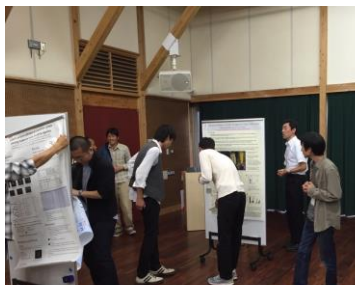# Research Activity Report
Supported by "Leading Graduate Program in Primatology and Wildlife Science"
(Please be sure to submit this report after the trip that supported by PWS.)

	2015. 06, 18
Affiliation/Position	Graduate School of Science, Kyoto University
Name	Masaya Tamura

1. Country/location of visit
Kyoto, Japan
2. Research project
Genome Science Course in spring
3. Date (departing from/returning to Japan)
2015. 06. 02 – 2015. 06. 07 (6days)
4. Main host researcher and affiliation
Graduate School of Science, 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.

In this course, I conducted bioinformatics by using whole genome of Japanese macaque (*Macaca fuscata yakui*). We learned, in this practice, the principle of Next generation sequencer and "Linux" commands for data processing.

After sequencing, I searched genomes relating to external shapes of Japanese macaque and focused on HMX1 gene that forms the external era. I found that three non-synonymous mutations occurred on this gene. However, I couldn't get good suggestion of the effect of these mutations on external era. In this analysis, I used only one reference (Rhesus macaque, *Macaca mulatta*), so I might well have to add other primate's references to solve this question.

I knew that there is much whole genome information of various species throughout this course. From now, many more whole genomes in many species will be analyzed. I'm looking at advance in this discipline.

There is no strong relation between contents of this course and my research in master's course. However the knowledge and technique gained from this practice will provide me with new viewpoint in my research.

Poster session of CTTBio

6. Others
I would like to thank Drs. T. Kishida and T. Hayakawa for their careful tutelage.