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.)

	2016. 6, 29
Affiliation/Position	Primate Research Institute/M1
Name	Akito TOGE

1. Country/location of visit

Kyoto

2. Research project

Genome Science Course

3. Date (departing from/returning to Japan)

2016. 05. 30 – 2016. 06. 07 (7 days)

4. Main host researcher and affiliation

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.

This is a schedule of Genome Science Course (Deer team, which I belonged to).

5/30 DNA extraction, PCR amplification
5/31 electrophoresis (for sexing), DNA extraction, PCR amplification
6/1 electrophoresis (for sexing), PCR product clean-up
6/2 PCR product clean-up, Running the samples using ABI3130x
6/3 Analyzing sequence data
(6/4 – 6/5 holidays)
6/6 preparation for poster presentation
6/7 poster presentation (International seminar)

We aimed to understand the way to analyze the DNA which is extracted from fecal samples. We conducted sex identification and mitochondrial haplotype identification.

(1)Sex identification
We used the region in the Amelogenin gene, which is located on sex chromosome and the length of which is different between X and Y chromosomes. In this region, male samples yield around 165 and 219 bands, while female ones yield 219 band only.
(2)Mitochondrial haplotype identification
We amplified the mitochondrial control region (D-loop) which sequence is highly polymorphic. We ran the samples using ABI3131x.

【Results】
(1) Sex identification
We used 47 fecal samples, and 2 samples mismatched the results using genetic marker with the observation data. These 2 feces were both collected from young deer, so sexing according to observation were probably wrong.
(2)Mitochondrial haplotype identification
We used 52 fecal samples, and we can't read the sequences from 3 fecal samples. From them, we identified the haplotypes of 45 individuals, but we can't identified clearly 4 ones. The haplotype which the most sika deer in Yakushima Island have is Type1 (38 individuals). Type2 is the second most haplotype (5 individuals). We found one individual of Type7 and 8 respectively.

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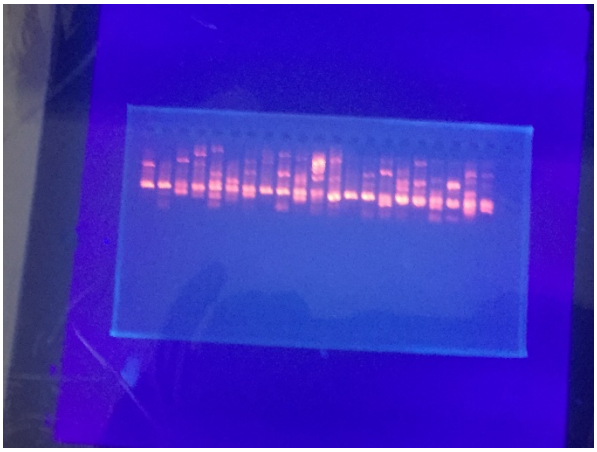
Through this course, I learned the way to extract DNA from fecal samples and to handle the extracted DNA. This was my first time to analyze the sequence data, but I understood how to do. In my research, I will analyze DNA sequences from fecal samples, so this course is very useful for me. I want to put this experience to good use.

Lab-work



electrophoresis

Group-photo (Deer team)

6. Others

This course was supported by PWS program. I appreciate it.