Giardia lamblia and trichomonas vaginalis flagella proteomic analysis.

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Abstract

Microtubules make up all eukaryotic flagella, which are propelled by dynein motor proteins. Every organism, on the other hand, has its own flagellar waveform, beat frequency, and general motility pattern. Recent research has revealed that, despite overall flagellar structure conservation, the distribution of tubulin post-translational modifications inside the flagella is different, which may contribute to variances in motility patterns. Using global, untargeted mass spectrometry, we investigated tubulin post-translational modification in the protozoan parasites *Giardia lamblia* and *Trichomonas vaginalis*. We show that tubulin monoglycylation is a flagella-specific alteration found in *G. lamblia* but not in *T. vaginalis*. We also discovered glutamylated tubulin in both *G. lamblia* and *T. vaginalis*. We were also able to locate previously unknown monoglycylation sites in -tubulin at E438 and E439 in *G. lamblia* using MS/MS. We analysed the flagellar proteome in *G. lamblia* and *T. vaginalis flagella* using isolated flagella and found 475 proteins in *G. lamblia* flagella and 386 proteins in *T. vaginalis flagella*. Overall, the flagellar proteomes and tubulin PTM sites in these species show potential mechanisms for regulating flagellar motility in these understudied protozoan parasites.

Keywords: *Trichomonas vaginalis*, Phagolysosome, Proteome, Cysteine peptidase, Glycosylation, Mannose 6-Phosphate receptor.

Introduction

Infection with *T. vaginalis* has a wide range of outcomes. Host immunity, nutritional condition, and the vaginal microbiota are all possible causes for these phenomena. Furthermore, changes in adherence and cytotoxicity capacity across *T. vaginalis* isolates are expected to result in variances in disease development [1]. *T. vaginalis* strains that are much more cytotoxic to host cells than laboratory-adapted strains have recently become available, providing the path for comparative research to find proteins that correlate with virulent phenotypes.

Despite the relevance of *T. vaginalis* surface proteins as a crucial interface for pathogen-host interactions, no systematic study of these parasite's surface proteins has been conducted [2]. *T. vaginalis* has a big genome that encodes a large proteome with a vast and diverse set of potential surface proteins. Sequence analysis tools that predict trans membrane protein topology, for example, found one or more transmembrane domains in *T. vaginalis* proteins. Furthermore, nearly 300 predicted transmembrane proteins share protein patterns with surface proteins from other pathogens that are known to contribute to mucosal colonisation and other pathogenic processes [3].

To identify candidates for specialised functional studies, a multitiered strategy employing complementing genomes and proteomics analysis is required due to the large number and diversity of potential surface proteins. For the enrichment and identification of surface proteins, biotinylation of proteins at the cell surface with an impermeable reagent followed by specific purification of these proteins with streptavidin has proved successful. Because of the low amount of membrane proteins in total cellular extracts, the high avidity binding of biotin to streptavidin considerably aids membrane protein separation [4].

This method was utilised to profile the *T. vaginalis* surface plasma membrane proteome and discover proteins that are differently expressed in adherent versus less adherent parasite strains. This is the first study that we are aware of that comprehensively identifies and characterises proteins on the surface of Trichomonas parasites. Differential expression could possibly explain why just a few proteins from other major gene families were found in our membrane proteome. In the proteome of 104 genes encoded in the genome, for example, only six ABC transporters were discovered. Nonetheless, in an organism like *T. vaginalis*, where several, big gene families are frequent, these findings highlight the significance of a proteomics method in identifying specific proteins for subsequent functional research. Proteomics is especially important because high-density microarrays for *T. vaginalis* are not currently available due to the genome's complexity and repetition [5].

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Conclusion

Phosphatases and adenylate/guanylate cyclases are important components of cell signalling, which allows cells to sense their surroundings. More research is needed to see if these proteins are involved in *T. vaginalis* adhesion to host cells directly or indirectly. Comprehensive characterization of the cell surface proteome of several parasite strains is a useful method for identifying possible novel surface adhesion factors. The information presented here will aid research into host-infection interactions, as well as genetic and strain differences that could explain the wide range of symptoms and disease progression seen in women infected with this pathogen.

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