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.)

	2019. 7 10
Affiliation/Position	University of Science /PhD student
Name	Muhammad Afif bin Yusof

1. Country/location of visit

Japan, Kyoto

2. Research project

Genome Science Course

3. Date (departing from/returning to Japan)

2019. 6. 3 – 2019. 6. 7 (5 days)

4. Main host researcher and affiliation

Dr. Miho Murayama, Professor at Wildlife Research Center, 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.

During this course, our group that consists of 6 people had conducted molecular labwork on genotyping of Yakushima's macaques faecal samples based on microsatellite data. By the end of this course, we have identified the sex of the collected faecal samples of Yakushima's macaques and several analyses were done.

First to Third Day of Lab work
The DNAs from the faecal samples were extracted and certain region of X and Y chromosomes were amplified. Then, the PCR amplification was done and the agarose gel electrophoresis was prepared for the sequencing which has been instructed by Murayama-sensei and her lab members.

Fourth to Fifth Day, Data Analysis and Poster making
The DNA bands for certain X and Y choromosome from the agarose gel electrophoresis was observed in order to determine the sex of Japanese macaques. From 39 samples, we only managed to determine the sex of 32 samples, 17 males (2 DNA band, with the length of each band 445 and 221 bp) and 15 female (1 DNA band, with length 445 bp), while the rest of them were unidentified because of lacks of DNA band and some of them have only the shorter band that was counted during the observation. Then, 10-microsatellite out of 16 having success rates more than 50% were selected for the GeneCap (individual identification) and GenAlEx 6 software (genetic diversity) for analysis. From the initial analysis result, we could only use 24 samples out of 39 that had succes rate above 50%. The further analysis showed that the samples exhibit random mating based on inbreed cofficient and some markers have P-value <0.05 due to allelic dropout event. As for relationship analysis, no results could be yielded due to insufficient data. It is advisible to add more number of polymorphic microsatellite markers in the future. The poster for CETBio Seminar was prepared after all the analysis were done later on that day.

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Through this experience, my laboratorium experience was enriched specifically in genotyping work and the statistical analysis and I could meet and interact with other people from different countries, have conversation about many things, like the culture in our country.

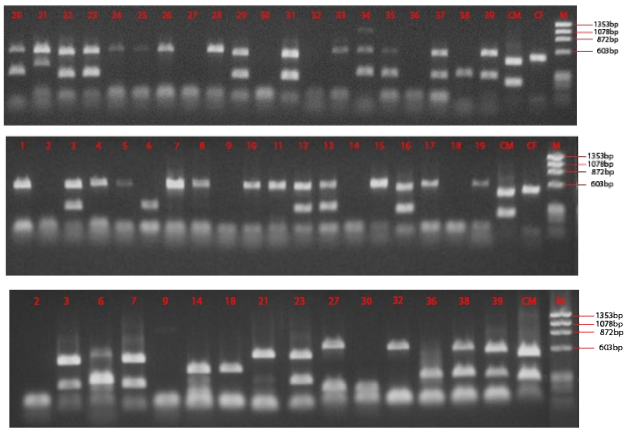

Fig. 1 Agarose gel electrophoresis reult for sex identification

Fig. 2 Group's discussion in analysing microsatellite genotyping data

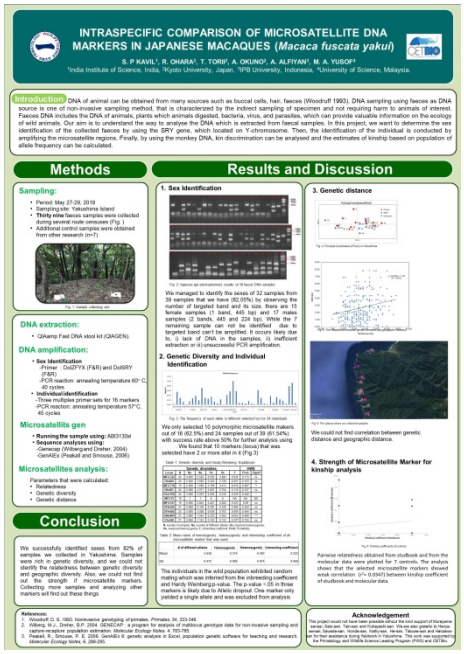

Fig 3. Poster for the presentation during seminar

6. Others

I would like express my gratitude to Dr. Miho Murayama, Dr. Sato, Mr. Taki, Mrs. Kobayashi and Ms. Sai, for sharing their knowledge, guidance and expertise during this course. This course was only made possible with financial support from PWS and WRC, Kyoto University. Thank you