Human microbiome in respiratory diseases

We would like to present with great pleasure this special issue of the *Annals of Translational Medicine*, "The Human Microbiome in Respiratory Diseases".

The microbiome refers to the community of microorganisms and their products that share a particular environment. The field of respiratory microbiome studies is still at an early stage, with most studies to date limited by the small number of samples, the lack of longitudinal samples and control subjects. Our current understanding of the role of the microbiome in the pathogenesis and progression of respiratory tract diseases is mainly based on classical culture techniques. However, they suffer from limitations, is a laborious process and the use of standard culture conditions only allows to grow 30% of the bacteria in the lungs. It is therefore understandable that, historically, the lungs have been considered sterile, despite their continuity with the upper respiratory tract, proximity to the gastrointestinal tract and continuous exposure to the environment. During the last decade, culture-independent techniques have emerged, most of them becoming accessible to the research groups. These techniques combined with advances in sequencing technologies have produced a powerful tool to investigate the role of bacteria in health and disease and have recently begun to shed more light on the role of bacteria as we will see in the following articles presented (1,2).

Understanding the role of the microbiome in respiratory diseases is a field that is becoming very relevant due to the wide range of applications that may have. Several studies that the lower airways and alveoli of patients with different lung diseases contain a microbiome different from that of healthy people and those changes in it are associated with the progression of the disease and the intermittent development of exacerbations (3).

As briefly summarized below, the articles of this special issue present three hot topics related to microbiome.

The fluctuating nature of the microbiome and all its constant interactions with different body systems makes it a promising target for translation into medical practice. Molecular techniques allow us to explore the diversity of the microbiome but it is also necessary to understand and analyze properly all the data that those techniques provide. Shankar examines different aspects of study design like choosing a representative population, including controls and determining the time and frequency of sample collection. It is also discussed the pros and cons of the two main techniques for measuring the microbiome: whole-genome sequencing and 16-S profiling and finally the bioinformatic analysis of the data obtained.

Hewitt and Molyneaux made a review of the role of microbiome in idiopathic pulmonary fibrosis (IPF). IPF is a fibrosing lung disease that causes an unyielding decline in the lung function followed by respiratory failure. There is no causative factor yet known and therefore, the treatment options are not optimal. Some studies suggest that changes from the normal an infective and aberrant microbiota that interacts with the host susceptible immune system, may contribute to the progressive development of the of fibrosis.

Finally, Monsó examines the lung microbiome of COPD patients during stable periods and exacerbations. The lower airways and alveoli of patients with COPD contain a different microbiome than healthy people, and changes in it are associated with the progression of the disease and the intermittent development of exacerbations. The microbiome of a healthy subject is diverse, comprising Firmicutes, Bacteroidetes and Proteobacteria as their most frequent phyla. However, the microbiome of COPD patients becomes less diverse, with an overrepresentation of the Proteobacteria phylum.

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Maria Ruiz-Rodriguez

Jordi Rello

Maria Ruiz-Rodriguez[1]

[1]*Department of Clinical Research & Innovation in Pneumonia and Sepsis, Vall d'Hebron Institute of Research (VHIR), Barcelona, Spain. (Email: maria94ruiz@gmail.com)*

Jordi Rello[2,3]

[2]*Centro de Investigación Biomédica en Red de Enfermedades Respiratorias (CIBERES), Madrid, Spain; [2]Department of Clinical Research & Innovation in Pneumonia and Sepsis, Vall d'Hebron Institute of Research (VHIR), Barcelona, Spain. (Email: jrello@crips.es)*