Student Free Design Activities (One Health Collaborative Training)
報告書 Report

報告者 [Reporter]

氏名 [Full Name]	Barnes David Atomanyi		
学年 [Year]	DC-4	E-mail	
所属 [Affiliation]	Division of Bioresources, IIZC		

担当教員 [Instructor]

氏名 [Full Name]	Prof. Chie Nakajima		
署名 [Signature]	中島千絵		
所属 [Affiliation]	Division of Bioresources, IIZC		
E-mail		電話 [Tel]	

活動報告 [Activity Report]

※活動内容が判る様な写真や図表を加えて下さい。/ Provide photos, tables and figures that clearly show the activities during the period.

タイトル [Course Title]	Student Free Design Activities – Module 3
実施期間 [Periods]	12th May – 17th May 2025
共同実施者 [Other participants]	None
言語 [Language]	English
実施場所 [Location]	Nakamura's Lab (Bioinformatics Center, Department of Infection Metagenomics)

申請時計画の実施報告 [Report how you carried out your plan in the application form]

Did you follow the schedule you initially planned? Did you get the outcome(s) you expected? Please describe what you did during the activity period in detail.

Yes, I generally followed the schedule I initially planned for the visit, and I was able to achieve the core outcomes I aimed for. Each day was structured to progressively build on my skills in NGS data analysis and to apply specific pipelines to my non-tuberculous mycobacteria (NTM) dataset from Ghana.

My trip to Osaka Research Institute for Microbial Diseases (RIMD), Prof. Shota Nakamura's laboratory closely aligned with the genomic component of my doctoral research on zoonotic tuberculosis and non-tuberculous mycobacteria (NTM) in Ghana. The primary goal was to deepen my expertise in advanced bioinformatics and genomic tools for analysing NTM isolates, particularly focusing on species identification, antimicrobial resistance (AMR) and virulence gene profiling. Additionally, this opportunity was meant to support the development of some collaborative efforts towards a research publication based on the genomic findings.

Picture with Prof. Nakamura (right)
Prof. Matsumoto (left)

I arrived in Osaka on May 12 and was warmly welcomed by Prof. Nakamura and his lab team. After an introduction to the lab's ongoing research and computational infrastructure, I was guided through the preliminary setup of my analysis environment. This included configuring a Linux-based system and installing relevant Python packages for

NGS data analysis.

Over the next few days, I engaged in hands-on training in various analytical tasks. On May 13, I began species identification of my Ghanaian NTM isolates using the lab's in-house pipeline, learning how to structure and manage large datasets effectively. The following day, I performed batch downloads and quality control of NTM sequencing data from the NCBI Short Read Archive (SRA), using tools such as fastQC and multiQC. This was accompanied by a preliminary demographic analysis of the isolates from Ghana, giving me an opportunity to contextualize the genomic data within field metadata. In total, I analyzed 16 NTM isolates and identified six potentially novel species. These isolates showed Average Nucleotide Identity (ANI) values similar to *Mycolicibacterium duvalii*, *Mycolicibacterium boenickei*, *Mycolicibacterium chitae*, among others, suggesting new taxonomic diversity in these animal-derived strains (Table 1).

Table 1 showing the ANI of Ghanaian NTM isolates

Lab ID	genus	species	strain	score	ANI %	misc
D.B 003	Mycolicibacterium	Mycolicibacterium duvalii	IP141180004	0.5802141	83.4263	sp. nov. #1
D.B 009	Mycolicibacterium	Mycolicibacterium boenickei	CCUG47580	0.3691532	87.9923	sp. nov. #2
D.B 010	Mycolicibacterium	Mycolicibacterium duvalii	IP141180004	0.6091334	83.4895	sp. nov. #1
D.B 012	Mycolicibacterium	Mycolicibacterium duvalii	IP141180004	0.5655913	83.6042	sp. nov. #1
D.B 016	Mycolicibacterium	Mycolicibacterium elephantis	852014-51730_SCH5271717	0.9034787	96.3339	
D.B 017	Mycolicibacterium	Mycolicibacterium duvalii	IP141180004	0.6572055	83.5917	sp. nov. #1
D.B 030	Mycolicibacterium	Mycolicibacterium duvalii	IP141180004	0.57956	83.5938	sp. nov. #1
D.B 031	Mycobacterium	Mycobacterium tuberculosis	18142	0.827836	99.5373	
D.B 040	Mycolicibacterium	Mycolicibacterium komanii	GPK 1020	0.8801817	92.6676	sp. nov. #3
D.B 075	Mycolicibacterium	Mycolicibacterium fortuitum	isolate_2	0.98796	98.5817	
D.B 091	Mycolicibacterium	Mycolicibacterium thermoresistibile	JCM6362	0.9091742	85.5347	sp. nov. #4
D.B 095	Mycobacterium	Mycobacterium grossiae	GK	0.1410646	76.3921	Non-NTM (RI
D.B 098	Mycolicibacterium	Mycolicibacterium chitae	NCTC10485	0.9921824	94.2553	sp. nov. #5
D.B 110	Mycolicibacterium	Mycolicibacterium duvalii	IP141180004	0.7089857	83.5457	sp. nov. #1
D.B 127	Mycolicibacterium	Mycolicibacterium sp. GF69	GF69	0.595063	86.0346	sp. nov. #6
D.B 131	Mycolicibacterium	Mycolicibacterium duvalii	IP141180004	0.6228532	83.5279	sp. nov. #1

On May 15th, In addition to mutation detection and AMR gene screening using different curated databases, I participated in a guided tour of the RIMD facilities. Prof. Matsumoto gave me a lecture on genome registration and public database submission protocols, which was particularly relevant for my future goals of contributing genomic data to international repositories. Later that day, we discussed the preliminary findings from my data and outlined possible directions for a collaborative manuscript.

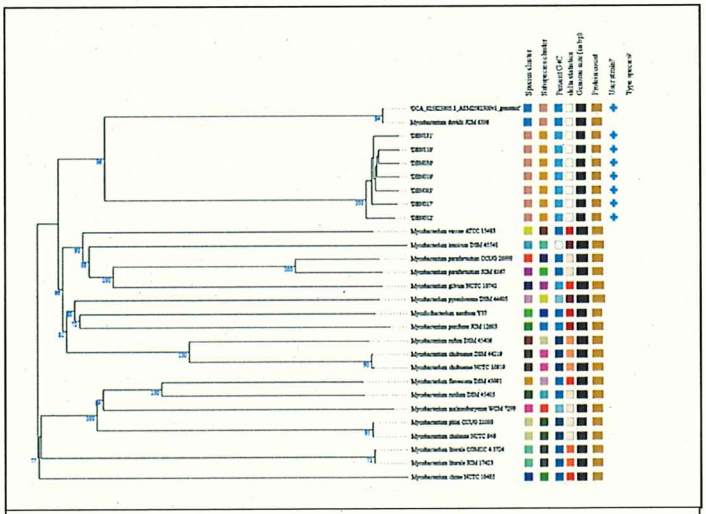

Fig 2: Phylogenetic tree generated using the TYGS platform, showing the position of a novel *Mycolicibacterium* species among its closest relatives.

I was also introduced to several integrated pipelines for processing short-read sequencing data. This included filtering, mapping, variant calling (both SNPs and INDELs), and annotation. I paid special attention to the analysis of pathogenicity-related genes within the NTM genomes. The day concluded with building a preliminary phylogenetic tree to explore evolutionary relationships and potential clusters among the Ghanaian isolates.

Although we did not specifically perform ancestral reconstruction for *Mycobacterium tuberculosis* complex (MTBC) lineages due to the focus on NTMs, the outcomes of the visit were aligned with and even exceeded my expectations. I also had a productive discussion with Prof. Nakamura regarding potential directions for publication based on the findings.

I departed from Osaka on May 17 with a sense of accomplishment and renewed clarity on how to structure and deepen the genomic components of my dissertation work.
In summary, I followed the planned schedule closely, gained hands-on experience with relevant tools, and made significant progress in the genomic analysis of my NTM isolates.

目的達成状況報告 [Report how you achieved your goal/objectives listed in the application form]

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Did you achieve all the goals you initially planned? If not, please describe why you failed to fulfill your objectives. Yes, I achieved nearly all the goals I initially planned for the visit. I successfully gained hands-on experience with advanced genomic analysis tools, learned how to analyze genes related to virulence and antimicrobial resistance in NTMs, and applied various bioinformatics pipelines to track genetic diversity and potential transmission patterns. Although we did not perform ancestral reconstruction or MTBC lineage calling as originally scheduled, this was due to a shift in focus toward NTM isolates, which were more relevant to my current dataset. This adjustment allowed for deeper analysis of NTMs and ultimately enhanced the relevance and impact of the visit.
One Health Approach実践報告 [Report how your activity could link to One Health Approach]
Did you have a chance to experience One Health approach (collaboration with people from other academic areas)? Please describe some of the examples of One Health approach you implemented in your activity. Otherwise, explain the possibility(ies) how you could link this activity to One Health approach for your future. During my time at Prof. Nakamura's lab, while the primary focus was microbial genomics, the visit fostered a meaningful One Health dialogue. The NTMs I brought for analysis were isolated from cattle in Ghana, offering a veterinary and environmental health dimension to a lab that primarily works with human NTM isolates. This contrast created a valuable space for interdisciplinary exchange, as many members of the lab were unfamiliar with the animal and environmental reservoirs of NTMs, especially in African settings. Our discussions highlighted the need to better understand the cultural and ecological contexts in which NTMs emerge and spread. The opportunity to share perspectives on zoonotic transmission and environmental exposure pathways in rural Africa helped broaden the scope of ongoing work in the lab. Looking ahead, I see strong potential to build on this foundation by integrating environmental and veterinary data from Ghana with genomic findings—advancing a true One Health approach to NTM research and control.
備考 [Remarks]

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