

**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.)

	2017. 11. 21
<b>Affiliation/Position</b>	Primate Research Institute / M1
<b>Name</b>	Tianmeng HE

<b>1. Country/location of visit</b>
Japan, Yakushima
<b>2. Research project</b>
Regional Distribution of mtDNA Haplotypes in Yakushima Macaques ( <i>Macaca fuscata yakui</i> )
<b>3. Date (departing from/returning to Japan)</b>
2017. 11. 05 – 2017. 11. 17 (13 days)
<b>4. Main host researcher and affiliation</b>
Prof. Hideki SUGIURA and Prof. KISHIDA Takushi, Wildlife Research Center of Kyoto University;
<b>5. Progress and results of your research/activity</b> (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>During the field course in Yakushima (5th - 11th, November) and genome course in Kyoto (13th – 17th , November), I was a member of monkey team. We conducted a brief research about the regional distribution of mtDNA haplotypes in Yakushima macaques (<i>Macaca fuscata yakui</i>).</p> <p>In Yakushima, we searched and followed monkey groups in coastal area in the west of the island as well as the highland area in the north of the island. We observed the behavior of monkeys and collected fecal DNA samples during the following. Then in the genome course, we used these samples for DNA extraction. After that, designated segment of mtDNA were amplified and sequenced for 37 samples. Finally, we analyzed the sequencing data with MEGA and QGIS to find out the regional distribution of haplotypes.</p> <p>We find haplotype Y1 is the commonest haplotype in Yakushima monkeys and is distributed around our sampling area. Y2 distributed in the south part of western coastal area. These results agreed with previous results of genome course in spring, 2017. We also found two new haplotypes in two samples which were collected in the north of western coastal area. Interestingly, the two samples came from the same individual. One of the samples was vomiting material, while the other was fecal sample. According to Prof. Kawamoto’s comment, one possible explanation of this phenomenon is heteroplasmy.</p> <p>Through this experience, I have learnt the basic methodology of fecal DNA samples collection and the genetic analysis of monkeys. I also have learnt how to use MAGE and QGIS. As a master student, I will conduct my own research in the western coastal area of Yakushima. Thus, I also used this opportunity to learn the environment of my future study sites as well as to get familiar with my future study subject.</p>
<b>6. Others</b>
I would like to express my appreciation to all the lectures in the course who provide patient guidance and advice over our work. I would also like to thank my teammates, the two weeks spent with them were enjoyable and fruitful. I would also like to appreciate all the staff who helped to run this course smoothly.