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The role of flagella in *Clostridium difficile* pathogenesis and biofilm formation: Comparison between a non-epidemic and an epidemic strain

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Clostridium difficile is a major cause of healthcare-associated infection and inflicts a considerable financial burden on healthcare systems worldwide. Disease symptoms range from self-limiting diarrhoea to fatal pseudomembranous colitis. Whilst *C. difficile* has two major virulence factors, toxin A and B, it is generally accepted that other virulence components of the bacterium contribute to disease. *C. difficilecolonises* the gut of humans and animals and hence the processes of adherence and colonisation are essential for disease onset. Bacteria within biofilms are protected from multiple stresses, including immune responses and antimicrobial agents. Increased antibiotic resistance and chronic recurrent infections have been attributed to the ability of bacterial pathogens to form biofilms. We have limited understanding of how the causative bacterium *C. difficilecolonizes* the host or how it can resist antibiotics and persist within the gut. Our work demonstrates the ability of this anaerobic pathogen to form complex biofilms, the involvement of important clostridial pathways in biofilm development and perhaps a connection between formation of spores which are believed to mediate persistence, and biofilm formation. Importantly, we show that bacterial sensitivity to antibiotics is reduced in clostridial biofilms. Biofilm formation may be a mechanism employed by *C. difficile* to survive in hostile environments such as the human gut. Here we tested this hypothesis by comparing flagellated parental strains to strains in which flagella genes were inactivated using ClosTron technology. Our focus was on a UK-outbreak, PCR-ribotype 027 (B1/NAP1) strain, R20291. We compared the flagellated wild-type to a mutant with a paralyzed flagellum and also to mutants (*fliC*, *fliD* and *flgE*) that no longer produce flagella *in vitro* and *in vivo*. Our results with R20291 provide the first strong evidence that by disabling the motor of the flagellum, the structural components of the flagellum rather than active motility, is needed for adherence and colonisation of the intestinal epithelium during infection. Comparison to published data on 630Δ*erm* and our own data on that strain revealed major differences between the strains: the R20291 flagellar mutants adhered less than the parental strain in vitro, whereas we saw the opposite in 630Δ*erm*. We also showed that flagella and motility are not needed for successful colonization in *vivo* using strain 630Δ*erm*. Finally we demonstrated that in strain R20291, flagella do play a role in colonisation and adherence and that there are striking differences between *C. difficile* strains. In addition, we also demonstrate that clinical *C. difficile* strains, 630 and the hypervirulent strain R20291, form structured biofilms in vitro, with R20291 accumulating substantially more biofilm. Employing isogenic mutants, we show those virulence-associated proteins, cwp84, and a putative quorum sensing regulator, luxS are all required for maximal biofilm formation by *C. difficile*. Interestingly, a mutant in spo0A, a transcription factor that controls spore formation, was defective for biofilm formation, indicating a possible link between sporulation and biofilm formation. Furthermore, we demonstrate that bacteria in clostridial biofilms are more resistant to high concentrations of vancomycin, a drug commonly used for treatment of CDI.

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