

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, 09
Affiliation/Position	Dept. of Biophysics, Div. of Biological Science, Graduate School of Science
Name	Mayu, ONODA

1. Country/location of visit
Japan, Kyoto
2. Research project
Genome Science Course (Whole Genome Group)
3. Date (departing from/returning to Japan)
2016. 05. 30 – 2016. 06. 07 (8 days)
4. Main host researcher and affiliation
Dr. Kishida, Assistant Professor at Wildlife Research Center of 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 actively participated in Whole Genome Group in this course.</p> <p>We mapped WGS (whole genome shotgun) sequences of single Yakushima macaque <i>Macaca fuscata yakui</i> (YM) provided by Japan Monkey Centre, to a reference genome of rhesus macaque <i>Macaca mulatta</i> (RM). Using an unique method previously reported, Pairwise sequentially Markovian coalescence (PSMC, Li H. and Durbin R. 2011), what we investigated are:</p> <ol style="list-style-type: none"> 1. Inference of population history of YMs in Yakushima. 2. Estimation of speciation events and time of YMs from rhesus macaques with the geographical history of Yakushima. 3. Isolation of specific genes from whole genome analysis with SNP (single nucleotide polymorphism) data. <p>A supercomputer of Kyoto University was used throughout this course. Details of the study were presented during the poster session in The 5th International Seminar on Biodiversity and Evolution: New Methodology for Wildlife Science held on 7th June, 2016. Here, I will just describe the entire picture of our research.</p> <p>Results:</p> <ol style="list-style-type: none"> 1. YMs were branched from rhesus macaques approximately 0.5 million years ago, which was accorded with earlier research. 2. Population of YM was recovered after the speciation time. 3. Population size was decreased approximately five thousand years ago. 4. Genome analysis did not give information about interesting genetic variation due to the speciation between YM and RM. <p>It is conceivable that YMs walked across a land bridge between Kyushu and Yakushima island during the last glacial age after the speciation. Also, the decline in the population size after migration is thought to be due to volcano eruptions in Kuchinoerabu island.</p> <p>What we have achieved:</p> <p>We learned basic techniques and concepts of WGS, PSMC, and population genetics with CUI (character user interface). For the future prospect, I hope to explore interesting genes involving in the speciation. This course was brought to me a great opportunity to think of an animal and its large-scale history, which will also help me study my own research from a deeper perspective.</p>

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Whole Genome group conducted this study in Kyoto University throughout the course all.



Photograph by Kota, KUROKI.
Whole genome analysis.



Photograph by Kei, HAZEHARA.
Actual sequence data.



Photograph by Kei, HAZEHARA.
During the discussion.

6. Others

First of all, I would like to express my deep gratitude for:

- Dr. Kishida and Matsushima-san for the intensive instruction during this course and strong supports.
- PWS leading program for this course.
- Whole Genome Group members for their cooperation to fully enjoy this course!
- My academic advisor Prof. Kiyokazu AGATA for providing me with this opportunity not only to interact with friends and professors, but also to do interesting research.