

The global rise in prevalence of obesity presents a challenge to public health and economies. Obesity has been associated with a variety of metabolic disturbances including dyslipidemia and insulin resistance; both are regarded as major risk factors for development of cardiovascular disease, nonalcoholic fatty liver disease, and cancer. Sedentary lifestyle and increased food consumption has been considered the main underlying causes for this obesity epidemic. Environmental and genetic factors have also been implicated including changes in the gut microbiota to play a role in the development of metabolic disorders. Intestinal bacteria play important physiological role in vital processes such as digestion, vitamin synthesis and metabolites production amongst others. It is believed that modulation of gut microbiota holds a therapeutic potential to treat the growing obesity epidemic. Bariatric surgical procedures are the most effective treatment for extreme obesity causing weight loss by restricting the amount of food the stomach can hold and malabsorption of nutrients. However, while any type of weight-loss intervention can impacts the gut microbiota composition, changes in the gut microbiota not always correlate with the amount of weight loss.

The aim of this project is to link the bacterial composition and metabolites in stool samples with the effectiveness of bariatric surgery in extremely obese patients and to modulate the progression of metabolic syndrome in the experimental mice models of obesity by transplantation of stool from obese patients. The bacteria will be identified and quantified through the comparative analysis of 16S RNA gene that is present in all bacteria while the metabolites will be surveyed with the technique called the mass spectrometry.

We expect that determining the bacterial and metabolites composition in stool associated with the response to a bariatric surgery and in animal models of obesity, will confirm the hypothesis about the modulating role of intestinal bacteria in the outcome of surgical weight loss intervention (in humans) and progression of metabolic syndrome (in mice). In addition, we may identify new markers, bacteria or metabolites, predicting the responsiveness to bariatric surgery. The results of this study will lay the groundwork for further research on the possibility of modulating the composition of the intestinal microbiota towards improving the effectiveness of treatment of obesity and obesity-linked co-morbidities.