Research Activity Report
Supported by "Leading Graduate Program in Primatology and Wildlife Science"

(Please be sure to submit this report after the trip that supported by PWS.)

	2017. 06. 30
Affiliation/Position	Wildlife Research Center/M1
Name	Moe Yanagi

1. Country/location of visit

Kyoto university, Kyoto. Japan

2. Research project

Genome science course

"The Diversity and Phylogeography of Mitochondrial DNA in Japanese Macaque (Macaca fuscata yakui) of Yakushima Island"

3. Date (departing from/returning to Japan)

2017.05.22- 2017.05.26 (5days)

4. Main host researcher and affiliation

Dr. Takushi Kishida, (Program-Specific Assistant Professor, Wildlife Research Centre of Kyoto University)

Kei Matsushima (lecturer)

5. Progress and results of your research/activity (You can attach extra pages if needed)

Please insert one or more pictures (to be publicly released). Below each picture, please provide a brief description.

During this genome science course, we conducted DNA analysis from fecal samples collected in Yakushima island. We investigated diversity and phylogeography of mitochondrial DNA of Japanese Macaque (*Macaca fuscata yakui*) of Yakushima Island. Finally, we prepared poster presentation for showing our result in The 6th International Seminar on Biodiversity and Evolution: Wildlife science by New Biologging studies. Our schedule was as follows :

2017/5/22-25: Extraction of DNA, PCR, Sequencing
2017/5/26: Analysis, preparation for poster presentation
2017/5/30: Poster presentation in international seminar

First, we extracted and purified mtDNA from fecal samples using QIAamp DNA stool mini kit (QIAGEN). We used nanodrop for estimating the concentration of the DNA per samples. Second, we used PCR for amplification of DNA. We confirmed the amplification by electrophoresis. Finally, we used a DNA sequencer to determine the sequence of mtDNA D-loop region. After all experiments, we analyzed the sequence using MEGA7, and prepared for poster presentation. We compared the result of distribution of each haplotype with the result of previous research (Hayashi and Kawamoto, 2006), in addition, we analyzed the relationship between success rate of experiments and condition of fecal samples, and the weather when we collected the samples.

As a result, we detected one of the haplotype which previously reported in higher elevation area in Yakushima. This is the first time to detect minor haplotype group in this area. It might suggest the expansion of this haplotype group. We need to confirm it by more surveys because we have few samples in this time, however, it is important information for conservation of genetic diversity for *Macaca fuscata yakui* in Yakushima.
Moreover, we found the success rate of DNA analysis were significantly related to the freshness of fecal samples. We had sunny days and a rainy day for collecting fecal samples, but it was not significantly related with success rate.

I was able to learn basic knowledge about DNA analysis from fecal samples of wildlife in this course. This was so useful time for me because I would like to conduct DNA analysis from fecal samples of wildlife too. It was great to have a kind lecturer and good members in this study. It was also memorable day of the presentation in the seminar.
These experiences must help my research in the future. Thank you so much.

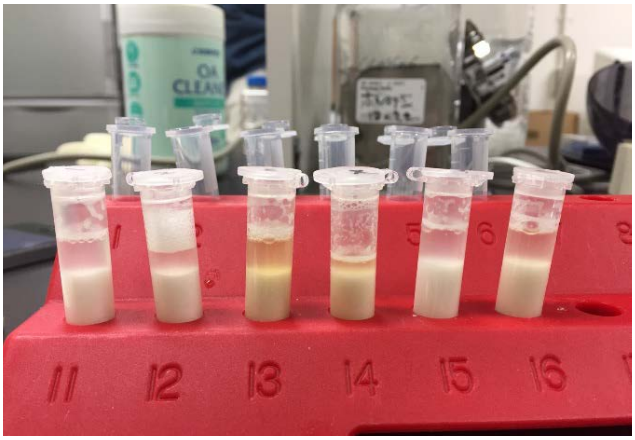

Fig 1. Extraction of DNA

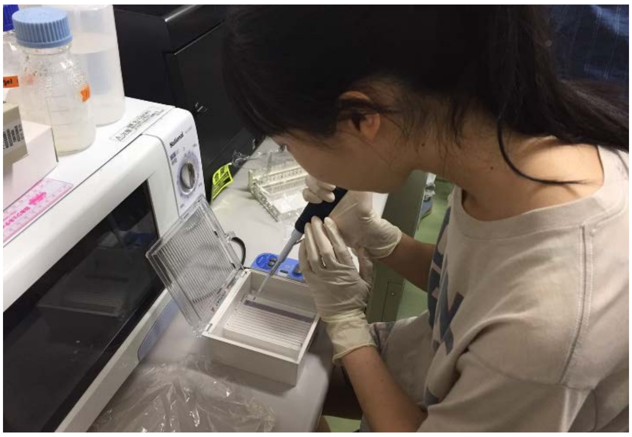

Fig 2. Electrophoresis

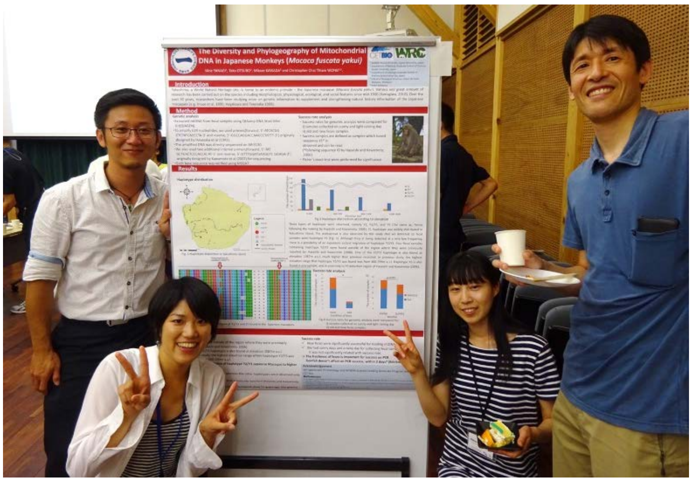

Fig 3. Poster presentation

6. Others

This science course was financially supported by the PWS leading graduate program, and the CET- Bio project. I appreciate to them for providing me this opportunity. I would also like to express my gratitude to all the lecturers, staffs and my team members.