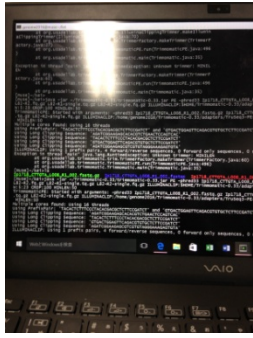


Research Activity Report
Supported by “Leading Graduate Program in Primatology and Wildlife Science”
(Please be sure to submit this report after the trip that supported by PWS.)

2016. June, 09	
Affiliation/Position	Department of Botany, Graduate School of Science, Kyoto University/M1
Name	Chung-Kun Lee

1. Country/location of visit
Japan/Kyoto
2. Research project
Genome Science Course (whole genome analyses)
3. Date (departing from/returning to Japan)
2016. May. 30 – 2016. June. 3 (5days)
4. Main host researcher and affiliation
Dr. Kishida, 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>I was a member of the whole genome analyses group, which aimed to analyze Yakushima macaque (<i>Macaca fuscata yakui</i>). We got results of following:</p> <ol style="list-style-type: none"> 1) Inference of Yakushima macaque population history by PSMC 2) Estimation of Yakushima macaque-rhesus macaque divergence time by PSMC 3) Exploration of genes related to Yakushima macaque’s characteristics by comparing SNPs with those of rhesus macaque. <p>Academic results were presented at the 5th International Seminar on Biodiversity and Evolution: New Methodology for Wildlife Science held on 7th June, so I do not describe the results here.</p> <p>We used Yakushima macaque’s genome data already obtained by chemical experiments, so all processes of this study were conducted <i>in silico</i>.</p> <p>We used command line interface, which was unfamiliar to us, because of the size of whole genome data. We gradually adapted to it with a lot of kind explanations. Most of calculation was conducted by a supercomputer.</p> <p>The genome data were numerous short sequences gained by shotgun method, and we synthesized complete genome sequence by mapping them to arranged rhesus macaque genome registered in NCBI. For about 3 days, we conducted arranging and converting the shotgun dataset, calculation of quality of the dataset, excluding too low quality data for analysis. Then we conducted PSMC analysis and gene exploration based on SNP data. Most of the processes were programmed calculations, but gene exploration required persistent effort.</p> <p>In my discipline, calculation by computer is necessary to analyze DNA data, so it will be helpful to experience the analysis with command line interface.</p>

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Display of my colleague



Analyzing members

6. Others

Genome Science Course was conducted with supports of PWS Leading Graduate Program. I express my gratitude to lecturers, group members, and everyone who supported us.