Report on visit to Poole lab (July 18 – Aug 31, 2018)

I am Nanditha Krishnan V and am from Dr. P. M. Reddy's lab. Our lab is one of the participating labs in the India UK Nitrogen Fixation Centre. We are interested in the screening and identification of rice varieties for enhanced di-/tri-carboxylic acid secretion and the effects of increased dicarboxylate secretion on the rhizosphere, rhizoplane and endosphere microbiome.

The work that I was associated with, during my tenure in Poole lab includes

1) **Use of bacterial biosensors for analysis of the composition of rice root exudates**

   An array of bioreporters were developed in *Rhizobium leguminosarum bv viciae* strain 3841 which can detect metabolites secreted by roots, in space and time (Pini *et al*., 2017). Fourteen bacterial lux fusion bioreporters, specific for sugars, amino acids, organic acids, flavonoids etc were tested to determine the composition of root exudates collected from different rice varieties. Among the 13 rice varieties tested, almost all varieties showed the presence of xylose, sucrose, fructose and myoinositol in their root exudates. Formate was present in all varieties except PB1 and tartarate was found in all varieties except PB1, Vandana and Salem Sanna. The presence of mannitol was only found in the root exudates of Taipei 309 and Vandana

2) **Metagenomic studies to understand the effect of organic acid secretion on rice root microbiome**

   From an array of rice cultivars screened for organic acid secretion from root exudates, we selected a representative set of five rice cultivars that secrete high, medium and low amounts of malate and/or citrate, to study the influence of these carboxylic acids on rice root microbiome composition, and structure and functional dynamics of microbial populations in rhizosphere. A pipeline was developed for metagenome analysis by Dr. Andrzej Tkacz. I was introduced to Linux coding for the analysis of sequenced data. Basics of MEGAN software and XLstat were also discussed. Commands for checking the quality of reads, finding the EE quality values, FLASH (fast length adjustment of short reads) to improve genomic assemblies, removing short length and long length reads, equalizing the number of reads in all the samples, sorting the reads into corresponding OTUs were also practised with the available sequence data

On a concluding note I would like to add that it was indeed a great pleasure and privilege for me, to work in Poole lab. The lab members were always ready to help especially Dr. Alison East, Dr. Vinoy Ramachandran and Dr. Beatriz John. I thank all lab members for this opportunity and look forward to work with you sometime in future as well. Many thanks once again for all your help and support.