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.)

	2015. 06, 29
Affiliation/Position	Universiti Malaysia Sabah/Ph.D candidate
Name	Esther Lonnie Baking

1. Country/locationof visit

Kyoto University, Japan

2. Research project

Genome Science Course

3. Date (departing from/returning to Japan)

1st of June 2015 to 5th of June 2015 (5 days)

4. Main host researcher and affiliation

Dr. Eiji Inoue (Kyoto Unviversity)

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 abrief

The Genome Course was conducted after the Yakushima field course in the laboratory at Kyoto University from 1st until 5th of June 2015. We analysed 44 DNA samples of deer feces that succesfully collected from Yakushima. This course was led by Dr. Inoue and assisted by Mr. Tajima and Mr. Yokoyama. The purpose of this course was to understand the way to analyze the DNA which is extracted from fecal samples focusing on sex identification, individual identification and kin discrimination using deer DNA.

At first, I was quite nervous to conduct laboratory work as I don't have such good experience of working in the lab. I also did not familiar with the machines, the protocols, buffers and other lab materials for genetic study purpose. However, with the help and motivation from other members of Deer team as well as getting clear instructions and explanation from Dr. Inoue, I managed to get through all the procedures smoothly.

During this course, we first did the DNA extraction from the samples of feces and proceeded to PCR amplification for sex identification and also individual identification for deer. For the deer samples, we amplified 16 microsatellite loci for the microsatellite information. Here, I have learned how to read the result from electrophoresis and was able to identify sex from the analyzed DNA samples. We have also run the genotyping protocols and determine the alleles using the Peak Scanner software. The genotypes data were entered into excel sheet with GenAlEx format and we calculated kinship of each identity of individuals.

As a result, we have ultimately reached our first objective of using DNA from fecal samples for individual identification. The DNA analyses went well and successfully enable us to identify individuals from all samples. We can also conclude that the higher and longer period of exposure of rain and ultraviolet rays, the lower success for the DNA extraction. We also found that the relationships among individuals from the DNA analysis are similar with the estimated relationships from our observations of behaviours in the

field.

In general, I learned many new things during this Genome Course. Though it seemed hard and I faced some difficulties during the course, I could say that studying a particular wildlife involving fieldwork and genetic research would be much more interesting as we could get different experiences and gain wider knowledge.

Photo 1: Putting primer into the agarose gel before the PCR amplification (photo by Kotoyo).

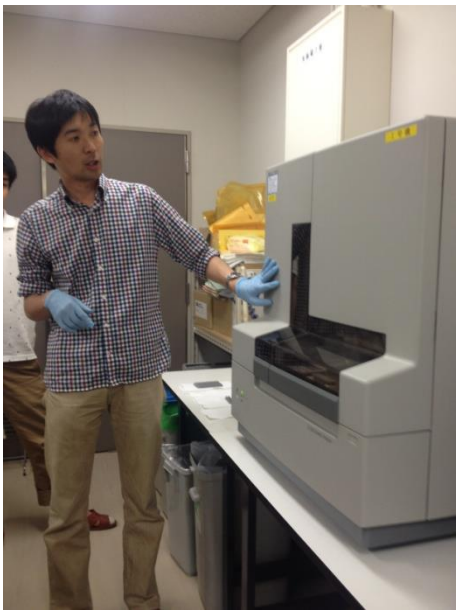

Photo 2: Dr. Inoue is briefing about the DNA sequencer.

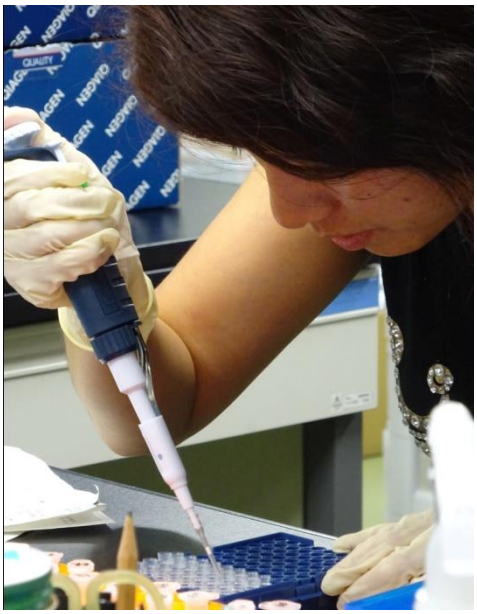

Photo 3: Carefully filling DNA samples in the 96 well plate.

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6. Others
Thank you very much to Wildlife Research Centre as the organizer of this course, Prof. Shiro Koshima, Dr. Sugiura, Dr. Agetsuma, Dr. Yoshimi, Dr. Inoue and not forgetting my own supervisor, Assoc. Prof Dr. Henry Bernard (UMS) for choosing me to participate this course.