

Abstract

The intestinal microflora is an extensive ecosystem of microorganisms that consists of symbiotic and pathogenic species. The microflora is responsible for many important functions in the human body. An unquestionable function is that it affects the health state of the host. The higher the biodiversity, the greater the benefit for the host. However, it is necessary to point out that this should not include a high diversity of pathogenic bacterial species. There are many "beneficial" species, especially from the *Bifidobacterium* and *Lactobacillus* families. In recent decades, the popularity of supplementing these "beneficial" species with various supplementary diets (e.g. probiotics) has been growing a lot. The presented diploma thesis deals with pilot studies of liquid commercial probiotic preparations from American companies Ascended Health (not available on the Czech market) and their effects on the human microbiome.

The study involved 9 volunteers who provided 70 fecal samples before, during, and after use of the studied products. Two methods were used to determine the biodiversity of intestinal bacterial species. Both are based on the identification by bacterial DNA that encodes gene 16S rRNA. The first method uses PCR-DGGE technique and then identification by Sanger sequencing. The second method is based on preparation of a library for next generation sequencing. The evaluation and the analysis of biodiversity was performed in the PC programme QIIME 2. The differences between the samples were determined based on the number of operational taxonomic unit. The study also monitors changes in the relative frequency of the most bacterial families and families supplied in probiotics.

Even though the study results are not always conclusive, it can be said, however, that the use of probiotic preparations increased the biodiversity of intestinal bacterial species of 6 donors. The biodiversity of these donors began to return to pre-use state after discontinuation of the probiotics. The most abundant families in faecal samples are *Bacteroidaceae*, *Lachnospiraceae* and *Ruminococcaceae*, the relative abundance of which was not affected by the use of probiotics. The analyzes did not show any change in the relative abundance of probiotic bacterial families in faecal samples during and after the use of commercial probiotic preparations.

Key words: intestinal microflora, 16S rRNA, commercial probiotics, biodiversity

[IN CZECH]