The human digestive system is home to an enormous number of microorganisms which can, in total, weigh up to 2 kilograms. The gastrointestinal microbiota consists primarily of bacteria, but there are also slightly less numerous populations of fungi, viruses, protozoa, or archaea. Their composition and abundance vary significantly in different sections of the gastrointestinal tract. The large intestine demonstrates the greatest activity, diversity and amounts of microbes. It is estimated that this part of the digestive tract is inhabited by up to 1,000 different species of microorganisms representing 45 genera and 17 families. Over the past few years, thanks to the development of methods based on molecular biology, complex interactions between microbes and the human body are understood better and better. Hence, there has been a visible increase in knowledge of the impact of the gut microbiota on the course of many diseases, such as inflammatory bowel disease, systemic connective tissue inflammation, anorexia, obesity, diabetes, or ailments associated with mental disorders such as depression, autism or Parkinson's disease. Recently, a lot of attention has been paid to the role of intestinal dysbiosis in the induction of Crohn's disease (CD). CD is a chronic autoimmune inflammatory disease of the gastrointestinal tract, with periods of exacerbation and remission. Despite the fact that the disease has been known for over a hundred years, the causes of its recurrence as well as its etiopathogenesis remain unexplained. Due to the fact that numerous studies show a disturbed composition of the gastrointestinal microbiota in patients with CD, there are hypotheses that the disease results from genetic and immunological disorders which, due to intestinal dysbiosis, result in overactivity of the immune system against microorganisms. Consequently, this leads to permanent, nonspecific lesions of the gastrointestinal mucous membrane. Many clinical observations support the participation of microorganisms in the pathogenesis of the disease. They involve, among others, improvements in patient health following the application of antibiotics and bowel cleansing procedures, alleviation of the disease symptoms or achieving remission due to modification of the gastrointestinal microbiota with the use of probiotic drugs, relapses due to food poisoning and gastrointestinal infections, absence of intestinal inflammation in experimental animals bred in sterile (germ-free) conditions, or remission in patients after fecal transplants from healthy individuals. So far, analyses of intestinal microbiota in CD patients have mainly focused on disorders within the bacterial biome. However, there is a lack of more comprehensive research, including archaeobiome or mycobiome, which are also part of the natural gut microbiome. This gap can be filled with this research project as it aims to determine the taxonomic composition of fungi and archaea colonizing the intestines of children with newly diagnosed CD compared to healthy people. Owing to the application of state-of-the-art molecular biology techniques, such as next-generation sequencing (NGS) or real-time PCR, an accurate and comprehensive quantitative and qualitative assessment of fungi and archaea of the digestive system will be possible, even for the ones that cannot be cultured on artificial media. These techniques are based on the analysis of DNA isolated directly from the microorganisms present in a given environment, using a molecular marker in the form of the rDNA sequence. The nucleotide sequences obtained will be subjected to bioinformatic analysis which, in turn, will allow for accurate assignment of the studied fungi and archaea to specific taxonomic groups. Undoubtedly, the composition of the microbiome significantly affects the maintenance of internal balance and good health, and quantitative and/or qualitative changes associated with microorganisms constitute an important factor inducing pathological processes. Due to the fact that both fungi and archaea are an important component of the gut microbiota, it is possible that a change in their numbers or composition could affect the incidence of certain diseases, in particular, CD, which is the research hypothesis of this project. If a difference is found in the composition and/or number of these microbes between the group of patients with CD and the healthy population, it will be a premise confirming the participation of these microorganisms in the development of the disease. Finding such a disparity will perhaps, in the future, make it possible to implement preventive measures in order to modify gastrointestinal tract microbiota using probiotics, targeted antibiotic therapy, antifungals or fecal transplantation, which could alleviate the symptoms of CD or even prevent the occurrence of the disease.