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Resolving the "lipid divide' by unravelling the evolution and role of fatty acid metabolic pathways in Archaea - Lipid Divide

Initiative: "Leben?" - Ein neuer Blick der Naturwissenschaften auf die grundlegenden Prinzipien des Lebens

(beendet)

Bewilligung: 09.07.2019

Laufzeit: 5 Jahre

Projekt-Website: https://www.uni-due.de/umb/enzym_projekte.php

Recent phylogenetic findings have led to a revised "Two Domains of Life Tree" model in which Eukarya evolved from within the Archaea. Thus, during eukaryogenesis the membrane lipids must have fundamentally changed from archaeal-type (isoprenoids ether-linked to glycerol-1-phosphate) to eukaryotic/ bacterial-type lipids (fatty acids (FAs) ester-linked to glycerol-3-phosphate). However, the functional and evolutionary basis for this elusive "lipid divide" is still obscure. The key to close this knowledge gap is to understand the evolutionary history and the presence and distribution of FAs in the archaeal lineages as well as the functional role of archaeal FA metabolic pathways and enzymes including their regulation. This project will provide these insights by unravelling the distinct functions as well as the degradation and biosynthesis of fatty acids in Archaea by a combination of molecular biology, biochemistry, transcriptomics, proteomics, metabolomics and lipidomics. These results will then be linked to a broad phylogenetic/phylogenomic approach to address the membrane lipid transition conundrum. Therefore, available and to be generated (meta)genomic sequence information from Archaea including the Asgard superphylum will be analyzed in a phylogenetic and phylogenomic framework and linked to novel biochemical, metabolic and proteomic insights. The project will therefore contribute to a fundamental understanding of one of the central unresolved questions in evolutionary biology, i.e. the lipid divide in eukaryogenesis.

Projektbeteiligte

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Open Access-Publikationen

The biology of thermoacidophilic archaea from the order Sulfolobales.
Potential of atmospheric pressure ionization sources for the analysis of free fatty acids in clinical and biological samples by gas chromatography-mass spectrometry