

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 CETbio, PWS.)

2018. 12, 11	
Affiliation/Position	Bogor Agricultural University/M2
Name	Vinna Windy Putri
1. Country/location of visit	
Japan, Primate Research Institute, Inuyama.	
2. Research project	
Genome Science Course	
3. Date (departing from/returning to Japan)	
2018. Nov. 12 – 2018. Nov. 16 (5 days)	
4. Main host researcher and affiliation	
Dr. Kishida: Wildlife Research Center.	
Dr. Hayakawa: Primate Research Institute.	
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 the Genome Course, we analyzed the fecal sample from Yakushima Field Course Fall 2018. We performed DNA extraction from the fecal samples which is quite new for me since I’m usually extracting DNA from tissue samples. We amplified the D-loop region from mtDNA using specific primers for monkey and deer. The final labwork step is sequencing the DNA target using Sanger’s dideoxy sequencing method. We were able to obtain good sequence data from both monkey and deer. We analyzed the sequence data using MEGA, DNASP, and NETWORK. From our result, we found three haplotypes from six Japanese Macaques haplotypes in Yakushima. We found slight changes in Japanese macaque haplotype distribution compared to the data from 16 years ago. As for deer, since there’s not many study about Yaku-sika deer genetics, so we focused on the Yaku-sika deer haplotype distribution in Yakushima in the present.</p>	
6. Acknowledgement	
<p>I would like to thank Dr. Kishida, Dr. Hayakawa and Ms. Yan for sharing their knowledge during this course. I also would like to thank PWS for organizing and supporting the Genome Science Course.</p>	