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.)

	2016.06.08
Affiliation/Position	Primate Rsearch Institute/M1
Name	Kei Hazehara

1. Country/location of visit

Graduate School of Science Bldg. No.1,Kyoto University

2. Research project

Study on Whole Genome Analysis (Genome science course)

3. Date (departing from/returning to Japan)

2016. 05. 30 – 2016. 06. 03 (5days)

4. Main host researcher and affiliation

Dr.Kishida, at Wildlife Research Center

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.

In this Genome Science Course, we analyzed the whole genome data of Yakushima macaque. By using the analysis data, we inferred the population size history of Yakushima macaque and estimated the rhesus macaque-Yakushima macaque divergence time. We also explored the gene resulting in the features of the Yakushima macaque. Whole genome analysis group was carried out in the following schedule.

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2016/5/30 Move to Kyoto
2016/5/31-2016/6/2 Data processing
2016/6/3 Divergence time estimation and gene exploration
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2016/5/30
We moved to Graduate School of Science Bldg.No.1,Kyoto University from Inuyama. Immediately we received a description of the machine and so on from Dr.Kishida.We processed most of the data by using a supercomputer. It was the first time I saw this computer. Then we took a lunch in the cafeteria. In the afternoon we received a brief description of the command line interface. I was anxious about conducting genome analysis because I didn't have such an experience. However, my friend helped me a lot.

2016/5/31-2016/6/2
We processed genome data.When we conducted genome analysis, we used the command table which I got in advance.Dr.Kishida always gave us description. Some analysis was conducted overnight.

2016/6/3
The population size history and divergence time estimation used PSMC Analysis. We got the results by PSMC analysis of Yakushima macaque and of *in silica* rhesus-Yakushima hybrid.I learned how to estimate divergence time instead of fossils. It was also interesting for to determining sex and to analyze paticular genes.I learned in detail about genes related to my interest to analyze them, so this time was very meaningful for me.Although I found mutations, I couldn't check the expression of these genes.
I enjoyed thinking that how the gene make our body and work with other factor.

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1. DNA sequence of Yakushima macaque   2. members typing commands.

6. Others

I would like to express my sincere gratitude to Dr.Kishida. I also thanks PWS for supporting this field work.