Research Activity Report
Supported by International Core of Excellence for Tropical Biodiversity Conservation focusing on Large Animal Studies(CETbio),
“Leading Graduate Program in Primatology and Wildlife Science”

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Affiliation/Position	Primate Models for Behavioural Evolution Lab, University of Oxford
Name	Mary Sadid

1. Country/location of visit

Japan, Primate Research Institute- Inuyama

2. Research project

Study on genetic diversity in Japanese macaques and deer, Genome Science Course

3. Date (departing from/returning to Japan)

2018.11.12-2018.11.16

4. Main host researcher and affiliation

Dr. Takashi Hayakawa Professor at Kyoto University, Primate Research Institute

5. Progress and results of your research/activity

Please insert one or more pictures (to be publicly released). Below each picture, please provide a brief description.

During this course based at the Primate Research Institute (PRI) I learnt how to carry out the extraction, amplification, purification and sequencing of DNA from faecal samples collected during the Yakushima Field Course (2018.11.03-2018.11.09) under the direction of Professor Hayakawa with the support of M2 student Yan san. As someone with limited genetic lab work experience this was an invaluable insight into the processing of genetic samples from start to finish.

Days 1-4: Lab work

We spent the first 4 days carrying out labwork to process our samples. We carried out DNA extraction, amplification (PCR), gel electrophoresis, purification, and next generation sequencing using the Sanger dye terminator method. In addition to having demonstrations from our instructors we were also encouraged to form mixed ability groups such that team members with more experience could offer further guidance- this proved to be incredibly useful and a great way to build up confidence in using new techniques!

Whilst waiting for the sequencing reaction to finish we were able to visit the Japan Monkey Centre with Dr Hayakawa, this was an interesting insight into the history of primates at the research centre as well as being a chance to see many primate species for the first time. Some of us also used our free time to visit Inuyama Castle and the surrounding area, the medieval castle had a lovely view of the city and we were even able to see the PRI from the building.

Day 5: Analysis

We spent the final day analyzing sequence data. This included using Mega7 to align sequences with reference haplotypes for macaques and deer to determine sample haplotype and establish how and if haplotype distribution differed from previous data sets. We also produced haplotype networks and population genetic measures such as nucleotide diversity (π). I was made aware of the challenges that come with using faecal samples-such as low quality sequences – and their possible solutions- e.g. using better-fitting primers for the target region. We interpreted our results and produced a poster for each species to present at the 8th International Seminar (2018.11.21).

Fig.1 View from Inuyama Castle

6. Others

My sincerest thanks to Dr Hayakawa and Yan san as well as to PWS for arranging and funding this enriching course.