During my stay in Kyoto, I conducted research in genomics using feces of monkeys collected on the island of Yakushima and Koshima. This study aimed to compare the constitution of the intestinal microbiota of monkeys of different groups and especially between different islands in order to try to estimate from the establishment of the microbiota if the animals have the same diet in different localities.

For this, we use collected samples to extract DNA and amplify the 16S gene region, considered a barcode in bacteria and it is mainly used for species identification. The genome training course aimed to teach us the techniques of sample preparation to use the next generation sequencing platforms, and especially as the data obtained by this new equipment should be analyzed. So, after preparation of the samples, they were injected into a flowcell used for sequencing in MiSeq equipment (Illumina).

Several teachers gave lectures and taught us how to analyze the data obtained by next-generation sequencing in new programs developed by them and using the R platform.

After the course, we analyzed data obtained with our samples and prepare a poster (Figure 1) with our results for data presentation at the 3rd International Seminar on Biodiversity and Evolution (Figure 2), where we also had the opportunity to know other works in the area of genomics performed by fellow students.

I am currently working on a report based on these results for publication.

In Brazil I am working with genetics for 14 years, but never had the opportunity to undertake work in the area of genomics. This course was very important for my career because I intend to use the techniques I learned in Japan in similar studies with samples from the Amazon.
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.)

Figure 1 – Poster with the results of the Genome Training Course presented in the International Seminar.
Figure 2 – Poster presentation at the 3rd International Seminar on Biodiversity and Evolution.