
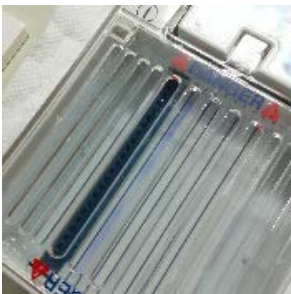


Research Activity Report
Supported by “Leading Graduate Program in Primatology and Wildlife Science”
 (Please be sure to submit this report after the trip that supported by PWS.)

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Affiliation/Position	Wildlife Research Center/M1
Name	Yutaro Sato

1. Country/location of visit
Japan/ Kyoto prefecture, Wildlife Research Center
2. Research project
Genome Science Course
3. Date (departing from/returning to Japan)
2017. 5. 22 – 2017. 5. 30 (6 days)
4. Main host researcher and affiliation
Dr. Miho Murayama, Professor at Wildlife Research Center, 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>The aim of this course was to analyze fecal samples from wild Yakushima macaques and acquire fundamental skills and knowledge of DNA analysis. Together with results of field work in Yakushima, we did a poster presentation at the 6th International Seminar on Biodiversity and Evolution: Wildlife science by New Biologging studies.</p> <p>This was the first time for me to do DNA analyses so it took a long time to perform each manipulation at first. Because of lecturers’ kind assistance, however, I gradually got used to doing the tasks. I learned how important it is to work while keeping in mind what to do next (Fig. 1).</p> <p>When we extracted DNA from fecal samples, I could not believe that DNA was inside the tube because it could not be seen. However, we could decide the base sequences after genome sequencing, which made me feel how wonderful the DNA analyses were.</p> <p>Regarding to the sexing, we could not obtain reliable results. The conditions (e.g. temperature or enzymes used) may have affected our results. I learned that just following the method determined beforehand was not enough to obtain the result.</p> <p>Finally, we compared the allele frequency of <i>COMT</i> among several regions and discussed in relation to the regional difference of social tolerance. Our results suggest that differences in the frequency of a single nucleotide polymorphism (SNP) may partially affect the regional difference in tolerance of Japanese macaques. Also, we found a haplotype, which was not reported in the previous study. In addition, we calculated</p>
 <p>Figure 1. Sampling tubes used in the analyses. Things which seemed trivial, such as how to label each tubes or how to line them up, affected how efficiently we did the experiments.</p>
 <p>Figure 2. The electrophoresis for sexing. Since we could not obtain reliable results by just one trial, we repeated the procedures changing some conditions of PCR or the thickness of the gel.</p>

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the heterozygosity and considered the genetic diversity of each region. We found that the genetic diversity may differ depending on the regions.

At the symposium, some people listened to us and they gave us some insightful comments. Since the regional difference of tolerance among Japanese macaques has been one of topics of interest, this practice was really fascinating. In this time, the samples from other regions such as Shodoshima Island or Kinkazan Island were provided by other researchers. I hope to observe macaques there with my own eyes in someday.

6. Others

I am grateful to Prof. Murayama, Mr. Sato, and Ms. Kobayashi at the Wildlife Research Center for their kind help. I also thank to the members of the same team, Ms. Yang, Ms. Oka, and Mr. Sakurai for their cooperation during the whole practice.