The role of Archaea in the human body

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 February 01, 2017 00:00 and March 19, 2017 23:59 (CEST)

Description

Background:

Trillions (10^{14}) of microbes live in and on the human body, forming the human microbial community. These complex communities contain taxa from all three domains of life (bacteria, eukaryotes and archaea) as well as viruses.

Scientists have shown that microorganisms associated with the human body play an important role in health maintenance (Morgan et al., 2013). Microbes help in energy harvest and storage, and have a variety of metabolic functions such as fermentation and absorbing undigested carbohydrates; they interact with the immune system and support the development of normal immune functions (Flint et al., 2012; Round and Mazmanian, 2009).

A special group of microorganisms, the archaea, have been poorly studied in relation to the human body. Archaea have been identified in the gastro-intestinal tract, the oral cavity and on the human skin (Dridi et al., 2011; Probst et al., 2013). The dominant archaea in the gastro-intestinal tract are the methanogens, representing almost 10% of all anaerobic microorganisms (Dridi et al., 2009). Methanogens are part of the commensal microbiota and form stable colonization within the human body and are often in syntrophic relationships with other bacteria. These microbes reduce the metabolic products resulted during fermentation leading to an increased efficiency of bacterial fermentation. Methanogens produce methane under anaerobic conditions by using bacterial fermentation products such as hydrogen, carbon dioxide, methanol, acetate and methylamines (Bang and Schmitz, 2015). These microbes are thought to be “key stone” species influencing the community composition and function, by keeping the hydrogen partial pressure at low levels. Much less is known on the human skin archaea, which belong to the thaumarchaeal phylum, and could be involved in skin surface ammonia turnover (Probst et al., 2013), or associated halophilic archaea (Khelaifia et al., 2016), that were even found in human milk samples (Jimenez et al., 2015).

Hypothesis and Objectives:

Hypotheses: *Archaea are normal components of the human microbiota. They are closely interacting with a number of different Bacteria. Archaea play a metabolic key role and their metabolic products can influence the host.*

Objectives:

- Visualization and quantification of Archaea in gut, oral and skin samples
- Detection of Archaea-colocalized and potential syntrophic bacteria
- Cultivation of human-associated Archaea
- Functional analysis of human-associated Archaea in the host system and in cultures

Methodology:

Visualization and quantification will be based on quantitative PCR, 16S rRNA gene sequencing, immunostaining techniques, fluorescence in situ hybridization. Detection of colocalized Bacteria will be based on immuno-capturing, FACS (fluorescence activated cell sorting) and sequencing. Cultivation will be done using our anoxic cultivation facilities (glove box and gas station). Functional analyses will/can be based on stable isotope probing, neuroimaging (in collaboration), transcriptomics and methane detection (gas chromatography).

References:

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