Abstract

Trichomonas vaginalis (Tv) is a parasitic protist and causative agent of Trichomoniasis, the most common non-viral sexually transmitted infection (STI), implicated in perinatal complications and increased rates of HIV transmission. Tv uses its four anterior flagella, composed of 9 outer microtubule doublets (OMD) forming a ring around a central pair of microtubules, to facilitate parasite motility and host cell adherence. The absence of a high-resolution OMD structure hampers our understanding of Tv flagella and its role in drug development. To tackle this challenge, we utilized cryo-electron microscopy (cryo-EM) to image the OMDs of Tv flagella. Here, we performed single particle analysis to resolve a structure of the OMD to 3.8 Å resolution and identified several uncharacterized internal and external proteins. We integrated Alphafold’s AI-based protein structure predictions with mass spectrometry data to create an atomic model of the previously unidentified protein TVAG_347810. This protein exhibits homology with the CFAP family, implying its potential involvement in molecular ruler interactions and precise docking of radial spoke proteins, flagellar beating frequency. Altogether, this work elucidates how Tv-specific protein densities provide stability and architecture in the OMD and offers structural basis for flagellar movement in trichomonads.

Summary and Conclusion

- High-resolution Reconstruction of Trichomonas vaginalis OMD
- Refinement of 8nm, 16nm, 48nm, and 96 nm repeating densities
- Fitting of Homologous Conserved Densities from Bovine Respiratory Cilia, Mouse Sperm Doublet Microtubule
- Novel Characterization of TVAG_347810

References and Acknowledgements

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