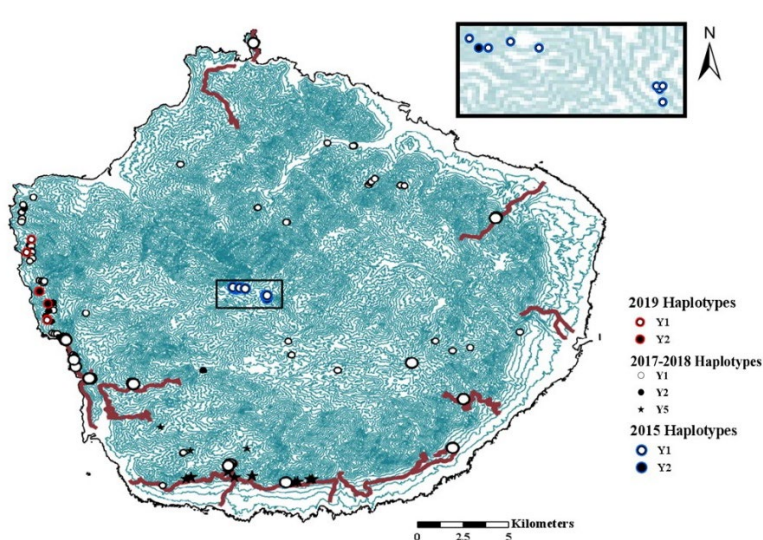


Research Activity Report
Supported by “Leading Graduate Program in Primatology and Wildlife Science”
 (Please be sure to submit this report after the trip that supported by PWS.)

2019. 06, 18	
Affiliation/Position	Primate Research Institute/M1
Name	David Fasbender

1. Country/location of visit
Japan, Kyoto University
2. Research project
Advanced Training in Laboratory Skills, Monkey Phylogeography Course
3. Date (departing from/returning to Japan)
Kyoto 2019. 06. 03 – 2019. 06. 07 & 2019.06.11
4. Main host researcher and affiliation
Kyoto University: Dr. Kishida (WRC)
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 lab course in Kyoto was a chance to see what the fecal samples collected in Yakushima could reveal about macaque phylogeography. We were guided through the steps of isolating the DNA from these samples and some older samples, amplifying the d-loop of the mtDNA, sequencing this amplified mtDNA and identifying haplotypes. At each step we were taught how to verify our success which was very helpful in the complicated process of mixing and isolating different samples and buffers while attempting to avoid contamination. It was exciting to see successful sequencing results from the cells on small fecal samples. Our results contributed to a bigger picture of range shifts of Yaku monkey populations: haplotypes that previously were only found in the lowlands (Hayaishi 2006) were now at high altitudes.</p> <p>The week after the lab work we presented results at the PWS international workshop in Kyoto. We learned about research from a diverse mix of study sites (from Brazil to Malaysia), study subjects (mycorrhizae, dolphins, snakes, etc.) and disciplines. It was fun to discover the main campus of Kyoto and inspiring to see the breadth of biology/ecology studies as Kyoto.</p> <p>I was relatively new to this type of lab-work and am grateful for such an opportunity to see how my field samples can help in the identification of sub-populations and ranges. This is especially useful as I work on unhabituated primates (bonobos), I hope to use what I learned here.</p> <div style="text-align: center;">  <p style="font-size: small;"> 2019 Haplotypes ● Y1 ● Y2 2017-2018 Haplotypes ○ Y1 ● Y2 * Y5 2015 Haplotypes ● Y1 ● Y2 </p> </div>
Map with our findings of the 2019 & 2015 haplotypes in relation to courses from the past two years

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6. Acknowledgements

Thank you very much PWS for this useful experience and thank you to Kishida-sensei and Naito-san for help in the lab and with analysis.