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.)

	2015.7.7
Affiliation/Position	Bioinformatics Center/M1
Name	Genki Yoshikawa

1. Country/location of visit

Kyoto University

2. Research project

Genome Science Course (Mushroom)

3. Date (departing from/returning to Japan)

2015.6.2 – 2015.6.8 (5days)

4. Main host researcher and affiliation

Dr. Fuse and Dr. Satoh, Kyoto University

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.

In Genome Science Course, we learned the techniques of sequencing and the species identification using DNA.

For each mushroom sample that was collected at Yakushima, we amplified the ITS2 region by PCR. The ITS region is DNA barcode marker for Fungi. We performed cycle sequencing on the PCR products and ran sequencer. Then, we constructed accumulation curve and bipartite graph. Each sequence were classified using BLAST search and Cladient, and species were identified. At the end of the course, these results were presented using poster at the international seminar.

Through this experience, I am able to learn the process of using the database from the actual sample. This learning will be of great help in the future my research.

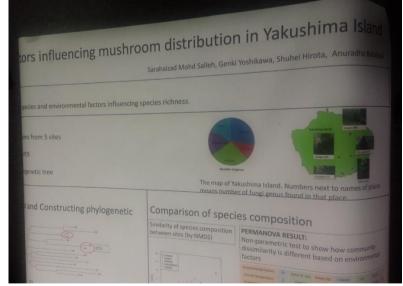


Figure. Poster used in a presentation

6. Others

I am grateful to Dr. Sato, Dr. Fuse, and everyone who helped me in this course.

Submit to: report@wildlife-science.org 2014.05.27 version