Characterization of the clade 4 non-toxigenic *C. difficile* isolate L-NTCD03 carrying the *cfr*(B) gene

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Abstract

Clostridioides difficile infection (CDI) is a toxin-mediated gastro-intestinal disease. Yet, *C. difficile* is a phylogenetically diverse species that includes many non-toxigenic strains. In general, these are understudied, despite having significant potential impact for our understanding of the colonization process and as therapeutic modalities. Here, we present an in-depth characterization – including the complete genome sequence - of the non-toxigenic *C. difficile* strain L-NTCD03. This strain belongs to PCR ribotype 416, clade 4 and multilocus sequence type 39. It is resistant to multiple antimicrobials, but not those used for treatment of CDI. We validated the relevance of the *cfr*(B) gene from this strain in antimicrobial resistance to clindamycin, linezolid, retapamulin and streptogramin A. We found the L-NTCD03 strain to be non-toxic in various assays. Altogether, L-NTCD03 is a promising candidate for developing into a live biotherapeutic product.

Introduction

The Gram-positive anaerobic spore-forming bacterium *Clostridioides difficile* is best known as a nosocomial pathogen and *C. difficile* infection (CDI) is regarded as an important cause of healthcare-associated infectious diarrhea (Leffler & Lamont, 2015, Smits *et al.*, 2016). In this context, in particular strains belonging to the fluoroquinolone resistant PCR ribotype 027 (RT027) are associated with increased morbidity and mortality (Warny *et al.*, 2005, He *et al.*, 2013). Nevertheless, recent years have seen an increase in CDI cases that are not linked to classical risk factors such as antibiotic use or healthcare exposure, and are community-acquired (Smits *et al.*, 2016, Viprey *et al.*, 2022). Strains belonging to different types than RT027, such as those belonging PCR ribotype 078 (RT078), which also occur in many animal species, may be associated with community-acquired disease (Goorhuis *et al.*, 2008, Viprey *et al.*, 2022). Thus, *C. difficile* can be considered a quintessential One Health pathogen (Lim *et al.*, 2020).

Considering its causative role in debilitating disease, much research has focused on the main virulence factors of *C. difficile:* toxin A (TcdA), toxin B (TcdB) and binary toxin (CDT) (Aktories *et al.*, 2017, Kordus *et al.*, 2022). Of note, whereas TcdA and/or TcdB is required for disease, CDT is mainly produced by a subset of

75 toxigenic *C. difficile* strains, including those belonging to the epidemic types RT027 and RT078 (Smits *et al.*,
76 2016).

77 *C. difficile* colonization does not always lead to disease. Importantly, a fraction of the population is
78 asymptomatically colonized by toxigenic *C. difficile* (Crobach *et al.*, 2018) and in particular in infants a high
79 prevalence of *C. difficile* is noted without apparent disease (Ferretti *et al.*, 2023, Mani *et al.*, 2023).
80 Additionally, *C. difficile* is not a universally pathogenic species; that is, non-toxigenic *C. difficile* (NTCD) strains
81 exist that lack the genes encoding TcdA, TcdB and CDT, such as those belonging to PCR ribotype 010 (RT010)
82 (Braun *et al.*, 1996, Monot *et al.*, 2015, Smits *et al.*, 2016). Though these isolates have not been found to
83 induce disease in humans and animals, it has been noted that they might act as reservoirs for antimicrobial
84 resistance genes. For instance, resistance to metronidazole is common in RT010 strains (Boekhoud *et al.*, 2020,
85 Boekhoud *et al.*, 2021) and over half the non-toxigenic isolates from Southeast Asia appeared to carry
86 antimicrobial resistance determinants on mobile genetic elements (Imwattana *et al.*, 2020).

87 *C. difficile* is a phylogenetically diverse species with isolates falling into at least 5 classical clades and 3
88 so called cryptic clades, that could be considered a separate genomospecies (Knight *et al.*, 2021). Epidemic
89 strains fall generally into clade 2 (RT027 and related strains) and clade 5 (RT078 and related strains). NTCD
90 have been reported in multiple clades, such as clade 1 (which includes RT010)(Baktash *et al.*, 2022), clade 4
91 (Imwattana *et al.*, 2020), clade C-I and clade C-II (Ducarmon *et al.*, 2023). Nevertheless, such strains are
92 generally understudied compared to the toxigenic counterparts.

93 There is epidemiological and experimental evidence that NTCD carriage is associated with lower
94 incidence of CDI, that NTCD colonization can prevent CDI disease and can reduce CDI recurrence in intestinal
95 models, animals and humans (Natarajan *et al.*, 2013, Gerding *et al.*, 2018, Etifa *et al.*, 2023). The strongest
96 evidence for use of NTCD as a therapeutic intervention is for strain M3 (a RT010 isolate) in humans (Villano *et*
97 *al.*, 2012, Gerding *et al.*, 2015, Sambol *et al.*, 2023) and strain Z31 (RT009) in piglets (Oliveira Junior *et al.*,
98 2019, Oliveira Junior *et al.*, 2019).

99 In addition to potential use as a live biotherapeutic product, NTCD could provide a chassis for
100 engineering of immune-epitopes and therefore serve as a potential vaccine (Hughes *et al.*, 2022, Wang *et al.*,
101 2022, Wang *et al.*, 2022), or be used to study aspects of CDI disease that are generally confounded by toxin-
102 mediated effects, such as early colonization events.

103 In light of the possible applications of NTCD, and the relative paucity of well-characterized NTCD
104 strains, we present here a detailed analysis of L-NTCD03, a clade 4 non-toxigenic *C. difficile* strain.
105
106
107 **Materials and Methods**
108
109 **Bacterial strains and growth conditions**
110 L-NTCD03 was isolated from fecal material of a healthy elderly subject negative for HIV-1, HIV-2, HCV, HBV, as
111 follows. Fecal material was stored in Stool Transport and Recovery (STAR) buffer and stored at -80C. Ethanol
112 treated material was inoculated into *C. difficile* enrichment modified broth (CDEB MOB; Mediaproducts NV,
113 Groningen, The Netherlands, cat no. 21.1295). After 6 days of growth at 37C under anaerobic conditions, the
114 culture was plated onto *C. difficile* selective growth medium (CLO; VWR International, cat.no. 43431). From
115 this medium, a colony was streaked to singles on a Tryptic Soy Sheep Blood medium (TSS; bioMérieux, cat.no.
116 43009,), and growth was harvested into glycerol-containing broth (Tritium Microbiology, cat. no. I200.36.0001)
117 for storage at -80°C.
118 Control strains belonging to PCR ribotype 027 (LL-027) and 078 (LL-078) were obtained from the
119 Leeds-Leiden collection (Knetsch *et al.*, 2012, Baktash *et al.*, 2022).
120 Strains were cultured in simulated ileal effluent medium (SIEM)(Minekus *et al.*, 1999, Wiese *et al.*,
121 2022), Brain-Heart Infusion (BHI) broth, BHI supplemented with yeast extract (BHI-Y; BHI with 0.5 % yeast
122 extract) or CDMN (Aspinall & Hutchinson, 1992) medium supplemented with 0.1% sodium taurocholate
123 (CDMNT).
124
125 **Molecular biology**
126 A genomic region including *cfr*(B) and its native promoter was amplified by PCR using Q5 polymerase (NEB)
127 and primers oIMM-01 and oIMM-02. The resulting PCR product was digested with KpnI and BamHI and cloned
128 into similarly digested pAP24 (Oliveira Paiva *et al.*, 2016). The resulting plasmid, pIMM03, was sequence
129 verified using primers NF793, NF794 (Fagan & Fairweather, 2011), oIMM-01, oIMM02, oIMM-03 and oIMM-04
130 was introduced using standard laboratory methods into strain 630Δ*erm* (van Eijk *et al.*, 2015, Roseboom *et al.*,
131 2023). Transconjugants were verified by PCR using primers oWKS-1070/oWKS-1071 (targeting chromosomal

132 *gluD*), oWKS-1387 and oWKS-1388 (targeting plasmid-located *traJ*) and oIMM-01/oIMM-02 (targeting *cfr*(B))
133 using appropriate controls. All oligonucleotide sequences are listed in **Table 3**.
134
135 **Antimicrobial susceptibility testing**
136 To determine minimal inhibitory concentrations (MIC) of a panel of antibiotics epsilometer tests
137 (Etests) were used. This panel consisted of cotrimoxazol, linezolid, metronidazole (Liofilchem), augmentin,
138 cefuroxime, ciprofloxacin, chloramphenicol, clindamycin, erythromycin, meropenem, moxifloxacin, penicillin,
139 rifampicin, tetracyclin, teicoplanin and vancomycin (bioMerieux). For this test, bacterial suspensions
140 corresponding to a turbidity of 1.0 McFarland unit were plated on Brucella blood agar supplemented with 5
141 mg L^{-1} hemin and 1 mg L^{-1} vitamin K (bioMerieux) plates, unless indicated otherwise. MIC values were
142 determined after 48 h of anaerobic incubation at 37°C as recommended by Clinical and Laboratory Standards
143 Institute (CLSI), including relevant control strains (CLSI, 2012). Fidaxomicin MIC was determined using the agar
144 dilution method according to CLSI guidelines on fresh Brucella Blood Agar supplemented with 5 mg L^{-1} hemin
145 and 1 mg L^{-1} vitamin K. Epidemiological cut-off values were used as defined by European Committee on
146 Antimicrobial Susceptibility Testing (EUCAST, 2026), when available.
147 MIC measurements for engineered strains (3 independent transconjugants) were performed on BHI-
148 yeast extract agar with either an E-test (clindamycin, linezolid) (bioMerieux or Liophilchem, respectively) or by
149 incorporating retapamulin (Sigma CDS023386) or streptogramin A/virginiamycin M1 (Sigma V2753) at 0-128
150 mg/L into the agar.
151
152 **PCR ribotyping**
153 Capillary gel electrophoresis ribotyping of L-NTCD03 was performed according to standardized protocols
154 (Fawley *et al.*, 2015). In short, 2µl of isolated DNA was added to 23 µl of the master mix which includes the 16S
155 and 23S primers and HotStart Taq Master Mix (Qiagen). Using a MyCycler thermocycler (Biorad), the resulting
156 DNA mix was subjected to an enzyme activation step at 95 °C for 15 minutes followed by 24 cycles of
157 amplification at 95 °C for 1 minute, 1 minute at 57 °C and 1 minute at 72 °C. Finally, the DNA mix was
158 subjected to 72 °C for 30 minutes. The sample was prepared for analysis by adding PCR product as 1 µl of PCR
159 product to 8.5 µl HiDi formamide (Applied Biosystems) and 0.5 µl of GeneScan™ 1200 LIZ marker (Thermo
160 Fisher) and samples was denatured at 95 °C for 5 minutes. To determine the ribotype, it was then analyzed

161 using the ABI3500XL (capillary length 50 cm) and the resulting *.fsa files were compared to a reference
162 database in BioNumerics (bioMérieux).
163
164 **Toxin ELISA**
165 To determine the productions of Toxin A and B, the *C. difficile* Tox A/B II™ kit (Techlab) was used according to
166 manufacturer's protocol with a minor modification. In short, the supernatants that were collected at 0, 24, 48,
167 72 and 96 h from growth curves in SIEM pH=5.8 and pH=6.8 were filtered using a UNIFILTER microplate device
168 (0.45 µm cellulose acetate filter, long drip, 96 wells, GE Health Care Life Sciences). The samples were applied to
169 the filter plate and centrifuged at 3220 G for 5 minutes at 4°C. The filtrates were used in the analysis as
170 described by manufacturer and the optical density was measured at 450 nm (OD_{450}). A threshold value of
171 OD_{450} of 0.12 was used determine whether toxins were present in the filtrate.
172
173 **Cell lines and culture conditions**
174 Human colorectal adenocarcinoma cells (Caco-2) were obtained from the American Type Culture Collection
175 (ATCC-HTB-37) and cultured in minimum essential medium (MEM, Gibco) supplemented with 10% bovine fetal
176 serum (10% FCS), 1% non-essential amino acids (NEAA, Lonza), 2 mM glutamine (Sigma Aldrich), 100 units/ml
177 penicillin (Sigma Aldrich), and 100 units/ml streptomycin (Sigma Aldrich). Epithelial-like, mucin-producing,
178 LS174T cells were obtained from Sigma Aldrich (87060401) and cultured in the medium described for Caco-2.
179 Both cells were grown to 80% confluency before experimental conditions were prepared.
180
181 ***In vitro* intestinal epithelial barrier model**
182 The apical side of Thincert 12 well cell culture inserts (PET, pore size 0.4 µm, Greiner Bio-one) were coated
183 with 250 µg/well purified human collagen type IV (OptiCol collagen Type IV, dissolved in 0.25% acetic acid, Cell
184 Guidance Systems) and washed with sterile PBS after 1-2 h incubation.
185 To mimic the human colon environment, an 80:20 ratio mixture of Caco-2 and LS174T in MEM
186 supplemented with 10% FCS, 1% non- NEAA, 2 mM glutamine, 100 U/ml penicillin, and 100 U/ml streptomycin
187 (cell culture medium) was prepared. To function as controls, 100:0 and 0:100 ratio mixtures of Caco-2 and
188 LS174T were prepared in cell culture medium. For all conditions, $1*10^5$ cells were seeded on the apical side of
189 the PET membrane. To mimic the intestinal environment, medium was present in both the basal compartment

190 (the well) and apical compartment (on top of the PET membrane) of the system. The systems were incubated
191 at 37°C and 5% CO2. The cells in this model were allowed to grow and differentiate for 21 days during which
192 the medium in both compartments was refreshed every other day.
193 To monitor the development of the *in vitro* intestinal epithelial barrier model, starting at T=0 the
194 transepithelial electrical resistance (TEER) values were measured using EVOM-2 resistance meter (World
195 Precision Instruments) every 7 days.
196 On day 21, the medium in the apical compartment of the system was replaced with a 10 times
197 diluted, in cell culture medium, supernatant harvested at 72 h in a growth curve of all of the strains in BHI-y
198 medium. This supernatant was incubated in the apical compartment for 1 hour at 37°C and 5% CO2, removed
199 afterwards and replaced with cell culture medium. In every condition, a control well was exposed to calcium
200 free medium (SMEM, Gibco) to determine as a positive control. TEER measurements were performed at 4
201 (only SMEM condition), 24, and 48 h post-exposure. Morphology was assessed under light microscopy every
202 24 hrs.
203
204 **Swine IsoLoop model**
205 We compared the effect of L-NTCD03 and LL-078 on intestinal mucosa *in vivo* in the pig IsoLoop model, a
206 translational surgical *in situ* ileal loop platform for host-microbiome-pathogen interface (Bayne *et al.*, 2025). 12
207 h before the start of the surgery, 1 ml was drawn from a culture in the exponential growth phase of either L-
208 NTCD-03 or LL-078 in BHI-y and inoculated into fresh, pre-reduced CDMNT medium and grown anaerobically at
209 37 °C. 10 ml of culture was aliquoted per loop and stored anaerobically at room temperature until injection
210 was required.
211 3-month-old, female pigs (*Sus scrofa*, mixed breed, 50-60kg) were used under USDA pain category D,
212 per Institutional Animal Care and Use Committee (IACUC) protocol IACUC-22-066 essentially as described
213 (Bayne *et al.*, 2025).
214 In short, the pig was placed in dorsal recumbency under general anesthesia. Ileal loops were rinsed
215 with sterile saline solution before treatment with an antibiotic cocktail (60 mg/L norfloxacin; 160 mg/L
216 moxalactam) for 30 minutes. After a saline rinse, each independent loop except for the most aboral segment
217 was inoculated using a tuberculin needle full thickness into the lumen. Upon recovery, animals were housed
218 under standard husbandry conditions with regular veterinary assessments to ensure welfare. The loops were

219 sampled at euthanasia by cutting the mesentery and immediately cooling the intestines on ice. On ice, the
220 loops were cut open one by one and a piece of tissue, including intestinal content, was fixed in 10% neutral
221 buffered formalin (VWR) before embedding in paraffin.
222 5µm-thick tissue sections were stained with hematoxylin and eosin. Microscopic analysis of
223 histopathologic features was conducted by a board-certified pathologist, blinded to sample identities. The
224 scoring rubric, including descriptive statistics applied, is provided as **Supplementary Information**, and raw data
225 of the scoring is included as **Supplementary Table 1**. Scores are reported as total histological score per ileal
226 loop (range 0-20), computed as the sum for four 0-5 ordinal components (epithelial necrosis, mucosal/lamina
227 propria edema, crypt abscess and neutrophils in villi/lamina propria). Statistical analyses of histological scores
228 were performed in Python (NumPy/SciPy); figures were generated with matplotlib. All tests were two sided
229 with $\alpha = 0.05$.
230
231 **DNA extraction and genome sequencing**
232 To extract pure high-molecular weight total DNA, a two-fold serial dilution of L-NTCD03 in BHI-Y medium was
233 prepared. After overnight incubation at 37°C in an anaerobic environment, 4mL of culture with an optical
234 density at 600nM between 0.6 and 0.8 was spun down and DNA was extracted from the cell pellet using the
235 500/G genomic tip kit (Qiagen), according to the instructions of the manufacturer. Quantity and quality of the
236 DNA was verified by gel electrophoresis on a 0.8% agarose gel, using the Qubit dsDNA high-sensitivity kit
237 (Qubit) and a Femto Pulse system (Agilent), according to the manufacturer's protocols.
238 PacBio sequencing libraries were generated according to the manufacturer's multiplexed microbial
239 library preparation protocol, part number 101-696-100, version 7, July 2020 release (Pacific Biosciences) using
240 the SMRTbell Express Template Prep Kit v2.0 with the following modifications: genomic DNA was sheared
241 using Speed 34 on the Megaruptor 3 (Diagenode) and an additional size selection step of 6-50kb fragments on
242 the Blue Pippin (Sage Science) was included for the final SMRT bell library. The libraries were sequenced on a
243 Sequel II platform (Pacific Biosciences) using the Sequel II Binding Kit v2.0, Sequencing Primer v4, Sequencing
244 Kit v2.0 and a 30hr movie time.

245

246 **Genome annotation and bioinformatics analyses**

247 De novo genome assembly was carried out using Hifiasm (version 0.16.1-r375; parameters '--hg-size 4m')
248 (Cheng *et al.*, 2021) and the start position was set to *dnaA* using Circlator fixstart (version 1.5.5 using default
249 parameters) (Hunt *et al.*, 2015). Completeness check was performed using Busco (version 5.2.2; parameters '-
250 m genome -l clostridia_odb10') (Manni *et al.*, 2021) and assembly statistics were calculated and visualised with
251 Quast (version 5.0.2; using NZ_CP076401 as reference genome)(Gurevich *et al.*, 2013). Finally, Prokka (version
252 1.14.6; parameters '--genus Clostridioides --species difficile --compliant')(Seemann, 2014) was used to
253 annotate the genome.

254 A database of AMR genes was constructed using the AMRFinder plus tool v3.10.23 (parameters "-n"
255 "–organism Clostridioides difficile", "—plus") to identify antimicrobial resistance (AMR) genes (Feldgarden *et*
256 *al.*, 2021). Minimal "% coverage of reference sequence" and "% Identity to refence sequence" were set to 60%
257 and 90% percent, respectively.

258 BacAnt (Hua *et al.*, 2021) and MobileElementFinder (Johansson *et al.*, 2021) were used to identify
259 putative transposable elements. progressiveMauve was used to align genome sequences (Darling *et al.*, 2010).

260 Multi-locus sequence typing (MLST) was performed using mlst (v2.19.0) with the PubMLST *C. difficile*
261 database updated to October 21, 2021, (Jolley *et al.*, 2018) and verified on December 1, 2025.

262 Genomic comparisons were made in Geneious R10 (BioMatters Ltd), and figures for publication were
263 prepared using CAGECAT (van den Belt *et al.*, 2023) and Adobe Illustrator 26.3.1.

264

265 **Data availability**

266 L-NTCD03 genome information is available under BioProject PRJEB62683 (raw reads: ERR11495271, assembly:
267 ERZ18456945). The annotated genome is OX637968.1.

268

269

270 **Results**

271

272 **L-NTCD03 belongs to a rare PCR ribotype, RT416**

273 As part of a study investigating carriage of multidrug resistant organisms and *C. difficile* in nursing homes
274 (Ducarmon *et al.*, 2021), fecal material was obtained from a healthy elderly subject. *C. difficile* was cultured
275 from this material as described in Materials and Methods. The resulting isolate was negative in a multiplex PCR
276 that targets the toxin genes *tcdA*, *tcdB, cdtA* and *cdtB* (Control, 2018), suggesting that the isolate was non-
277 toxigenic. Hereafter, the isolate is referred to as L-NTCD03.
278 We performed capillary electrophoresis PCR ribotyping (Fawley *et al.*, 2015) of L-NTCD03 through the
279 Dutch Expertise Center for *C. difficile*, hosted at the LUMC. We initially failed to obtain a ribotype assignment,
280 as the banding pattern was not present in our database. The *.fsa files were shared with the *Clostridioides*
281 *difficile* Ribotyping Network Laboratory (CDRN; PHE Microbiology Services, Leeds, UK), and they determined
282 the isolate to belong to PCR ribotype 416. Since this identification, no other isolates were identified with the
283 same ribotype in the Dutch National Expertise Center for *C. difficile* infections. This suggests a prevalence in
284 the Netherlands that is below 0.01% on the basis of the number of strains typed since then.
285
286 **L-NTCD03 is susceptible to clinically used antimicrobials**
287 To determine whether L-NTCD03 the minimal inhibitory concentration for different antimicrobials, we
288 performed antimicrobial susceptibility testing using agar dilution (for fidaxomicin) or Etest (augmentin,
289 cefuroxime, chloramphenicol, clindamycin, cotrimoxazol, erythromycin, linezolid, metronidazole, meropenem,
290 moxifloxacin, penicillin, rifampicin, tetracyclin, teicoplanin and vancomycin) methods on Brucella Blood Agar
291 (BBA), as recommended by CLSI (CLSI, 2012). Out of the 17 antimicrobials tested, L-NTCD03 demonstrated
292 elevated MICs for cefuroxime, chloramphenicol, ciprofloxacin, erythromycin, linezolid, rifampicin and
293 tetracycline (**Table 1**). In contrast, the strain is susceptible to antimicrobials that are used in CDI therapy -
294 fidaxomicin, vancomycin and metronidazole – as well as several others (**Table 1**). As BBA is a suboptimal
295 medium for determining resistance to metronidazole, we also retested the isolate on recently recommended
296 Fastidious Anaerobe Agar supplemented with horse blood (Freeman *et al.*, 2025); this confirmed susceptibility
297 to metronidazole (data not shown). These results demonstrate that L-NTCD03 would likely be suppressed or
298 eradicated using standard antimicrobial therapy for CDI, but not by certain other antimicrobials that increase
299 susceptibility for CDI.
300
301 **Supernatant from L-NTCD03 does not contain detectable toxin A and B**

302 To confirm the absence of toxins, as suggested by the multiplex PCR result, we assessed the presence of TcdA
303 and TcdB in culture supernatant using an enzyme-coupled immune assay (Techlab). We used a medium that
304 mimicks the physiological conditions in the gut: simulated ileal effluent medium, SIEM (Minekus *et al.*, 1999,
305 Wiese *et al.*, 2022).
306 During 96 h of growth in SIEM, toxin levels were below the limit of detection for all supernatants
307 derived from L-NTCD03, as well as for the reference non-toxigenic strain LL-010 (**Figure 1A**). In contrast, toxins
308 were readily detected in culture supernatants derived from the toxigenic reference strains LL-027 and LL-078
309 (**Figure 1A**).
310
311 **Supernatant from L-NTCD03 does not affect transepithelial electrical resistance**
312 Though our results clearly indicate the absence of TcdA and TcdB, we considered that there could be other
313 factors that affect epithelial integrity, not detected in our assays so far. For this reason, we assessed the effect
314 of culture supernatant derived from L-NTCD03, LL-010, LL-027 and LL-078 in an *in vitro* model for epithelial
315 integrity. In this model, a mixture of Caco2 and mucin-producing LS174T cells is grown in a transwell system
316 and the transepithelial electrical resistance (TEER), a proxy for epithelial integrity, is measured using
317 electrodes.
318 The TEER values gradually increased over the first 14 days of incubation, consistent with cells growing
319 to confluency, and stabilized between days 14 and 21 (**Figure 1B**). When filtered supernatants from 72h-
320 cultures in BHI were applied to the cell layer, no drop in TEER was observed for the non-toxigenic strains (LL-10
321 and L-NTCD03), whereas LL-027 and LL-078 derived supernatants resulted in a significant decrease (**Figure 1B**).
322 Similar results were obtained when only LS174T cells or Caco2 cells were used (data not shown). This shows
323 that no other factors are produced by the non-toxigenic *C. difficile* strains that affect TEER in this cellular
324 model.
325
326 **L-NTCD03 grows similar to other isolates in a simulated ileal effluent medium**
327 To assess the growth and sporulation of L-NTCD03 in relation to well-characterized common subtypes of *C.*
328 *difficile* in SIEM, we monitored the total number of colony forming units (CFU) per milliliter (mL) over a period
329 of 14 days. Spore formation was monitored by enumeration of ethanol resistant CFUs.
330 Growth of L-NTCD03 was indistinguishable from LL-010, LL-027 and LL-078 for the first 6 h, during

331 which the number of CFU/mL increased ~3 log (**Figure 1C**). During stationary phase, we observed a lower total
332 cell count of ~10^7 CFU/mL, for all strains (**Figure 1C**).
333 No spore production was found during the first 6h of growth in SIEM (**Figure 1D**). For LL-010 and LL-
334 027 spores were detectable at 24h, but for L-NTCD03 and LL-078 spores were first found at the 48h-timepoint.
335 Beyond this point, sporulation dynamics were comparable between all strains **Figure 1D**).
336 Thus, under the conditions tested, L-NTCD03 shows robust growth and sporulation, in line with other
337 *C. difficile* strains.
338
339 **Phenotype microarrays show a common carbon utilization profile for L-NTCD03**
340 In order to assess the carbon utilization by L-NTCD03 we performed phenotype microarrays on Biolog PM1 and
341 PM2 plates, and analyzed the results using AMIGA software, as described previously (Midani *et al.*, 2021). We
342 used an arbitrary cut-off of 1.5-fold increase in or a 2-fold decrease in optical density to define differential
343 growth. We observed stimulated growth on the carbon sources N-Acetyl-D-Glucosamine, D-Mannose, D-
344 Mannitol, D-Fructose, alpha-D-Glucose, N-AcetylNeuraminic Acid, D-Melezitose, D-Tagatose and D-
345 Glucosamine (**Supplemental Table S1**). A decreased cell density was observed in the presence of Glyoxylic Acid
346 and Glycyl-LGlutamic Acid (**Supplemental Table S1**).
347 In parallel experiments, we observed similar profiles for representative strains from PCR ribotype 010,
348 027 and 078 (data not shown)(Collins *et al.*, 2018, Midani *et al.*, 2025). We conclude that L-NTCD03 carbon
349 utilization is similar to that of other *C. difficile* isolates.
350
351 **L-NTCD03 does not induce *C. difficile*-associated intestinal lesions in the swine IsoLoop model**
352 We have previously demonstrated the utility of the swine IsoLoop model for assessing *C. difficile*–associated
353 lesions in a translationally relevant gut microbiota–pathogen interface (Bayne *et al.*, 2025). Using this platform,
354 we compared the effects of L-NTCD03 in relation to the effects induced by the toxigenic reference strain LL-
355 078.
356 We inoculated multiple loops in the same animal (one animal per strain, either LL-078 or L-NTCD03),
357 and compared the histology to control loops without *C. difficile* and normal ileum (**Figure 2)**. Loops inoculated
358 with LL-078 showed signs of inflammation, whereas those inoculated with L-NTCD03 were comparable to the
359 control loop (**Figure 2A**). The total histological score (further detailed in the Methods section of this

360 manuscript) of samples derived from loops inoculated with LL-078 were significantly higher than those derived
361 from , whereas the histology of L-NTCD03 derived samples was comparable to that of control loops (**Figure 2B**
362 and **Supplemental Table 1**).
363
364 **L-NTCD03 is an ST39 (clade 4) isolate carrying a *cfr*(B) resistance gene**
365 *C. difficile* is a phylogenetically diverse species, with isolates falling into at least 5 classical (CDI-associated)
366 clades and 3 so called cryptic clades, that have been proposed to form separate genomospecies (Knight *et al.*,
367 2021). To place the L-NTCD03 in phylogenetic context, we reconstructed the complete genome sequence of
368 the strain using Pacific Biosciences circular consensus sequencing (BioProject PRJEB62683). After assembly, the
369 resulting genome showed a single circular contig of 4,318,385 bp – indicating the absence of
370 extrachromosomal elements - and an average [G+C]-content of 28,91%. Reference assembly of short-read
371 (Illumina) sequence data did not identify any nucleotide variants (data not shown), underscoring the quality of
372 the assembly.
373 We derived the 7-gene multilocus sequence type of our isolate using PubMLST (Griffiths *et al.*, 2010,
374 Jolley *et al.*, 2018). L-NTCD03 was found to belong to ST39 (*adk* 3, *atpA* 7, *dxr* 10, *glyA* 8, *recA* 7, *sodA* 2, *tpi*
375 10), which falls into clade 4. A core genome phylogenetic tree of representative isolates of different *C. difficile*
376 clades using Panaroo and IQTree confirmed this placement (data not shown)(Minh *et al.*, 2020, Tonkin-Hill *et*
377 *al.*, 2020, Baktash *et al.*, 2022).
378 We performed automated annotation of the genome sequence using Prokka (Seemann, 2014). This
379 resulted in 3,844 predicted coding sequences, 88 tRNAs, 34 rRNAs, 1 tmRNA and 8 repeat regions. As
380 expected, no complete genes corresponding to the toxin genes *tcdA*, *tcdB*, *cdtA* and *cdtB* were detected; in
381 stead the PaLoc insertion site conforms to what has been described for clade 4 strains (115bp insertion)(Dingle
382 *et al.*, 2014).
383 We used AMRfinderPlus to identify antimicrobial resistance genes in the L-NTCD03 genome
384 (Feldgarden *et al.*, 2022). We found 14 putative antimicrobial resistance genes, which are associated with 12
385 different classes of antibiotics (**Supplemental Table 2**); ten of these might be linked to the phenotypically
386 observed reduced susceptibility/resistance (**Table 1**).
387 Though *cfr*(B) has been implicated in antimicrobial resistance of *C. difficile* to PhLOPSa (phenicol,
388 lincosamide, oxaxolidinone, pleuromutilin and streptogramin A) antimicrobials (Marin *et al.*, 2015, Stojkovic *et*

389 *al.*, 2019), a direct causal role for this gene in resistance to these antimicrobials has not been shown to date.
390 Therefore, we cloned the *cfr*(B) gene under its native promoter in a shuttle plasmid and introduced this
391 plasmid into the commonly used *C. difficile* laboratory strain 630Δ*erm* (Hussain, 2005, van Eijk *et al.*, 2015). We
392 assessed antimicrobial susceptibility using Etest and found that introduction of *cfr*(B) increased the minimal
393 inhibitory concentration for clindamycin, linezolid, retapamulin and streptogramin A (**Table 2**) in comparison
394 to a control strain carrying a similar plasmid that carried the reporter gene *sluc*^{opt} (Oliveira Paiva *et al.*, 2016)
395 rather than *cfr*(B). The MIC increased >128-fold for clindamycin (from 2 mg/L to >256 mg/L), 12-fold for
396 linezolid (from 1 mg/L to 12 mg/L), 64-fold for retapamulin (from 0.125 mg/L to 16 mg/L) and 8-fold for
397 streptogramin A (from 2 mg/L to 16 mg/L) in the presence of *cfr*(B). We observed no change in MIC for
398 vancomycin and metronidazole (data not shown). This result indicates that *cfr*(B) can indeed confer resistance
399 to lincosamide, oxazolidinone, pleuromutilin and streptogramin antimicrobials in *C. difficile*, consistent with
400 expectations (Marin *et al.*, 2015, Stojkovic *et al.*, 2019).
401
402 **The genome of L-NTCD03 harbors several putative mobile genetic elements**
403 The BacAnt annotation server (Hua *et al.*, 2021) identified two putative transposable elements, with homology
404 to Tn*4451* (GenBank U15027; 94.57% identity and 100% coverage; bp 524023-530368) and Tn*5405* (GenBank
405 U73027; 99.84% identity and 95.97% coverage; bp 551080-553654). Of note, the *catP* gene is contained on the
406 former, suggesting a potential for transmission of this resistance determinant. MobileElementFinder
407 (Johansson *et al.*, 2021), in addition to Tn*4551*, identifies a chromosomal region with homology to Tn*6009*
408 (GenBank EU399632; identity 99.95% and coverage 100%; bp 268640-270528). Comparison with a closely
409 related clade 4 genome (DSM 29629, GenBank NZ_CP016104) reveals that this is in fact a 17.9-kb transposon
410 highly similar to Tn*916*, which has inserted in a gene (*pdeR*) encoding a GGDEF domain containing protein (in L-
411 NTCD03 this gene is split into two ORFs: LLHAOGBK_00311 and LLHAOGBK_00328) (**Figure 3**). The transposon
412 (**GenBank OR192611**) is also found in several *Streptococcus* and *Enterococcus* genome assemblies (data not
413 shown), and was assigned the number Tn*7696* by the transposon registry (Tansirichaiya *et al.*, 2019).
414 Compared to Tn*916*, Tn*7696* has a 120-bp in-frame deletion in the gene encoding a putative endopeptidase
415 p60 precursor (ORF14 in Tn*916*, LLHAOGBK_00319 in L-NTCD03) as well as several SNPs.
416 Finally, we employed two tools to predict i) putative phages (Wishart *et al.*, 2023) and ii) genomic
417 islands (Bertelli *et al.*, 2017). This identified two possible complete (pro)phages in L-NTCD03, with homology to

418 phiCDHM19 (NC_028996; bp 664975-719994) and phiC2 (NC_09231; bps 2626715-2687566) both of which are
419 also predicted with high confidence by geNomad (Camargo *et al.*, 2024), and 2 large (bp 490582-569665 and
420 3900143-3992891) plus several small regions that are likely horizontally acquired.
421 Overall, the complete genome sequence suggests a clear relation with other clade 4 *C. difficile*
422 isolates, and a significant contribution of horizontal gene transfer to its genetic content.
423
424
425 **Discussion**
426
427 Here, we provided a characterization of L-NTCD03, isolated from a healthy elderly subject. We confirmed that
428 this isolate does not express the large clostridial toxins *tcdA* and *tcdB*, using ELISA, and showed that
429 supernatants derived from an L-NTCD03 culture do not induce a loss of TEER in a trans-well model of colonic
430 epithelium. Additionally, data from the swine IsoLoop model suggest that there is no induced pathology in
431 loops inoculated with L-NTCD03 compared to controls. The loop experiment provides insight into strain
432 behavior within a translationally relevant, *C. difficile*–predisposing intestinal environment, using a customized
433 dysbiotic gut segment that enables precise local control of the bacterial inoculum, bile acid milieu, and other
434 key microenvironmental parameters. The data is in line with the genomic analysis, which shows a lack of
435 identifiable toxin genes, including the binary toxin locus. Together, these data strongly suggest that L-NTCD03
436 is unlikely to induce disease.
437 The high-quality complete genome generated for L-NTCD03 as part of this work, allowed us to place
438 the PCR ribotype 416 strain in clade 4. The most closely related publicly available genome at the time of
439 analysis is DSM 29629 (Riedel *et al.*, 2017)(CP016104.1). Like L-NTCD03, this strain was non-toxigenic and
440 assigned to clade 4, however, it is listed as ribotype SLO 235. At present it is unknown if the ribotyping
441 patterns for SLO 235 and RT416 (as determined by capillary ribotyping and assigned at the CDRN) are similar or
442 the same. Interestingly, in the manuscript describing DSM 29629 the authors note metabolic versatility
443 between 17 different *C. difficile* strains that does not appear to necessarily follow the 5 major phylogenetic
444 clades (clade) or PCR ribotypes tested. In the present work, we find that L-NTCD03 demonstrated a carbon
445 utilization profile that is quite similar to that of other *C. difficile* strains under the conditions tested. We have
446 to note that this was assessed at a single concentration and we cannot rule out that differences may exists at

447 alternative concentrations, similar to what has been noted for other *C. difficile* strains belonging to other
448 ribotypes (Collins *et al.*, 2018, Midani *et al.*, 2025).
449 We have determined the phenotypic antimicrobial resistance profile for 17 antimicrobials and found
450 that several could be explained by genetic determinants identified in the complete genome of L-NTCD03.
451 Some of these determinants appear to be associated with mobile genetic elements (Bannam *et al.*, 1995,
452 Derbise *et al.*, 1997, Soge *et al.*, 2008, Hua *et al.*, 2021), supporting the view that NTCD strains may act as a
453 reservoir for resistance determinants (Imwattana *et al.*, 2020). As observed also by others for NTCD strains
454 (Imwattana *et al.*, 2020), we also observed resistance to rifampicin and ciprofloxacin in L-NTCD03. It is
455 interesting to speculate that high levels of resistance in NTCD may relate to prolonged carriage, or reflect
456 antibiotic use in geographic areas where these strains are common. Rifampicin, for instance, is commonly used
457 in the treatment of tuberculosis patients. For clade 4 strains, high prevalence in Asia has been noted
458 (Imwattana *et al.*, 2020) but such strains are also more broadly found (Viprey *et al.*, 2022). Notably, though the
459 *nimB*-Cd resistance gene was identified (**Supplemental Table 2**), we observed no resistance to metronidazole.
460 Consistent with this, *nimB* is commonly found in susceptible isolates of *C. difficile* and L-NTCD03 lacks the
461 P*nimB*^{G} mutation associated with increased *nimB* expression and inducible metronidazole resistance (Olaitan
462 *et al.*, 2023). It also highlights the putative nature of automated identification of antimicrobial resistance
463 determinants.
464 Finally, we identified the *cfr*(B) gene in L-NTCD03. The *cfrB* gene encodes a rRNA methyltransferase
465 that confers multidrug resistance by ribosomal target modification and, in addition to *C. difficile*, has been
466 found in *Enterococcus* spp and methicillin-resistant *Staphylococcus aureus*. We showed that this gene can
467 confer resistance to clindamycin (>256 mg/L), linezolid (12 mg/L), repatamulin (16 mg/L) and streptogramin A
468 (16 mg/L) in the RT012 laboratory strain 630Δ*erm* (van Eijk *et al.*, 2015). Our data confirm that *cfr*(B) is a
469 legitimate PhLOPSa (phenicol, lincosamide, oxazolidinone, pleuromutilin, streptogramin A) resistance gene.
470 We were unable to establish whether *cfr*(B) plays a role in phenicol resistance, though, as L-NTCD03 also
471 contains the *catP* (chloramphenicol resistance gene) and the plasmid we used to introduce the *cfr*(B) gene in
472 our laboratory strain also carries a *catP* resistance determinant (Fagan & Fairweather, 2011, Oliveira Paiva *et*
473 *al.*, 2016). We have, however, independently observed that *catP*-negative clinical isolates that carry *cfr*(B)
474 demonstrate elevated chloramphenicol MICs compared to isolates that lack *cfr*(B), suggesting that *cfr*(B) also
475 affects chloramphenicol MICs. Though it has previously been shown that *cfr* gene carriage can be associated

476 with linezolid resistance in *C. difficile* (Marin *et al.*, 2015, Stojkovic *et al.*, 2019) or lead to an increase in MIC for
477 certain antibiotics when expressed in a heterologous host (Hansen & Vester, 2015), to our knowledge, the
478 present study is the first direct demonstration of this function for *cfr*(B) as a PhLOPSa resistance gene in this
479 organism.
480
481
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489
490 **Declaration of interest statements**
491 The authors declare that the research was conducted in the absence of any commercial or financial
492 relationships that could be construed as a potential conflict of interest.
493
494 **Author contributions**
495 BN, EJK and WKS conceived the study. CH and IMJGS performed typing and susceptibility testing, BN
496 performed characterization of L-NTCD03 in *in vitro* and cellular assays. RHAMV and SLK performed PacBio
497 sequencing. SN and QRD performed bioinformatics analyses. CKB and RAB performed the Biolog experiments.
498 JB, CC, MLM, AL, BS, AR and SM conducted the animal experiments. FY performed the histological scoring. EB,
499 SM and TO reviewed the histology. WKS, TO, SM and EJK supervised work. BN and WKS drafted the
500 manuscript. All authors edited the manuscript and agreed to its submission.
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502
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685 **Table 1. Antimicrobial susceptibility of L-NTCD03**
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Antibiotic	MIC (mg/L)[a]	EUCAST (T)ECOFF (mg/L)	Putatively associated AMR gene[b]
Augmentin	0.25	-	-
Cefuroxime	>256	-	*blaCDD*
Chloramphenicol	>256	-	*catP, cfr(*B*)*
Ciprofloxacin	>32	(32)	*gyrB*_S366A
Clindamycin	>256	16	*cfr*(B), *cplR*
Cotrimoxazole	0.06	-	-
Erythromycin	48	4	*erm*(52)
Fidaxomicin	0.06	0.5	-
Linezolid	6	-	*cfr*(B)
Meropenem	1	(8)	-
Metronidazole	0.06	2	-
Moxifloxacin	1	4	-
Penicillin	0.75	-	*blaCDD*
Rifampicin	>32	0.004	*rpoB*_R505K
Tetracycline	2	(0.25)	*tet*(M)
Teicoplanin	1	-	*vanZ1*
Vancomycin	0.38	2	-

687 [a] MICs were determined using Etest, except for fidaxomicin (where agar dilution was used) as described in
688 Materials and Methods
689 b EUCAST Epidemiological Cut-off (ECOFF) are given without, tentative epidemiological cut-off (TECOFF) values
690 are given within brackets (EUCAST, 2026).
691 [c] AMR gene content was determined using AMRFinderPlus (Feldgarden *et al.*, 2021). Genes not shown in table
692 are the aminoglycoside resistance genes *ant(6)-Ia*, *sat4*, *aph(3')-IIIa*, *blaAHM*, *nimB*-Cd. The latter is omitted
693 here for as the allele identified does not a contain the resistance associated promoter mutation (see
694 Discussion).
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701 **Table 2. Table 1. Minimal inhibitory concentrations of *C. difficile* 630Δ*erm*-derived strains carrying different**

702 **plasmids.**

plasmid	antimicrobial MIC (mg/L)			
	clindamycin	linezolid	retapamulin	streptogramin A
pAP24 (control)	2	1	0.125	2
pIMM03 (*cfr*(B))	>256	12	16	16

703 Experiments were performed at n>3, with results consistent between experiments. Clindamycin and linezolid

704 MICs were determined by Etest, and MICs for retapamulin and streptogramin A were determined by modified

705 agar dilution (see Methods).

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707

708 **Table 3**. **Oligonucleotides**

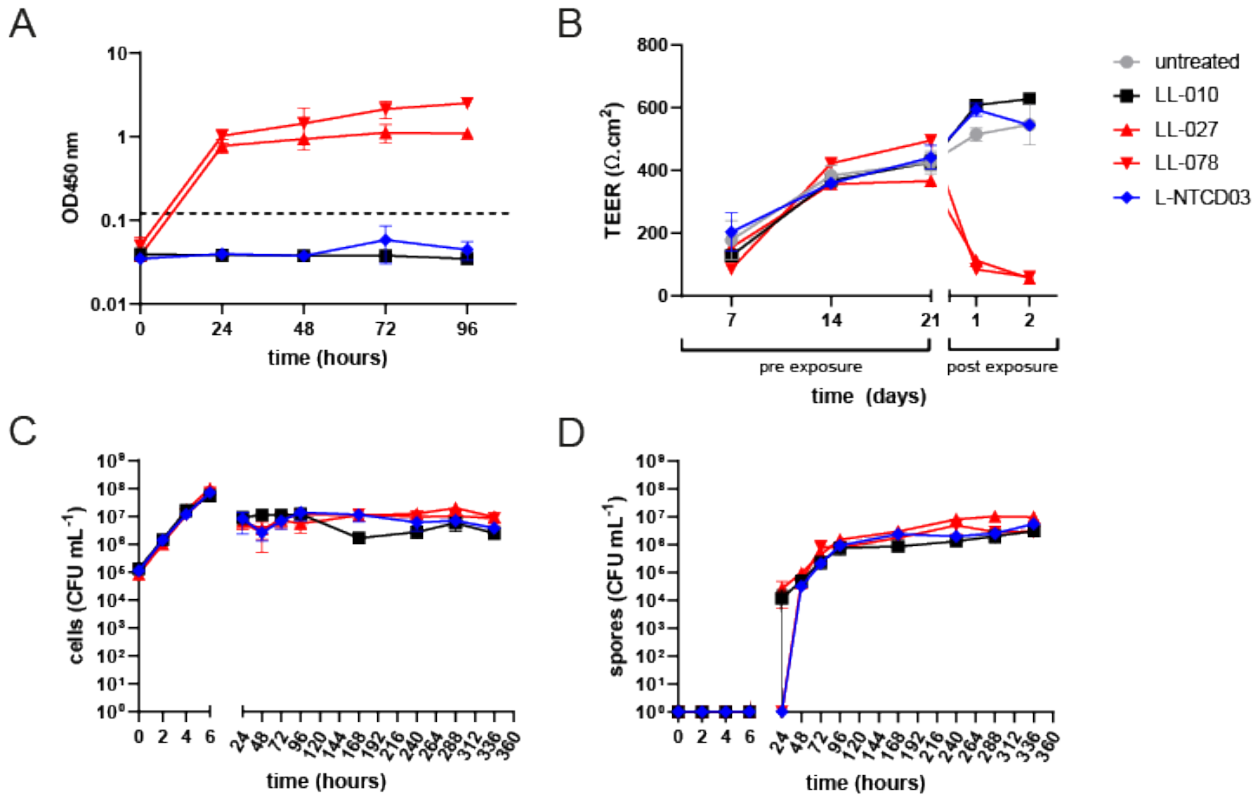
Oligonucleotide	Sequence (5'>3')	Reference
16S-F	TET[#]-GTGCGGCTGGATCACCTCCT	(Fawley *et al.*, 2015)
23S-R	CCCTGCACCCTTAATAACTTGACC	(Fawley *et al.*, 2015)
NF793	CACCTCCTTTTTGACTTTAAGCCTACGAATACC	(Fagan & Fairweather, 2011)
NF794	CACCGACGAGCAAGGCAAGACCG	(Fagan & Fairweather, 2011)
oIMM-001	CTACGGTACCCTCTACCTAATAGCCACAGGAG	This study
oIMM-002	GATGGGATCCTCACTGCATCCGCAATTC	This study
oIMM-003	GTTAATTGAGGAGTTTGGAGAATCG	This study
oIMM-004	CACATCTGATAATGGGTAGCGTTC	This study
oWKS-1070	GTCTTGGATGGTTGATGAGTAC	(Boekhoud *et al.*, 2020)
oWKS-1071	TTCCTAATTTAGCAGCAGCTTC	(Boekhoud *et al.*, 2020)
oWKS-1387	CAGATGAGGGCAAGCGGATG	(Boekhoud *et al.*, 2020)
oWKS-1388	CGTCGGTGAGCCAGAGTTTC	(Boekhoud *et al.*, 2020)

709 [#] TET: 5-tetrachlorofluorescein

710 **Figure Legends**

711

712 **Figure 1. L-NTCD03 is a non-toxigenic *C. difficile* strain. A.** L-NTCD03 does not show production of toxins in an
713 ELISA assay. The dotted line indicates the threshold value indicated by the manufacturer for defining toxin
714 production. **B**. Culture supernatant from L-NTCD03 does not lead to a reduction in transepithelial resistance as
715 measured in a Caco2/LS174T cellular model that was matured for 21 days (pre-exposure) before applying
716 culture supernatant (post exposure). **C**. Growth of L-NTCD03 is similar to other *C. difficile* strains. Colony
717 forming units (CFU) per milliliter culture were determined by a droplet-plating method. **D**. Spore formation of
718 L-NTCD03 is similar to other *C. difficile* strains. Spores were enumerated after ethanol treatment using a
719 droplet plating method. Values indicated are the mean and standard error of the mean of n=3 biological
720 replicates. LL-010 is a non-toxigenic control strain and LL-027 and LL-078 are toxigenic controls.



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723 **Figure 2. L-NTCD03 does not induce pathology in the swine IsoLoop model. A.** Representative images from
724 histological analyses. Tissues samples were formalin fixed and paraffin embedded, sectioned and hematoxylin
725 and eosin stained. No significant *C. difficile*-associated lesions are observed in the control loop (an ileal loop
726 that was antibiotic-treated but not inoculated with *C. difficile*), normal ileum (not a loop but control for
727 surgical integrity of the loops) and the loop inoculated with L-NTCD03. In contrast, the loop inoculated with LL-
728 078 (toxigenic strain, positive control for *C. difficile* pathology) showed blunting of the villi with epithelial
729 necrosis, neutrophilic infiltration of lamina propria, and crypt abscesses. **B**. Combined histological scores for
730 the different samples. A bar plot depicting the mean histological score with standard error of the mean is
731 given, with individual datapoints depicted. Prespecified contrasts (see Supplementary Information) are shown
732 with brackets, with asterisks indicating the raw p-value magnitude, for readability (**: $p < 0.01$) , while
733 significance is determined by Holm adjustment across the three prespecified tests.
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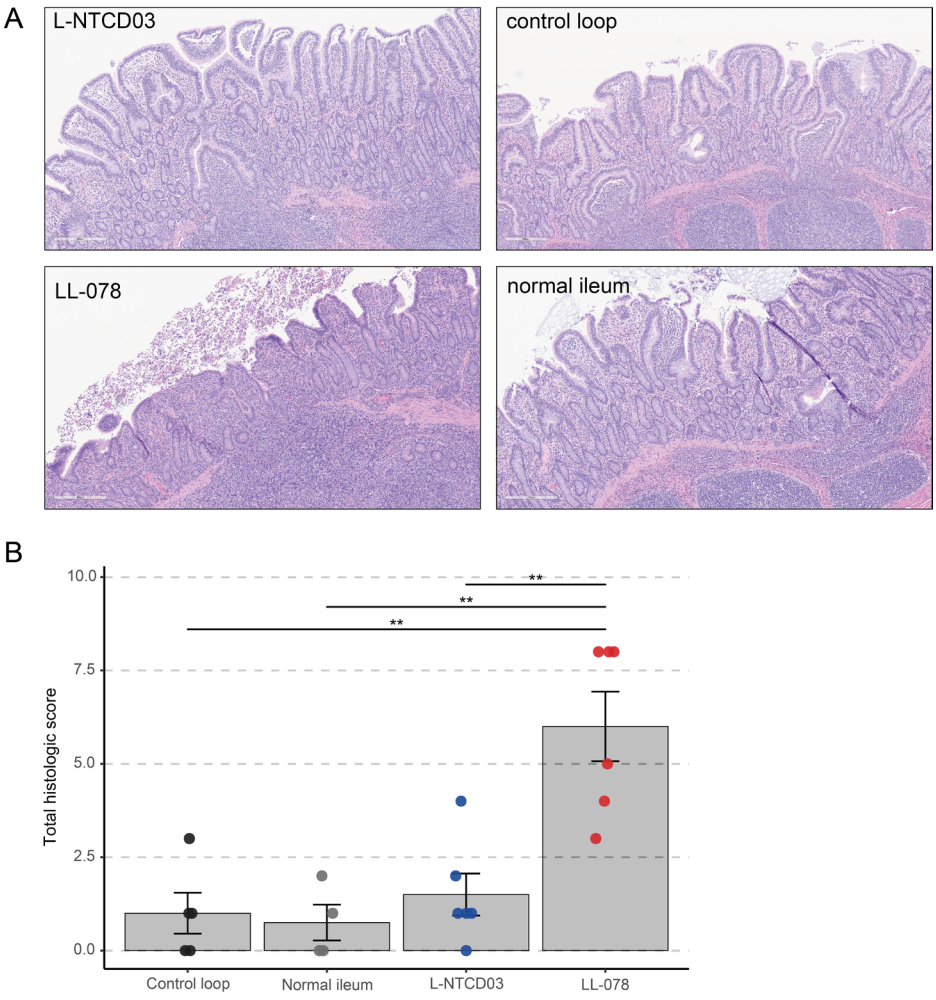

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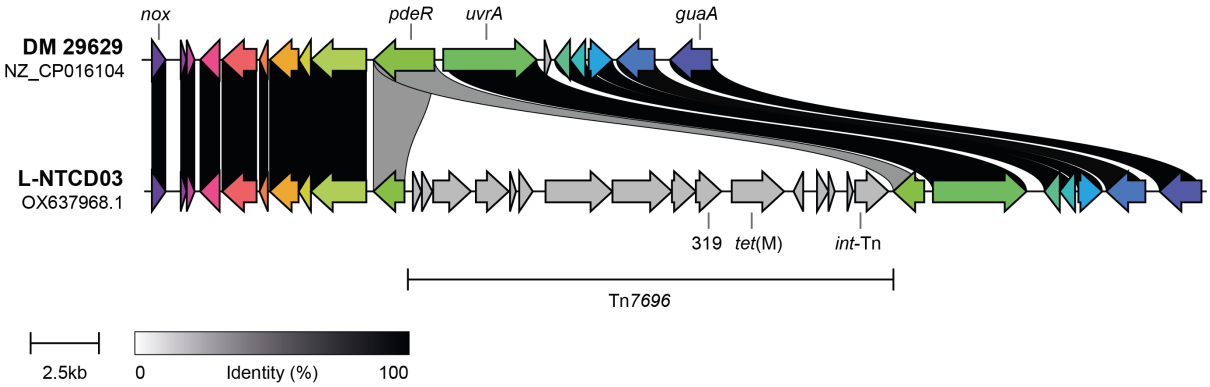
737 **Figure 3. L-NTCD03 harbors the novel transposon Tn*7696*.** Comparison of a region of the genome of L-NTCD03
738 with the genome of the closely related clade 4 strain DSM 29629 (GenBank NZ_CP016104). The insertion of
739 Tn*7696* into the *pdeR* gene (LLHAOGBK_00328 and LLHAOGBK_00311/CDIF29629_RS01565) is evident. Tn*7696*
740 harbors the tetracycline resistance gene *tet*(M) and an integrase (*int*-Tn), like Tn*916*. The gene with locus tag
741 LLHAOGBK_00319 (see main text) is abbreviated to 319 for simplicity. Colors and linkages indicate homology
742 between genes. *nox* encodes a predicted NADH dehydrogenase/nitroreductase (LLHAOGBK_00337/
743 CDIF29629_RS01610), *uvrA* an excinuclease (LLHAOGBK_00310/CDIF29629_RS01560) and *guaA* a glutamine-
744 hydrolyzing GMP synthase (LLHAOGBK_00305/CDIF29629_RS01525).
745



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Supplementary information

Histological scoring

H&E-stained sections from each ileal loop were graded for four components present in the dataset: epithelial necrosis, edema (mucosal/lamina propria), crypt abscess, and neutrophils in villi/lamina propria. A fifth field, submucosal edema, was also recorded but was invariant (0 in this experiment) and therefore excluded from totals.

Each component used an ordinal 0–5 scale with shared anchors; the best matching description was assigned:

- Epithelial necrosis: 0 = absent; 1–2 = scattered villus-tip necrosis; 3 = multifocal epithelial lifting/patchy denudation; 4–5 = broad denudation/ulceration with diffuse surface loss.
- Edema (mucosal/lamina propria): 0 = none; 1–2 = subtle to mild expansion; 3 = clear expansion with villus blunting; 4 = marked expansion; 5 = diffuse expansion with severe blunting/separation.
- Crypt abscess: 0 = none; 1–2 = rare crypts with a few intraluminal neutrophils/debris; 3 = several crypts with clear pus; 4–5 = numerous/widespread abscesses across fields.
- Neutrophils in villi/lamina propria: 0 = no neutrophils; 1= scattered individual cells; 2 = multifocal small clusters; 3 = multifocal large clusters; 4 = confluent clusters; 5 = sheets/near-diffuse infiltration. (Field counts may aid consistency; final grade is by pattern/severity.)

Total histologic score: per loop, the sum of the four variable components (range 0–20); higher totals indicate greater injury. Each loop was treated as the experimental unit; scoring was performed blinded to group identity.

Statistical analyses

Outcome and unit. The primary endpoint was the total histologic score per ileal loop (range 0–20), computed as the sum of four 0–5 ordinal components: epithelial necrosis, mucosal/lamina propria edema, crypt abscess, and neutrophils in villi/lamina propria. Submucosal edema values were invariant and excluded from totals. Each loop was the experimental unit; scoring was blinded to group.

Descriptive statistics. Group data are summarized as median [Q1–Q3]. Figures display mean ± SEM with per loop jittered points.

Global comparison. Overall heterogeneity among Control loop, Normal Ileum, L-NTCD03 and LL-078 was assessed with the Kruskal–Wallis test (two sided, $\alpha = 0.05$) using mid ranks with tie correction.

Primary prespecified contrasts. The biological comparisons of primary interest were LL-078 vs Control loop, LL-078 vs Normal ileum, and LL-078 vs L-NTCD03. Each was tested using a two sided Mann–Whitney U test (Wilcoxon rank sum). Multiplicity was controlled across these three tests using the Holm procedure (family wise $\alpha = 0.05$). For each contrast we report the Holm adjusted p value and the rank biserial correlation (r) as an effect size.

784 **Supplementary Table 1. Histopathological analysis of the pig-ileal loop experiments.**

	Epithelial necrosis	Edema	Crypt abscess	Submucosal edema	Neutrophils in villi/lamina propria	Total histological score
Control loop	0	0	0	0	0	0
Control loop	0	1	0	0	0	1
Control loop	0	1	1	0	1	3
Control loop	0	0	0	0	0	0
Control loop	0	1	0	0	0	1
Normal ileum	0	1	1	0	0	2
Normal ileum	0	0	0	0	0	0
Normal ileum	0	0	0	0	0	0
Normal ileum	0	1	0	0	0	1
L-NTCD03	1	1	1	0	1	4
L-NTCD03	0	1	0	0	0	1
L-NTCD03	0	0	0	0	0	0
L-NTCD03	0	1	1	0	0	2
L-NTCD03	0	1	0	0	0	1
L-NTCD03	0	1	0	0	0	1
LL-078	2	2	2	0	2	8
LL-078	2	2	2	0	2	8
LL-078	3	1	2	0	2	8
LL-078	2	1	1	0	1	5
LL-078	2	1	0	0	1	4
785 LL-078	1	1	0	0	1	3

786

787 **Supplementary Table 2. Antimicrobial resistance genes of L-NTCD03.**

Start	Stop	Strand	Locus tag	Resistance gene	Name	Class	Subclass	Alignment length	Reference length	Reference sequence	Coverage	Identity
4145	6043	+	LLHAOGBK_00005	gyrB_S366A	Clostridioides difficile quinolone resistant GyrB	quinolone	quinolone	633	633	WP_003434229.1	100	99,84
95557	99270	+	LLHAOGBK_00126	rpoB_R505K	Clostridioides difficile rifampin resistant RpoB	rifamycin	rifampin	1238	1238	WP_003436174.1	100	99,76
272459	274375	-	LLHAOGBK_00317	tet(M)	tetracycline resistance ribosomal protection protein Tet(M)	tetracycline	tetracycline	639	639	WP_000691736.1	100	99,69
334396	335442	+	LLHAOGBK_00374	cfr(B)	23SrRNA (adenine(2503)-C(8))-methyltransferase Cfr(B)	lincosamide/oxazolidinone/phenicol/pleuromutilin/streptogramin	chloramphenicol/clindamycin/linezolid/retapamulin/streptogramin B/virginiamycin	349	349	WP_002405682.1	100	99,71
526699	527319	+	LLHAOGBK_00554	catP	type A-11 chloramphenicol O-acetyltransferase CatP	phenicol	chloramphenicol	207	207	WP_002570989.1	100	100
548779	549684	+	LLHAOGBK_00577	ant(6)-Ia	aminoglycoside nucleotidyltransferase ANT(6)-Ia	aminoglycoside	streptomycin	302	302	WP_001255864.1	100	100
549684	550223	+	LLHAOGBK_00578	sat4	streptothricin N-acetyltransferase Sat4	streptothricin	streptothricin	180	180	WP_000627290.1	100	100
550319	551110	+	LLHAOGBK_00579	aph(3')-IIIa	aminoglycoside O-phosphotransferase APH(3')-IIIa	aminoglycoside	amikacin/kanamycin	264	264	WP_001096887.1	100	100
1530614	1532263	+	LLHAOGBK_01435	cplR	ABC-F type ribosomal protection protein CplR	lincosamide/pleuromutilin/streptogramin	clindamycin/lincomycin/retapamulin/virginiamycin	550	550	AJP12342.1	100	97,82
2811949	2812410	+	LLHAOGBK_02605	nimB-Cd	putative 5-nitroimidazole reductase NimB-Cd	nitroimidazole	nitroimidazole	154	155	CBE03766.1	99,35	100
3057328	3057834	-	LLHAOGBK_02836	vanZ1	glycopeptide resistance protein VanZ1	glycopeptide	vancomycin	169	169	CAJ68095.1	100	99,41
3344140	3345051	-	LLHAOGBK_03095	blaAHM	AHM family subclass B3-like metallo-beta-lactamase	beta-lactam	carbapenem	304	304	WP_011860980.1	100	97,7
3874110	3875045	-	LLHAOGBK_03550	blaCDD	CDD family class D beta-lactamase	beta-lactam	beta-lactam	312	308	WP_021361759.1	100	96,15
3965200	3966126	-	LLHAOGBK_03629	erm(52)	23SrRNA (adenine(2058)-N(6))-methyltransferase Erm(52)	macrolide	macrolide	309	309	WP_002571018.1	100	100

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