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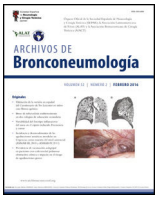

Editorial

The Microbiome and Asthma☆

Microbioma y asma

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In 2016, a group of scientists from the University of Düsseldorf published a genetic portrait of the ancestor of all living beings which they called LUCA, the last universal common ancestor. This ancestor was a unicellular organism similar to bacteria, which, according to these researchers, might have been the original common point of all bacteria, archaea, and eukaryotes.[1] It therefore seems reasonable to think that the relationship between humans and bacteria is not one that has developed over time, but instead dates back to a common ancestral nexus.

Since the 1980s, the prevalence of diseases in developed countries has changed. A decrease in the incidence of infectious diseases, due to the use of antibiotics and vaccines, has been accompanied by an alarming increase in the incidence of diseases with an autoimmune component, such as inflammatory bowel disease, type 1 diabetes, and asthma.[2] This inverse relationship appears to be caused by changes in the intestinal microbial colonization that occurs in the first few weeks of human life.[3]

The development of massive sequencing platforms capable of analyzing entire metagenomes by rapidly and inexpensively amassing DNA sequencing data has solved the problems inherent to conventional methods of culture-based diagnosis. This has enabled scientists to determine which types of microorganisms, not just bacteria, are present in the different organs of the human body, and how they interact with the host.[4]

It is estimated that the gut microbiome contains 150 genes more than the human being, and that there is a constant interaction between the two which, under normal circumstances, thrive in symbiosis. Circumstances such as country of origin,[5] manner of birth (vaginal or cesarean),[6] the use of antibiotics, or feeding with breast milk or formula,[7] can influence the establishment of the intestinal microbiota. This first contact of our intestines with bacteria will mark the development of the immune system, and may predispose us to or protect us from the appearance of some diseases.[8] Thus, a lower intestinal microbial diversity in childhood is associated with an increased risk of allergic diseases, such as atopic dermatitis, eczema, or asthma.[9] In contrast, greater exposure to certain microorganisms reduces the likelihood of developing these entities.[10] This is known today as the microflora hypothesis,[11] and is a variant of the hygiene hypothesis proposed by Strachan in 1989.[12]

The intestinal microbiota, which is initially unstable, undergoes dynamic changes up to the age of 3 years, when it stabilizes, creating an intestinal microbiota similar to that of the adult. It plays a leading role in human health, helping to maintain intestinal homeostasis and adequate protection against certain pathogens, while exercising a nutritional and metabolic effect and physiological and immunological activity.[13]

The lower airway is one of the least populated surfaces in the human body in terms of bacteria. Both the intestinal and respiratory microbiota develop simultaneously after birth. There is a constant cross-communication between these 2 compartments, and fluctuations in the populations of certain bacteria occur in a similar manner in both. Diet has also been shown to have an impact not only on the composition of the intestinal microbiota, but also on the respiratory microbiota.

In patients with chronic respiratory diseases, the respiratory microbiota presents some specific phenotypes that differ from those of healthy individuals,[14] and there is a close relationship between low microbial diversity in the gut during childhood and allergic asthma.[9] Various studies have also shown that contact with certain environmental microorganisms and the habitat of farms are associated with a decreased risk of developing asthma and atopy.[10]

Although we know less about how viral or bacterial infections that cause many of the exacerbations of chronic respiratory diseases modify the respiratory microbiota of diseases such as COPD, recent studies in this area have highlighted the relationship between infections by certain respiratory viruses in childhood and predisposition to asthma. This relationship is stronger when the infections were caused by respiratory syncytial virus and less when caused by human rhinovirus.[15] Very recent data show that the inflammatory response triggered by respiratory syncytial virus infection in childhood varies depends on the composition of the nasopharyngeal microbiome. This produces 2 different clusters of immune response, which are associated with a greater probability of wheezing during the first and second year of life.[16] Modifying the composition of the nasopharyngeal microbiome to reduce the inflammatory response provoked by exposure to respiratory syncytial virus is a promising hypothesis that has yet to be tested.

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The same occurs with a high-fiber diet, which we know to be important for maintaining intestinal health, since it fosters favorable colonization and the production of short-chain fatty acids. However, there is no sound evidence that increased consumption of fiber reduces the incidence of asthma.

All these data point toward a window of therapeutic opportunity in the first few weeks of life that could modify the subsequent appearance of allergic diseases, including asthma.

Despite all this rapid progress, our understanding of "healthy" intestinal microbiota, the optimal intestinal colonization patterns that help to establish tolerance, and the numerous and complex interactions between the host and the microbiota is still incomplete. This may explain the inconsistencies in studies that have aimed to manipulate the microbiota in the treatment and prevention of different allergic diseases. Microbiota and, in particular, markers of microbiota activity must still be identified. In the near future, we should be able to use these markers in the diagnosis, treatment, and prevention of chronic diseases such as asthma.

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