

The knowledge and results of previous studies of the intestinal microbiome are limited and incomplete, especially in relation to intestine diseases like the Irritable Bowel Syndrome (IBS). It is estimated that 50% of all patients with gastrointestinal symptoms suffer from IBS, although statistics are not relevant to the epidemiological situation, because IBS is often mistakenly diagnosed. The disease affects both sexes, however the incidence of IBS among women is two times more common than among men population. It is estimated that IBS is the second reason, just after colds, that cause absence from work. Moreover IBS is the reason of every second gastrological consultation. The etiology of IBS is not fully known. The diagnosis of IBS is a diagnosis of "exclusion" - consisting of eliminating other diseases with similar and / or the same symptoms or signs [World Gastroenterology Organisation, 2015]. Recent scientific reports suggest that intestinal microflora may have a great importance in the IBS pathogenesis. The IBS, due to problems related to the degree of its severity, the lack of both precise diagnostic criteria and effective therapy, and the number of diagnosed cases in recent times, can be classified as a disease of civilization. However, knowledge of the intestinal ecosystem composition of our body is still very limited. Currently available data do not clearly state whether and how microbes can influence the occurrence of gastrointestinal symptoms identified in patients with IBS.

The hypothesis of this project assumes the existence of difference in qualitative composition of the microorganisms constituting the intestinal microflora in patients with IBS and control individuals without any gastro-intestinal disorders.

The aim of this project is the identification of intestinal microbiota specific for patients suffering from IBS. The obtained results will allow for detailed analysis of the bacterial element of microbiota among IBS patients and unaffected individuals, and thus the influence of intestinal microflora on the gastrointestinal pain experienced by IBS patients.

The hypothesis will be verified using methods of molecular biology, sequencing of 16S rRNA (next generation sequencing, NGS) using technology Illumina Miseq.

As a result of a research project, it will be possible to assess the bacterial element of intestinal microbiome, which may have an important influence on the pathogenesis of IBS. In addition, the project aim is to prove the correlation between the bacterial microflora of the intestinal dysbiosis among female and male subjects, and the occurrence of specific gastrointestinal symptoms in patients with IBS.

The obtained results may become the basis for the prevention and implementation of new diagnostic criteria necessary for the classification and further treatment of IBS patients.