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Microbiome analyses in chronic rhinosinusitis

In this edition of Rhinology we feature the work of Connell and colleagues from Australia on chronic rhinosinusitis that describes an interesting new pipeline to characterize the bacterial composition of microbiota [1]. We are constantly exposed to a multitude of micro-organisms in the environment and our immune system has the important task discerning and fighting off potential threats. In most people the immune system is doing its job properly and prevents anything untoward from happening. On occasion, a microbe slips by the first (innate) level of defense and we might suffer from an infection. This then activates the second layer of (the adaptive) defense tasked to clear this infection. Sometimes the immune system gets its wrong and starts a full-out defense against something harmless, and an allergy is born. The task of the immune system of doing what is right is even more difficult than it might seem at first sight. In addition to these incidental potential threats, our mucosal surfaces are lined with commensal bacteria which contributes to the complexity of our environment. This collection of bacteria or microbiome has become a major focus of research, as the composition of this microbiome seems related to the health state of the individual. Originally the relationship between the gut microbiome and the development of asthma and allergy was the main focus. In recent years, the focus has been broadened to include the microbiome of the upper and lower airways. In addition to allergy, our field has also been given more and more attention to studying the microbiome in chronic rhinosinusitis [2]. An important driver for all this research is the realization that the composition of the microbiome may have consequences for the development of disease states and that the microbiome might be a target for treatment [3]. To characterize the composition of the microbiome there are different options. Initially bacterial cultures have been used, but given the potential difficulty associated with growing specific bacterial species, this was soon replaced with DNA-based techniques. One such technique leverages the relative species uniqueness of the rDNA sequence of one or more of the nine hypervariable regions in 16S gene, a gene that encodes part of the bacterial ribosome. A relative low-cost alternative (IS-pro) uses a collection of phylum-specific primers that span the 16S-23S rDNA interspace regions that have distinct lengths in different bacterial species. The technique described in the current edition of Rhinology by Connell and co-workers determines the DNA sequence of a larger region of the 16S gene and they show that for chronic rhinosinusitis they are able to identify more bacterial species than when the more traditional 16S sequence method was used [1]. Indeed, all species they were able to culture from CRS patients, were also picked up by their microbiome analysis pipeline. Something the traditional 16S sequence method was not able to do. Sequencing more than a (small) defined region does have the benefit that it might resolve potential ambiguities between bacterial species with (very) similar variable regions in the 16S gene. However, this does not necessarily mean that this method is now the silver bullet to solve all microbiome questions. A side-by-side comparison of the traditional and extended sequence method shows that ratios between bacterial species can differ between both methods, without being able to tell what ratio is the correct one. Although the third option of microbiome characterization (IS-pro) was not used, it would not be farfetched to think that this outcome would yet again be slightly different from the two methods discussed in this paper. What we feel that the important take-home messages are: (a) every approach comes with its own strengths and weaknesses, (b) as a consequence, there is no silver bullet, and (c) a new important analysis pipeline has become available that could benefit all microbiome/bacteria-related research [4].



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