

Microbiome complexity and staphylococcus aureus in chronic rhinosinusitis



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Chronic Rhinosinusitis is affecting major social group and despite intensive analysis has an unknown etiology and pathophysiology which lasts longer than three months (2, 4). CRS leads to vital morbidity in young and old adults, impacting considerably upon quality of life (6). Microbe infection is a primary cause or ensuing issue of inflammatory in CRS disease (3). The abnormal innate immune function in patient may be responsible for presence of polymicrobial bacterial biofilms in CRS (1). In molecular method there is no need of axenic cultivation for example DNA sequencing, polymerase chain reaction (PCR) and microarrays and in contrast is the conventional culture technique. Molecular method can explain better about complexity of microbial community (4).

By using 16S rRNA gene sequencing procedures that's conventional culture and culture-independent, the main objective for experimentation is to compare both methodology to spot the composition and variety of microbes in patients suffering from chronic rhinosinusitis(CRS). We hypothesized that culture of bacteria and DNA pyrosequencing would with great extend have contemporaneous outcome, even supposing that sequencing would determine higher bacterial diversity and CRS patient's sinonasal microbiomes would make a difference in diversity and composition when compared with non-CRS control(1).

For obtaining the results methods were followed sequentially. Swabs as samples were collected with patient's convenience who were undergoing endoscopic sinus surgery (ESS) and sent for routine aerobic/anaerobic

culture and further placed at -80°C . Later DNA based techniques were used step by step 1) purification of swab heads 2) DNA extraction and PCR. 3) Quantitative PCR 4) Pyrosequencing using GS-FLX instrument 5) Ribosomal database project (RDP) classifier was used for genus level taxonomic calls. 6) Basic local alignment search tool (BLAST) was used for precision in species level taxonomy. 7) BIODIV software tool used for Standard ecological indices of diversity, richness and evenness. All statistical analysis was done by using R statistical package. Samples of CRS patients and non-CRS control were distinguished and composition of microbiomes were checked by Morisita-Horn index using Adonis function. Later demographic characteristics were compared by use of analysis of variance (ANOVA) for continuous and categorical outcomes with operational taxonomic unit (OTU) prevalence (1).

The result of this introductory analysis suggests that bacterial culture and 16s rRNA gene Pyrosequencing of CRS patients and controls yield broadly congruent outcomes, although importantly diversity in more amount particularly of Anaerobic groups was observed in culture -independent than culture dependent. Also, a lot of microbial communities are found in CRS patients when compared with CRS controls along with *Staphylococcus aureus* in immense quantity which relate to atopic disease including allergic rhinitis and atopic dermatitis which has poor outcomes (1, 8).

In conclusion the results proved that complex bacterial community plays vital role in etiology of CRS (1). As limited data of mechanism of microbes is probably the best obstacle in understanding the causes and improved treatments for CRS (7). After this study we would reveal additional

understanding of the role of microorganisms in CRS, it's vital to characterize <https://assignbuster.com/microbiome-complexity-and-staphylococcus-aureus-in-chronic-rhinosinusitis/>

the microbes comprehensively for examining the particular host immunological responses to the organisms. The systematic studies will lead to importance of these microbes in the disease phenotype. Additionally, our research can provide vital information for the choice of antimicrobial therapies, and modify the determination of the effectiveness of such treatments (1, 2). Ultimately, understanding the causes of variation among the sinus microbiota could cause a lot of personalised treatment choices for CRS (5). With great experts with us including Dr. Sergio Pereira and Dr. Todd Kingdom and support of NIH we have successfully completed our preliminary research and once if we are granted further, we assure you faster completion of work.

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