Rector's Office
Auenbruggerplatz 2, A-8036 Graz

Gerald Auer
Public relations and event management

gerald.auer@medunigraz.at
Tel +43 / 316 / 385-72023
Fax +43 / 316 / 385-72030

Press release
For immediate publication

Gut health: New research findings as a treasure trove of data for science
First comprehensive description of the human archaeome published

Graz, 11 January 2022: Analysis of the medical benefits of the microbiome appears to resemble the proverbial search for a needle in a haystack since the number of microorganisms on and in our body is unimaginably large. A team of researchers from the Medical University of Graz and Kiel University have analyzed extensive microbiome data to demonstrate the share of archaea in the microbial colonization of the gut. The initial findings on their functional characteristics and the role they play in our health have now been published in the internationally renowned journal "Nature Microbiology." The researchers from Kiel and Graz provide a unique source of scientific data for future research.

Archaea: The great unknowns in the human microbiome

In recent years, researchers around the world have investigated the connections between the composition and function of the body's microbiome and the development of disease. Most of this research has concentrated on bacteria, whose different species dominate the microbiome in number. A special group of microorganisms has received little attention until now: the archaea. Although the archaea make up on average "only" 1.2 percent of the entire gut microbiome, previous studies have shown that they have tremendous regulatory effects on the microbiome.

An international research team of scientists from Kiel University (CAU), the Medical University of Graz and other international partner institutions in Great Britain and France have now planned to characterize the insufficiently profiled "archaeome" of the human gut using comprehensive genome data from large cohorts at different locations worldwide. With this survey, the scientists working with Ruth Schmitz-Streit, CAU, and Christine Moissl-Eichinger, Med Uni Graz, would like to increase knowledge of this group of microorganisms. They were able to identify previously unknown archaea species and prominently publish their research findings in the internationally renowned journal "Nature Microbiology."

Archaea in the gut more diverse and less "international" than expected

The new analysis provides the first comprehensive description of the human archaeome. Researchers exploited data sources from numerous existing microbiome studies that included the complete genetic information of individual microbial colonization of the gut of participating subjects. "First, we were able to determine that the human archaeome is much more diverse than previously known and independent of external factors such as geography, sex or age, most people host a core population of roughly the same species," stresses Cynthia Chibani, a scientific staff member in Ruth Schmityz-Streit's working group. "In addition to a large number of newly discovered species, we were able to identify unknown viruses that can infect the archaea."

Archaea leave behind an individual fingerprint

In addition to the simple list of species, the researchers also searched for connections to known patterns in the genetic information of the archaea. They examined more than 28,000 so-called protein clusters that indicate significant correlations between archaeal colonization in the gut and sociodemographic characteristics of the human hosts. "Based on the presence of certain species and the proteins they produce, conclusions can be drawn about age groups or lifestyles," explains Alexander Mahnert, Med Uni Graz, who conducts bioinformatic analysis with Cynthia Chibani. "At present, such significant correlations with regard to potential archaeome-associated symptoms cannot be reliably construed," say the two researchers.

Further research on inflammatory bowel disease in sight

Another important finding was the splitting of the previously identified species Methanobrevibacter smithii into two clades at the species level. M. smithii and its new "sister" Ca. Methanobrevibacter intestini are widespread in a large number of individuals. The interaction between these two closely related species and its importance for human health must still be investigated. The connection between these methane-forming archaea with diseases such as colon cancer or inflammatory bowel disease has not been clearly explained. The research now being published increases understanding of the human archaeome and provides a more extensive genome and protein catalog for future analysis.

Science is just at the beginning of identifying the full diversity of the archaea. "The archaea catalog presented here and its associated protein catalog (1.8 million proteins) are a unique resource that can be exploited in the future development of new research questions," stresses Christine Moissl-Eichinger, who is actively driving archaea research forward along with her colleagues in Kiel. "These approaches include the study of the physiology and metabolism of the newly identified archaea or the nature of their communication with the human host." Any future investigation of the functional aspects of the archaeome will require the development of new analysis methods since they are mainly tailored to bacterial species as well as the specific culturing of archaea from the human gut. "Our work makes a significant contribution to the understanding of the human microbiome as a complex, multilayered network of bacteria, archaea, fungi and viruses," summarizes Ruth Schmitz-Streit. In future studies, the researchers hope to gradually discover the impact that the archaea have on human physiology and their potential contribution to the development of disease.

Further information and contact
Christine Moissl-Eichinger
Professor of Interactive Microbiome Research
Medical University of Graz
Diagnostic and Research Institute of Hygiene,
Microbiology and Environmental Medicine
Tel.: +43 316 385 73770
christine.moissl-eichinger@medunigraz.at

Publication
A catalogue of 1,167 genomes from the human gut archaeome; Nature Microbiology 2021
https://www.nature.com/articles/s41564-021-01020-9