Promoting healthy diets by reducing the fat, sugar, and salt content in processed foods and increasing physical activity are key supports for obesity prevention. The booster of these supportive fundamentals is an increased consumption of fruit and vegetables taking into consideration that some of them inhibit the uptake of glucose and fructose or lipids through the inhibition of digestive enzymes. Polyphenols, as plant-derived, non-nutrient products, are characterized by appetite/hunger-suppressing and/or satiety/fullness-increasing properties. It is worth noting that even short-term consumption of diets composed of animal or plant products influences the structure and activity of the human gut and overwhelms inter-individual differences in microbial gene expression. It was previously demonstrated that the microbiota from lean or obese twins induces similar phenotypes in mice. Bacterial invasion and phenotypic rescue of obese mice were diet-dependent. Processes that shape the gut microbiota are believed to be mostly niche-driven, and the nutrient landscape dictates which organisms successfully colonize and persist in the gut. On the other hand, it has been already known that bacteriophages are the most abundant biological entities. These bacterial viruses by infection and replication in bacterial cells are the first factors determining the number of bacterial populations. Phage mixtures were first employed in 1919 to treat bacterial illnesses by killing the pathogenic and opportunistic pathogenic bacteria in the intestine, showing more advantages over antibiotic treatment. The challenges faced in bacterial modeling are the movement of the microbe population toward the desired bacterial population and attacking the target by overcoming their antimicrobial strategies. Since 1958 when Joshua Lederberg received the Nobel Prize for his discoveries of gene exchange in bacteria, the mechanism of gut microbiota shaping is not known. The question about the influence of phytochemicals on bacterial phages and nucleases as the possible way for gut microbiota shaping is raised in the proposed project.

It is more and more considered that the leakage of the intestinal barrier and the disruption of the gut microbiome are increasingly recognized as key factors in different pathophysiological conditions, such as obesity, diabetes mellitus, irritable bowel syndrome, inflammatory bowel disease, and chronic liver diseases. Any alterations of the intestinal epithelial barrier open the way for excessive passage of lipopolysaccharides (LPS), which are membrane components of Gram-negative bacteria. A high-fat diet increases the proportion of an LPS-containing microbiota in the gut. There is evidence that nutrients profoundly impact the development of a functioning microbiota, as well as a leaky gut syndrome and chronic low-grade inflammation might be significantly limited by a plant-rich diet.

In everyday diet, a wide range of phytochemicals directly affect the gut barrier, which might be a useful tool for assuring the protection of epithelium against pathogenic bacteria. The natural sources of these phytochemicals are homemade or commercial juices, teas, and tinctures prepared, *inter alia*, from fruits of sea buckthorn, Japanese quince, and Cornelian cherry. They are the representative source of compounds from the classes of flavonoids and carotenoids, proanthocyanidins, iridoids, and anthocyanins, which provide potentially bioactive, polyphenolic metabolites after gastrointestinal digestion. Some of these products are characterized by low bioavailability and are hypothesized to affect gut microbiota composition.

The aim of the proposed study is an assessment of intestinal integrity, LPS leakage, proteins of adipose tissue, and lipid profile in model rats treated with a high-fat diet and extracts from fruits of sea buckthorn, Japanese quince, and Cornelian cherry. The expression of proteins crucial for intestinal integrity and the uptake of glucose and lipids will be determined in the rat intestinal tissue. The changes in gut microbiota and bacterial viruses after extract treatment will be established. The special goal of this study will be an evaluation of the potential inhibition of bacterial enzymes from classes of nucleases by extracts or their major constituents. Determining the role of plant-derived products in the shaping of the microbiome through the influencing bacterial viruses and nucleases will be a novel insight into diet-microbiome interactions and the mechanism of niche colonization.

In conclusion, finding a relation between specific extract constituents and gut microbiota composition concerning the prevention of leaky gut syndrome and metabolic disorders is the main expected result of the study. It will also expand the discussion on the mechanism responsible for shaping the intestinal microflora through the modulation of viruses or bacterial nucleases and the prebiotic properties of plant materials, in particular sea buckthorn, Japanese quince, and Cornelian cherry fruits, which probably prevent the development of metabolic endotoxemia. In light of increasing antibiotic resistance, we believe that the results of the project will allow us to highlight the forgotten phage therapy and plant-derived products as useful tools for the regulation of gut microbiota in *e.g.* post-antibiotic therapy.