Research Activity Report
Supported by "Leading Graduate Program in Primatology and Wildlife Science"

	2018. 6. 9
Affiliation/Position	Wildlife Research Center (D1)
Name	Kristin Havercamp

1. Country/location of visit

Wildlife Research Center, Kyoto, Japan

2. Research project

PWS Genome Science Course

3. Date (departing from/returning to Japan)

2018. 5. 28 – 2018. 6. 1 (5 days)

4. Main host researcher and affiliation

Murayama-sensei, Kobayashi-san & Sato-san; WRC, 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.

The goal of the Genome Course was to learn how to analyze DNA extracted from fecal samples we collected in Yakushima. First we conducted sex identification of our samples, then we surveyed the catechol-O-methyltransferase (*COMT*) gene. This is a candidate gene which may affect the behavior of Japanese macaques; some populations are despotic while others are egalitarian. *COMT* gene is associated with aggressive traits in humans and macaque carriers of haplotype 3 (HT3; C-T) show higher cortisol excretion, which may affect aggressive behavior. We compared the allele frequency of macaques in Yakushima with other populations (Shodoshima, Koshima & Kinkazan). Our results showed that HT4 (T-T) exists only in the Shodoshima population, thus confirming that this population contains a unique composition of haplotypes. We also showed that HT3 (C-T) frequency was highest in Kinkazan. However, more behavioral and/or hormonal data are needed, as well as samples, for future investigations.

Day 1 (5/28)
We extracted DNA from fecal samples, ran PCR amplification for sexing and sequencing and prepared the agarose gel.

Day 2 (5/29)
We ran the agarose gel electrophoresis and were able to successfully identify the sex of less than half of our samples, so we decided to re-do it to check our results. We also prepared and sequenced the samples.

Day 3 (5/30)
We analyzed our sequence data and found that it was not very successful, so we re-sequenced in hopes that we could get a better result. We also prepared the samples from the other monkey group (#2) because we wanted to obtain a larger sample size that covered our entire sampling efforts in Yakushima.

Day 4 (5/31)
Our sequencing results were successful, so we moved on to sequence the samples from monkey group 2.

Day 5 (6/1)
We analyzed our sequence data from monkey group 2 samples and began to interpret our results and create our poster.

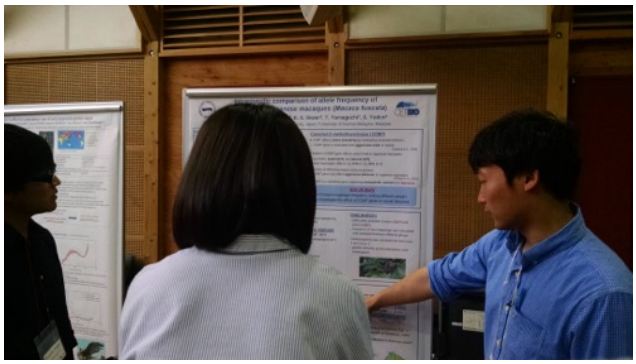
Day 6-8 (6/2-4)
We met to continue to analyze and interpret our results and create the poster for the international seminar.

Day 9 (6/5)
We presented our work at the 8th International Seminar on Biodiversity and Evolution: Wildlife Science by Environmental DNA Analysis.

During this course I learned how to extract DNA from fecal samples, run agarose gel electrophoresis to identify the sex

of unknown (individual) samples, conduct PCR amplification and run the 3130xl sequencer Genetic analyzer, and finally use FinchTV to analyze the data from the sequencer. I really enjoyed working in the laboratory and continuing to collaborate with other students and the visiting CETBio international researchers, as well as getting the chance to learn from Murayama-sensei, Kobayashi-san and Sato-san.

Elan presenting at the seminar.



山口様 explaining our poster.

6. Others

I am thankful to PWS for providing me with the opportunity to participate in the Genome Course, to Murayama-sensei, Kobayashi-san and Sato-san for all their (much needed!) support throughout the week and to the other students in "monkey group 1".