Abstract

Intestinal microflora could be considered a “forgotten” organ of the human body. In the gastrointestinal tract, xenobiotics (including drugs) can be converted into their active or inactive forms by intestinal microorganisms via various metabolic pathways. This, in turn, affects their biological activity. The variability of microorganisms in the hosts intestines leads to diverse metabolic reactions of xenobiotics. Thus, the resulting metabolites may vary across host organisms. It is almost imperative to keep this fact in mind while studying and testing new drugs, as well as dietary supplements, because many microbial metabolites can have serious implications for host organisms, especially when administered orally.

In this work, mutual interaction between myricetin and faecal bacteria originating from human intestines was studied under various conditions. For the experiments, a high performance liquid chromatography (HPLC) method was used to determine the rate of myricetin degradation and the potential formation of dihydromyricetin as a reductive metabolite. The effect of myricetin on the growth of faecal bacteria was studied by PCR-DGGE. From the isolated DNA of the bacteria, the DNA sequence corresponding to 16S rRNA was amplified by the PCR method. The PCR products were then separated on a denaturing gradient polyacrylamide gel.

Carrying out the experiments we found that myricetin was degraded by faecal bacteria under anaerobic conditions in McDougall’s buffer and in BHI medium in 10 and 3 hours, respectively. Within the same time (3 hours), myricetin was degraded under aerobic conditions in McDougall’s buffer. Employing the HPLC, it was shown that dihydromyricetin is not a reduced myricetin metabolite. Finally, using the PCR-DGGE method, it was found that the flavonoid studied herein affects the growth of bacteria.

Keywords: bacteria, intestines, flavonoid, metabolism