

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.)

2018 NOV 28	
Affiliation/Position	Wildlife Research Center/M1
Name	Annegret Moto Naito
1. Country/location of visit	
Kyoto University Primate Research Institute, Aichi Prefecture	
2. Research project	
Inuyama genome course	
3. Date (departing from/returning to Japan)	
2018. NOV. 12 – 2018. NOV. 16 (5 days)	
4. Main host researcher and affiliation	
Dr. Hayakawa (PRI), Dr. Kishida (WRC)	
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>In mid-November, I participated in the genome field course at the Primate Research Institute as a part of the PWS program, together with 7 other students from Kyoto University and abroad (from the CET Bio program).</p> <p>During this course, we analyzed the fecal samples obtained in Yakushima the week before. We extracted DNA from each Japanese macaque and Yakushima sika deer sample, amplified (PCR) and sequenced the mitochondrial control region. Most samples yielded satisfactory/decent results, despite some fecal samples being slightly old or run over by vehicles, etc, and we were able to use the sequences for further analysis. After completing the laboratory work, we performed phylogenetic and population genetic analysis in software including MEGA and DNAsp. Specifically, for the Japanese macaques, we compared the distribution of haplotypes on Yakushima Island to data collected 16 years ago, in hopes to track movements of haplotypes over time. For sika deer, very little genetic research has been done especially in Yakushima, so instead of tracking changes in haplotype distribution over time, we focused on their phylogeography. We decided to compare the sequences of Yakushima sika deer to those of neighbouring islands and Kyushu to see how different their sequences are. I was mostly involved in analyzing the deer data, and it was very interesting to learn about the biogeographic history of this species and how it was reflected in their mtDNA sequences.</p> <p>When we had spare time, people who had analyzed deer vocalizations in Yakushima continued to work on this analysis as well, so it was a busy but fruitful week of research.</p> <p>The results from these analyses were presented at the 9th International Seminar on Biodiversity and Evolution in Kyoto. I took part in preparing 3 posters, and it was very rewarding to share our research from an intense two-week field and lab work.</p>	
6. Acknowledgements	
I thank Dr. Hayakawa, Dr. Kishida, Dr. Sugiura, Ms. Agetsuma, and Ms. Yan for their guidance and support. I am indebted to PWS for organizing and funding this trip.	