

SOL 2010, The 7th Solanaceae Conference

Prof. RP Sharma¹, Prof. JP Khurana²,

¹University of Hyderabad, Hyderabad, ²University of Delhi South Campus, New Delhi,

Solanaceae is a family that represents major vegetables that are a regular part of our diet, such as potato, tomato, brinjal and chilies. Additionally, it also comprises of a large number of ornamental and medicinal plants. Recognizing importance of Solanaceae for our daily nutritional needs, an international initiative named SOL was launched in 2004 to sequence the genome of tomato as a representative plant of Solanaceae. Since then the SOL community is meeting annually to discuss the progress of genome sequencing and its potential use in improving desired traits in tomato and other species of Solanaceae. Right from inception of SOL India has joined this effort, with support of DBT, and has participated in sequencing chromosome five of tomato and also contributed to sequencing efforts. After the last SOL 2009 meeting that was held in New Delhi in 2009 with support of DBT, it was the turn of UK to host the SOL 2010 meeting. SOL 2010 was held from September 5-9, 2010 at the port city of Dundee. This British city had very strong links with India during 19th and 20th century, when its economy largely depended on factories processing raw jute imported from India.

Nearly 300 scientists from 27 different countries participated in the SOL meeting at Dundee. The presentations at the meeting highlighted a strong common

thread running through most of the talks. It was apparent that the sharing of the material and information generated through the collective sequencing efforts has catalyzed speedy progress in the area of functional genomics of Solanaceae. This aspect was very clearly highlighted in the inaugural talk by David Baulcombe where he used the introgression lines of tomato consisting of segments of genome of wild relative *S. pennelli*. His group found that an atypical class of 22nt sRNA initiates secondary sRNA production in plants. He predicted that in heterologous parent the novel secondary sRNA would be produced. Using introgression lines (ILs) of tomato where small regions of the *S. pennelli* genome were introgressed all along the tomato genome, he confirmed the presence of hybrid-specific sRNAs and their role in suppression of gene expression. His results in fact added a new dimension to molecular basis of hybrid vigor.

Since the inception of SOL initiative, there has been a strong emphasis of integration of biodiversity of Solanaceae along with genome sequencing. The fusion of both areas is now bringing its dividends as the wild relatives and natural accessions can contribute the desired genes that can improve the traits of crop plants related to disease resistance, yield and nutritional value. Several

talks during the meeting highlighted use of these resources. Neelima Sinha used genomics approach to understand natural variation in leaf morphology of tomato and its relationship to ambient light. Her talk highlighted how the availability of genome sequence information of tomato and use of NGS allowed them to characterize the leaf shape using transcriptome sequencing. Using massively parallel sequencing, they acquired genome-wide mRNA sequence and SNP information in wild and domesticated tomato to make genetic networks regulating leaf morphology and light mediated development.

The advent of next generation sequencing along with near completion of sequencing of two major crop plants, tomato and potato, have led to similar efforts to sequence chilies and tobacco, wherein information from these two genomes would allow them for a faster annotation of genes, as Solanaceae members have high degree of synteny in their genome. This also highlighted that, in a year or two, the transcriptome sequencing is likely to replace the currently used microarray technology. With availability of NGS more laboratories have shifted to sequencing of whole transcriptome of different organs of tomato, a tool that is likely to make rapid advances in functional genomics with its integration with

▶ proteomics. This approach was highlighted by Joselyn Rose in his multi-pronged strategy to examine the cuticle of tomato fruit at the level of assembly, structure and functions, using cell type-specific transcriptome and proteome profiling, and the characterization of cuticles from mutant tomato lines and wild tomato species.

Several talks highlighted use of natural mutations as well as induced mutations, using available tools of reverse genetics. The focus of these talks was mainly on regulation of tomato fruit ripening. Indian contribution supported by DBT under Functional Genomics of tomato was reported in two talks. First talk reported that the photoreceptor phototropin 1 is a new player that not only regulates shelf life of tomato fruits; it also increases the lycopene content of fruits. Second talk described the polymorphism of different genes using EcoTILLING in Indian tomato accessions, with particular emphasis on ACS-2 gene regulating ethylene biosynthesis during fruit ripening. It was reported that the apricot mutant that has intense orange color in the ripe fruit causes an alteration in the carotenoid pathway, along with increased production of antioxidant naringenin chalcone in the epidermis of the fruit. Using a dominant transposon-tagged tomato mutant it was shown that OrrDs encoding a NDH-M subunit, that is part of the NADH dehydrogenase (Ndh) complex, is also essential for the fruit ripening process. These studies highlighted that the use of mutants can bring about the desired changes in the

metabolic profile of tomato to suit specific nutritional needs.

Deliberations on the assembly and analyses of the genome sequences of both tomato and potato, where Indian scientists also participated, were. India has made a significant contribution towards sequencing of the tomato genome, primarily through the support from the DBT. The pseudomolecules for the respective chromosomes have been developed by amalgamating the data obtained using both conventional and NGS technologies. With the completion of tomato and potato genome sequencing and its publication expected in the next few months, the focus of SOL is shifting to functional genomics and sequencing of the natural

accessions, mutants and the wild relatives using NGS. The momentum is gathering to launch initiatives like SOL 100 and SOL 1000 to sequence the genomes of that many numbers of Solanaceae species, with emphasis on ornamentals and medicinal plants as well. Gradually, a systems biology approach is being developed that would integrate all omics platforms in one and would help to improve the crop plants. The SOL community is now poised to exploit the genome sequence information for the benefit of mankind. The next one decade would be most challenging but also exciting, as the dividends of above efforts would become some available. ■

