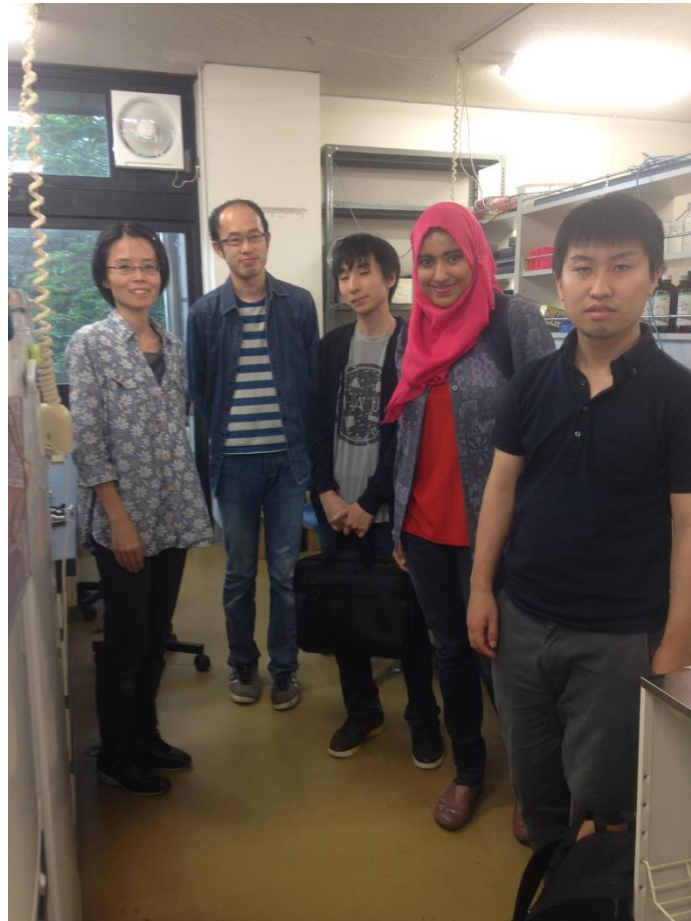


**Research Activity Report**  
**Supported by “Leading Graduate Program in Primatology and Wildlife Science”**  
 (Please be sure to submit this report after the trip that supported by PWS.)

	2015. 06, 19
<b>Affiliation/Position</b>	School of Biological Sciences, Universiti Sains Malaysia (Ph.D candidate)
<b>Name</b>	Sarahaizad Mohd Salleh

<b>1. Country/location of visit</b>
Kyoto University, Japan
<b>2. Research project</b>
Genome training course of mushroom species in Yakushima Island, Japan.
<b>3. Date (departing from/returning to Japan)</b>
2015.05.14 – 2015.06.15 (32 days)
<b>4. Main host researcher and affiliation</b>
Dr. Hirotooshi Sato (CER Kyoto University)
<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>The genome mushroom course was held at North Campus, Kyoto University from June, 2 until June, 8 2015. During this visit, I choose to participate in genome training course of mushroom species. It was my first experience conducting a genome training course, thus, I’m very excited since I know it will give me a new knowledge and new exposure which will gives benefits in my future project. I’ve been taught on how to extract DNA mushroom species using the specific chemicals and advanced equipment which is totally new for me. For example: using a pipetman, running the latest version of PCR machine, and electrophoresis machine.</p> <p>Since I’m inexperience in genome course, the lecturer, Sato-san has teaches me patiently in detail on how to cut the mushroom sample and running the further methods in extracting the mushroom’s DNA. During the course, we analyze 96 mushrooms samples, which have been collected in Yakushima Island previously. The procedures that I’ve learn in extracting the mushroom species involved:</p> <ol style="list-style-type: none"> <li>1. Procedure for DNA extraction</li> <li>2. Reagent used for DNA extraction</li> <li>3. Procedure for PCR</li> <li>4. Procedure for electrophoresis</li> <li>5. Procedure for purifying PCR products</li> <li>6. Procedure for cycle sequencing</li> <li>7. Procedure for denature of cycle sequencing products.</li> </ol> <p>In addition, I’ve been exposed to Mega6 software, R packages software, BLAST search, and BLAST using Claident. All this software in new for me and I found that the softwares are important in analyzing the mushroom DNA sequences. During DNA sequence analyzing, I’ve been taught on how to cut and trim the DNA sequences manually and how to generate the phylogenetic tree using Mega6 software. I also had been taught on how to match the DNA sequences database by using BLAST search, which helps compares the nucleotide or protein sequence to sequence database and calculate the significant matches. I’ve also been taught to identify cryptic species using R packages software, and identifying species not represented in International Nucleotide Sequence Database (INSD) using a BLAST using Claident.</p> <p>Through this experience, I’ve developed a clear vision and knowledge on genome analysis, which will be of great help, in my future conservation of sea turtle project in Malaysia.</p> <p>In conclusion, I’m totally satisfied with this one-week genome course due to the input that I’ve learn is highly valuable.</p>
<b>6. Others</b>
I would like to send my gratitude to Dr. Takaya Iwasaki, Dr. Hirotooshi Sato, Yoriko Sugiyama, and Yuki Matsutani for helping me during mushroom field science course in Yakushima Island. Meanwhile, thanks to WRC staffs for organizing my personal training with Dr. Hideoki Nishizawa, who helps in giving the positive comments and suggestion regarding the Ph.D project based on sea turtles.

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The mushroom team members with Dr. Hirotohi Sato (second from left) during genome mushroom training course.