

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. 02	
Affiliation/Position	University Malaysia Sabah/ Graduate student
Name	Nurul Ain Mohd Sharif
1. Country/location of visit	
Wildlife Research Centre, Kyoto University, Japan	
2. Research project	
Sex identification and haplotype identification from fecal samples of sika deers	
3. Date (departing from/returning to Japan)	
30.5.2016 to 3.6.2016 (7 days)	
4. Main host researcher and affiliation	
Miho Inoue-Murayama (Professor, Wildlife Research Center of 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.	
<p>As I was in deer team during Yakushima field course, I also part of deer team for genome course. For this genome course, we used the fecal samples collected from our field work. There were three objectives we tried to achieved from this course:</p> <ol style="list-style-type: none"> 1. To identify the sex using genetic markers and genotype mitochondrial haplotype from non-invasive samples. 2. To analyse relationship between social interactions and mitochondrial types. 3. To measure rate of successful sequencing mitochondrial DNA from fecal samples under various conditions. <p>On our first day, we were divided into three smaller groups which consist of three to four people which assist by two instructors. We started with DNA extraction of fecal samples and doing the PCR amplification and agarose gel preparation. In second day, we viewed our PCR product under gel electrophoresis, however no band was detected. Thus, we did another trial and repeat the procedure using other fecal samples. After we obtained the band, the product was selected for sequencing. We repeated this step until 4th day. On our last day of genome course, we analysed the data using MEGA 7 software for haplotype identification. The results from this Yakushima field work and genome course were combined and will be presented at International Seminar on Biodiversity and Evolution on 7th June 2016.</p> <p>From this course, I've learned how to analyse the samples from non-invasive samples which was different from my previous study where I get the samples from tissue of the crabs. This fecal technique are useful and should be used widely to avoid threatened or harm the animals.</p>	

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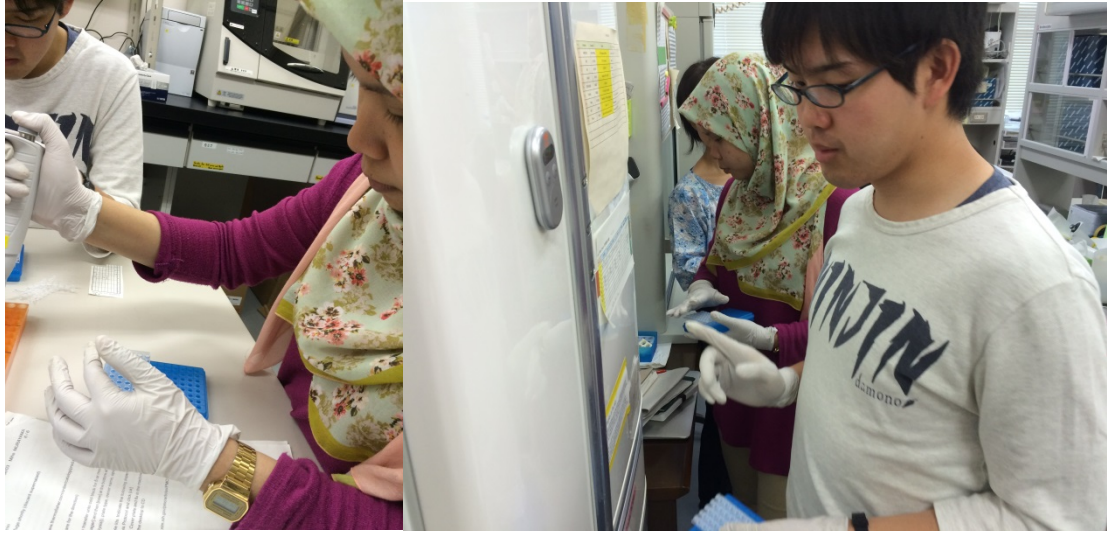


Figure 1: Genome course

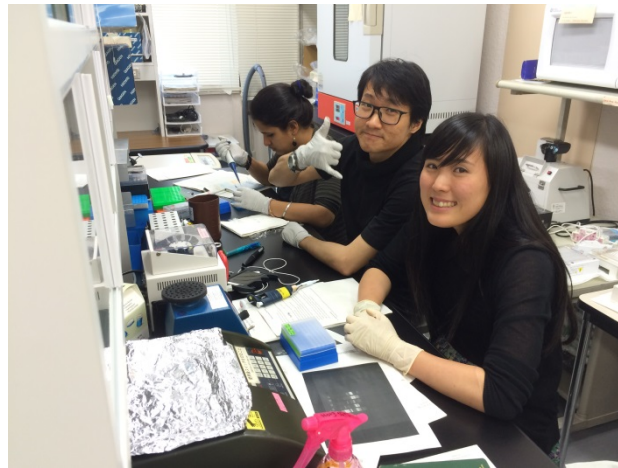


Figure 2: Other deer team members for genome course

6. Others

I would like to thank Murayama sensei, staffs and graduate students for helping me during this course. Thank you.