

# The archaeome in gastrointestinal disorders - AGAD

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## Summary

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Supervisor: Prof. Dr. Christine Moissl-Eichinger  
Availability: This position is available.  
Offered by: Medical University of Graz  
Application deadline: Applications are accepted between July 15, 2019 00:00 and September 15, 2019 23:59 (Europe/Zurich)

## Description

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### Background:

The human microbiome is composed of various microorganisms, including bacteria, small eukaryotes, fungi, viruses/phages, and archaea. A shortcoming of most studies is the focus on the bacteriome in most studies, and the ignorance of other components, in particular archaea. Not a single archaeal pathogen is known yet, thus, their medical relevance is considered negligible, resulting in a reduced effort to understand their role. Consequently, the human archaeome remains uncharted territory of microbiome research, and many questions with respect to potential pathogenicity, genetics, function and interactions with host and other microbes remain unanswered. With the exception of detrimental health effects of methane, causal relationship between the presence/abundance of (specific) archaea and an individual pathology has not been proven yet. However, (methano-) archaea represent an important, highly interactive hub in the human microbiome and serve as strong indicators of the microbiome status *per se*.

### Hypothesis and Objectives:

We recognized two different phenomena, which we address in more detail in order to understand the abundance, diversity, role and impact of the human archaeome in the gastrointestinal tract. More specific, we will address methane-overproduction in adults and the role of archaea in acute appendicitis in adolescents. We hypothesize that methane-overproducers possess a different abundance and/or composition of their archaeome and/or that the corresponding methanoarchaea possess a different activity/physiology/genomic inventory. Moreover we hypothesize intra-microbiome networks (bacteria-archaea-fungi) are composed differently with respect to function and profile. Following our observation that archaea make between 22 and 70% of all microbial signatures in appendix samples, we hypothesize increased abundance and a functional role of archaea in acute appendicitis.

### Methodology:

We will use the above-mentioned settings (whereas the methane over-producers serve as models for more detailed studies and the appendicitis part is more explorative) to answer specific questions on the abundance, diversity, role and impact of Archaea in the GIT, by using a combination of molecular quantitative methods, amplicon/metagenome/genome sequencing (Illumina Mi/HiSeq, NanoPore technology, genome reconstruction and annotation), metatranscriptomics, metabolomics, targeted cultivation and isolates characterization. More specifically, we will address the following goals:

- Determine archaeal abundance and diversity
- Analyze archaeal interaction with bacteria, fungi and the human host
- Assess archaeal genetic and functional profiles
- Cultivate and characterize human-associated archaea

The successful PhD candidate requires skills in anaerobic cultivation of microorganisms and basic knowledge in microbiome data processing.

### References:

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