Research Activity Report Genome Training Course - Kyoto University, 2014

	2014. June, 08
Affiliation/Position	PhD Student, Centre for Ecological Sciences, Indian Institute of Science, Bangalore
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1. Country/location of visit

Kyoto University, Japan

2. Research project

Olfactory and taste receptors in the Yakushima macaque. An investigation using non-invasive sampling and next-generation sequencing.

3. Date (period of stay in Japan)

2014. May. 12 – 2014. June. 13 (32 days)

4. Main host researcher and affiliation

Dr. Shiro Kohshima, 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.

It was a smooth transition from field boots in Yakushima to a lab coat in the genome training course, where we got a bird's eye view of the multi-disciplinary research being conducted by Kyoto University. The role of our group's work in the larger research framework was clearer as a result of the field exposure prior to the genomics work. The aim of our project was to understand the diversity in taste and olfactory receptors in *Macaca fuscata yakui*, a macaque endemic to the Yakushima island. This piece of work fits into the larger story of feeding ecology in Yakushima monkeys, in revealing how a unique suite of taste and olfactory receptors may drive diet preferences in them. Understanding the mechanism of diet preference at a molecular level complements the information that behavioural studies and fecal analysis of diet have provided so far. It also allows us to understand the evolution of these receptors in the Yakushima macaque, when compared to other closely related species.

To meet our objectives, we used the powerful tool of Next-Generation Sequencing (NGS) to obtain sequences of taste and olfactory receptor genes in individuals of Yakushima macaques. We prepared a DNA library enriched for the taste and olfactory receptor genomic region, sequenced it and then aligned these sequence reads with a reference *Rhesus* macaque DNA sequence to identify single nucleotide polymorphisms. I learnt several new procedures during this process, the most important being library preparation for NGS and post-NGS data processing. Though I have learnt about Next-Generation Sequencing in theory, carrying out DNA library preparation in person has made the procedure clearer in my mind. It also gave me the opportunity to handle several high-end lab instruments which I don't have access to in my home institution. The analysis of sequence data was the best part of my experience, where I was extensively using the Linux platform for the first time. A clear set of instructions, having ready troubleshooting help at hand and encouragement from our lecturers to explore the software programs independently made it a hurdle-free and enjoyable learning experience.

This lab experience is directly relevant to my PhD research at the Centre for Ecological Sciences, Indian Institute of Science. I plan to use Restriction-site Associated DNA (RAD) sequencing - an extension of routine NGS, to understand population genetic structure in marine gastropods in the Indian coastline. A substantial part of the lab procedure and bio-informatics in RAD sequencing is common with what I have already learnt in the genome training course at Kyoto University. This experience has given me a jump-start to design my own lab-work, providing me with an overview of the work-flow associated with NGS.

6. Others

A great, big thank you to all the members of the host genome group - Kutsuma-San, Tsuji-San, Yagi-San, Agetsuma-San, Kashima-San and Kishida-San. This is not a routine acknowledgement note at the end of a document because it is expected to be written. I really mean it most sincerely when I sav I have had the greatest fun working with you all. I think we made an amazing team, wheels in perfect unison. JJGUU!



Some late night trepidation while our poster gets its final touches. Agetsuma-San's expression captures it all!