

温泉環境に生息する微生物のメタゲノム解析
Metagenomic Analyses of Microbes in Hot Springs

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研究成果概要

During the fiscal year 2022 I conducted a study using the Kyoto supercomputer to analyze metagenome data obtained from iron-rich hot springs in the Akita and Aomori prefectures of Japan. This research aimed to identify the metabolic capabilities of the microbial communities present in these extreme environments.

The supercomputer allowed me to analyze large amounts of sequencing data, which resulted in the identification of various metabolic pathways present in the hot springs' microbial communities. Through this analysis, we discovered that these communities have a diverse range of metabolic capabilities, including the ability to use iron as an electron donor for energy production.

This research provided new insights into the metabolic capabilities of microbial communities in extreme environments, which could have significant implications for understanding the roles of these communities in biogeochemical cycles and potentially in biotechnological applications.

A model for carbon cycling, nitrogen cycling and sulfur cycling was generated for all the samples in the study and graphical representation such as the one presented in Fig 1. were generated.

The following biogeochemical cycling figure was able to be made thank to the use of the supercomputer and provided useful insight which will help in writing a paper during 2023.

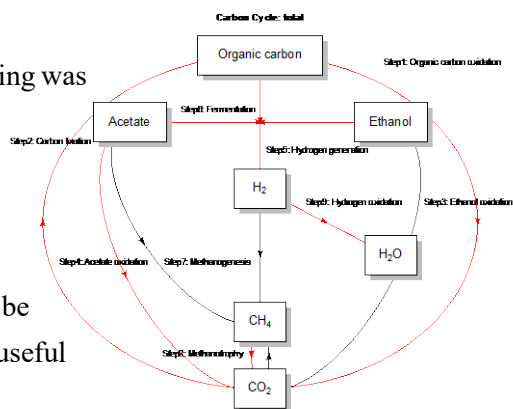


Fig1. Carbon cycling in iron rich springs