

Abstract

The microflora located on the surface of and inside the human body is a very large system. The intestinal microflora of the gastrointestinal tract is a very important and still not fully explored area. The intestinal microflora consists of many types of bacteria, viruses, fungi or some single-cell eukaryotic heterotrophic organisms. The intestinal microflora is involved, for example, in the synthesis of vitamins, digestion of polysaccharides or in the storing of fats. It is significantly involved in the metabolism of foreign substances and digestion of food. The activity of foreign substances can influence the composition of the intestinal microflora. It must not be forgotten that the composition of the intestinal microflora differs in separate individuals and is changeable during life. The metabolism of foreign substances in relation to the human organism is a subject of global studies. This work is devoted to the metabolism of myricetin and its influence on the digestive tract of a healthy individual and a person with celiac disease. It is also studied whether myricetin affects the biodiversity of intestinal bacteria.

The collected stool samples from donor A (a person with celiac disease) and B (a healthy control) were incubated at 0, 3 and 6 hours in McDougall buffer with myricetin. They were also investigated through the RP-HPLC method. The task was to determine whether the added myricetin was metabolized by the cultivated bacteria to a next metabolite (e.g. dihydromyricetin). In the analysis, the decrease of myricetin was detected within 6 hours for both provided samples, however, none of the samples detected dihydromyricetin.

The effect of myricetin on the biodiversity of the cultivated bacteria was monitored in both stool samples during a period of 72 hours. A PCR method followed by a denaturing gradient gel electrophoresis (DGGE) was used for the analysis. Myricetin was found to have influenced the composition of the bacteria in the sampled faeces during the 72-hour cultivation.

After the DGGE, the bacterial DNA was amplified through the PCR method and sent for sequencing to the SEQme company. Through comparison with sequence databases it was possible to determine the types of involved bacteria from some of the obtained sequences. A match was found, for example, with *Eubacterium rectale* or *Escherichia coli*. In addition, there has been evidence of diversity in the representation of bacterial species in the stool samples of both donors.

Key words: intestinal microflora, myricetin, metabolism, biodiversity, celiac disease

(In Czech)