北海道大学
One Health フロンティア卓越大学院プログラム
One Health Allyコース
One Health on-site Training報告書

Hokkaido University
WISE Program for
"One Health Frontier Graduate School of Excellence"
One Health Ally Course
One Health on-site Training Report from

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

報告者 [Reporter]

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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]	Module 3
実施期間 [Periods]	May 19th – 23rd, 2025
共同実施者 [Other participants]	-
言語 [Language]	English
実施場所 [Location]	Rakuno Gakuen University, Hokkaido, Japan

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 followed the schedule I initially planned, and I achieved the outcomes I expected. During the activity period, I participated in both wet lab and dry lab sessions regarding antimicrobial resistance.

Day 1: Upon arrival at the Laboratory of Food Microbiology and Food Safety, Professor Usui kindly provided a brief introduction to his laboratory and an overview of the current antimicrobial resistance situation in livestock in Japan. We then discussed the planned activities and schedule in detail. He also provided laboratory documents and reference materials related to the upcoming experiments, which enabled me to study and prepare in advance. The experimental work began with the preparation of LB agar, followed by the inoculation of 50 bacterial isolates onto the prepared plates. The plates were then incubated overnight at 37°C for bacterial growth. In the afternoon, I conducted metagenomic analysis using sequencing data from one of Usui sensei's previous studies. This experiment was a mock analysis, so I primarily focused on learning how to analyze the data. I used the Galaxy Australia website for this analysis. Initially, I struggled with the tool—QIIME2—and realized that carefully reading the instructions before starting the analysis was necessary.

Day 2: In the morning, I attended a journal club presentation by undergraduate students. Then, I examined the bacterial culture plates from the previous day to assess the growth of the isolates. In the afternoon, I picked up bacterial colonies from the plates and inoculated them into a 96-well plate. Additionally, Usui sensei provided a detailed explanation of the plasmid reconstruction pipeline he employed in his previous study. For this activity, I was able to use data from my earlier experiments.

Figure 1. Bacterial inoculation in a 96-well plate

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Figure 2. Plates for agar dilution method

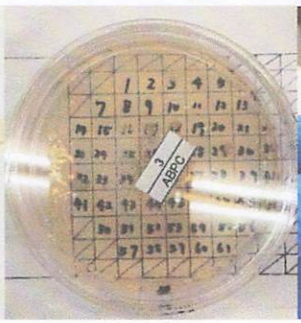

Figure 3. Agar dilution plate

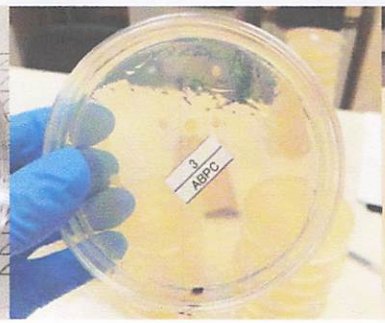

Figure 4. Agar dilution plate

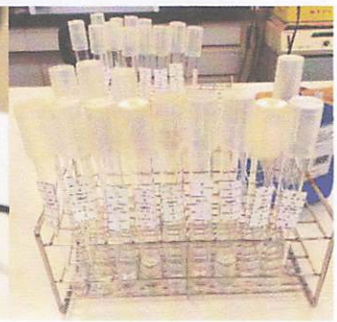

Figure 5. Dilution tubes for agar dilution method

Day 3: I began the day by preparing master mix, dilution tubes, and Petri dishes for the agar plate dilution assay. In the afternoon, I presented my PhD research to Usui sensei, Fukuda sensei, and Deepika san (PhD student). I appreciated the opportunity to engage in a productive discussion with them. During the session, Usui sensei posed questions related to One Health, which provided an excellent opportunity for me to practice critical thinking about this interdisciplinary concept. Following the presentation, Deepika san and I proceeded with the agar plate dilution and broth microdilution assays.

Day 4: I examined the plates from both assays and subsequently determined the MIC values. Also, Usui sensei provided a form for recording the results. In the afternoon, I continued with the metagenomic analysis; however, I was unable to complete the analysis that day and therefore planned to finish it on the final day.

Day 5: I presented the results of the MIC assays to Usui sensei, followed by a discussion about the findings. We also discussed strategies for plasmid reconstruction. As this work could not be completed that day, I planned to resume and finish it the following week. For the metagenomic analysis, I successfully completed the mock dataset. However, since it was an example, I recognized the need for more self-learning to further develop my understanding and strengthen my analytical skills.

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

Did you achieve all the goals you initially planned? If not, please describe why you failed to fulfill your objectives.

I was unable to complete the plasmid reconstruction during the scheduled activity. However, I plan to finalize it within one week, as the task involves dry-lab work and can be completed in my own computer at HU-IIZC. Usui sensei already provided the necessary documents and kindly explained the procedures to me. If I have any problems, he said I can email him to discuss them.

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.

One of the objectives of this activity is to learn how to analyze metagenomic data. This skill is particularly relevant to the One Health approach, as metagenomic analysis can reveal the presence of antimicrobial resistance genes and bacterial pathogens among the microbial community in complex environments shared by humans, animals, and ecosystems. After graduation, I plan to apply this approach in my future interdisciplinary research to investigate microbial dynamics and resistance transmission in agricultural and environmental settings. For example, metagenomic analysis can be used to monitor the microbiota of livestock and detect resistance patterns that may affect both animal and human health. It also offers insight into how resistance genes disseminate through environmental reservoirs, such as soil and water.

In addition, I aim to integrate phenotypic analysis, such as minimum inhibitory concentration (MIC) assays, with *in silico* metagenomic approaches to obtain a more comprehensive understanding of AMR in my country. The combination of these methods will provide a stronger evidence base for addressing AMR from both functional and genetic perspectives within the One Health framework.

備考 [Remarks]

※ 報告書を作成後、担当教員に確認をお願いし署名をもらってください。PDFファイルとしてVetlogから提出