adherence and

invasion of epithelial cells along with more progressive gastritis and proximal duodenitis in two

in vivo mouse models[75, 76]. However, the role of CDT in driving different diarrheal symptoms

is not well understood. Previous studies have assessed CDT production with HeLa cells among *C.*

jejuni strains from clinical or poultry sources and have reported variability, although none had a

diarrheal manifestation associated with any of the strains[77-79]. Additionally, IL-8 secretion, a

hallmark of initial epithelial response to *C. jejuni* contact[80-82] and a potent chemoattractant and

cellular activator[81] also did not differ significantly between diarrheal manifestation groups at 24

hours post-infection. Although not statistically significant, strain to strain variation was observed

among bloody/inflammatory strains with D33a and NCTC11168 having lower IL-8 levels than

M129 and A9a. Watery diarrhea associated strains showed less variation between strains with only

A13a and A14a having lower IL-8 levels than other watery diarrhea associated strains. Few studies

have looked at differences in IL-8 secretion across *C. jejuni* strains and this is the first study to

assess IL-8 secretion by *C. jejuni* strains with known diarrheal manifestations in the neonatal piglet

model. One study using bloody/inflammatory diarrhea associated strain NCTC11168 and human

colitis strain L115 showed no difference in IL-8 secretion by T84 cells[83], while another study

looked at IL-8 secretion between *C. jejuni* strains from poultry and human sources and found no

difference in IL-8 secretion by T84 cells between groups[84]. However, IL-8 secretion is not based

solely on the invasive or adherent capability of *C. jejuni* strains, as it can also be activated by CDT

production[81, 82], indicating that early chemokine responses may not correlate with longer-term

invasive or inflammatory phenotypes. Furthermore, our findings that both bloody/inflammatory

and watery diarrhea associated strains produce similar levels of CDT and elicit comparable IL-8

responses despite significant differences in invasion. This variation highlights the importance of

considering strain-level differences when evaluating the inflammatory potential of *C. jejuni* and

suggests that multiple mechanisms may drive IL-8 secretion in the host.

Strain A9a, originally recovered from a poultry processing plant in Kansas, USA[85], is

associated with bloody/inflammatory diarrhea in the neonatal piglet model. A9a demonstrated the

highest levels of adherence, invasion, and intracellular survival to intestinal epithelial cells

compared to all other *C. jejuni* strains. While its CDT production was comparable to many of the

other *C. jejuni* strains, A9a showed the highest stimulation of IL-8 secretion from T84 cells, results

that support IL-8 production due to high adherence and invasion even with similar levels of CDT.

A9a also caused the most pronounced disruption to epithelial barrier integrity, with the steepest

decline in TEER, the highest FITC-dextran permeability, and the greatest translocation of *E. coli*

DH5α across Caco-2 BBE monolayers over 72 hours. Finally, A9a had the highest survivability

within macrophages across all time points, reflecting its resilience against innate immune

responses. Despite its strong *in vitro* virulence potential, A9a was not hypervirulent in the piglet

model[21]. Instead, it produced bloody/inflammatory diarrhea at similar levels to the other strains

in this study, 81-176, M129, D33a and NCTC11168, suggesting that multiple factors may drive

the severity of diarrhea. *C. jejuni* strain variation has been observed in other studies, such as Ex114,

a *C. jejuni* strain that was found to be 25 times more invasive than reference strain 81116, which

is a relatively low invader[16]. Consistent with our findings, the same study reported that increased

invasiveness was not linked to enhanced adhesion, and motility levels were similar between highly

and minimally invasive strains. In other studies, stain 81-176, sourced from a raw milk

outbreak,[86] is widely regarded as a highly invasive clinical isolate and has been shown to cause

robust epithelial invasion in cell lines[53, 87] and animal models[88] as well as produce disease

in humans[89]. Yet its performance varies between laboratories depending on passage history[53,

55, 90]. Repeatedly passages reduced the invasiveness and serum survival of 81-176[91].

Similarly, while strain NCTC11168 is a reference strain in *C. jejuni* research, its virulence is

known to diminish with laboratory passage, leading to reduced motility, invasion and colonization

capacity *in vitro*[56] in addition to altering *in vivo* virulence in the neonatal piglet model[35]. Our

findings support these previous reports that strain-dependent variation plays a key role in

pathogenicity.

This strain-to-strain variations observed in this study, even among strains associated with

a particular diarrheal manifestation in the neonatal piglet model, highlight the inherent complexity

and plasticity of *C. jejuni* virulence[92-95]. This study also underscores the need for population-

scale studies integrating phenotypic data with comparative genomics to identify combinations of

traits that drive disease severity. One such study that performed a comparative genomic analysis

on 67 *C. jejuni* and 12 *C. coli* strains, identified the *Campylobacter jejuni*-integrated elements

(CJIEs) originally identified in *C. jejuni* strain RM1221, were variably present across other

Campylobacter strains[96]. These genomic elements, some of which included prophages and

mobile genetic elements, contribute to functional differences that may affect virulence, stress

response, or host interaction. Notably, Parker et al reported that coding sequences within CJIEs

were highly variable, highlighting a potential genomic mechanism for the phenotypic diversity

observed in our assays[96]. This supports our findings that even within clinically defined groups,

virulence phenotypes can differ, potentially due to underlying genomic heterogeneity. One

limitation of this study is that the number of strains included was limited, but they were well-

characterized and associated with consistent clinical phenotypes in a validated *in vivo* neonatal

piglet model. Our *in vitro* assays cannot fully replicate host complexity, but the consistency of

results across multiple models strengthens confidence in the observed trends. Future work should

integrate whole-genome sequencing, transcriptomic profiling, and *in vivo* validation to identify the

molecular determinants responsible for these virulence phenotypes.

In summary, *C. jejuni* strains associated with bloody/inflammatory diarrhea exhibit a

distinct virulence profile characterized by epithelial invasion, intracellular survival, barrier

disruption, and macrophage persistence (**Fig 8**). Together, enhanced invasion and intestinal

damage, intracellular survival, and macrophage survivability provide a functional explanation for

the more severe pathology observed in the piglet model by bloody/inflammatory strain and, by

extension, potentially in human infections. By linking *in vivo* disease phenotypes to mechanistic

in vitro traits, our findings advance understanding of *C. jejuni* pathogenesis and provide a

framework for developing targeted diagnostics, risk-based screening tools, and novel therapeutic

interventions. Furthermore, the strain-to-strain variation observed in this study, even within groups

associated with the same *in vivo* diarrheal manifestation, present that caution is needed when

interpreting the results of experiments that utilize only a few *C. jejuni* strains.

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in sample processing and other aspects of the study.

Ethics statement

This study did not involve the use of animals or human participants. The *Campylobacter jejuni*

strains used in this study were previously characterized in a neonatal piglet model under approved

animal use protocols, as described in Law et al and Cooper et al. No new *in vivo* experiments were

conducted for this study.

Data availability statement

All relevant data are within the manuscript and its supplementary files.

Author Contributions

JB: Conceptualization, methodology, experimentation, formal analysis, writing – original draft,

and review & editing. **KKC:** Conceptualization, methodology, resources, funding acquisition,

project administration, supervision, writing, and review & editing. **CP:** Writing, and review &

editing. **BP:** Writing, and review & editing.

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the manuscript.

Competing interests

The authors declare no competing interests.

Tables

Table 1. *Campylobacter jejuni* strains utilized in this study

Strain	Source	Sequence Type (ST)	Clonal Complex	Diarrheal Manifestation
NCTC11168	Clinical	ST43	ST-21	Bloody and/or Inflammatory
81-176	Clinical	ST604	ST-42	Bloody and/or Inflammatory
M129	Clinical	ST353	ST-353	Bloody and/or Inflammatory
A9a	Poultry	ST2827	ST-460	Bloody and/or Inflammatory
D33a	Poultry	ST459	ST-42	Bloody and/or Inflammatory
RM1221	Poultry	ST354	ST-354	Watery
S3	Poultry	ST354	ST-354	Watery
D42a	Poultry	ST21	ST-21	Watery
A14a	Poultry	ST1212	ST-607	Watery
A13a	Poultry	ST1212	ST-607	Watery

 Figure Legends

Fig 1. Gross pathology associated with different diarrheal outcome caused by different

strains of *Campylobacter jejuni* based on previous challenge in colostrum deprived neonatal

piglet model. (A) Gross pathology of the intestinal tract of neonatal piglets infected with *C. jejuni*

strains associated with watery diarrhea manifestation. (B) Gross pathology of the intestinal tract

of neonatal piglets infected with *C. jejuni* strains associated with bloody and/or inflammatory

diarrhea manifestation. Piglet studies were conducted prior to this study and were described

previously in Law et al and Cooper et al[21, 35].

Fig 2. Average percent invasion of intestinal epithelial cell line Caco-2 BBE. (A) Invasion

across all ten *C. jejuni* strains. Bars labeled with different letters indicate statistically significant

differences (p < 0.05) based on Dunn's post hoc test following a Kruskal-Wallis analysis. Shared

letters denote groups that are not significantly different from each other. (B) Invasiveness of Caco-

2 BBE cells by *C. jejuni* strains grouped by diarrheal manifestation (**, p = 0.0014).

Fig 3. Intracellular survival over 24 hours in T84 cells. (A) Average percent survival within

T84 cells by strain. Bars labeled with different letters indicate statistically significant differences

(p < 0.05) based on Dunn's post hoc test following a Kruskal-Wallis analysis (n = 3). Shared letters

denote groups that are not significantly different from each other. (B) Percent T84 24-hour

intracellular survival by *C. jejuni* strains grouped by diarrheal manifestation (***, p = 0.0007).

Strain 81-176 is not included in this data set.

Fig 4. Adherence to intestinal epithelial cell lines. (A) Adherence of each *C. jejuni* strain to

INT407 cells. Bars labeled with different letters indicate statistically significant differences ($p <$

0.05) based on Dunn's post hoc test following a Kruskal-Wallis analysis (n = 3). Shared letters

denote groups that are not significantly different from each other. (B) Adherence to INT407 cell

by *C. jejuni* strains grouped by diarrheal manifestation ($p = 0.20$). (C) Adherence of each *C. jejuni*

strain to Caco-2 BBE cells (n = 3). (D) Adherence to Caco-2 BBE cells by *C. jejuni* strains grouped

by diarrheal manifestation ($p = 0.14$).

Fig 5. Change in the transepithelial electrical resistance (TEER) over 24, 48 and 72 hours.

(A) Change in TEER for each *C. jejuni* strain over 24-, 48- and 72-hours. Those labeled with

different letters indicate statistically significant differences ($p < 0.05$) based on Dunn's post hoc

test following a Kruskal-Wallis analysis (n = 3). Shared letters denote groups that are not

significantly different from each other. (B) Change in TEER across *C. jejuni* strains grouped by

diarrheal manifestation at 24 hours (****, $p < 0.0001$), 48 hours (****, $p < 0.0001$), and at 72

hours (****, $p < 0.0001$). Mock infection represents Caco-2 BBE cells that contained only sterile

cell culture media.

Fig 6. The fluorescence of FITC-Dextran flow through after 72 hours of infection with *C.

jejuni strains.** (A) Average FITC-Dextran fluorescence intensity of each *C. jejuni* strain. Bars

labeled with different letters indicate statistically significant differences ($p < 0.05$) based on

Dunn's post hoc test following a Kruskal-Wallis analysis (n = 3). Shared letters denote groups that

are not significantly different from each other. (B) There was a highly significant difference

between the watery and bloody/inflammatory diarrhea associated strains (**, p = 0.0027). Mock

infection represents Caco-2 BBE cells that contained only sterile cell culture media.

Fig 7. Survivability of *C. jejuni* strains in J774A.1 macrophages over 24, 48 and 72 hours. (A)

Survivability by each *C. jejuni* strain over 24 hours. Bars labeled with different letters indicate

statistically significant differences (p < 0.05) based on Dunn's post hoc test following a Kruskal-

Wallis analysis. Shared letters denote groups that are not significantly different from each other.

Average percent survivability was calculated based on three biologically independent assays with

two technical replicates (n = 3). (B) Macrophage survivability of *C. jejuni* strains grouped by

diarrheal manifestation over 24 hours (p = 0.23). (C) Survivability by each *C. jejuni* strain over

48-hours. (D) Macrophage survivability of *C. jejuni* strains grouped by diarrheal manifestation

over 48 hours (*, p = 0.011). (E) Survivability of *C. jejuni* strains over 72 hours. (F) Macrophage

survivability of *C. jejuni* strains grouped by diarrheal manifestation over 72 hours (p = 0.43).

Fig 8. Proposed lifestyles of *C. jejuni* strains associated with watery or bloody/inflammatory

diarrhea. Watery diarrhea associated strains live an extracellular lifestyle where they attach to

enterocytes and produce CDT toxin. They are poor invaders, disrupting the tight junctions between

epithelial cells to a minimal degree, although commensal bacterial such as *E. coli* are translocated.

Those that do weakly invade, do not survive long term intracellularly and are effectively removed

by macrophages. Bloody/inflammatory diarrhea associated strains support an intracellular lifestyle

where they attach to and invade enterocytes, significantly disrupting the tight junctions between

those enterocytes. Bloody/inflammatory diarrhea associated strains can evade killing by

macrophages for longer periods of time, promoting infection and contributing to more severe

patient symptoms. Figure created in BioRender.

Supplementary Figure Legends

Supplementary Fig S1. Invasion of INT407 cells. (A) Invasion across all ten *C. jejuni* strains.

Bars labeled with different letters indicate statistically significant differences ($p < 0.05$) based on

Dunn's post hoc test following a Kruskal-Wallis analysis. Shared letters denote strains that are not

significantly different from each other. (B) Invasiveness of INT407 cells by *C. jejuni* strains

grouped by diarrheal manifestation (***, $p = 0.0006$).

Supplementary Fig S2. Average percent invasion of intestinal epithelial cell line T84. (A)

Invasion of T84 cells across all ten *C. jejuni* strains. Bars labeled with different letters indicate

statistically significant differences ($p < 0.05$) based on Dunn's post hoc test following a Kruskal-

Wallis analysis. Shared letters denote groups that are not significantly different from each other.

(B) Invasiveness of *C. jejuni* strains grouped by diarrheal manifestation (**, $p = 0.0063$).

Supplementary Fig S3. Adherence to T84 cells. (A) Adherence to T84 cells by *C. jejuni* strains.

Bars labeled with different letters indicate statistically significant differences ($p < 0.05$) based on

Dunn's post hoc test following a Kruskal-Wallis analysis. Shared letters denote groups that are not

significantly different from each other ($n = 3$). Strain 81-176 was not included in this data set. (B)

Adherence to T84 cells by *C. jejuni* strains grouped by diarrheal manifestation ($p = 0.90$). Strain

81-176 is not included in this data set.

Supplementary Fig S4. Cytolethal Distending Toxin (CDT) production at 37°C and 42°C.

(A) CDT toxin production at 37°C and 42°C by *C. jejuni* strains. (B) CDT production *C. jejuni*

strains grouped by diarrheal manifestation at 37°C ($p = 0.74$) and 42°C ($p = 0.086$). CDT

production was not significantly different when performed at 37°C compared to 42°C for watery

diarrhea associated strains ($p = 0.65$) or bloody/inflammatory diarrhea associated strains ($p = 0.12$).

Supplementary Fig S5. IL-8 Production following 24-hour incubation with *C. jejuni* strains.

(A) IL-8 production in pg/ml of *C. jejuni* strains. Bars labeled with different letters indicate

statistically significant differences ($p < 0.05$) based on Dunn's post hoc test following a Kruskal-

Wallis analysis. Shared letters denote groups that are not significantly different from each other.

Strain 81-176 is not included in this data set. Mock infection represents Caco-2 BBE cells that

contained only sterile cell culture media. (B) IL-8 production in pg/ml of *C. jejuni* strains grouped

by diarrheal manifestation ($p = 0.61$). Mock infection represents Caco-2 BBE cells that contained

only sterile cell culture media. Strain 81-176 is not included in this data set.

Supplementary Fig S6. Translocation of *Escherichia coli* through Caco-2 BBE cell monolayers. (A) 6-hour co-culture incubation with *C. jejuni* strains. Bars labeled with different letters indicate statistically significant differences ($p < 0.05$) based on Dunn's post hoc test following a Kruskal-Wallis analysis. Shared letters denote groups that are not significantly different from each other. (B) 6-hour co-culture incubation with *C. jejuni* strains grouped by diarrheal manifestation ($p = 0.66$). Mock infection represents Caco-2 BBE cells that contained only sterile cell culture media. (C) Pre-infection with *C. jejuni* for 72 hours followed by 3-hour exposure to *E. coli* through Caco-2 BBE cells by strain ($n = 3$). (D) Pre-infection with *C. jejuni* for 72 hours followed by 3-hour exposure to *E. coli* through Caco-2 BBE grouped by diarrheal manifestation ($p = 0.30$).

References

1.   Organization WH. Global View of Campylobaceriosis, Report of an Expert Consultation. 2012.
2.   Walter EJS, Cui Z, Tierney R, Griffin PM, Hoekstra RM, Payne DC, et al. Foodborne Illness Acquired in the United States—Major Pathogens, 2019. Volume 31, Number 4. 2025. PubMed PMID: April.
3.   Schorling E, Knorr S, Lick S, Steinberg P, Brüggemann DA. Probability of sequelae following *Campylobacter* spp. infections: Update of systematic reviews and meta-analyses. Public Health Challenges. 2023;2(4):e145. doi: 10.1002/puh2.145.
4.   Nyati KK, Nyati R. Role of *Campylobacter jejuni* infection in the pathogenesis of Guillain-Barré syndrome: an update. Biomed Res Int. 2013;2013:852195. Epub 20130813. doi: 10.1155/2013/852195. PubMed PMID: 24000328; PubMed Central PMCID: PMCPMC3755430.
5.   Peters S, Pascoe B, Wu Z, Bayliss SC, Zeng X, Edwinson A, et al. *Campylobacter jejuni* genotypes are associated with post-infection irritable bowel syndrome in humans. Commun Biol. 2021;4(1):1015. Epub 20210830. doi: 10.1038/s42003-021-02554-8. PubMed PMID: 34462533; PubMed Central PMCID: PMCPMC8405632.
6.   Kotloff KL, Nataro JP, Blackwelder WC, Nasrin D, Farag TH, Panchalingam S, et al. Burden and aetiology of diarrhoeal disease in infants and young children in developing countries (the Global Enteric Multicenter Study, GEMS): a prospective, case-control study. Lancet. 2013;382(9888):209-22. Epub 20130514. doi: 10.1016/s0140-6736(13)60844-2. PubMed PMID: 23680352.

7.   Investigators TM-EN. The MAL-ED Study: A Multinational and Multidisciplinary
Approach to Understand the Relationship Between Enteric Pathogens, Malnutrition, Gut
Physiology, Physical Growth, Cognitive Development, and Immune Responses in Infants and
Children Up to 2 Years of Age in Resource-Poor Environments. Clinical Infectious Diseases.
2014;59(suppl_4):S193-S206. doi: 10.1093/cid/ciu653.
8.   Haque MA, Platts-Mills JA, Mduma E, Bodhidatta L, Bessong P, Shakoor S, et al.
Determinants of *Campylobacter* infection and association with growth and enteric inflammation
in children under 2 years of age in low-resource settings. Sci Rep. 2019;9(1):17124. Epub
20191120. doi: 10.1038/s41598-019-53533-3. PubMed PMID: 31748573; PubMed Central
PMCID: PMCPMC6868199.
9.   Pogreba-Brown K, Baker A, Ernst K, Stewart J, Harris RB, Weiss J. Assessing risk
factors of sporadic *Campylobacter* infection: a case-control study in Arizona. Epidemiol Infect.
2016;144(4):829-39. doi: 10.1017/s0950268815002162. PubMed PMID: 26828241.
10.   Igwaran A, Okoh AI. Human campylobacteriosis: A public health concern of global
importance. Heliyon. 2019;5(11):e02814. Epub 20191114. doi: 10.1016/j.heliyon.2019.e02814.
PubMed PMID: 31763476; PubMed Central PMCID: PMCPMC6861584.
11.   Harvey P, Battle T, Leach S. Different invasion phenotypes of *Campylobacter* isolates in
Caco-2 cell monolayers. J Med Microbiol. 1999;48(5):461-9. doi: 10.1099/00222615-48-5-461.
PubMed PMID: 10229543.
12.   Ruiz-Palacios G, Torres N, Ruiz-Palacios B, Torres J, Escamilla E, Tamayo J. Cholera-
like enterotoxin produced by *Campylobacter jejuni*: characterisation and clinical significance.
The Lancet. 1983;322(8344):250-3.
13.   Johnson WM, Lior H. Toxins produced by *Campylobacter jejuni* and *Campylobacter*
coli. Lancet. 1984;1(8370):229-30. doi: 10.1016/s0140-6736(84)92155-x. PubMed PMID:
6141372.
14.   Apel D, Ellermeier J, Pryjma M, Dirita VJ, Gaynor EC. Characterization of
Campylobacter jejuni RacRS reveals roles in the heat shock response, motility, and maintenance
of cell length homogeneity. J Bacteriol. 2012;194(9):2342-54. Epub 20120217. doi:
10.1128/JB.06041-11. PubMed PMID: 22343300; PubMed Central PMCID: PMCPMC3347078.
15.   Turonova H, Briandet R, Rodrigues R, Hernould M, Hayek N, Stintzi A, et al. Biofilm
spatial organization by the emerging pathogen *Campylobacter jejuni*: comparison between
NCTC 11168 and 81-176 strains under microaerobic and oxygen-enriched conditions. Front
Microbiol. 2015;6:709. Epub 20150713. doi: 10.3389/fmicb.2015.00709. PubMed PMID:
26217332; PubMed Central PMCID: PMCPMC4499754.
16.   Fearnley C, Manning G, Bagnall M, Javed MA, Wassenaar TM, Newell DG.
Identification of hyperinvasive *Campylobacter jejuni* strains isolated from poultry and human
clinical sources. J Med Microbiol. 2008;57(Pt 5):570-80. doi: 10.1099/jmm.0.47803-0. PubMed
PMID: 18436589.
17.   Hofreuter D, , Novik V, , Galán JE, . Metabolic Diversity in *Campylobacter jejuni*
Enhances Specific Tissue Colonization. 2008.
18.   Poly F, Ewing C, Goon S, Hickey TE, Rockabrand D, Majam G, et al. Heterogeneity of a
Campylobacter jejuni protein that is secreted through the flagellar filament. Infect Immun.
2007;75(8):3859-67. Epub 20070521. doi: 10.1128/IAI.00159-07. PubMed PMID: 17517862;
PubMed Central PMCID: PMCPMC1951984.
19.   Meurens F, Summerfield A, Nauwynck H, Saif L, Gerdts V. The pig: a model for human
infectious diseases. Trends Microbiol. 2012;20(1):50-7. Epub 20111205. doi:

10.1016/j.tim.2011.11.002. PubMed PMID: 22153753; PubMed Central PMCID:
PMCPMC7173122.

20.   Boosinger TR, Powe TA. *Campylobacter jejuni* infections in gnotobiotic pigs. Am J Vet
Res. 1988;49(4):456-8. PubMed PMID: 3377304.

21.   Law BF, Adriance SM, Joens LA. Comparison of in vitro virulence factors of
Campylobacter jejuni to in vivo lesion production. Foodborne Pathog Dis. 2009;6(3):377-85.
doi: 10.1089/fpd.2008.0183. PubMed PMID: 19278341.

22.   Canibe N, O'Dea M, Abraham S. Potential relevance of pig gut content transplantation
for production and research. Journal of Animal Science and Biotechnology. 2019;10(1):55. doi:
10.1186/s40104-019-0363-4.

23.   van der Laan JW, Brightwell J, McAnulty P, Ratky J, Stark C. Regulatory acceptability
of the minipig in the development of pharmaceuticals, chemicals and other products. J
Pharmacol Toxicol Methods. 2010;62(3):184-95. Epub 20100616. doi:
10.1016/j.vascn.2010.05.005. PubMed PMID: 20601024.

24.   Lodemann U, Amasheh S, Radloff J, Kern M, Bethe A, Wieler LH, et al. Effects of Ex
Vivo Infection with ETEC on Jejunal Barrier Properties and Cytokine Expression in Probiotic-
Supplemented Pigs. Dig Dis Sci. 2017;62(4):922-33. Epub 20161219. doi: 10.1007/s10620-016-
4413-x. PubMed PMID: 27995406.

25.   Gefeller EM, Martens H, Aschenbach JR, Klingspor S, Twardziok S, Wrede P, et al.
Effects of age and zinc supplementation on transport properties in the jejunum of piglets. J Anim
Physiol Anim Nutr (Berl). 2015;99(3):542-52. Epub 20140721. doi: 10.1111/jpn.12232. PubMed
PMID: 25039419.

26.   Lodemann U, Dillenseger A, Aschenbach JR, Martens H. Effects of age and controlled
oral dosing of Enterococcus faecium on epithelial properties in the piglet small intestine. Benef
Microbes. 2013;4(4):335-44. doi: 10.3920/bm2013.0004. PubMed PMID: 24311317.

27.   Harvey RB, Young CR, Ziprin RL, Hume ME, Genovese KJ, Anderson RC, et al.
Prevalence of *Campylobacter* spp isolated from the intestinal tract of pigs raised in an integrated
swine production system. J Am Vet Med Assoc. 1999;215(11):1601-4. PubMed PMID:
14567422.

28.   Taylor D, Olubunmi P. A re-examination of the role of Campylobacter fetus subspecies
coli in enteric disease of the pig. The Veterinary Record. 1981;109(6):112-5.

29.   Vítovec J, Koudela B, Štěrba J, Tomancová I, Matyáš Z, Vladík P. The gnotobiotic piglet
as a model for the pathogenesis of *Campylobacter jejuni* infection. Zentralblatt für Bakteriologie.
1989;271(1):91-103. doi: 10.1016/s0934-8840(89)80058-1.

30.   Abuoun M, Manning G, Cawthraw SA, Ridley A, Ahmed IH, Wassenaar TM, et al.
Cytolethal distending toxin (CDT)-negative *Campylobacter jejuni* strains and anti-CDT
neutralizing antibodies are induced during human infection but not during colonization in
chickens. Infect Immun. 2005;73(5):3053-62. doi: 10.1128/IAI.73.5.3053-3062.2005. PubMed
PMID: 15845513; PubMed Central PMCID: PMCPMC1087314.

31.   Watson RO, Galán JE. *Campylobacter jejuni* survives within epithelial cells by avoiding
delivery to lysosomes. PLoS Pathog. 2008;4(1):e14. doi: 10.1371/journal.ppat.0040014. PubMed
PMID: 18225954; PubMed Central PMCID: PMCPMC2323279.

32.   Stamps BW, Kuroiwa J, Isidean SD, Schilling MA, Harro C, Talaat KR, et al. Exploring
Changes in the Host Gut Microbiota During a Controlled Human Infection Model for
Campylobacter jejuni. Frontiers in Cellular and Infection Microbiology. 2021;11. doi:
10.3389/fcimb.2021.702047.

33.   Cody AJ, McCarthy NM, Wimalarathna HL, Colles FM, Clark L, Bowler IC, et al. A
longitudinal 6-year study of the molecular epidemiology of clinical *Campylobacter* isolates in
Oxfordshire, United kingdom. J Clin Microbiol. 2012;50(10):3193-201. Epub 20120718. doi:
10.1128/JCM.01086-12. PubMed PMID: 22814466; PubMed Central PMCID:
PMCPMC3457434.
34.   Babakhani FK, Bradley GA, Joens LA. Newborn piglet model for campylobacteriosis.
Infect Immun. 1993;61(8):3466-75. doi: 10.1128/iai.61.8.3466-3475.1993. PubMed PMID:
8335377; PubMed Central PMCID: PMCPMC281024.
35.   Cooper KK, Cooper MA, Zuccolo A, Joens LA. Re-sequencing of a virulent strain of
Campylobacter jejuni NCTC11168 reveals potential virulence factors. Res Microbiol.
2013;164(1):6-11. Epub 20121006. doi: 10.1016/j.resmic.2012.10.002. PubMed PMID:
23046762.
36.   Rubinchik S, Seddon A, Karlyshev AV. Molecular mechanisms and biological role of
Campylobacter jejuni attachment to host cells. Eur J Microbiol Immunol (Bp). 2012;2(1):32-40.
Epub 20120317. doi: 10.1556/EuJMI.2.2012.1.6. PubMed PMID: 24611119; PubMed Central
PMCID: PMCPMC3933988.
37.   Monteville MR, Yoon JE, Konkel ME. Maximal adherence and invasion of INT 407 cells
by *Campylobacter jejuni* requires the CadF outer-membrane protein and microfilament
reorganization. Microbiology (Reading). 2003;149(Pt 1):153-65. doi: 10.1099/mic.0.25820-0.
PubMed PMID: 12576589.
38.   Konkel ME, Hayes SF, Joens LA, Cieplak W, Jr. Characteristics of the internalization
and intracellular survival of *Campylobacter jejuni* in human epithelial cell cultures. Microb
Pathog. 1992;13(5):357-70. doi: 10.1016/0882-4010(92)90079-4. PubMed PMID: 1297914.
39.   Fauchere JL, Rosenau A, Veron M, Moyen EN, Richard S, Pfister A. Association with
HeLa cells of *Campylobacter jejuni* and *Campylobacter coli* isolated from human feces. Infect
Immun. 1986;54(2):283-7. doi: 10.1128/iai.54.2.283-287.1986. PubMed PMID: 3770943;
PubMed Central PMCID: PMCPMC260156.
40.   Newell DG, McBride H, Saunders F, Dehele Y, Pearson AD. The virulence of clinical
and environmental isolates of *Campylobacter jejuni*. J Hyg (Lond). 1985;94(1):45-54. doi:
10.1017/s0022172400061118. PubMed PMID: 3973380; PubMed Central PMCID:
PMCPMC2129391.
41.   Peterson MD, Mooseker MS. Characterization of the enterocyte-like brush border
cytoskeleton of the C2BBe clones of the human intestinal cell line, Caco-2. J Cell Sci. 1992;102
(Pt 3):581-600. doi: 10.1242/jcs.102.3.581. PubMed PMID: 1506435.
42.   Hughson EJ, Cutler DF, Hopkins CR. Basolateral secretion of kappa light chain in the
polarised epithelial cell line, Caco-2. J Cell Sci. 1989;94 (Pt 2):327-32. doi:
10.1242/jcs.94.2.327. PubMed PMID: 2516089.
43.   Lea T. Caco-2 Cell Line. In: Verhoeckx K, Cotter P, López-Expósito I, Kleiveland C,
Lea T, Mackie A, et al., editors. The Impact of Food Bioactives on Health: in vitro and ex vivo
models. Cham (CH): Springer

Copyright 2015, The Author(s). 2015. p. 103-11.
44.   Sambuy Y, De Angelis I, Ranaldi G, Scarino M, Stammati A, Zucco F. The Caco-2 cell
line as a model of the intestinal barrier: influence of cell and culture-related factors on Caco-2
cell functional characteristics. Cell biology and toxicology. 2005;21:1-26.
45.   Peterson MD, Bement WM, Mooseker MS. An in vitro model for the analysis of
intestinal brush border assembly. II. Changes in expression and localization of brush border

proteins during cell contact-induced brush border assembly in Caco-2BBe cells. J Cell Sci.
1993;105 (Pt 2):461-72. doi: 10.1242/jcs.105.2.461. PubMed PMID: 8408277.
46.   Dharmsathaphorn K, McRoberts JA, Mandel KG, Tisdale LD, Masui H. A human
colonic tumor cell line that maintains vectorial electrolyte transport. Am J Physiol. 1984;246(2
Pt 1):G204-8. doi: 10.1152/ajpgi.1984.246.2.G204. PubMed PMID: 6141741.
47.   Devriese S, Van den Bossche L, Van Welden S, Holvoet T, Pinheiro I, Hindryckx P, et
al. T84 monolayers are superior to Caco-2 as a model system of colonocytes. Histochemistry and
Cell Biology. 2017;148(1):85-93. doi: 10.1007/s00418-017-1539-7.
48.   Konkel ME, Joens LA. Adhesion to and invasion of HEp-2 cells by *Campylobacter* spp.
Infect Immun. 1989;57(10):2984-90. doi: 10.1128/iai.57.10.2984-2990.1989. PubMed PMID:
2550368; PubMed Central PMCID: PMCPMC260759.
49.   Rivera-Amill V, Kim BJ, Seshu J, Konkel ME. Secretion of the virulence-associated
Campylobacter invasion antigens from *Campylobacter jejuni* requires a stimulatory signal. J
Infect Dis. 2001;183(11):1607-16. Epub 20010501. doi: 10.1086/320704. PubMed PMID:
11343209.
50.   Russell RG, Blake DC, Jr. Cell association and invasion of Caco-2 cells by
Campylobacter jejuni. Infect Immun. 1994;62(9):3773-9. doi: 10.1128/iai.62.9.3773-3779.1994.
PubMed PMID: 8063393; PubMed Central PMCID: PMCPMC303030.
51.   Konkel ME, Talukdar PK, Negretti NM, Klappenbach CM. Taking Control:
Campylobacter jejuni Binding to Fibronectin Sets the Stage for Cellular Adherence and Invasion.
Frontiers in Microbiology. 2020;11. doi: 10.3389/fmicb.2020.00564.
52.   Everest PH, Goossens H, Butzler JP, Lloyd D, Knutton S, Ketley JM, et al. Differentiated
Caco-2 cells as a model for enteric invasion by *Campylobacter jejuni* and *C. coli*. J Med
Microbiol. 1992;37(5):319-25. doi: 10.1099/00222615-37-5-319. PubMed PMID: 1433253.
53.   Yao R, Burr DH, Doig P, Trust TJ, Niu H, Guerry P. Isolation of motile and non-motile
insertional mutants of *Campylobacter jejuni*: the role of motility in adherence and invasion of
eukaryotic cells. Mol Microbiol. 1994;14(5):883-93. doi: 10.1111/j.1365-2958.1994.tb01324.x.
PubMed PMID: 7715450.
54.   Doig P, Yao R, Burr DH, Guerry P, Trust TJ. An environmentally regulated pilus-like
appendage involved in *Campylobacter* pathogenesis. Molecular Microbiology. 1996;20(4):885-
94.
55.   Yao R, Burr DH, Guerry P. CheY-mediated modulation of *Campylobacter jejuni*
virulence. Mol Microbiol. 1997;23(5):1021-31. doi: 10.1046/j.1365-2958.1997.2861650.x.
PubMed PMID: 9076738.
56.   Gaynor Erin C, Cawthraw S, Manning G, MacKichan Joanna K, Falkow S, Newell Diane
G. The Genome-Sequenced Variant of *Campylobacter jejuni* NCTC 11168 and the Original
Clonal Clinical Isolate Differ Markedly in Colonization, Gene Expression, and Virulence-
Associated Phenotypes. Journal of Bacteriology. 2004;186(2):503-17. doi: 10.1128/jb.186.2.503-
517.2004.
57.   Novik V, Hofreuter D, Galán JE. Identification of *Campylobacter jejuni* genes involved
in its interaction with epithelial cells. Infect Immun. 2010;78(8):3540-53. Epub 20100601. doi:
10.1128/iai.00109-10. PubMed PMID: 20515930; PubMed Central PMCID: PMCPMC2916286.
58.   Day WA, Jr., Sajecki JL, Pitts TM, Joens LA. Role of catalase in *Campylobacter jejuni*
intracellular survival. Infect Immun. 2000;68(11):6337-45. doi: 10.1128/iai.68.11.6337-
6345.2000. PubMed PMID: 11035743; PubMed Central PMCID: PMCPMC97717.

59.   De Melo MA, Gabbiani G, Pechère JC. Cellular events and intracellular survival of
Campylobacter jejuni during infection of HEp-2 cells. Infect Immun. 1989;57(7):2214-22. doi:
10.1128/iai.57.7.2214-2222.1989. PubMed PMID: 2731988; PubMed Central PMCID:
PMCPMC313863.
60.   Kiehlbauch JA, Albach RA, Baum LL, Chang KP. Phagocytosis of *Campylobacter jejuni*
and its intracellular survival in mononuclear phagocytes. Infect Immun. 1985;48(2):446-51. doi:
10.1128/iai.48.2.446-451.1985. PubMed PMID: 3988342; PubMed Central PMCID:
PMCPMC261341.
61.   Gundogdu O, Mills DC, Elmi A, Martin MJ, Wren BW, Dorrell N. The *Campylobacter*
jejuni Transcriptional Regulator Cj1556 Plays a Role in the Oxidative and Aerobic Stress
Response and Is Important for Bacterial Survival In Vivo. Journal of Bacteriology.
2011;193(16):4238-49. doi: doi:10.1128/jb.05189-11.
62.   Gundogdu O, da Silva DT, Mohammad B, Elmi A, Mills DC, Wren BW, et al. The
Campylobacter jejuni MarR-like transcriptional regulators RrpA and RrpB both influence
bacterial responses to oxidative and aerobic stresses. Frontiers in Microbiology. 2015;Volume 6 -
2015. doi: 10.3389/fmicb.2015.00724.
63.   Srinivasan B, Kolli AR, Esch MB, Abaci HE, Shuler ML, Hickman JJ. TEER
measurement techniques for in vitro barrier model systems. J Lab Autom. 2015;20(2):107-26.
Epub 20150113. doi: 10.1177/2211068214561025. PubMed PMID: 25586998; PubMed Central
PMCID: PMCPMC4652793.
64.   Gerkins C, Hajjar R, Oliero M, Santos MM. Assessment of Gut Barrier Integrity in Mice
Using Fluorescein-Isothiocyanate-Labeled Dextran. J Vis Exp. 2022;(189). Epub 20221118. doi:
10.3791/64710. PubMed PMID: 36468715.
65.   MacCallum A, Hardy SP, Everest PH. *Campylobacter jejuni* inhibits the absorptive
transport functions of Caco-2 cells and disrupts cellular tight junctions. Microbiology (Reading).
2005;151(Pt 7):2451-8. doi: 10.1099/mic.0.27950-0. PubMed PMID: 16000735.
66.   Hofreuter D, Tsai J, Watson RO, Novik V, Altman B, Benitez M, et al. Unique features
of a highly pathogenic Campylobacter jejuni strain. Infect Immun. 2006;74(8):4694-707. doi:
10.1128/IAI.00210-06. PubMed PMID: 16861657; PubMed Central PMCID:
PMCPMC1539605.
67.   Mills DC, Gundogdu O, Elmi A, Bajaj-Elliott M, Taylor PW, Wren BW, et al. Increase in
Campylobacter jejuni invasion of intestinal epithelial cells under low-oxygen coculture
conditions that reflect the in vivo environment. Infect Immun. 2012;80(5):1690-8. Epub
20120221. doi: 10.1128/iai.06176-11. PubMed PMID: 22354027; PubMed Central PMCID:
PMCPMC3347453.
68.   Brás AM, Ketley JM. Transcellular translocation of *Campylobacter jejuni* across human
polarised epithelial monolayers. FEMS Microbiology Letters. 1999;179(2):209-15. doi:
10.1111/j.1574-6968.1999.tb08729.x.
69.   Konkel ME, Mead DJ, Hayes SF, Cieplak W, Jr. Translocation of *Campylobacter jejuni*
across human polarized epithelial cell monolayer cultures. J Infect Dis. 1992;166(2):308-15. doi:
10.1093/infdis/166.2.308. PubMed PMID: 1634802.
70.   Kalischuk LD, Inglis GD, Buret AG. *Campylobacter jejuni* induces transcellular
translocation of commensal bacteria via lipid rafts. Gut Pathog. 2009;1(1):2. Epub 20090203.
doi: 10.1186/1757-4749-1-2. PubMed PMID: 19338680; PubMed Central PMCID:
PMCPMC2653720.

71.   Kalischuk LD, Leggett F, Inglis GD. *Campylobacter jejuni* induces transcytosis of
commensal bacteria across the intestinal epithelium through M-like cells. Gut Pathogens.
2010;2(1):14. doi: 10.1186/1757-4749-2-14.
72.   Lara-Tejero M, Galán JE. A bacterial toxin that controls cell cycle progression as a
deoxyribonuclease I-like protein. Science. 2000;290(5490):354-7. doi:
10.1126/science.290.5490.354. PubMed PMID: 11030657.
73.   De Rycke J, Oswald E. Cytolethal distending toxin (CDT): a bacterial weapon to control
host cell proliferation? FEMS Microbiol Lett. 2001;203(2):141-8. doi: 10.1111/j.1574-
6968.2001.tb10832.x. PubMed PMID: 11583839.
74.   Gu J, Lin Y, Wang Z, Pan Q, Cai G, He Q, et al. *Campylobacter jejuni* Cytolethal
Distending Toxin Induces GSDME-Dependent Pyroptosis in Colonic Epithelial Cells. Frontiers
in Cellular and Infection Microbiology. 2022;12. doi: 10.3389/fcimb.2022.853204.
75.   Fox James G, Rogers Arlin B, Whary Mark T, Ge Z, Taylor Nancy S, Xu S, et al.
Gastroenteritis in NF-κB-Deficient Mice Is Produced with Wild-Type *Camplyobacter jejuni* but
Not with *C. jejuni* Lacking Cytolethal Distending Toxin despite Persistent Colonization with
Both Strains. Infection and Immunity. 2004;72(2):1116-25. doi: 10.1128/iai.72.2.1116-
1125.2004.
76.   Jain D, Prasad KN, Sinha S, Husain N. Differences in virulence attributes between
cytolethal distending toxin positive and negative *Campylobacter jejuni* strains. Journal of
Medical Microbiology. 2008;57(3):267-72. doi: https://doi.org/10.1099/jmm.0.47317-0.
77.   Pickett CL, Pesci EC, Cottle DL, Russell G, Erdem AN, Zeytin H. Prevalence of
cytolethal distending toxin production in *Campylobacter jejuni* and relatedness of
Campylobacter sp. cdtB gene. Infect Immun. 1996;64(6):2070-8. doi: 10.1128/iai.64.6.2070-
2078.1996. PubMed PMID: 8675309; PubMed Central PMCID: PMCPMC174038.
78.   Talukder KA, Aslam M, Islam Z, Azmi IJ, Dutta DK, Hossain S, et al. Prevalence of
virulence genes and cytolethal distending toxin production in *Campylobacter jejuni* isolates from
diarrheal patients in Bangladesh. J Clin Microbiol. 2008;46(4):1485-8. Epub 20080220. doi:
10.1128/jcm.01912-07. PubMed PMID: 18287317; PubMed Central PMCID:
PMCPMC2292937.
79.   Eyigor A, Dawson KA, Langlois BE, Pickett CL. Cytolethal distending toxin genes in
Campylobacter jejuni and *Campylobacter coli* isolates: detection and analysis by PCR. J Clin
Microbiol. 1999;37(5):1646-50. doi: 10.1128/jcm.37.5.1646-1650.1999. PubMed PMID:
10203548; PubMed Central PMCID: PMCPMC84865.
80.   Hickey TE, Baqar S, Bourgeois AL, Ewing CP, Guerry P. *Campylobacter jejuni*-
stimulated secretion of interleukin-8 by INT407 cells. Infect Immun. 1999;67(1):88-93. doi:
10.1128/IAI.67.1.88-93.1999. PubMed PMID: 9864200; PubMed Central PMCID:
PMCPMC96281.
81.   Zheng J, Meng J, Zhao S, Singh R, Song W. *Campylobacter*-induced interleukin-8
secretion in polarized human intestinal epithelial cells requires *Campylobacter*-secreted
cytolethal distending toxin- and Toll-like receptor-mediated activation of NF-kappaB. Infect
Immun. 2008;76(10):4498-508. Epub 20080721. doi: 10.1128/IAI.01317-07. PubMed PMID:
18644884; PubMed Central PMCID: PMCPMC2546826.
82.   Hickey TE, McVeigh AL, Scott DA, Michielutti RE, Bixby A, Carroll SA, et al.
Campylobacter jejuni cytolethal distending toxin mediates release of interleukin-8 from
intestinal epithelial cells. Infect Immun. 2000;68(12):6535-41. doi: 10.1128/IAI.68.12.6535-
6541.2000. PubMed PMID: 11083762; PubMed Central PMCID: PMCPMC97747.

83.   MacCallum AJ, Harris D, Haddock G, Everest PH. *Campylobacter jejuni*-infected human
epithelial cell lines vary in their ability to secrete interleukin-8 compared to in vitro-infected
primary human intestinal tissue. Microbiology (Reading). 2006;152(Pt 12):3661-5. doi:
10.1099/mic.0.29234-0. PubMed PMID: 17159219.
84.   Van Deun K, Haesebrouck F, Heyndrickx M, Favoreel H, Dewulf J, Ceelen L, et al.
Virulence properties of *Campylobacter jejuni* isolates of poultry and human origin. J Med
Microbiol. 2007;56(Pt 10):1284-9. doi: 10.1099/jmm.0.47342-0. PubMed PMID: 17893162.
85.   Malik-Kale P, Raphael BH, Parker CT, Joens LA, Klena JD, Quiñones B, et al.
Characterization of genetically matched isolates of *Campylobacter jejuni* reveals that mutations
in genes involved in flagellar biosynthesis alter the organism's virulence potential. Appl Environ
Microbiol. 2007;73(10):3123-36. Epub 20070316. doi: 10.1128/aem.01399-06. PubMed PMID:
17369342; PubMed Central PMCID: PMCPMC1907099.
86.   Korlath JA, Osterholm MT, Judy LA, Forfang JC, Robinson RA. A point-source
outbreak of campylobacteriosis associated with consumption of raw milk. J Infect Dis.
1985;152(3):592-6. doi: 10.1093/infdis/152.3.592. PubMed PMID: 4031557.
87.   Bacon DJ, Alm RA, Burr DH, Hu L, Kopecko DJ, Ewing CP, et al. Involvement of a
plasmid in virulence of *Campylobacter jejuni* 81-176. Infect Immun. 2000;68(8):4384-90. doi:
10.1128/IAI.68.8.4384-4390.2000. PubMed PMID: 10899834; PubMed Central PMCID:
PMCPMC98329.
88.   Pei Z, Burucoa C, Grignon B, Baqar S, Huang XZ, Kopecko DJ, et al. Mutation in the
peb1A locus of *Campylobacter jejuni* reduces interactions with epithelial cells and intestinal
colonization of mice. Infect Immun. 1998;66(3):938-43. doi: 10.1128/iai.66.3.938-943.1998.
PubMed PMID: 9488379; PubMed Central PMCID: PMCPMC107999.
89.   Black RE, Levine MM, Clements ML, Hughes TP, Blaser MJ. Experimental
Campylobacter jejuni infection in humans. J Infect Dis. 1988;157(3):472-9. doi:
10.1093/infdis/157.3.472. PubMed PMID: 3343522.
90.   Corcionivoschi N, Clyne M, Lyons A, Elmi A, Gundogdu O, Wren BW, et al.
Campylobacter jejuni Cocultured with Epithelial Cells Reduces Surface Capsular
Polysaccharide Expression. Infection and Immunity. 2009;77(5):1959-67. doi:
doi:10.1128/iai.01239-08.
91.   Corcionivoschi N, Clyne M, Lyons A, Elmi A, Gundogdu O, Wren BW, et al.
Campylobacter jejuni cocultured with epithelial cells reduces surface capsular polysaccharide
expression. Infect Immun. 2009;77(5):1959-67. Epub 20090309. doi: 10.1128/iai.01239-08.
PubMed PMID: 19273563; PubMed Central PMCID: PMCPMC2681765.
92.   Taboada EN, Acedillo RR, Carrillo CD, Findlay WA, Medeiros DT, Mykytczuk OL, et
al. Large-scale comparative genomics meta-analysis of *Campylobacter jejuni* isolates reveals
low level of genome plasticity. J Clin Microbiol. 2004;42(10):4566-76. doi:
10.1128/jcm.42.10.4566-4576.2004. PubMed PMID: 15472310; PubMed Central PMCID:
PMCPMC522315.
93.   Woodcock DJ, Krusche P, Strachan NJC, Forbes KJ, Cohan FM, Méric G, et al. Genomic
plasticity and rapid host switching can promote the evolution of generalism: a case study in the
zoonotic pathogen *Campylobacter*. Scientific Reports. 2017;7(1):9650. doi: 10.1038/s41598-
017-09483-9.
94.   Hofreuter D, Tsai J, Watson Robert O, Novik V, Altman B, Benitez M, et al. Unique
Features of a Highly Pathogenic *Campylobacter jejuni* Strain. Infection and Immunity.
2006;74(8):4694-707. doi: 10.1128/iai.00210-06.

95.   Leonard EE, 2nd, Tompkins LS, Falkow S, Nachamkin I. Comparison of *Campylobacter*
jejuni isolates implicated in Guillain-Barré syndrome and strains that cause enteritis by a DNA
microarray. Infect Immun. 2004;72(2):1199-203. doi: 10.1128/iai.72.2.1199-1203.2004. PubMed
PMID: 14742576; PubMed Central PMCID: PMCPMC321608.
96.   Parker Craig T, Quiñones B, Miller William G, Horn Sharon T, Mandrell Robert E.
Comparative Genomic Analysis of *Campylobacter jejuni* Strains Reveals Diversity Due to
Genomic Elements Similar to Those Present in C. jejuni Strain RM1221. Journal of Clinical
Microbiology. 2006;44(11):4125-35. doi: 10.1128/jcm.01231-06.

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Figure 1

Figure 2

Figure 3

Figure 4

Figure 5

Figure 6

Figure 7

Figure 8