

**Research Activity Report**  
**Supported by “JSPS Core-to-Core Program(International Core of Excellence for Tropical Biodiversity Conservation focusing on Large Animal Studies )” “Leading Graduate Program in Primatology and Wildlife Science”**

(Please be sure to submit this report after the trip that supported by CETbio,PWS.)

	2018.06.07
<b>Affiliation/Position</b>	Master student/ School of Sociology and Anthropology, Sun Yat-sen University
<b>Name</b>	Gu Ningxin

<b>1. Country/location of visit</b>
Japan/Kyoto
<b>2. Research project</b>
Genome Science Course (Phylogeography of Yakushima Macaques Inferred from Mitochondrial DNA)
<b>3. Date (departing from/returning to Japan)</b>
2018.05.28/2018.06.01
<b>4. Main host researcher and affiliation</b>
Dr. Kishida Takushi; Wildlife Research Center, 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>In the Genome Science course of 2018 spring (2018.5.28-6.1), we conduct a research about phylogeography of Yakushima macaques(<i>Macaca fuscata yakui</i>) inferred from mitochondrial DNA.</p> <p>Our experiment samples came from previous Yakushima field course which are collected from feces and preserved in lysis buffer, and we also have the GPS data of sampling sites. QIAamp stool mini kit is used to extract and purify DNA. The accuracy of our pipetting is important for the DNA's quality. And using the same primer of Hayaishi and Kawamoto (Hayaishi and Kawamoto,2016), we conducted PCR amplification for target segment of mitochondrial DNA. Then we took use of BigDye XTerminator Purification Kit to prepare for sequencing. Sanger sequencing method was chosen for our research because of the purpose. In my laboratory, we don't have sequencer and all that I can do are the steps from beginning to PCR. Learning the process of sequencing is helpful to deepen my understanding for the principle of sanger sequencing method. After getting the sequences, Kishida sensei taught us how to use MEGA 7.0 to analyze them. Reading and correcting the 'n' sites is not so easy for me. Maybe I need more practice in this part, but the best way is to improve the quality of sequencing by regulating experiment operation. Learning how to analyze data is really essential for my research of rhesus macaques (<i>Macaca mulatta</i>), and thank PWS to give me such a chance to attend the genome science course.</p>
<b>6. Others</b>

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I would like to express my appreciation to KISHIDA Takushi sensei and MATSUSHIMA Kei san to teach and help us with so much patience. Also thank all my teammates: Seema Sheesh LOKHANDWALA, NAKANO Katsumitsu and TAKI, Yuto. It's so lucky for me to meet these kind people.