2019 Helmholtz – OCPC – Program

for the involvement of postdocs in bilateral collaboration projects

PART A

Title of the project: Microbial transformation of dietary fatty acids into active metabolites in the gut

Helmholtz Centre and institute: Helmholtz Zentrum München; Research Unit for Comparative Microbiome Analysis

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Description of the project:

The anaerobic degradation of dietary lipids by the gut microbiome is so far not well understood, despite its suggested importance for the formation of important metabolites which trigger health and disease. We postulate that the lipid composition and diet complexity affect the overall structure and function of the gut microbiome (metagenome), whereas the overall dietary composition (C:N:P ratio) mainly determines the activity pattern of the gut microbiome (metatranscriptome). Furthermore, we assume that genetic disposition of the host strongly modulates the diversity of fatty acid degraders in the gut and, depending on fatty acid structure, impacts the flexibility of the gut microbiome to degrade these compounds originating from different types of diet. Therefore, the objectives of this project are (a) to identify key players which catalyze the anaerobic degradation of dietary fatty acids in the gut, (b) to investigate the consequences of different dietary inventions for the community composition and activity of microbiota triggering the anaerobic degradation of dietary fatty acids, and (c) to identify key metabolites formed by the degraders and define those acting as a driver for microbe-microbe and host-microbe interactions. To identify major degraders and to reconstruct important pathways of the anaerobic transformation of fatty acids differing in the degree of saturation, dietary formulations varying in C:N:P ratios will be supplemented with ^{13} C-labelled fatty acids (C18:0, C18:1, C18:2, C18:3, C20:4). This will be applied first *in vitro* using anaerobic fermenter systems with minimal consortia and fecal samples, and then *in situ* using wild-type as well as mice models relevant for inflammation (Crohn`s disease). By means of meta-genomic and meta-transcriptomic analysis, we will identify those microbes utilizing the fatty acids within complex microbial communities. Comparative untargeted metabolomics (SWATH-MS) of the ^{13}C-labelled and non-labelled systems, followed by targeted quantitative lipidomics using stable isotope dilution analysis (SIDA) will further specify the metabolites formed during anaerobic fatty acid transformation with special emphasis on unknown metabolites and bacterially generated lipid derivatives.

Description of existing or sought Chinese collaboration partner institute:

So far there is no direct contact in this field with partners from China established, but we are strongly looking for collaborators. As our experience is on Microbiome Research it would be beneficial to collaborate with partners who have profound knowledge on host responses and immunology in murine models, as well as clinicians working on acute and chronical inflammatory gut diseases

Required qualification of the post-doc:

- PhD in Microbiology, Microbial Ecology, Microbiome Research
- Experience with Next generation sequencing of microbiomes and use of different bioinformatics pipelines; knowledge of tools for integrative big data analysis
- Additional skills in Immunology and nutrition would be welcome