T2R2 東京科学大学 リサーチリポジトリ
Science Tokyo Research Repository

論文 / 著書情報
Article / Book Information

題目(和文)	鉄に富む温泉環境における微生物生態の地球化学的変動要因：メタゲノム解析と機械学習アプローチ
Title(English)	Investigating Geochemical Drivers of Microbial Ecology in Iron-Rich Hot Springs: Metagenomic and Machine Learning Approaches
著者(和文)	LiHau Fatima
Author(English)	Fatima Li Hau
出典(和文)	学位:博士(理学), 学位授与機関:東京科学大学, 報告番号:甲第217号, 授与年月日:2025年3月26日, 学位の種別:課程博士, 審査員:上野 雄一郎,横山 哲也,尾﨑 和海,MC　GLYNN SHAWN ERIN,癸生川 陽子,Gilbert Alexis
Citation(English)	Degree:Doctor (Science), Conferring organization: Institute of Science Tokyo, Report number:甲第217号, Conferred date:2025/3/26, Degree Type:Course doctor, Examiner:,,,,,
学位種別(和文)	博士論文
Category(English)	Doctoral Thesis
種別(和文)	審査の要旨
Type(English)	Exam Summary

Powered by T2R2 (Science Tokyo Research Repository)

（博士課程）

論文審査の要旨及び審査員

報告番号	甲第　　号		学位申請者氏名		LI HAU Fatima	
論文審査 審 査 員		氏　名	職　名		氏　名	職　名
	主査	上野 雄一郎	教授	審査員	McGLYNN Shawn	准教授
	審査員	横山 哲也	教授			
		GILBERT Alexis	准教授			
		尾﨑 和海	准教授			

論文審査の要旨（2000 字程度）

The thesis is entitled " Investigating Geochemical Drivers of Microbial Ecology in Iron-Rich Hot Springs: Metagenomic and Machine Learning Approaches" and contains 5 chapters. This work contains research on the microbiological communities and geochemical properties of five iron rich carbonate hot springs in Japan and additionally a comparative approach of hot springs in New Zealand based on machine learning. The candidate compared the genetic and geochemical information from the studied hot springs in order to find relationships between them. The studied hot springs may be similar to some conditions in Earth history and the findings are discussed in the context of the possible ecology of ancient environments.

In the “Introduction”, the candidate reviewed current understandings about the chemistry of the early ocean and summarized the timeline of biological evolution. Ferrous iron is expected to be more abundant in early Earth’s oceans, and the candidate reviewed contemporary analog sites which have been treated as having the potential to host microbial ecosystems which may be similar to some on the early Earth. While stratified lakes were introduced as areas which have been an international research focus, the candidate proposed ferrous iron rich hot springs as more appropriate analogs to investigate the impact of light and the contributions of phototrophic microbes.

In Chapter 2, "Bulk metagenome analysis of iron rich hot springs of Japan", the candidate investigated the geochemistry and microbial inhabitants of the five studied hot springs. Geochemical analyses showed that the springs were all elevated in temperature and iron with variable salinity. Carbon isotopes of the inorganic and organic fractions were also reported. The microbial inhabitants documented by amplicon sequencing at each site were variable between the sites and were dominated by a limited taxonomic group. Using metagenomic sequencing, the candidate was able to construct models of biochemical transformations occurring at the sites including C, N, and S cycling. The genetic capacity for these transformations was compared using the perspective of gene count abundances. Gene presence was related to geochemical parameters by performing a canonical correspondence analysis, where for example the operation of anoxygenic photosynthetic organisms was observed to be related to increased pH values. A major conclusion from this chapter was that while the microbial taxonomy is variable between the sites, the overall patterns in elemental cycling is similar. “Kowakubi” hot spring was observed to contain an abundance of organisms which are not involved in iron cycling and instead are involved in hydrogen and methane cycling, indicating that iron is not necessarily the primary driver of microbial activity.

In Chapter 3, " Species-level contributions to the biogeochemical cycles in iron rich hot springs", the candidate investigated the recovered Metagenome Assembled Genomes (MAGs) from the study sites. 242 medium to high quality MAGs were obtained and contained 9 unreported orders indicating that the study sites harbor previously unexplored microbial groups. The species level contributions as viewed from the MAG perspective were discussed as were potential implications for the early Earth. The individual genomes recovered were observed to have flexibility in their utilization of electron donor/acceptor pairs suggesting the organisms are able to live in dynamic environments. Six of the cyanobacterial genomes contained genes associated with anoxygenic photosynthesis with sulfide as the electron donor; although sulfide was not detected in the data presented in Chapter 2, this finding motivates further research on the sulfur cycle of these springs. The metabolic characteristics of the genomes recovered was compared and displayed phylogenetically, and the gene phylogenies encoding enzymes involved in major transformations in the C, N, and S cycles was compared.

In Chapter 4, "Prediction of microbial community assemblages using machine learning”, the candidate explored the application of machine learning to predicting microbial community membership and activity. Due to the requirement of using large datasets in this type of analysis, the candidate did not use the data from the above discussed chapters but instead focused on a large dataset of microbe and geochemistry of ~1019 hot springs. This work was conducted collaboratively in the group of Prof. Bowman at Scripps Oceanography Institute. A Random Forest regression was used and showed predictive capability for temperature and pH. To increase the predictive ability the candidate suggested supplementation of more geochemical parameters.

Chapter 5 provided a summary of the main findings and interpretations. The thesis synthesized knowledge of Earth-Life evolution and provided new data and interpretation of ancient Earth analog sites. It is judged to be of sufficient quality for the degree of Doctor of Science.

注意：「論文審査の要旨及び審査員」は、東工大リサーチリポジトリ（T2R2）にてインターネット公表されますので、公表可能な範囲の内容で作成してください。