

ABSTRACT

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Title of rigorous thesis: Analysis of flagellar proteins in *C. difficile* isolates of clinically relevant PCR-ribotypes

Background: Strains of *C. difficile* of known human *epidemiologic importance* are associated with severe clinical features of *C. difficile* infection (CDI). In this study, a panel of eight different PCR-ribotypes (RTs) with their proteins released *in vitro* were subjected to analysis. The aim of this work is to monitor the relationship between secretions of individual proteins associated with flagellar formation and function in *C. difficile* strains of variable virulence.

Methods: Within our research, a combination of tandem mass spectrometry with liquid chromatography was used. The semi-quantitative analysis employed label free quantification (LFQ) approach.

Results: From the quantifiable proteins, 17 were significantly increased in functional annotations. Among them, several known factors connected with flagellar assembly and other functions were identified. Higher expression of selected flagellar proteins clearly distinguished RTs 027, 176, 005 and 012, confirming the pathogenic role of the assembly in CDI.

Conclusion: The outcome of this work was different observations of individual flagellar proteins in various strains differentiated by increased potential for virulence.

Keywords: *Clostridium difficile*, label-free quantification, virulence factors, toxins A/B, flagellins.