

DESCRIPTION FOR THE GENERAL PUBLIC

The community of microorganisms that inhabit the human body is referred to as microbiota. Bacteria are the main element of this collection. It is estimated that the human microbiota contains about 10 times more bacteria than human cells. The most numerous group is the microflora of the gastrointestinal tract, especially its final section – the colon. It is considered a peculiar ecosystem which has a substantial impact on the functioning of the human body. In contrast, the term microbiome now refers to all genomes of microorganisms living in and on the human body. Frequently, however, the term microbiome is used to mean microbiota. The significance and role of the gut microbiota is more and more well-known and helps to explain the course and causes of many diseases such as inflammatory bowel disease, diabetes, or obesity. There are also hypotheses that in patients with celiac disease (CD) the microflora composition is disturbed in comparison with healthy subjects. Celiac disease, also called celiac sprue, is the most widespread type of food intolerance and, at the same time, is characterized by the most severe course. It is an immune-mediated disease, which means that it results from a strong immune response in the gastrointestinal tract to a plant protein introduced into the body (called gluten). It is predominantly found in certain grains (wheat, rye, and barley) and when it is part of the diet of a person who has a certain genetic predisposition, it causes an excessive immune reaction. Consequently, in the long run, the disease leads to atrophy of the intestinal villi, and in the end, to intestinal malabsorption. CD can manifest itself at any age; however, it is usually diagnosed in childhood. Currently, the only effective treatment for the disease is a strict adherence to a diet devoid of gluten. Consumption of gluten generates an immune response, which has to affect the state of the intestinal flora. On the other hand, the composition of the gut microflora stimulates the intestinal immune system, referred to as GALT, which under physiological conditions should lead to a balance between the host organism and microbiota. So far, the analysis of the intestinal microbiota in patients with celiac disease has covered only a few studies focusing on selected groups of bacteria. It was demonstrated, among other things, that in the course of CD and gluten-free diet, there is a reduction in the number of bacteria belonging to the species *Lactobacillus* and *Bifidobacterium*, considered a reservoir of strains with probiotic potential. However, there is a shortage of more comprehensive studies, covering the whole human gut microbiome, which consists of over 1,000 bacterial species. This gap can be filled by the presented research project. Through analysis of specimens derived from both the upper gastrointestinal tract (fragments of duodenal mucosa taken during gastroscopy) as well as the lower gastrointestinal tract (stool samples) and the application of modern methods for molecular diagnostics, it is planned to carry out detailed research on the intestinal microflora with regard to qualitative and quantitative composition of bacteria and selected fungi in children with newly diagnosed celiac disease as compared to healthy children. There is also a plan to assess the gut microbiome in terms of the degree of adherence to a gluten-free diet in children with celiac disease. Such a comprehensive analysis is possible through the use of state-of-the-art methods for molecular diagnostics. To identify the type and number of bacteria and fungi, metagenomic next-generation sequencing (NSG) will be used, which is the analysis of DNA isolated directly from microorganisms present in a given environment (without prior culture on artificial media) with the use of a molecular marker in the form of rDNA sequence (encoding rRNA gene – a component of the small ribosomal subunit of prokaryotes and eucaryotes). Finally, the resulting nucleotide sequences will be subjected to bioinformatic analysis enabling each bacterium to be classified into a given taxonomic group. Obtaining scientific data pointing to a possible link between celiac disease and microbiome may allow the application of preventive measures (in the form of suitable antibiotics or probiotics) in order to modify the gastrointestinal flora. Such actions might prevent the development of disease in genetically susceptible individuals or alleviate the symptoms in individuals already suffering from CD.