
LETTER TO THE EDITOR

YOUR IDENTITY IS YOUR PROFILE OF MICROBIOTA

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With strong interest and enthusiasm, as a staunch reader of *Romanian Archives of Microbiology and Immunology*, I read the invaluable review entitled "SPONDYLOARTHRTIS AND THE INTESTINAL MICROBIOTA", written by Daniela CRISTEA *et al.* and published in Volume 77, Issue 2, April-June, 2018 of *Romanian Archives of Microbiology and Immunology*. The authors of this review, had a deep look into the role of the microbial pattern of intestinal microbiota in the occurrence of spondyloarthritis [1].

I believe that they are quite right. In recent years by the progress in science and technology, we now know that a large portion of our bodies, including alimentary tract (comprising gut and mouth), urogenital tract, nasal cavity and the skin are captured by useful microorganisms termed microbiota. These microorganisms involve both culturable and viable but not culturable aerobes and anaerobes. The local microbiota or normal flora in different parts of our bodies include hundreds of types of microbial agents, each tract having its own particular microbial pattern. The microbial communities and populations in our bodies consist of not only bacteria, but also archaea, fungi, protozoa and viruses. The normal, natural and appropriate composition of colonized microbiota in their own situations and places

within the human body guarantees the host's health and freshness.

But the occurrence of dysbiosis (improper replacements in the population of microbiota) results in destructive effects on the related part of body. In other words, by the appearance of dysbiosis in human body the host will experience unfavorable and unsuitable pathologic consequences. But the question is why? In recent golden years several advanced techniques like Next Generation Sequence (NGS) technologies have been applied for detection and identification of different types of microbiota and microbiome (genomic structure of microorganisms). Furthermore, the combination of sequencing technologies and in particular 16S rRNA sequencing technique in parallel with metagenomics, shotgun sequencing and bioinformatics has offered us an ideal promise regarding decoding human body's microbiota profiles. In this regard, a 70-kg individual adult's body may consist of 3×10^{13} cells while the total number of colonized bacterial microbiota in the same body is estimated at about 3.9×10^{13} cells. So, the role of microbial pattern of microbiota in an individual's body in association with the host's vital condition cannot be ignored. The predisposing factors of age, diet, environment, infectious diseases and type of delivery at birth (C-section or vaginal delivery)

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determine the microbial pattern of microbiota. Interestingly, any inappropriate changes in composition of microbiota pertaining to any anatomical places in human body have depth chaotic effects on immune system responses. This improper occurrence results in disruption, dysregulation and dysfunction in immune system responses and interactions. For example, unfavored changes in composition of microbiota on skin or within the intestine ecosystem have direct correlation with autoimmune diseases of psoriasis and inflammatory bowel disease (IBD), respectively. Psoriatic arthritis (PSAR) as a kind of chronic spondyloarthritis is a well-known comorbidity of psoriasis. According to previous surveys, there is an interesting similarity between the composition of microbiota in the guts of patients with IBD and PSAR with unknown reasons [1-6].

So, prevention, control and treatment of different diseases including autoimmune diseases will be possible when the human body's composition of microbiota is completely recognized. Deciphering of the entire profile of the individual's microbiota enables us to have a new means for prevention, control and treatment of a wide range of diseases. This ability is directly dependent on application of advanced technologies e.g. NGS, metagenomics, shotgun sequencing and bioinformatics. It seems that effective means to

decode individual's profile of microbiota is the golden key for promise!

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