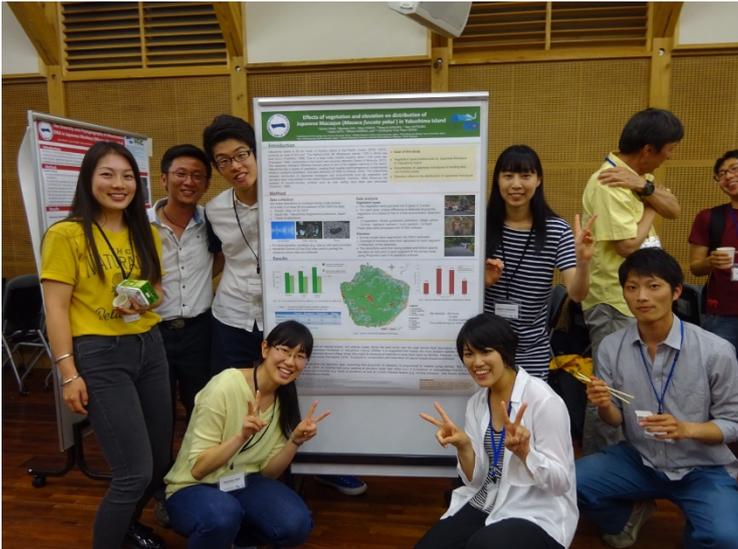


Research Activity Report
Supported by “Leading Graduate Program in Primatology and Wildlife Science”
 (Please be sure to submit this report after the trip that supported by PWS.)

2017. 06. 09	
Affiliation/Position	
Name	Mikaze KAWADA

1. Country/location of visit						
Kyoto University						
2. Research project						
Genome PWS course						
3. Date (departing from/returning to Japan)						
2017. 05. 22 – 2017. 05.29 (5days)						
4. Main host researcher and affiliation						
Prof. Takushi Kishida and Mr. Kei Matsushima						
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>This course followed the Yakushima Field Course. We analyzed haplotype of Yakushima macaque (<i>Macaca fuscata yakui</i>) mtDNA D-loop region.</p> <p>Schedule of our activities</p> <table style="margin-left: 20px; border: none;"> <tr> <td style="padding-right: 20px;">22th ~ 27th</td> <td>DNA sequencing and analysis</td> </tr> <tr> <td>28th</td> <td>preparation for presentation</td> </tr> <tr> <td>29th</td> <td>presentation</td> </tr> </table>	22th ~ 27th	DNA sequencing and analysis	28th	preparation for presentation	29th	presentation
22th ~ 27th	DNA sequencing and analysis					
28th	preparation for presentation					
29th	presentation					
						
<p>The genetic diversity of yakushima macaque is said low in previous study. We compared the distribution of Yakushima macaque’s mtDNA morphororphism in 2017 and it in 2006 (Hayaishi and Kawamoto) and we analyzed success rate for genetic analysis.</p> <p>We observed 3 types of haplotype, namely Y1, Y2/Y3, and Y5 (the same as, so following the naming by Hayaishi and Kawamoto, 2006) and these haplotypes were detected outside of the region where they were previously reported by Hayaishi and Kawamoto (2006). One of the Y2/Y3 was also found at much higher elevation (1087m) than previous record. The distribution of Y2/Y3 might expand to higher elevation. Y1 was distributed widely, while the other haplotypes were observed only in restricted areas. Y5 was found in same area that previously reported by Hayaishi and Kawamoto (2006). Some haplotypes has still remained since 10years ago, but genetic diversity is still low.</p> <p>New feces were significantly successful for genetic analysis, whereas the weather when we collect fecal samples was not significantly related with success rate. That’s why we have to collect samples from newer feces.</p>						

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This was the first time that I sequence DNA. I have studied molecular biology by only text book, so I couldn't have clearly image of DNA sequencing until when I actually doing in this course. Furthermore, I have not made poster for presentation and presented at the International seminar until doing in this course. This course was really inforamative for me. I learned many techniques and knowledge in this course and I'm sure in future this experiments will be helpful for me.

6. Others

I'm very thanks to PWS for providing me this opportunity. I would also like to thank Dr. Kisida, and Mr. Matsushima for teaching us.