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.)

	2017. July, 5
Affiliation/Position	Primate Research Institute/M1
Name	Shohei Shibata

1. Country/location of visit

Primate Research Institute, Inuyama, Japan

2. Research project

Genome Science Course

3. Date (departing from/returning to Japan)

2017 May 22 – 2017 May 26

4. Main host researcher and affiliation

Dr. Takashi Hayakawa, Dr. Munehiro Okamoto and Mr. Akito Toge, Primate Research Institute, 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.

Following the Field Science Course, I had the opportunity to attend the Genome Science Course. During this course, we analyzed DNA sequence of ticks collected in the field course.

May 22: DNA extraction
May 23: PCR amplification, Electrophoresis
May 24: PCR amplification, Electrophoresis, Running the DNA Sequencer(Failed)
May 25: PCR amplification, Running the DNA Sequencer
May 26: Data analysis and preparation for poster presentation
May 30: Poster presentation (CETBio)

Obtaining DNA sequences
First, we extracted DNA from ecto-parasite samples collected in the field course. Second, we amplified the DNA by using polymerase chain reaction (PCR). The result of PCR was confirmed by electrophoresis. After that, we purified the PCR products. Finally, we obtained the DNA sequences using purified PCR products by running the sequencer.

Bioinformatics analysis
We analyzed the sequencing product by using FinchTV and MEGA7. First, we corrected and integrated each forward and reverse sequence of the samples to build the sequence without impurities by using FinchTV. Next, we compared sequences with reference sequences from NCBI by the alignment function in MEGA7. Finally, we constructed a phylogenetic tree by using the Neighbour-Joining method in MEGA7. The phylogenetic tree suggested that ticks we collected in field course are classified in three species. There is the possibility that one of them is a new species.

Presentation
We integrated the results of this course with that of the field course and made a poster and presented our results at the CETBio 6th International Seminar on Biodiversity and Evolution.

Through this course, I learned the difficulties of DNA analysis without issue. We failed to obtain the DNA sequences once, so we repeated the PCR amplification and running the sequencer. This process was very time consuming. However, I could also learn how DNA analysis is effective. I am glad for this learning opportunity.

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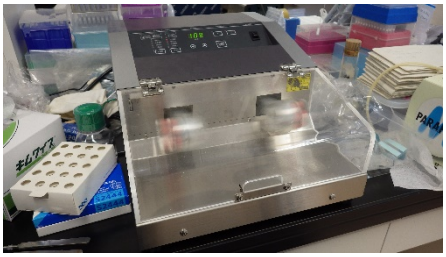
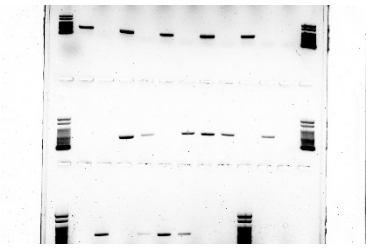
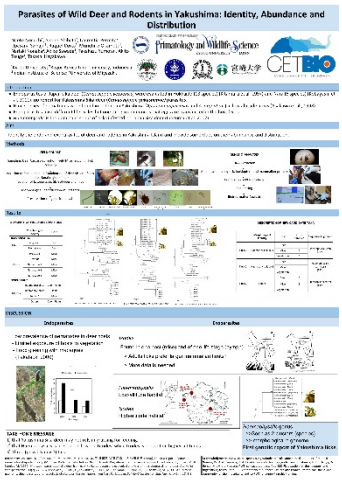
Cutting tick sample



Smashing samples



Result of electrophoresis



Presentation Poster

6. Others

I would like to thank the PWS program for supporting this course..

I also would like to express my appreciation to Lecturers of Parasite Group.