

Abstract

Introduction: Physiological microflora is characterised by wide diversity. The microbial community is mostly composed of bacteria, but also includes fungi, archaea and viruses. Anaerobic commensal bacteria (Firmicutes and Bacteroidetes) dominate 90% of the colon. The composition and products of the gut microbiota have a significant effect on an individual's immune system, and their interactions may ultimately promote immune tolerance or inflammatory immune response. Blood cell transplantation (HSCT) and its associated standard procedures of conditioning, antibiotic exposure and dietary prophylaxis represent modification and disruption of the gut microbiota leading to the development of some serious post-transplant complications affecting the OS (overall survival) and TRM (treatment related mortality) of patients.

Objectives: The aim of this work was to investigate the representation of individual bacterial strains in patients undergoing allogeneic HSCT, as well as the effect of transplantation on the composition and diversity of their gut microbiota.

Methods: Stool samples were obtained from 52 patients who underwent an allogeneic hematopoietic cell transplant at the Institute of Hematology and Blood Transfusion in Prague. A cut-off date for the first sample was set for the start of hospitalisation, generally in the pre-treatment period, while a second sample was taken in the post-transplant period until the end of hospitalisation. The molecularly genetic method PCR 16S of the bacteria ribosomal gene was used for the analysis of the microbiota, followed by sequencing of individual bacterial taxa with the NGS method (new generation sequencing). Testing of the samples took place at the Institute of Animal Physiology and Genetics (IAPG) of the Academy of Sciences of the Czech Republic.

Results: The gut microbiota is a highly dynamic system that in allo HSCT recipients is accompanied by the loss of some bacterial taxons in a very short time after transplantation. While pre-transplant patients dominate the Clostridia class of the Firmicutes strain post-transplant, Bacilli class monodominance occurs, with the expansion of *Enterococcus* spp. At the same time, there is a reduction in diversity in transplant patients and a decrease in some genera and species of bacterial microorganisms.

Conclusion: In this study, allo HSCT has been shown to have an effect on change in the composition and diversity of patients' gut microbiota.

Keywords: HSCT, gut microbiota, NGS, prebiotics, probiotics, SCFA