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.)

	2014.06.12
Affiliation/Position	Centre for Ecological Sciences, Indian Institute of Science / PhD Student
Name	Vani Dahiya

1. Country/location of visit

Japan/ Kyoto

2. Research project

Training course on metagenomic analysis of animal fecal DNA

3. Date (departing from/returning to Japan)

2014. 05. 29 – 2014. 06. 5 (8 days)

4. Main host researcher and affiliation

Wildlife Research Centre and Faculty of Science, Kyoto University

5. Progress and results of your research/activity

The objective of this training course was to analyze the plant species composition of mammalian (deer, money and weasel) fecal samples collected during the Yakushima field course. The first part of this training included wet lab work which comprised learning DNA extraction, purification, amplification and creation of the final "library" for MiSeq operation. We also quantified DNA using Nanodrop and Qubit methods. In the latter half of the training we learnt about metagenomic data generation from Next Generation Sequencer, the processing of the sequenced data using terminal operations (lecture by Dr. Tanabe) and finally performing statistical analyses of the data using R to identify patterns (lecture by Dr. Kadowaki). We could identify 46 families and 66 species of plants from the fecal samples. This number is quite high in comparison to the number of species identified by direct observation of feeding behaviour and dry analyses of fecal samples. The genome training course was a great platform to get hands on training in basic and advanced lab techniques and analyses methods.

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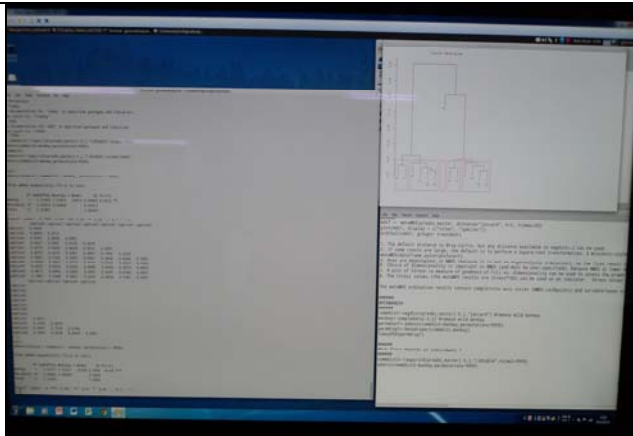(Please be sure to submit this report after the trip that supported by PWS.)

Fig 1. Analyzing the sequences generated from MiSeq

Fig 2. Participants at the genome training course

6. Others

Acknowledgements