NIVB Meeting 2022

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Institute of Organic Chemistry and Biochemistry of the CAS

Masaryk University

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GUT MICROBIOME DIVERSITY OF PORCINE PERITONITIS MODEL OF SEPSIS

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Animal models are essential in understanding of the mechanisms of sepsis moreover the development and the assessment of emerging therapies. In clinically relevant porcine model, however, a significant variability in the host response has been observed among animals. Thus, there is a strong demand to better understand the potential sources of this heterogeneity. In this study, we compared faecal microbiome composition of 12 animals. Three samples were collected at different time points from each animal. Bacteriome was subjected to 16S rDNA profiling. A significant difference in bacterial composition was associated with the season ($p<0.001$) but not with the sex of the pig ($p = 0.28$), the timing of sample collection ($p = 0.59$), or interactions thereof (all $p > 0.3$). The season batch explained 55% of the total variance in the bacteriome diversity. The season term was highly significant from the high-resolution level of the bacterial amplicon sequencing

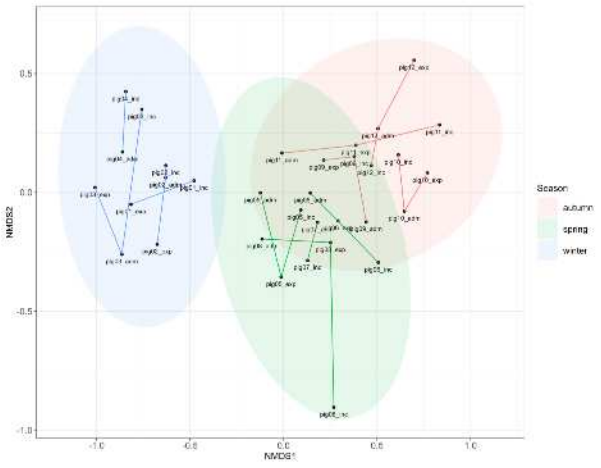

Fig. 2. **Non-metric multidimensional scaling on the quantitative Bray-Curtis dissimilarity (beta diversity – dissimilarity between communities).** Testing was performed by PERMANOVA at the genus level. Pigs are identified according to their numbers and the time of their admission into the animal facility ("pig*Nr*_adm"), immediately before the experiment ("pig*Nr*_exp"), and after incubation in isotonic saline before peritonitis induction ("pig*Nr*_inc").

variants up to the level of phylum. The diversity of the microbiome composition could significantly influence experimental model of sepsis, and studies are warranted to demonstrate the effects of gut microbiome diversity on the host-response. If confirmed, control of the gut microbiome should become a standard part of the pre-clinical sepsis experiments.

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