

## **Report of the 2011 International Conference on Soil Omics 20-11 November 2011, Nanjing, China**

The 2011 International Conference on Soil Omics was held from 20-22 November at Nanjing Agricultural University with more than 200 in attendance. Drs. Quirong Shen and Paolo Nannipieri were the organizers. More than 30 presentations were made by scientists from throughout the world. The keynote address on “Mining Soil Metagenomes for Meaning” was given by Dr. James Tiedje. The main topics covered in the other presentations were: functional soil microbiology, soil omics, and soil microbial diversity and community structure. The presentations illustrated that pyrotagged sequencing has become the standard for the taxonomic description of microbial communities in soils and is rapidly being adapted for use with functional genes as well. Updates were given on several on-going soil shotgun metagenomics studies, such as those being done at the Rothamsted site in the UK and the prairies of the US, which are generating terrabases of sequence data, largely using the Illumina platform. The quantity of this short-read data is taxing current bioinformatics approaches and is also limited by the existing annotated gene databases. Metagenomic research on soil viruses was also reported. Reports were given on early results from studies applying metatranscriptomics, metaproteomics, and metabolomics to soil systems. The challenge of integrating these different omics methods was pointed out, including questions related to the synchronicity and linearity of the connections between genes, transcripts, and proteins. The omics-related research was complemented with several reports of more targeted studies of functional genes and transcripts related to specific biogeochemical processes, such as ammonia oxidation, denitrification, and methane production and consumption. Applications of omics and related methods to organism-organisms interactions and biological control of plant pathogens were also described.

The conference concluded with a discussion about the needs of the community of soil omics researchers. The following were identified:

- Continue to move on to other omics and their integration
- More reference genomes of soil microorganisms are needed
- Community should adhere to metadata standards of the GSC
- Ensure that the large quantities of data are in accessible archives
- Identify the questions that omics data are best suited to answer
- A resource for getting answers to technical questions
- Analysis pipelines should be coordinated and harmonized
- Analysis tools for interpreting the data need to be developed
- A central “theory” for microbial ecology
- Improve annotation of existing databases and future entries

Progress on addressing these needs might be facilitated by a coordinated effort of the community in the spirit of the TerraGenome consortium that originally promoted the intensive sequencing effort of the Rothamsted soil metagenome and the establishment of metadata standards for soil metagenome research. The newly established TerraGenome RCN may provide a mechanism for working on some of these issues as well as helping to sponsor future international conferences on soil omics.

Submitted by Dr. David D. Myrold, Oregon State University