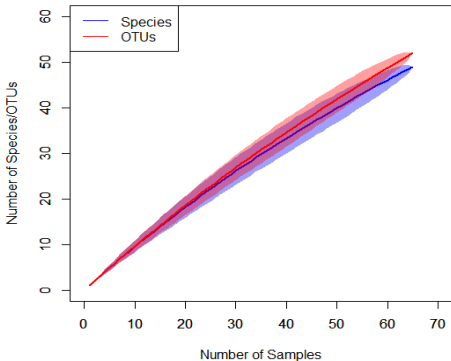


Research Activity Report
Supported by “Leading Graduate Program in Primatology and Wildlife Science”
 (Please be sure to submit this report after the trip that supported by PWS.)

2015. 06, 24	
Affiliation/Position	CES,IISc, India
Name	Anuradha Batabyal

1. Country/location of visit
Kyoto, Japan
2. Research project
Genome Science Course
3. Date (departing from/returning to India)
2015. 05. 15 – 2015. 06. 15 (30 days)
4. Main host researcher and affiliation
Dr. Shiro Koshima, Professor at 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>During this visit, I conducted research on identification of mushrooms collected from Yakushima Island. The DNA was extracted from each sample and a specific regions in the DNA called the ITS region was amplified using PCR and later sequencing was done for this region of the DNA. It is used in mushroom species identification. We analysed 96 samples and after sequencing constructed phylogenetic tree (Neighbor-Joining method) and calculated pairwise distance (p-distance) for each sample. We quantified Operational Taxonomic Units (OTUs) from the p-distnces and samples which had p-distance less than 0.03 were grouped into same OTU. We found 52 OTUs from all our samples. A species accumulation curve was made with OTUs and morphologically identified species and it was found that the OTU curve had a steeper slope than the morphologically defined species curve. Thus it shows that there are more OTUs than we had defined by morphology. A bipartite graph was also constructed to check for cryptic species and 4 morphologically defined species were found to be cryptic in nature. An estimation of species richness was also calculated by using various indices like chao and jackknife. We got OTU richness estimation of 126.42 from jack2 index.</p> <p>To find out how many species actually are represented in the International Nucleotide Sequence Database by doing manula BLAST and also BLAST search by Cladient software. We found that 5 samples could only be identified till phylum level and 22 samples could only be identified till order from the 96 samples analysed.</p> <p>Through this experience, I have developed a clear vision on various protocols used to identify a species genetically and also this gave an idea about how much is known for a species internationally. It seems that mushroom identification needs a lot of work and through our study we are able to add a lot of new undescribed sequences to the international database.</p>
 <p style="text-align: center;">Species/OTU Accumulation curve</p>
6. Others

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.)