Identification of microbiota-derived tryptophan immunometabolism as an individual driver of systemic immunity in chronic inflammatory diseases (additional funding for refugee scholars)

Initiative: Förderangebot für geflohene Wissenschaftler:innen aus Afghanistan

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Chronic inflammatory barrier disease (CID), such as inflammatory bowel disease (IBD), rheumatoid arthritis (RA) and psoriasis (Pso) are a growing health burden in industrialized countries with deep socioeconomic impact on the affected patients and the healthcare system. Intestinal dysbiosis has been identified as a common risk factor for the development of CID, however the mechanistic link on how disturbances in the gut ecology contribute to disease development are unknown. The aim of this project is to generate cross-sectional datasets of patients with IBD, RA and Pso and to combine clinical data with serum (targeted metabolomics) and fecal microbiota analysis (16s, metagenome) to understand the impact of gut microbiology on the metabolism of the amino acid tryptophan and seek to identify a common microbial core set that causally affects tryptophan immunometabolism in CID.

Projektbeteiligte

Dr. Konrad Aden
Universitätsklinikum Schleswig-Holstein
Campus Kiel
Klinik für Innere Medizin I
Institut für klinische Molekularbiologie
Kiel