

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 2

Affiliation/Position	IPB University /M2
Name	Achmad Alfyan

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.
<p>During this course, me and some other students conducted research on genotyping the Yakushima’s macaques based on microsatellite data. Our team used this opportunity identifying sex of Yakushima’s macaque samples from the faecal samples and do some kinship analysis.</p> <p>First to Third Day, Lab work</p> <p>We extracted Yakushima’s macaque DNA from faecal samples, amplified certain region of X and Y chromosome and also amplified some microsatellites, did agarose gel electrophoresis (for X and Y PCR result) and micarosatellite genotyping (for microsatellite PCR result) accompanied by Murayama-sensei and other member of her lab.</p> <p>Fourth to Fifth Day, Data Analysis and Poster making</p> <p>We observed the DNA band of certain region of X and Y chromosome (identifying sex of Yakushima’s macaque) and the chromatogram of the microsatellite data. Sex identifying was done by observing the number of DNA band and its size in the agarose gel, from 39 sample we could only determined 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 lenght 445 bp), while 7 remaining were unidentified (no DNA band or only the shorter band that was observed). Microsatellite data was analyzed using GeneCap (for individual identification) and GeneAlex (for genetic diversity ananalysis) software. From the initial analysis result we could only use 24 samples out of 39 and 10 microsatellite markers out of 16 for further analysis due to this samples and markers had succes rate above 50%, 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, we could not do that due to insufficient data, we needed to add more number of polymorphic microsatellite markers. Beside we did analysis we also prepared the poster for CETBio Seminar.</p>

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.)

Through this experience, my laboratory 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.

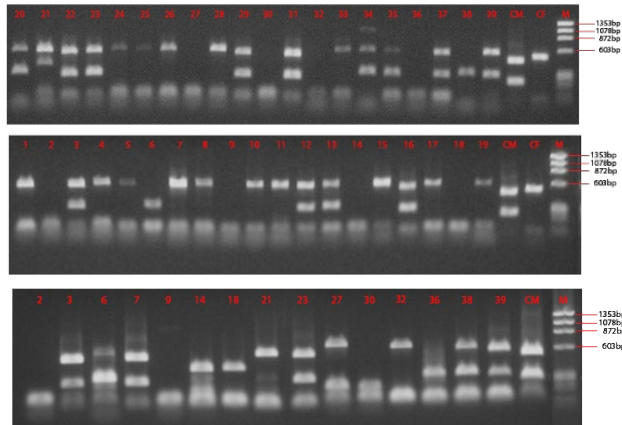


Fig. 1 Agarose gel electrophoresis result for sex identification

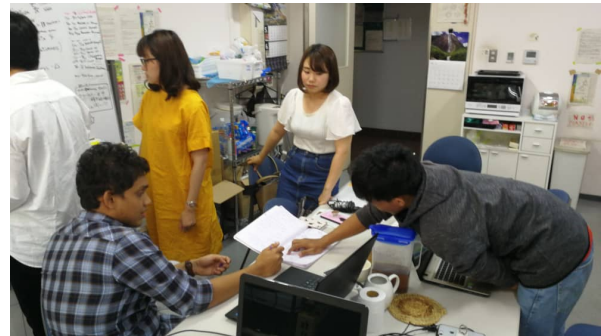


Fig. 2 Group's discussion in analysing microsatellite genotyping data

6. Others

I would like to thank Dr. Miho Murayama, Dr. Sato, Mr. Taki, Mrs. Kobayashi and Ms. Sai, for sharing their knowledge and also their guidance during this course. And also I would like to thank to PWS for organizing and supporting the Genome Science Course.