

**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, 14
<b>Affiliation/Position</b>	Universiti Sains Malaysia
<b>Name</b>	Nur Munira Azman

<b>1. Country/location of visit</b>
Kyoto University, Japan
<b>2. Research project</b>
Study on insect DNA sequencing by using Sanger-sequencing technology.
<b>3. Date (departing from/returning to Japan)</b>
2014. 05. 29 – 2014. 06. 05 (8 days)
<b>4. Main host researcher and affiliation</b>
<ol style="list-style-type: none"> <li>1. Professor Teiji Sota (Zoology Department, Kyoto University)</li> <li>2. Professor Okamoto (Zoology Department, Kyoto University)</li> <li>3. Professor Munehiro Okamoto (Primate Research Institute, Kyoto University)</li> </ol>
<b>5. Progress and results of your research/activity</b> (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.
<p>During genome training course, I was in the insect DNA sequencing team. I chose this team because I want to learn basic DNA sequencing since this is my first experience to do the DNA sequencing. In Kyoto University, we start to analyse DNA sample from insect specimens. I'm very excited to learn to DNA sequencing because everything is new for me. Basically, insect DNA sequencing involved three main steps. First extraction of total genomic DNA using QIAGEN DNeasy, followed by PCR-amplification of barcoding sequence (mitochondrial COI gene region) and the last step was Dye-terminator reaction and sequencing.</p> <p>Through this experience, I have developed my skill on how to do insect DNA sequencing. I also had a chance to try many advanced equipments such as multi-pipet and latest version of PCR machine. As far as what I know, according to friend of mine who study on microbiology in our university, she told me multi-pipet is very expensive and we can't afford to buy them for our laboratory. Thus, this was an excellent opportunity for me to get exposed on various advance techniques and equipments.</p> <p>After the sequencing is done, I have been taught how to match the DNA sequences with sequence databases by using BLAST. This program helps to compare nucleotide or protein sequences to sequence databases and calculates the statistical significance of matches. Finally we were able to identify members of gene families. I also have been taught how to generate phylogenic tree by using Mega6 software. We also produced a phylogenic tree which combines insect DNA sequencing data with insect metagenome group in order to identify the insects that contain in monkey feces which are probably ate by monkey.</p> <p>I also enjoyed the series of lectures by Prof. Tanabe and Dr. Kohmei. I also met Dr. Kohmei personally during free time activity to discuss about my project and he help me by suggesting several analysis for my PhD. Project.</p> <p>I would like to thank to all Professors, friends from Japan, Malaysia, Brazil, Tanzania and India which involved in this course. Million thanks to Professor Sota, Professor Okamoto, Professor Munehiro Okamoto and post-doc who really work hard to teach and help us during this training.</p>

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Figure 1: My team members and Professors during the training course

**6. Others**