

## FMT ALTERS CAECAL DYSBIOSIS IN PGF ANIMAL MODEL WITH INDUCED ULCERATIVE COLITIS

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Keywords: transplantation faecal microbiota (FMT), dextran sodium sulphate (DSS), ulcerative colitis, pseudo germ-free animal model, dysbiosis

### Objectives

Modulation of intestinal microbiota by a transplant of faecal microbiota in pseudo germ-free (PGF) animal model with chemically induced acute ulcerative colitis (UC).

### Methods

This experimental study conducted with the approval of State Veterinary and Food Administration, SR (No. 4073/18-221/3) was carried out on SPF (specific pathogen free) mice (females) of BALB/c line. Collection of biological material from potential stool donors was approved by the Ethical committee of the UHLP in Kosice, SR (No. 14/2018/OVaV). The PGF animal model with reduced intestinal microbiota was obtained by 5-day selective antibiotic decontamination of the gastrointestinal tract of model animals. Modelling of the acute UC involved chemical induction of UC by exposure of mice to DSS at 5 % concentration followed by 5-day therapy of mice by a transplant of faecal microbiota obtained from a human donor. DNA sequencing process was carried out using platform Illumina MiSeq (2 x 250 bp) and online platform Silva NGS was used for further processing.

### Results

NGS analysis of caecal microbiota of PGF mice with induced UC (DSS-FMT) revealed that transplantation of FMT resulted in a considerable shift in the

representatives of microbiota toward strain Firmicutes (92.32 %) and suppression of strain Bacteroidetes (5.91 %). There was observed a pronounced reduction in the originally dominant genus *Roseburia* from 95 % to 11.71 % in favour of genera from the original microbiota of mice represented by *Lachnospiraceae* NK4A136 (25.18 %), non-classified *Lachnospiraceae* (24.86 %), *Lachnospiraceae* UCG 006 (4.33 %), *Lachnoclostridium* (5.17 %), as well as a more diverse mixture of representatives originating from FMT of the human donor, such as the genera *Barnesiella*, *Parabacteroides*, *Butyricoccus* and *Blautia*. Alpha diversity revealed that after FMT therapy the highest diversity within the taxonomic classification of strains was recorded in animals with induced UC in comparison with control group without induction of UC (FMT).

### Conclusion

The experiment with transplantation of human faecal microbiota confirmed an obvious restorative effect of FMT therapy on composition of dysbiotic intestinal microbiota. Transmission of pathogenic microorganisms was not confirmed in the animals neither was observed multiplication of representatives involved in development of UC.

Acknowledgement: APVV-16-0176, VEGA 1/0015/21.