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**The structure, function and stability of the sinonasal microbiome during health and chronic rhinosinusitis****Brett Wagner Mackenzie**

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Chronic rhinosinusitis (CRS) is characterized by persistent inflammation of the sinonasal mucosa. The condition is highly prevalent (~5%) causing significant morbidity and considerable treatment-associated costs to healthcare systems. CRS is a complex, heterogeneous disease resulting from interactions between a patient's genetics, mucosal immune system and sinonasal microbiome. The pathogenic role of the microbiome in CRS remains incompletely understood. With the aim of providing a context for CRS-related microbiome research, I will present results from a variety of traditional culture-based and molecular techniques that we have employed to explore the roles of both individual bacterial strains and microbial communities. Amplicon sequencing of the bacterial and fungal communities has shed light on the dysbiotic, fragmented CRS bacterial community and the natural temporal variability in healthy subjects. Shotgun metagenomic sequencing was used to provide total

microbial community information, revealing the presence of bacteriophages and bacterial strain-level diversity in patients with CRS. I will highlight the substantial challenges associated with metagenomic shotgun sequencing in low biomass sinonasal samples and describe the advantages of such an approach. This research contributes to our current understanding of the role of the microbiome in CRS and will help inform multifaceted, cross-disciplinary studies that aim to develop more effective treatments for CRS.

**Speaker Biography**

Brett Wagner Mackenzie recently finished her PhD at the School of Medicine, Department of Surgery at The University of Auckland in Auckland, New Zealand. Her thesis focuses on the role of the human sinonasal microbiome in chronic rhinosinusitis and how to better understand the role of the sinonasal microbiome during health and disease. Her research interests include host-microbiome interactions and microbial community network stability and response to disturbance.

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