

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.)

	2014. 06. 15
Affiliation/Position	Institute for Tropical Biology and Conservation Universiti Malaysia Sabah / Master student
Name	Sabilah binti Tahir

1. Country/location of visit	Japan, Kyoto
2. Research project	Study on Plant (Ferns – DNA analysis for the gametophytes collected in Yakushima Island)
3. Date (departing from/returning to Japan)	2014. 05. 11 – 2014. 06. 13 (33days)
4. Main host researcher and affiliation	Dr. Shizuka Fuse (Professor at Kyoto University), Dr. Hirotooshi Sato (Professor at Kyoto University) and Dr. Wataru Shinohara (Professor at Kagawa University)
5. Progress and results of your research/activity (You can attach extra pages if needed)	<p>Please insert one or more pictures (to be publicly released). Below each picture, please provide a brief description.</p> <p>During this visit, I was involved in conducting research on “Plant Group” which focusing on the diversity of ferns in Yakushima Island. We have collected large amount of gametophytes especially from the third sampling sites which were at the Hanaage river basin. During the genome training course, our group was supervised by Dr. Sato, Dr. Fuse and also Dr. Shinohara. We learnt how to identify the species of fern-prothallia that were collected in Yakushima Island by using DNA barcoding technique. This was done by using a short standardized DNA sequence (a sequence of chloroplast <i>rbcL</i> gene). This technique is useful for identifying species of an organism that found from the environment. For most fern species in Japan, reference barcode sequences are available from the online DNA database. We learnt many process in DNA analysis included the DNA extraction, PCR, Electrophoresis, Purification of PCR products, Cycle Sequencing and also the application of samples to genetic analyzer. At the end of the process, we were very excited to have the most endangered and endemic species of fern which is the <i>Haplopteris yakushimensis</i> and this meant that our goal has been succeeded. From the 48 samples of gametophytes being analyzed, only 38 DNA sequence obtained. We identified 7 species and 9 genera. A total of 4 gametophyte samples were identified as <i>Haplopteris forrestiana</i> which could be the <i>Haplopteris yakushimensis</i>, the recently reported new and endangered species endemic to Yakushima Island. We also found 1 sample of <i>Haplopteris sp.</i> that had three different base pairs from the possible <i>Haplopteris yakushimensis</i>, which could be the other or new species closely related to <i>Haplopteris yakushimensis</i>.</p>

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Fig 1: Electrophoresis machine used in the genome training course

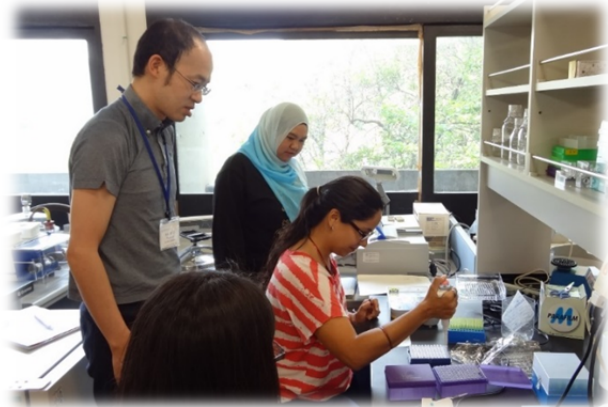


Fig 2: Students performing the electrophoresis procedure which was supervised by Dr. Sato

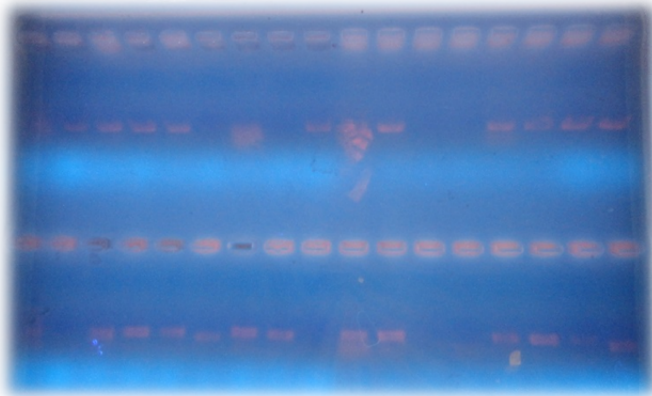


Fig 3(above) Fig 4 (below) :
The appearance of the DNA band from different primer on the agarose gel.

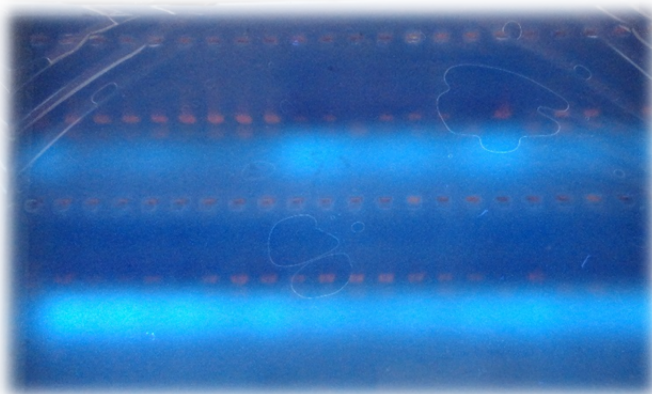


Fig 5 : Students performing the DNA barcode sequences which were available from the online DNA database

6. Others

We also had 1 day class/ lecture with Prof. Dr. Akifumi S. Tanabe for the Sequence processing by using the LINUX. This is mainly very useful for the metagenome course.