

Expanding the HOMD to Include Nasal- and Skin-associated Bacteria

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Chronic rhinosinusitis (CRS) affects >5% of Americans and is almost universal in post-pubertal cystic fibrosis (CF) patients; however, the composition and genetic diversity of the bacterial communities (microbiome) in CRS remain understudied. The human nose and sinuses naturally harbor both harmless bacteria (commensals) and bacteria that can cause infections (pathogens), with these often belonging to the same group (genus). Therefore, to achieve clinically relevant results, microbiome studies based on DNA sequencing must distinguish between closely related bacteria inhabiting the same body site. The Human Oral Microbiome Database (HOMD) is an outstanding resource for identification and classification of species of bacteria present in the mouth. We propose to expand HOMD to include bacteria from adult and pediatric sinonasal and skin microbiomes in health and disease. We will use the expanded HOMD, in conjunction with new bioinformatic approaches, to reanalyze at a higher resolution published sinonasal microbiome studies from healthy vs. CRS subjects and to compare the sinus microbiome in CF vs. non-CF CRS. Doing this, we will determine whether there are harmless bacteria that have a negative, or positive, relationship with pathogens in these types of CRS. We hypothesize that some of these harmless bacteria are in fact beneficial to humans (mutualists) and can block pathogen colonization or shift pathogen behavior towards living peacefully with the human host. This work will provide medical researchers with a useful tool for future sinonasal and skin microbiome studies and could help to develop novel strategies to control pathogen colonization and prevent/treat infections, e.g., CRS.