

Session 5: Impact of diet on gut microbiota

P-167 Impact of vegetables species and fibre contents on intestinal fermentation patterns in a humanized *in vitro* model of the gastro-intestinal tract

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Obesity and associated pathologies have dramatic consequences on patients' lives and high societal costs. Because of the role of intestinal dysbiosis and microbiota make-up on the pathogenesis of obesity, several strategies such as eating prebiotics and dietary fibre supplements are investigated to reshape intestinal microbial communities of obese patients. Beyond supplements, dietary fibre is supplied through plant ingredients in the meals. In the multidisciplinary research project Food4Gut, the use of vegetables rich in specific targeted dietary fibre, namely fructans, is being scrutinized for its ability to induce positive changes in the intestinal ecophysiology. Because expected effects might differ according to the content in dietary fibre and fructans, the soluble:insoluble ratio, as well as the cooking of the vegetables, the fermentation patterns of several vegetables are being investigated in a dual *in vitro* model combining enzymatic hydrolysis to an *in vitro* fermentation step using faecal inoculums from humans, to evaluate the performance of gut microbiota, in modulating metabolic functions. Six vegetables were sampled from three different producers (N=3) and steamed for 20 to 30 min.: Jerusalem artichoke, salsify, asparagus, pumpkin, fennel and swede. They were chosen because they display a diversity of contents in fructans, soluble (SDF) and insoluble dietary fibre (IDF). Steamed vegetable samples and burgers from local fast food restaurants (negative control) were hydrolysed *in vitro* with porcine pepsin and pancreatin to mimic digestion in the upper gut and indigested fibrous residues were recovered using a 6kDa dialysis membrane. Subsequently, *in vitro* fermentation is being run with independent faecal inoculums from obese and lean patients (N=4). Fermentation kinetics over 24h as well as short-chain fatty acids production and profiles will be compared according to the individual donor and the vegetable species and multivariate analysis used to explore the relationships between donor characteristics, vegetable species and composition and fermentation patterns.

P-168 Diet with different protein source alters microbiota composition and host metabolomic response in mice.

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Diets are known to influence intestinal functions, mainly by modulating the gut microbiota composition and diversity and thereby influencing the metabolic activity of the residing gut microbiota and their "crosstalk" with host cells in the mucosal layer. However, the composition and population dynamics of the microbiota in the small intestine as influenced by the use of different dietary protein sources, remains largely unknown. Therefore, this study was designed to address key questions concerning the effects of the use of different dietary protein sources on gut function and microbiota. We used casein, partially delactosed whey powder, spray dried porcine plasma, soybean meal, wheat gluten meal and yellow meal worm as dietary protein sources. Soybean meal based (SBM) diet served as reference to make comparisons with the other experimental diets. Mouse experiments were performed to evaluate effects of dietary protein source on intestinal mucosal genome-wide gene expression, intestinal microbiota composition using 16S rRNA gene sequencing, and metabolite composition in blood and urine using mass spectrometry analysis. Previously, we already reported on the dramatic effect of dietary protein sources on local and systemic immune parameters. Here, we provide evidence that dietary protein sources also induce significant changes in the taxonomic composition of gut microbiota and in the relative abundance of several microbial taxa (families, species). This analysis revealed that SBM distinctively influenced microbiota composition, compared to other dietary protein sources. Interestingly, we detected increased concentrations of metabolites in blood and urine which could be associated with the metabolic capacity of intestinal microbiota. We conclude that protein sources in animal diets not only affect local and systemic immune parameters but also "host" metabolic parameters.