

Review Article

Virulence Factors of *Clostridioides (Clostridium) difficile* Linked to Recurrent Infections

Laura Tijerina-Rodríguez,¹ Licet Villarreal-Treviño,¹ Rayo Morfín-Otero ,²
Adrián Camacho-Ortiz ,³ and E. Garza-González ³

¹Departamento de Microbiología e Inmunología, Facultad de Ciencias Biológicas, Universidad Autónoma de Nuevo León, San Nicolás de los Garza, Mexico

²Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara,

Hospital Civil de Guadalajara “Fray Antonio Alcalde” e Instituto de Patología Infecciosa y Experimental, Guadalajara, Mexico

³Hospital Universitario “Dr. José Eleuterio González”, Universidad Autónoma de Nuevo León, Monterrey, Mexico

Correspondence should be addressed to E. Garza-González; elvira_garza_gzz@yahoo.com

Received 1 July 2019; Revised 2 December 2019; Accepted 7 December 2019; Published 24 December 2019

Academic Editor: José Ramón Blanco

Copyright © 2019 Laura Tijerina-Rodríguez et al. This is an open access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

From 20 to 30% of *Clostridioides (Clostridium) difficile* infection (CDI), patients might develop recurrence of the infection (RCDI) and, after the first recurrence, the risk of further episodes increases up to 60%. Several bacterial virulence factors have been associated with RCDI, including the elevated production of toxins A and B, the presence of a binary toxin CDT, and mutations in the negative regulator of toxin expression, *tcdC*. Additional factors have shown to regulate toxin production and virulence in *C. difficile* in RCDI, including the accessory-gene regulator *agr*, which acts as a positive switch for toxin transcription. Furthermore, adhesion and motility-associated factors, such as Cwp84, SlpA, and flagella, have shown to increase the adhesion efficiency to host epithelia, cell internalization, and the formation of biofilm. Finally, biofilm confers to *C. difficile* protection from antibiotics and acts as a reservoir for spores that allow the persistence of the infection in the host. In this review, we describe the key virulence factors of *C. difficile* that have been associated with recurrent infections.

1. Introduction

Clostridioides (Clostridium) difficile infection (CDI) is the leading cause of healthcare-associated diarrhea worldwide. In 2011, increased CDI was reported in the United States by the Centers for Disease Control with an estimated 453 000 infections (83 000 had at least one recurrence) and 29 000 deaths [1].

CDI severity has increased in the last decade with outbreaks in the United States, Canada, the United Kingdom, Western Europe, Japan, Korea, China, Hong Kong, and some countries of Latin America. This increased severity has been coincident with the spread of the epidemic strain designated as North American Pulsed (NAP)-field type 01, restriction endonuclease analysis (REA) as group BI, (BI/RT-027/BI), and polymerase chain reaction (PCR) ribotype (RT) 027 (NAP1/BI/027) [2–8].

From 2008 to 2014, CDI cases declined considerably in the United Kingdom, from 55,498 to 13,361, as a result of a surveillance scheme implemented by the National Health Service, including antibiotic stewardship, improvement protocols for infection control in hospitals, and the creation of the *C. difficile* ribotyping network in aims to prevent CDI transmission and control epidemic strains [9–13].

However, CDI is not only of worldwide concern due to ribotype 027 but also due to the emergence of other virulent strains, including ribotypes 027, 078, 001, 176, 020, 002, and 106, in many populations [1, 14–17].

2. Recurrence of CDI

Primary CDI is predominantly treated with standard antibiotic therapy, including metronidazole, vancomycin, and fidaxomicin, the more recently FDA-approved drug,

TABLE 1: Summary of presumptive virulence factors associated with recurrent *C. difficile* infections.

Factor	Mechanism/function	Risk/association	Source
<i>tcdC</i> and binary toxin	Production of elevated toxin A and B levels in hypervirulent strains	Increased pathogenicity <i>in vivo</i> and <i>in vitro</i>	[37]
<i>agr1</i> locus (accessory-gene regulator)	Positive regulation of toxin A and toxin B production, independent of <i>tcdC</i>	Regulation of virulence, associated with increased colonization	[38–41]
Biofilm	Survival niche of <i>C. difficile</i> with multispecies communities	Long persistence/protection of <i>C. difficile</i>	[36, 42–46]
	Accumulation of toxins and biomass in variant strains regulated by quorum sensing		
	Accumulation of spores	Reduced susceptibility to antibiotics	[45, 47]
SlpA (S-layer protein A)	Presence and low molecular weight subunits with sequence variability in hypervirulent strains	Increased adhesion to gut mucosa	[48–52]
Cwp84 (cell wall protein 84)	Cleavage of adhesins, such as SlpA, for the paracrystalline layer assembly	Release and dissemination of <i>C. difficile</i> in the host	[49, 52]
	Degradation of several extracellular matrix proteins (fibronectin, laminin, vitronectin)	Increase adhesion and colonization	[48, 49, 53]
	Production of thicker biofilm in strains with high proteolytic activity associated to Cwp84	Enhanced virulence and host-pathogen adherence; maintenance of CDI	[54, 55]
Flagella	Presence of posttranscriptional modifications in flagellin and flagellar cap proteins	Increased biofilm, adherence, and cell internalization, associated with efficient colonization <i>in vivo</i>	[42, 56, 57] [58]
Spores	Development of structural morphotypes of outermost exosporium layers (thin or thick)	Associated to host-spore interactions, differences in affinity to epithelial cells	[12, 45, 59, 60]
	Expression of the sporulating regulator <i>spo0A</i> is associated with high spore production and biofilm formation	Transmission of CDI and maintenance of <i>C. difficile</i> in the host, despite the antibiotic treatment	[42, 45, 59, 61–63]

depending on severity [18]. Nevertheless, 20–35% of patients may develop the recurrence of symptoms, which is defined as a recurrent infection (RCDI) [19–23]. After the first recurrent episode, patients are more likely to have subsequent recurrences, and by the third episode, risk of recurrence can reach 60% [24, 25]. Several studies have evaluated administration of fidaxomicin versus vancomycin and metronidazole for RCDI patients, with lower recurrent episodes and fewer deaths for fidaxomicin [18, 26, 27].

3. Relapse and Reinfection

RCDI may occur due to relapse, defined as the persistence of the same strain causing the initial infection, or reinfection, defined as the acquisition of a genotypically distinct *C. difficile* strain from an exogenous source [28]. Furthermore, patients with ribotype 027 strains present a higher risk of relapse than those with other ribotypes [7].

4. Ribotypes Associated with Relapse or Reinfection

The glycosylating toxins, toxin A (TcdA) and toxin B (TcdB), are primarily responsible for the symptoms associated with CDI and are the key mediators of pathogenesis [29]. These

toxins have been shown to bind to the cell surface and translocate to the cytosol of the host epithelial cells where they glycosylate and inactivate important GTPases (including Rho, Rac, and Cdc42), leading to actin cytoskeleton alternations, cell rounding, apoptosis, and cell death [30, 31].

Several studies have shown elevated sporulation rates in epidemic strains, including the hypervirulent NAP1/BI/027 strain [32]. Also, these strains have been found to contain increased levels of toxins, which are associated with deletions in the toxin negative regulator *tcdC* (18 bp and 39 bp deletions for the 027 and 078 strains, respectively) in *in vitro* models [33, 34]. However, in more complex models, the 027 strain has been shown to have a longer growth cycle, where toxin production starts slightly earlier than that of other strains, and toxins tend to accumulate [35, 36].

Hypervirulent *C. difficile* also produces a third toxin called binary *C. difficile* toxin (CDT). CDT is a transferase that can irreversibly ADP-ribosylate actin and promote disruption of the actin cytoskeleton [31]. The presence of CDT and mutations in *tcdC* increases the risk of RCDI (odds ratio (OR), 5.3; 95% confidence interval (CI), 3.52–6.09) (Table 1) [2, 64].

RCDI is more frequent in patients infected with the 027 strain than in those infected with non-027 strains ($P < 0.001$). Besides, the clinical cure rate has been reported to be lower in 027-infected patients than in those with non-

027 infections when treated with fidaxomicin ($P = 0.007$) or vancomycin ($P = 0.02$) [3].

5. Antibody Response to Toxin A

In several studies, the immune response to toxins A and B has been described, with higher titers of immunoglobulins IgG antitoxin A in asymptomatic carriers than noncarriers, and higher titers of IgG and IgM against toxin A and toxin B, but regression analysis showed significance for recurrent infection and low antitoxin A for 027 and primarily for all types with patients with little antitoxin B ($P = 0.02$) [65, 66].

Patients with a single episode of CDI had higher concentrations of serum IgM against toxin A on day 3 of initial CDI than those with RCDI ($n = 22$; $P = 0.004$). On day 12, patients who had a single episode of diarrhea ($n = 7$) had higher serum IgG values against toxin A than those with RCDI ($n = 9$; $p = 0.009$). IgG response to toxin A (12 days after onset of CDI) during an initial episode confers protection against recurrence (OR, 48.0; 95% CI, 3.5–663) [25]. Nevertheless, CDI patients who received neutralizing antibodies against toxin A showed no difference in the frequency of recurrence in comparison with CDI patients receiving placebo (17% and 18%, respectively, $P = \text{NS}$) [67].

6. Biofilm Production

Bacterial biofilms are associated with antimicrobial resistance, act as a survival niche, and protect bacteria, which can be in a dormant form with prolonged growth rates deep within the biofilm structure. Biofilms have been reported for several *Clostridium* species, including *C. perfringens*, *C. thermocellum*, and *C. acetobutylicum* [68, 69]. Similarly, *C. difficile* growth has shown well-organized communities on abiotic surfaces and well-structured biofilms *in vitro* and *in vivo* [42, 61, 70], with differences in the level of biofilm production between some strains in monoculture biofilms [42, 71]. In addition, a range of studies has characterized the supernatant and the polymeric composition and architecture of the biofilm matrix in *in vivo* and *in vitro* models, which is composed of extracellular DNA, polysaccharides, and proteins similar to *B. subtilis* biofilm [42, 54, 61, 72].

Notably, in a chemostat gut model, *C. difficile* (vegetative and spore forms) has been shown to participate in multispecies communities forming a robust biofilm that accumulates toxins. In addition, this biofilm is a potential reservoir for the reestablishment of *C. difficile* after primary antimicrobial therapy has finished, when gut levels of antimicrobials are at sub-minimal inhibitory concentration [36, 43, 44]. Furthermore, the biofilm matrix showed a preferential localization of spores that have a higher resistance to some antibiotics (metronidazole and vancomycin) (Table 1). Taken together, these observations may explain the long-term persistence of strains involved in primary and/or recurrent CDI [42, 45].

7. Regulation by Quorum Sensing

Quorum sensing (QS) is the regulation of gene expression of virulence factors (biofilm production, attachment, motility,

toxin production, and sporulation) in response to environmental changes due to cell-to-cell communication. It is mediated by small diffuse molecules known as autoinducers produced by individual bacteria. The level of autoinducers is cell-density dependent: when the density is high, autoinducers are detected by other bacteria, enabling them to coordinate physiological activities [38, 73, 74].

Orthologues of the accessory-gene regulator (Agr) ACDB, the global regulatory locus that encodes AgrA, have been found within the genome of most *C. difficile* isolates, including the hypervirulent strain 027/BI/NAP1. AgrA has critical roles in controlling gene expression and enhancing the production of colonization factors and exoproteins essential for the pathogenic process [38, 39]. Furthermore, it is the transcriptional regulator of the best-understood QS system in Gram-positive bacteria, including *Staphylococcus aureus* [39].

C. difficile production of toxins A and B are controlled by an Agr-quorum signaling system mediated through a small thiolactone that can be detected in stools of CDI patients [40]. Some strains encode two Agr loci in their genomes (*agr1* and *agr2*), with the first being present in all strains and the second being present in a few strains. It has been shown that the *agr1* mutant cannot produce both toxins and that toxin production can be restored with the wild type *agr1*. Furthermore, it has been demonstrated that the *agr1* mutant can colonize but cannot cause disease in a murine CDI model (Table 1) [39, 75].

8. Sporulation and Germination

Another key virulence factor involved in *C. difficile* pathogenesis and colonization is spore production, with differences in germination rates being lower in spores from biofilm than those from a vegetative culture [45]. Spore production is mediated by the master regulator of the sporulation pathway (*spo0A*). In mice infected with sporulating and nonsporulating *C. difficile* strains (*spo0A* mutants), no recurrence of CDI was found after vancomycin treatment, and the *spo0A* mutant infection was not transmissible between hosts [59]. *Spo0A* mutants are associated with defective biofilm formation and low sporulation in biofilms (0.0001%), suggesting an essential link between *Spo0A* and biofilm production, such as that seen in *Bacillus subtilis* [42, 61, 62].

The production and accumulation of spores within *C. difficile* biofilms are likely to be significantly associated with RCDI, with further germination of vegetative toxin-producing cells after cessation of antibiotic therapy. Metabolically dormant spore forms can protect *C. difficile* from adverse conditions, such as nutrient starvation, antimicrobial agents, disinfectants, heat, and desiccation, and help the bacteria survive attacks of phagocytic cells [76]. Furthermore, antibiotic treatment triggers the excretion of higher sporulation of *C. difficile* in mice. Therefore, in most cases, when antibiotic therapy is stopped, a recovery occurs and the super-shedder state of *C. difficile* is suppressed [77].

A novel exosporial layer has been found in spores from biofilms, composed of fine fibers and darkly staining

granules. This layer is surrounded by a thin layer and is acquired after mother cell lysis; it has been found in 027 strains associated with multiple recurrent episodes of CDI (Table 1) [45, 59, 60]. The specific role of these structural differences of the exosporium in spores is not clear. A previous study showed that the *C. difficile* R20291 strain (RT-027) showed higher affinity to the host cell membrane and microvilli of intestinal epithelial cells [78], suggesting that the differences in composition of the exosporium of *C. difficile* spores might regulate the adherence to intestinal cells of the host (Table 1) [78–80]. Additional studies are needed to determine the role of the structural properties of the *C. difficile* layer and spore exosporium for the development of recurrent infection.

9. Adhesion Factors

Several nontoxigenic factors involved in the virulence and infection processes have been described, including surface proteins (cell wall and surface layer (S-layer) proteins), pili, flagellin, flagellar cap, and fibronectin-binding proteins [42, 53].

The S-layer protein A (SlpA) is the predominant outer surface and has shown to be the major contributor of *C. difficile* adherence to epithelial cells *in vitro*. SlpA is cleaved after translation in high and low molecular weight (HMW and LMW) subunits for the assembly of the paracrystalline layer. Interstrain sequence variability of LMW subunits has been associated with higher adhesion efficiency in hypervirulent strains [48–51].

The cell wall protein 84 (Cwp84) is one of the primary proteases that is exported by the cell and cleave several adhesins such as SlpA for the assembly of the paracrystalline layer and the degradation of extracellular matrix proteins (fibronectin, laminin, and vitronectin). This degradation triggers the release and dissemination of *C. difficile* in the host, which are related to the recurrence of infection (Table 1) [49, 81–83].

Cwp84 is present in all *C. difficile* strains, and those with the highest proteolytic activity are associated with stronger adhesion and production of thicker biofilm, planktonic growth defect, and virulence *in vivo* [49, 72]. In addition, a recent study found overexpression of *cwp84* in a biofilm model from recurrence causing strains, this phenomenon was not observed in the biofilm produced by nonrecurrent strains [84], suggesting an association with recurrent infection.

SlpA cleavage could be accomplished by other proteases in the absence of *cwp84*, such as *cwpV*, *cwp66*, and *cwp13* [49, 52]. These findings suggest an essential role of some surface proteins associated with increased host-pathogen adherence, which may be related to the maintenance of CDI.

In addition to propulsion, motility components provide bacteria with other advantages, such as adherence and cell internalization. *C. difficile* possesses peritrichous flagella, which induce the adhesion and establishment of the bacteria including the strains without complete and functional flagella as a result of mutations [56, 57, 85–87]. The filament from *C. difficile* flagella is mostly composed of single flagellin

subunits and flagellar cap proteins, both of which are modified posttranslationally. Therefore, as a consequence of a noncomplete functional flagella, these components do not confer motility but enhance binding of *C. difficile* to abiotic surfaces, as well as reduced biofilm formation, leading to the attenuation of colonization and relapse *in vivo*, suggesting a role of flagella in the process of adherence and biofilm formation independent to motility (Table 1) [42, 56, 57].

10. Concluding Remarks

RCDI development is associated with hypervirulent strains and may be attributed to a high rate of sporulation and the maintenance of spores encased in a *C. difficile* biofilm, which is resistant to antibiotic therapies. Besides, several adhesion-related proteins are involved in RCDI development and the establishment of the infection.

Antibiotics have been demonstrated to disrupt colonic microbiota, placing the patient at a high risk of further recurrent episodes. Further studies on RCDI development are needed to assess the correlation of these potential virulence traits and the persistence of *C. difficile* infection.

Conflicts of Interest

The authors declare that there are no conflicts of interest regarding the publication of this paper.

References

- [1] F. C. Lessa, Y. Mu, W. M. Bamberg et al., “Burden of *Clostridium difficile* infection in the United States,” *New England Journal of Medicine*, vol. 372, no. 9, pp. 825–834, 2015.
- [2] D. B. Stewart, A. S. Berg, and J. P. Hegarty, “Single nucleotide polymorphisms of the *tcdC* gene and presence of the binary toxin gene predict recurrent episodes of *Clostridium difficile* infection,” *Annals of Surgery*, vol. 260, no. 2, pp. 299–304, 2014.
- [3] L. A. Petrella, S. P. Sambol, A. Cheknis et al., “Decreased cure and increased recurrence rates for *Clostridium difficile* infection caused by the epidemic *C. difficile* BI strain,” *Clinical Infectious Diseases*, vol. 55, no. 3, pp. 351–357, 2012.
- [4] I. T. Balassiano, E. A. Yates, R. M. C. P. Domingues, and E. O. Ferreira, “*Clostridium difficile*: a problem of concern in developed countries and still a mystery in Latin America,” *Journal of Medical Microbiology*, vol. 61, no. 2, pp. 169–179, 2012.
- [5] P. N. Wiegand, D. Nathwani, M. H. Wilcox, J. Stephens, A. Shelbaya, and S. Haider, “Clinical and economic burden of *Clostridium difficile* infection in Europe: a systematic review of healthcare-facility-acquired infection,” *Journal of Hospital Infection*, vol. 81, no. 1, pp. 1–14, 2012.
- [6] A. C. Clements, R. J. S. Magalhães, A. J. Tatem, D. L. Paterson, and T. V. Riley, “*Clostridium difficile* PCR ribotype 027: assessing the risks of further worldwide spread,” *The Lancet Infectious Diseases*, vol. 10, no. 6, pp. 395–404, 2010.
- [7] R. Morfin-Otero, E. Garza-Gonzalez, S. A. Aguirre-Diaz et al., “*Clostridium difficile* outbreak caused by NAP1/BI/027 strain and non-027 strains in a Mexican hospital,” *The Brazilian Journal of Infectious Diseases*, vol. 20, no. 1, pp. 8–13, 2016.
- [8] M. Warny, J. Pepin, A. Fang et al., “Toxin production by an emerging strain of *Clostridium difficile* associated with

- outbreaks of severe disease in North America and Europe," *The Lancet*, vol. 366, no. 9491, pp. 1079–1084, 2005.
- [9] J. S. Brazier, R. Raybould, B. Patel et al., "Distribution and antimicrobial susceptibility patterns of *Clostridium difficile* PCR ribotypes in English hospitals, 2007–08," *Euro-surveillance*, vol. 13, no. 41, 2008.
- [10] B. I. Duerden, "Contribution of a government target to controlling *Clostridium difficile* in the NHS in England," *Anaerobe*, vol. 17, no. 4, pp. 175–179, 2011.
- [11] K. E. Dingle, X. Didelot, T. P. Quan et al., "Effects of control interventions on *Clostridium difficile* infection in England: an observational study," *The Lancet Infectious Diseases*, vol. 17, no. 4, pp. 411–421, 2017.
- [12] M. H. Wilcox, N. Shetty, W. N. Fawley et al., "Changing epidemiology of *Clostridium difficile* infection following the introduction of a national ribotyping-based surveillance scheme in England," *Clinical Infectious Diseases*, vol. 55, no. 8, pp. 1056–1063, 2012.
- [13] J. Freeman, J. Vernon, S. Pilling et al., "The ClosER study: results from a three-year pan-European longitudinal surveillance of antibiotic resistance among prevalent *Clostridium difficile* ribotypes, 2011–2014," *Clinical Microbiology and Infection*, vol. 24, no. 7, pp. 724–731, 2018.
- [14] O. Nyc, M. Krutova, A. Liskova, J. Matejkova, J. Drabek, and E. J. Kuijper, "The emergence of *Clostridium difficile* PCR-ribotype 001 in Slovakia," *European Journal of Clinical Microbiology & Infectious Diseases*, vol. 34, no. 8, pp. 1701–1708, 2015.
- [15] N. Cassir, N. Fahsi, G. Durand, J.-C. Lagier, D. Raoult, and P.-E. Fournier, "Emergence of *Clostridium difficile* tcdC variant 078 in Marseille, France," *European Journal of Clinical Microbiology & Infectious Diseases*, vol. 36, no. 10, pp. 1971–1974, 2017.
- [16] M. Rupnik, A. Tambic Andrasevic, E. Trajkovska Dokic et al., "Distribution of *Clostridium difficile* PCR ribotypes and high proportion of 027 and 176 in some hospitals in four South Eastern European countries," *Anaerobe*, vol. 42, pp. 142–144, 2016.
- [17] H. Pituch, P. Obuch-Woszczatynski, D. Lachowicz et al., "Hospital-based *Clostridium difficile* infection surveillance reveals high proportions of PCR ribotypes 027 and 176 in different areas of Poland, 2011 to 2013," *Eurosurveillance*, no. 38, p. 20, 2015.
- [18] L. C. McDonald, D. N. Gerding, S. Johnson et al., "Clinical practice guidelines for *Clostridium difficile* infection in adults and children: 2017 update by the infectious diseases society of America (IDSA) and society for healthcare epidemiology of America (SHEA)," *Clinical Infectious Diseases*, vol. 66, no. 7, pp. 987–994, 2018.
- [19] S. Aslam, R. J. Hamill, and D. M. Musher, "Treatment of *Clostridium difficile*-associated disease: old therapies and new strategies," *The Lancet Infectious Diseases*, vol. 5, no. 9, pp. 549–557, 2005.
- [20] D. W. Eyre, A. S. Walker, D. Wyllie et al., "Predictors of first recurrence of *Clostridium difficile* infection: implications for initial management," *Clinical Infectious Diseases*, vol. 55, no. 2, pp. S77–S87, 2012.
- [21] I. Lowy, D. C. Molrine, B. A. Leav et al., "Treatment with monoclonal antibodies against *Clostridium difficile* toxins," *New England Journal of Medicine*, vol. 362, no. 3, pp. 197–205, 2010.
- [22] C.-A. D. Burnham and K. C. Carroll, "Diagnosis of *Clostridium difficile* infection: an ongoing conundrum for clinicians and for clinical laboratories," *Clinical Microbiology Reviews*, vol. 26, no. 3, pp. 604–630, 2013.
- [23] T. Beinortas, N. E. Burr, M. H. Wilcox, and V. Subramanian, "Comparative efficacy of treatments for *Clostridium difficile* infection: a systematic review and network meta-analysis," *The Lancet Infectious Diseases*, vol. 18, no. 9, pp. 1035–1044, 2018.
- [24] L. V. McFarland, G. W. Elmer, and C. M. Surawicz, "Breaking the cycle: treatment strategies for 163 cases of recurrent *Clostridium difficile* disease," *The American Journal of Gastroenterology*, vol. 97, no. 7, pp. 1769–1775, 2002.
- [25] L. Kyne, M. Warny, A. Qamar, and C. P. Kelly, "Association between antibody response to toxin A and protection against recurrent *Clostridium difficile* diarrhoea," *The Lancet*, vol. 357, no. 9251, pp. 189–193, 2001.
- [26] D. W. Crook, A. S. Walker, Y. Kean et al., "Fidaxomicin versus vancomycin for *Clostridium difficile* infection: meta-analysis of pivotal randomized controlled trials," *Clinical Infectious Diseases*, vol. 55, no. 2, pp. S93–S103, 2012.
- [27] T. J. Louie, M. A. Miller, K. M. Mullane et al., "Fidaxomicin versus vancomycin for *Clostridium difficile* infection," *New England Journal of Medicine*, vol. 364, no. 5, pp. 422–431, 2011.
- [28] M. Mac Aogáin, G. Moloney, S. Kilkenny et al., "Whole-genome sequencing improves discrimination of relapse from reinfection and identifies transmission events among patients with recurrent *Clostridium difficile* infections," *Journal of Hospital Infection*, vol. 90, no. 2, pp. 108–116, 2015.
- [29] A. Shen, "Clostridium difficile toxins: mediators of inflammation," *Journal of Innate Immunity*, vol. 4, no. 2, pp. 149–158, 2012.
- [30] M. M. Awad, P. A. Johanesen, G. P. Carter, E. Rose, and D. Lyras, "Clostridium difficile virulence factors: insights into an anaerobic spore-forming pathogen," *Gut Microbes*, vol. 5, no. 5, pp. 579–593, 2014.
- [31] K. Aktories, C. Schwan, and T. Jank, "Clostridium difficile toxin biology," *Annual Review of Microbiology*, vol. 71, no. 1, pp. 281–307, 2017.
- [32] M. Merrigan, A. Venugopal, M. Mallozzi et al., "Human hypervirulent *Clostridium difficile* strains exhibit increased sporulation as well as robust toxin production," *Journal of Bacteriology*, vol. 192, no. 19, pp. 4904–4911, 2010.
- [33] T. Akerlund, I. Persson, M. Unemo et al., "Increased sporulation rate of epidemic *Clostridium difficile* Type 027/NAP1," *Journal of Clinical Microbiology*, vol. 46, no. 4, pp. 1530–1533, 2008.
- [34] A. Goorhuis, D. Bakker, J. Corver et al., "Emergence of *Clostridium difficile* infection due to a new hypervirulent strain, polymerase chain reaction ribotype 078," *Clinical Infectious Diseases*, vol. 47, no. 9, pp. 1162–1170, 2008.
- [35] J. Freeman, W. Fawley, S. Baines, and M. Wilcox, "Measurement of toxin production by *Clostridium difficile*," *The Lancet*, vol. 367, no. 9515, pp. 982–983, 2006.
- [36] J. Freeman, S. D. Baines, K. Saxton, and M. H. Wilcox, "Effect of metronidazole on growth and toxin production by epidemic *Clostridium difficile* PCR ribotypes 001 and 027 in a human gut model," *Journal of Antimicrobial Chemotherapy*, vol. 60, no. 1, pp. 83–91, 2007.
- [37] S. P. A. Stawicki, S. D. Moffatt-Bruce, H. M. Ahmed et al., "Retained surgical items: a problem yet to be solved," *Journal of the American College of Surgeons*, vol. 216, no. 1, pp. 15–22, 2013.
- [38] G. P. Carter, D. Purdy, P. Williams et al., "Quorum sensing in *Clostridium difficile*: analysis of a luxS-type signalling system," *Journal of Medical Microbiology*, vol. 54, no. 2, pp. 119–127, 2005.

- [39] M. J. Martin, S. Clare, D. Goulding et al., "The *agr* locus regulates virulence and colonization genes in *Clostridium difficile* 027," *Journal of Bacteriology*, vol. 195, no. 16, pp. 3672–3681, 2013.
- [40] C. Darkoh, H. L. DuPont, S. J. Norris et al., "Toxin synthesis by *Clostridium difficile* is regulated through quorum signaling," *MBio*, vol. 6, Article ID e02569, 2015.
- [41] M. D. Zilberberg, K. Reske, M. Olsen, Y. Yan, and E. R. Dubberke, "Development and validation of a recurrent *Clostridium difficile* risk-prediction model," *Journal of Hospital Medicine*, vol. 9, no. 7, pp. 418–423, 2014.
- [42] T. Thapa, R. Leuzzi, Y. K. Ng et al., "Multiple factors modulate biofilm formation by the anaerobic pathogen *Clostridium difficile*," *Journal of Bacteriology*, vol. 195, no. 3, pp. 545–555, 2013.
- [43] G. S. Crowther, C. H. Chilton, S. L. Todhunter et al., "Development and validation of a chemostat gut model to study both planktonic and biofilm modes of growth of *Clostridium difficile* and human microbiota," *PLoS One*, vol. 9, Article ID e88396, 2014.
- [44] G. S. Crowther, C. H. Chilton, S. L. Todhunter et al., "Comparison of planktonic and biofilm-associated communities of *Clostridium difficile* and indigenous gut microbiota in a triple-stage chemostat gut model," *Journal of Antimicrobial Chemotherapy*, vol. 69, no. 8, pp. 2137–2147, 2014.
- [45] E. G. Semenyuk, M. L. Laning, J. Foley et al., "Spore formation and toxin production in *Clostridium difficile* biofilms," *PLoS One*, vol. 9, no. 1, Article ID e87757, 2014.
- [46] C. C. Yu, W. J. Gao, J. S. Yang et al., "Can tranexamic acid reduce blood loss in cervical laminectomy with lateral mass screw fixation and bone grafting: a retrospective observational study," *Medicine*, vol. 96, no. 5, Article ID e6043, 2017.
- [47] M. C. Zanella Terrier, M. L. Simonet, P. Bichard et al., "Recurrent *Clostridium difficile* infections: the importance of the intestinal microbiota," *World Journal of Gastroenterology*, vol. 20, no. 23, pp. 7416–7423, 2014.
- [48] P. Spigaglia, A. Barketi-Klai, A. Collignon et al., "Surface-layer (S-layer) of human and animal *Clostridium difficile* strains and their behaviour in adherence to epithelial cells and intestinal colonization," *Journal of Medical Microbiology*, vol. 62, no. 9, pp. 1386–1393, 2013.
- [49] L. de la Riva, S. E. Willing, E. W. Tate, and N. F. Fairweather, "Roles of cysteine proteases Cwp84 and Cwp13 in biogenesis of the cell wall of *Clostridium difficile*," *Journal of Bacteriology*, vol. 193, no. 13, pp. 3276–3285, 2011.
- [50] M. M. Merrigan, A. Venugopal, J. L. Roxas et al., "Surface-layer protein A (SlpA) is a major contributor to host-cell adherence of *Clostridium difficile*," *PLoS One*, vol. 8, no. 11, Article ID e78404, 2013.
- [51] S. Péchiné, C. Denève, A. Le Monnier, S. Hoys, C. Janoir, and A. Collignon, "Immunization of hamsters against *Clostridium difficile* infection using the Cwp84 protease as an antigen," *FEMS Immunology & Medical Microbiology*, vol. 63, no. 1, pp. 73–81, 2011.
- [52] A.-J. Waligora, C. Hennequin, P. Mullany, P. Bourlioux, A. Collignon, and T. Karjalainen, "Characterization of a cell surface protein of *Clostridium difficile* with adhesive properties," *Infection and Immunity*, vol. 69, no. 4, pp. 2144–2153, 2001.
- [53] C. Denève, C. Janoir, I. Poilane, C. Fantinato, and A. Collignon, "New trends in *Clostridium difficile* virulence and pathogenesis," *International Journal of Antimicrobial Agents*, vol. 33, no. 1, pp. S24–S28, 2009.
- [54] I. Poquet, L. Saujet, A. Canette et al., "*Clostridium difficile* biofilm: remodeling metabolism and cell surface to build a sparse and heterogeneously aggregated architecture," *Frontiers in Microbiology*, vol. 9, p. 2084, 2018.
- [55] J. Woods, L. Boegli, K. R. Kirker et al., "Development and application of a polymicrobial, in vitro, wound biofilm model," *Journal of Applied Microbiology*, vol. 112, no. 5, pp. 998–1006, 2012.
- [56] A. Tasteyre, M.-C. Barc, A. Collignon, H. Boureau, and T. Karjalainen, "Role of FliC and FliD flagellar proteins of *Clostridium difficile* in adherence and gut colonization," *Infection and Immunity*, vol. 69, no. 12, pp. 7937–7940, 2001.
- [57] A. Faulds-Pain, S. M. Twine, E. Vinogradov et al., "The post-translational modification of the *Clostridium difficile* flagellin affects motility, cell surface properties and virulence," *Molecular Microbiology*, vol. 94, no. 2, pp. 272–289, 2014.
- [58] N. Y. Choi, S. Y. Kang, and K. J. Kim, "Artemisia princeps inhibits biofilm formation and virulence-factor expression of antibiotic-resistant bacteria," *BioMed Research International*, vol. 2015, Article ID 239519, 7 pages, 2015.
- [59] L. J. Deakin, S. Clare, R. P. Fagan et al., "The *Clostridium difficile* spo0A gene is a persistence and transmission factor," *Infection and Immunity*, vol. 80, no. 8, pp. 2704–2711, 2012.
- [60] D. Paredes-Sabja, A. Shen, and J. A. Sorg, "*Clostridium difficile* spore biology: sporulation, germination, and spore structural proteins," *Trends in Microbiology*, vol. 22, no. 7, pp. 406–416, 2014.
- [61] L. F. Dawson, E. Valiente, A. Faulds-Pain, E. H. Donahue, and B. W. Wren, "Characterisation of *Clostridium difficile* biofilm formation, a role for Spo0A," *PLoS One*, vol. 7, Article ID e50527, 2012.
- [62] M. A. Hamon and B. A. Lazazzera, "The sporulation transcription factor Spo0A is required for biofilm development in *Bacillus subtilis*," *Molecular Microbiology*, vol. 42, no. 5, pp. 1199–1209, 2001.
- [63] Y. Zou, J. Woo, and J. Ahn, "Cellular and molecular responses of *Salmonella* Typhimurium to antimicrobial-induced stresses during the planktonic-to-biofilm transition," *Letters in Applied Microbiology*, vol. 55, no. 4, pp. 274–282, 2012.
- [64] D. B. Stewart, A. Berg, and J. Hegarty, "Predicting recurrence of *C. difficile* colitis using bacterial virulence factors: binary toxin is the key," *Journal of Gastrointestinal Surgery*, vol. 17, no. 1, pp. 118–125, 2013.
- [65] R. Viscidi, B. E. Laughon, R. Yolken et al., "Serum antibody response to toxins A and B of *Clostridium difficile*," *Journal of Infectious Diseases*, vol. 148, no. 1, pp. 93–100, 1983.
- [66] L. Kyne, M. Warny, A. Qamar, and C. P. Kelly, "Asymptomatic carriage of *Clostridium difficile* and serum levels of IgG antibody against toxin A," *New England Journal of Medicine*, vol. 342, no. 6, pp. 390–397, 2000.
- [67] B. A. Leav, B. Blair, M. Leney et al., "Serum anti-toxin B antibody correlates with protection from recurrent *Clostridium difficile* infection (CDI)," *Vaccine*, vol. 28, no. 4, pp. 965–969, 2010.
- [68] F. Napoli, G. Olivieri, M. E. Russo, A. Marzocchella, and P. Salatino, "Butanol production by *Clostridium acetobutylicum* in a continuous packed bed reactor," *Journal of Industrial Microbiology & Biotechnology*, vol. 37, no. 6, pp. 603–608, 2010.
- [69] Z.-W. Wang, S.-H. Lee, J. G. Elkins, and J. L. Morrell-Falvey, "Spatial and temporal dynamics of cellulose degradation and biofilm formation by *Caldicellulosiruptor obsidiansis* and *Clostridium thermocellum*," *AMB Express*, vol. 1, no. 1, p. 30, 2011.

- [70] G. Donelli, C. Vuotto, R. Cardines, and P. Mastrantonio, "Biofilm-growing intestinal anaerobic bacteria," *FEMS Immunology & Medical Microbiology*, vol. 65, no. 2, pp. 318–325, 2012.
- [71] V. Pantaleon, M. Monot, C. Eckert et al., "*Clostridium difficile* forms variable biofilms on abiotic surface," *Anaerobe*, vol. 53, pp. 34–37, 2018.
- [72] V. Pantaleon, A. P. Soavelomandroso, S. Bouttier et al., "The *Clostridium difficile* protease Cwp84 modulates both biofilm formation and cell-surface properties," *PLoS One*, vol. 10, Article ID e0124971, 2015.
- [73] M. B. Miller and B. L. Bassler, "Quorum sensing in bacteria," *Annual Review of Microbiology*, vol. 55, no. 1, pp. 165–199, 2001.
- [74] J. A. Thompson, R. A. Oliveira, A. Djukovic, C. Ubeda, and K. B. Xavier, "Manipulation of the quorum sensing signal AI-2 affects the antibiotic-treated gut microbiota," *Cell Reports*, vol. 10, no. 11, pp. 1861–1871, 2015.
- [75] C. Darkoh, C. Odo, and H. L. DuPont, "Accessory gene regulator-1 locus is essential for virulence and pathogenesis of *Clostridium difficile*," *MBio*, vol. 7, no. 4, 2016.
- [76] D. Paredes-Sabja, G. Cofre-Araneda, C. Brito-Silva et al., "*Clostridium difficile* spore-macrophage interactions: spore survival," *PLoS One*, vol. 7, Article ID e43635, 2012.
- [77] T. D. Lawley, S. Clare, A. W. Walker et al., "Antibiotic treatment of *Clostridium difficile* carrier mice triggers a supershedder state, spore-mediated transmission, and severe disease in immunocompromised hosts," *Infection and Immunity*, vol. 77, no. 9, pp. 3661–3669, 2009.
- [78] P. Mora-Uribe, C. Miranda-Cardenas, P. Castro-Cordova et al., "Characterization of the adherence of *Clostridium difficile* spores: the integrity of the outermost layer affects adherence properties of spores of the epidemic strain R20291 to components of the intestinal mucosa," *Frontiers in Cellular and Infection Microbiology*, vol. 6, p. 99, 2016.
- [79] D. Paredes-Sabja and M. R. Sarker, "Adherence of *Clostridium difficile* spores to Caco-2 cells in culture," *Journal of Medical Microbiology*, vol. 61, no. 9, pp. 1208–1218, 2012.
- [80] J. Barra-Carrasco, V. Olguin-Araneda, A. Plaza-Garrido et al., "The *Clostridium difficile* exosporium cysteine (CdeC)-rich protein is required for exosporium morphogenesis and coat assembly," *Journal of Bacteriology*, vol. 195, no. 17, pp. 3863–3875, 2013.
- [81] M. R. Sarker and D. Paredes-Sabja, "Molecular basis of early stages of *Clostridium difficile* infection: germination and colonization," *Future Microbiology*, vol. 7, no. 8, pp. 933–943, 2012.
- [82] S. V. Seddon and S. P. Borriello, "Proteolytic activity of *Clostridium difficile*," *Journal of Medical Microbiology*, vol. 36, no. 5, pp. 307–311, 1992.
- [83] C. Deneve, C. Delomenie, M.-C. Barc, A. Collignon, and C. Janoir, "Antibiotics involved in *Clostridium difficile*-associated disease increase colonization factor gene expression," *Journal of Medical Microbiology*, vol. 57, no. 6, pp. 732–738, 2008.
- [84] L. Tijerina-Rodriguez, L. Villarreal-Trevino, S. D. Baines et al., "High sporulation and overexpression of virulence factors in biofilms and reduced susceptibility to vancomycin and linezolid in recurrent *Clostridium* [*Clostridioides*] *difficile* infection isolates," *PLoS One*, vol. 14, no. 7, Article ID e0220671, 2019.
- [85] E. Stevenson, N. P. Minton, and S. A. Kuehne, "The role of flagella in *Clostridium difficile* pathogenicity," *Trends in Microbiology*, vol. 23, no. 5, pp. 275–282, 2015.
- [86] S. T. Baban, S. A. Kuehne, A. Barketi-Klai et al., "The role of flagella in *Clostridium difficile* pathogenesis: comparison between a non-epidemic and an epidemic strain," *PLoS One*, vol. 8, no. 9, Article ID e73026, 2013.
- [87] T. C. Dingle, G. L. Mulvey, and G. D. Armstrong, "Mutagenic analysis of the *Clostridium difficile* flagellar proteins, FliC and FliD, and their contribution to virulence in hamsters," *Infection and Immunity*, vol. 79, no. 10, pp. 4061–4067, 2011.



Hindawi

Submit your manuscripts at
www.hindawi.com

