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.)

	2017.06.01
Affiliation/Position	Sun Yat-sen University/D2
Name	Danhe Yang

1. **Country/location of visit**

Japan/Kyoto,(Kyoto University WRC)

2. **Research project**

Genome Science Course(Genetic analyses of Yakushima macaque: group comparison of allele frequency in *COMT*gene)

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

2017. 05. 22 – 2014. 05. 26 (5 days)

4. Main host researcher and affiliation

Pro. Murayama, Ms. Kobayashi, Mr. Sato, WRC, 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.

This genome course is extension of Yakushima field course. We use the sample that collected from Yakushima. COMT gene as a candidate gene to affect behavior of Japanese macaques which previous study has shown before. And COMT is modulator of dopaminergic neural transmission. So, Our aim is to understand the way to analyze the DNA which is extracted from fecal samples, and we only use DNA from monkeys, that could provide valuable information on the ecology of wild animals.The purpose of this course were to compare allele frequency in COMT gene of Yakushima monkeys with other group monkeys in Japan, which are from Kinkazan, Koshima, Shodoshima, respectively. Also, to discuss the relationships between polymorphisms and the regional difference in tolerance.
During the Yakushima, 25 fecal samples were collected, and since we wanted to compare to others 3 regions', then used additional control samples and data that other researchers provided. In this course, we use the region which is located on sex chromosome and the length of which is different between X and Y chromosomes. However, after we finished for sex identification, results turned out not so suitable for analyzing due to insufficient samples.We ran several times on sequence with different PCR amplification, and used Finch TV for analyzing sequence data.
We found that 2 individuals in Shodoshima had a haplotype(HT4:T-T SNPs), which did not shown at the precious study, and as for the T-allele frequency in intron 4, Shodoshima and Yakushima were higher than Koshima. Compared to heterozygosity of each group, it shown that Ho-introns in Shodoshima and Yakushima were lower than that in Kinkazan, maybe it's related to genetic diversity between mainland and island areas. Also, in all sites, ho-exons were higher than he-exons.
I really appreciate that Pro. Murayama, Mr. Sato and Ms. Kobayashi, for their patient and careful. It was a great and unique experience for person like me never had a chance to work at lab.

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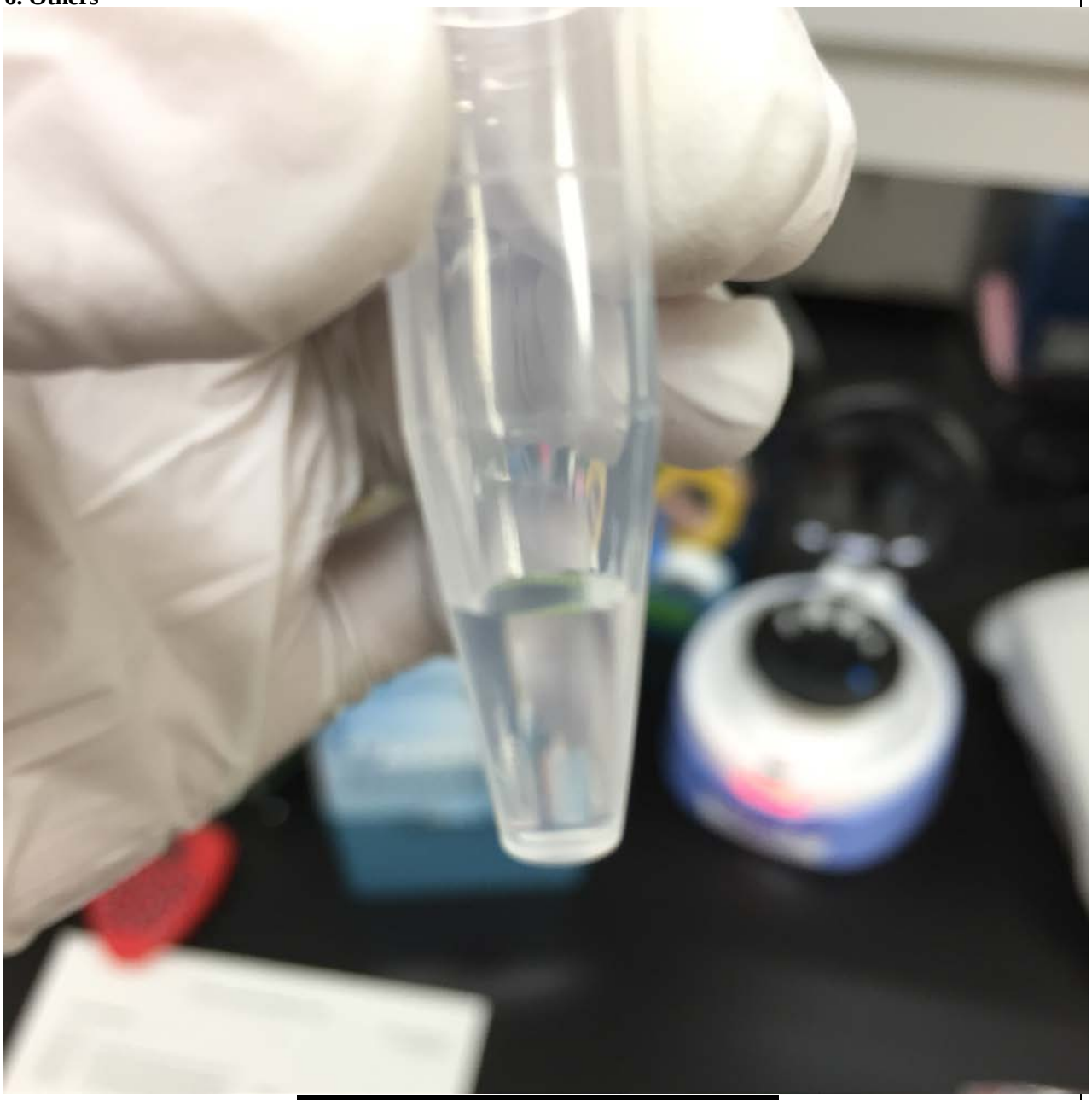
6. Others



DNA were extracted successfully for the first time

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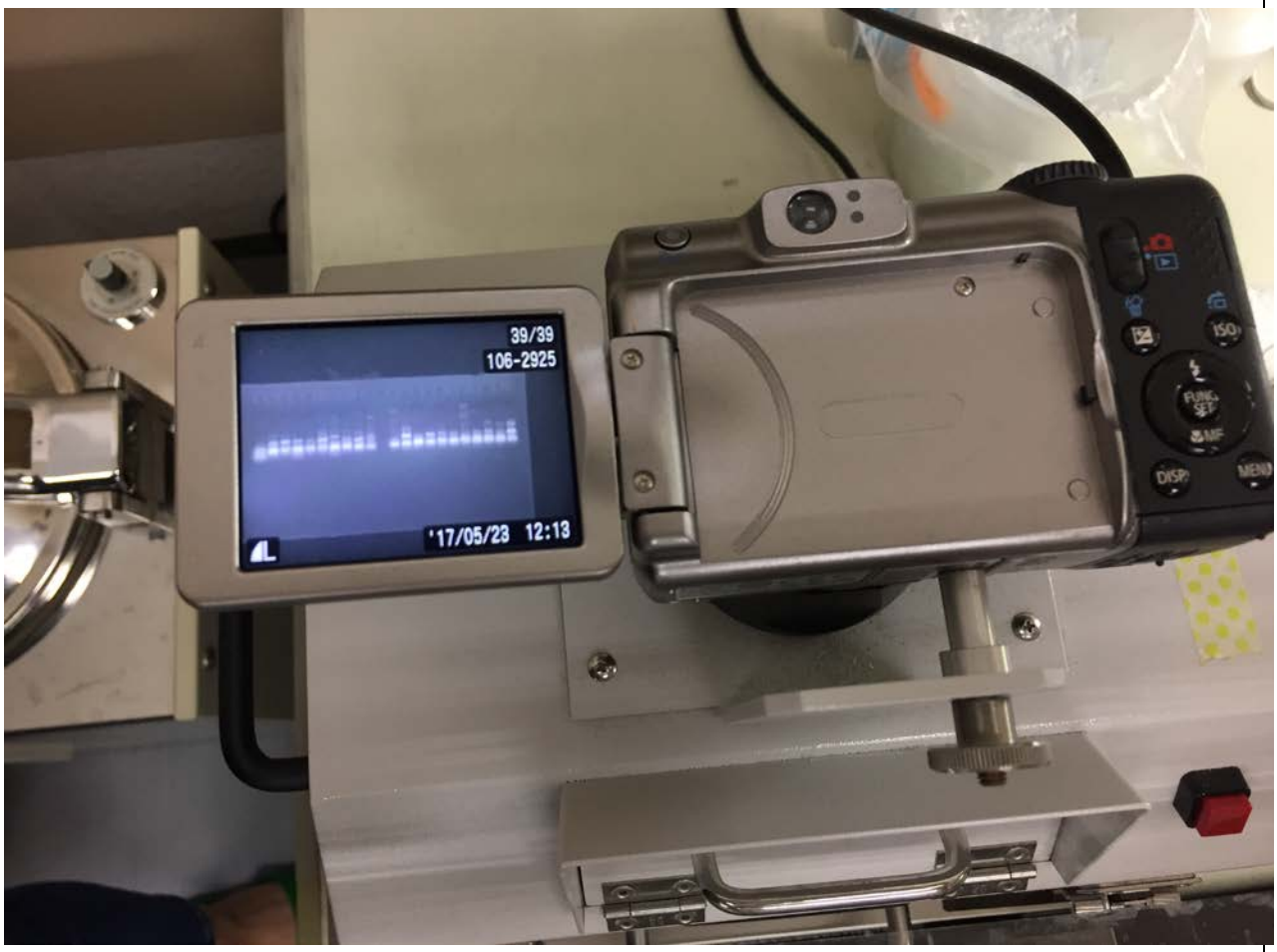

Sex identification after using agarose gel electrophoresis

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