Research Activity Report
Supported by "Leading Graduate Program in Primatology and Wildlife Science"

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Affiliation/Position	Science Officer, School of Biological Sciences, Universiti Sains Malaysia
Name	Mohd Abdul Muin Md Akil

1. Country/location of visit

Kyoto University, Japan.

2. Research project

Genome Training Course

3. Date (departing from/returning to Japan)

2014.05.29 – 2014.06.05

4. Main host researcher and affiliation

Professor at Shiro Koshima, Wildlife Research Centre, Kyoto University

5. Progress and results of your research/activity

Genome training course 2014 was held for 8 days. This training requires each personnel to choose one among a few titles of genome course prepared by the instructor, in accordance to their level of experience with genome research. The course namely are:

Next Generation Sequencing (Medium to expert level)

1. Monkey host genome
2. Insect genome
3. Plant Genome
4. Gut microbiota

Sanger Direct Sequencing (Beginner level)

1. Plant DNA
2. Insect DNA

During this training course, I have chose to do Insect Genome using Next Generation Sequencing. Next generation sequencing method is new to me, so the learning process is quite tough, as we need to learn and analyze many samples in such a short time.

Samples used were the DNA samples taken during the Yakushima Island fieldwork. For insects genome, we used the fecal samples stored in RNA later buffer. We also added a few samples from leopard feces and giant oarfish gut samples. In total, 21 samples were used.

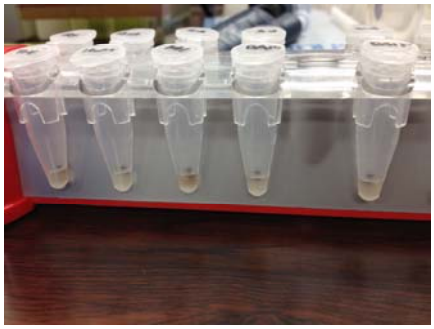
DNA extraction and purification from fecal samples were done using QiaAmp DNA Stool mini kit and a standard protocol prepared by the instructor. Extracted DNA was quantified using NanoDrop and Qubit dsDNA HS Assay Kit. Prior to the sequencing, Agilent Tapestation was used to measure the quality of the DNA in each sample. Samples with good results will be put into Illumina MiSeq next generation sequencer.

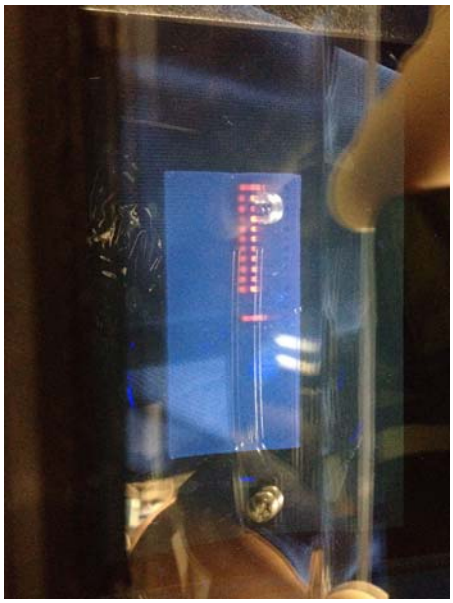
After the sequencing result is out, Claident software and R statistical package were used to analyze and summarize the results.

For insect genome, the result is not so good where we only find one good match for the insect DNA obtained from the Claident database. As for the matching with Insect DNA group result, we also only get one good result with 99.7% match.

In conclusion, I really enjoy this training and I learnt many new techniques and methods in DNA extractions and analysis. Hopefully I can use it for my future research and study.

6. Others





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I would like to extend my gratitude especially to Prof. Shiro Kohshima and Wildlife Research Centre for inviting me to participate in this training. I also would like to thank all of the lecturers and mentors involved with this training. Your valuable guidance and knowledge sharing during this training will always remain in my mind and forever be appreciated. To my supervisor, Associate Prof. Shahrul Anuar, thanks a lot for choosing me as one of the representative for Universiti Sains Malaysia. The knowledge and experience gained from this training will be shared and used to further enlighten our knowledge on wildlife research and conservation.

Thank you.