

**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.)

2015.6.12

<b>Affiliation/Position</b>	PRI/M1
<b>Name</b>	Shintaro Ishizuka

**1. Country/location of visit**

The Building#1 of the Faculty of Science, North Campus, Kyoto University

**2. Research project**

Genome science training

**3. Date (departing from/returning to Japan)**

2015.6.2-9 (7days)

**4. Main host researcher and affiliation**

Dr. Kishida and Dr. Hayakawa, Kyoto University

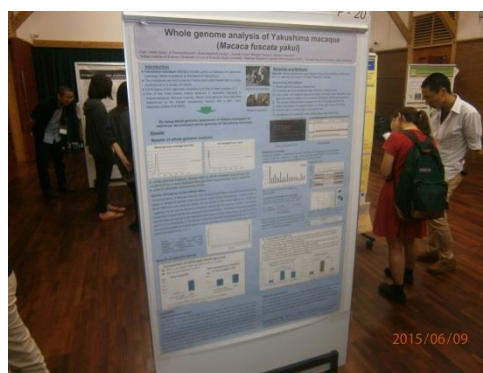
**5. Progress and results of your research/activity** (You can attach extra pages if needed)

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

From 2th to 9th in June, I attended genome science training. I was a member of whole genome group and analyzed whole genome of Yakushima macaque. In this course, sequencing data was obtained in last year by next generation sequencer (Illumina Miseq). These data was assembled through de novo program and mapped by referencing to whole genome of rhesus macaque, one of the closest related species. By these treats we got information about whole genome of Yakushima macaques. In our team, each of us analyzed what each member feels interested in by respectively. And I investigated about major histocompatibility complex (MHC). MHC is a genome region relating with immune system of all vertebrates. And it is said that MHC is very polymorphic because these polymorphism enables MHC molecular to combine various antigens, which has been adaptive. So I investigated differences of diversity between in MHC and in whole genome. I compared MHC with whole genome about heterozygosity, which is an index of genetic diversity, and non-synonymous mutation at heterozygous sites. As a result, these were significantly higher in MHC than in whole genome. This result may suggest that as often be said, traits of heterozygous genotype in MHC might have been selected. Though it was the small part that I could analyze of whole genome, I want to analyze more and particularly want to estimate past population size of Yakushima macaques based on whole genome sequence data.



Analysis for sequence data



Poster in symposium

**6. Others**

This program was supported by PWS Leading Program. I would like to appreciate this program and Dr. Kishida and Dr. Hayakawa.