

### Scientists as communicators

There seems to be a consensus over the view that both scientists and journalists are significant for the communication of science. A strong scientist–media interface can therefore help strengthen the process of science communication. In the UK efforts are being made to train scientists for better communication. One such course is being run by the Royal Society in London (<http://royalsociety.org/Communication-and-Media-Training/>).

Australia also conducts media training workshops for scientists (<http://www.scienceinpublic.com.au/>).

Though the general perception is that most scientists cannot communicate well, a recent article (<http://www.nature.com/news/2011/110126/full/469445a.html>) in *Nature* calls it a myth and propounds, ‘Of course scientists can communicate’.

It also goes on to add that ‘scientists are not the only people to blame for a prob-

lem in communication’. Here, I cannot agree more with Tim Radford when he writes, ‘Those who can think clearly can usually write clearly: thoughts have value only when expressed, and the more clearly they are expressed, the greater their potential value’.

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### MEETING REPORT

## Solanaceae conference\*

To take stock of the understanding of genetics, molecular biology and breeding efforts for solanaceous crops, the Solanaceae Conference (SOL) is being regularly organized every year, starting in 2004, when the first SOL was held at Wageningen, The Netherlands. The 7th SOL held at Dundee, Scotland, was attended by about 250 scientists belonging to as many as 30 countries. This conference was important because significant amount of work has been done in Solanaceae genomics research since the last conference in 2009 and particularly with the near completion of the tomato and potato genome sequencing projects.

The symposium began with a welcome address by Howard Davies (Deputy Director, Scottish Crop Research Institute (SCRI), Dundee) and SOL 2010 organizing committee members mentioning the rationale behind organizing the 7th SOL meeting. David Baulcombe (University of Cambridge, Cambridge) discussed about the genome interactions in hybrid *Solanum* species and RNA silencing. He showed that there are hybrid-specific small RNAs (sRNAs) associated with suppression of gene expression and epigenetic modification of the genic DNA. However, they are absent in the F<sub>1</sub> hybrids and present only in F<sub>2</sub> and intro-

gression lines. These hybrid-specific sRNAs may influence transgressive phenotypes in hybrids, including those affecting agronomic characteristics.

The conference comprised of the following themes: SOL biodiversity and evolution; Plant growth and development; The SOL genomes; Biotic stress; Abiotic stress; Translational genomics and molecular breeding; Informatics and computational biology; Tools and emerging technologies; Tomato; Potato; Other Solanaceae species; Metabolomics and proteomics, and Functional genomics and systems biology and SGN workshop.

As expected in the current post-genomics era, the major emphasis throughout the symposium was on biotechnology/genomics/metabolomics/proteomics/systems biology and their implication on the study of genetics for solanaceous crops improvement. Mario Vallejo-Marin (University of Stirling, Stirling) discussed how the interaction between anther morphology and pollinator behaviour in heterantherous *Solanum* determines the fate of pollen. Andrew R. Leitch (Queen Mary University, London) spoke on the evolution of allopolyploids in the genus *Nicotiana*. In other presentations, emphasis was laid on the study of plant growth and development, and status of SOL genomes sequencing. Mondher Bouzayen (Université de Toulouse, Toulouse) spoke on the tomato Auxin Response Factor (ARF8) which is central to the mechanism controlling

fruit-set initiation. One session was devoted to ‘The SOL genomes’. Giovanni Giuliano (Casaccia Research Center, Rome) presented the status of tomato genome sequencing and about the large-scale genome duplication and synteny. He reported that 33,926 predicted proteins are in agreement with previous estimates of tomato gene number. An average gene density of ~23.4 kb/gene reflects the occurrence of large ‘gene deserts’. C. R. Buell (The Potato Genome Sequencing Consortium, Michigan State University, Michigan) presented an overview of the potato genome sequencing. Buell and his group have annotated the potato genome and are currently analysing the transcriptome and genes critical to potato biology. He emphasized on the timely release of the potato genome sequence data that will provide the entire Solanaceae research community an opportunity to exploit the genome sequence for fundamental and applied biological studies, including plant breeding. N. Ivanov (Philip Morris International, Neuchâtel) talked about the challenges of tobacco genome sequencing and assembly. He concluded by saying that a successful high-quality assembly of such a complex genome requires the use of a physical map to overcome the challenges of polyploidy and high repeat content. Doil Choi (Seoul National University, Seoul) talked about the progress of pepper genome sequencing project. Choi and his group have assembled the 1270 pepper BAC sequences generated by Roche/454 FLX,

\*A report on the 7th Solanaceae Conference (SOL) held during 5–9 September 2010 at Dundee, Scotland and jointly organized by the Scottish Crop Research Institute and the UK-SOL.

resulting in 34,743 contigs, with average contig size of 2707 bp, and total length 0.94 Gb. Bicheng Yang (BGI–Shenzhen) talked about Pan Genome, with a target of sequencing 1000 plant and animal reference genomes.

Severe losses are caused by various biotic and abiotic stresses in solanaceous crops and understanding the different aspects of resistance is important. The third day of the conference was devoted to: (i) biotic stress, (ii) abiotic stress and (iii) translational genomics and molecular breeding. The session on biotic stress focused on various aspects of pathogen effectors in breeding and disease resistance (Sophien Kamoun, The Sainsbury Laboratory, Norwich), hormonal signalling in defence responses (Chuanyou Li, Chinese Academy of Sciences, Beijing), mapping of QTL associated with virus resistance (Palchamy Kadirvel, The World Vegetable Center, Tainan), and isolation of resistance gene (Ken-Taro Sekine, Iwate Biotechnology Research Center, Iwate). The session on abiotic stress focused on various aspects of improving water-use efficiency through transgenic and QTL approaches. Andrew Thompson (University of Warwick, Warwick) described the importance of abscisic acid, a key modulator of plant responses to water deficit and maintenance of a favourable plant water status. Menachem Moshelion (Hebrew University of Jerusalem, Rehovot) presented the role of aquaporins in improving plant vigour, abiotic stress tolerance and yield production. He proposed that the regulation mechanism controlling cellular water and CO<sub>2</sub> permeability might have a role in determining the whole-plant hydraulic conductance, and thus its abiotic stress tolerance. Rachael Symonds (The World Vegetable Center) described a new protocol to assess the comparative drought tolerance of different plant genotypes in comparable soil moisture conditions. He discussed about QTL analysis and candidate gene approaches for identification of genes associated with drought stress tolerance in tomato. Jocelyn Rose (Cornell University, Ithaca) described that cuticles make an important contribution to tomato fruit softening, both directly as a mechanical support and indirectly through the regulation of transpiration and water status, as well as resistance to microbial infection. Another important session of the conference focused on translational genomics and

molecular breeding, in which Ester van der Knaap (The Ohio State University, Wooster) discussed classification of tomato varieties based on germplasm class, fruit-shape category, fruit-shape genes and genetic clusters. Walter de Jong (Cornell University) described the development of SNP markers in elite germplasm for applied potato breeding under the SolCAP programme. Laura Toppino (Unità di Ricerca per l'Orticoltura, Montanaso Lombardo) talked about gene-containment system based on artificial microRNA-mediated inactivation of two general transcription factors in *Solanum melongena*. Christiane Gebhardt (Max-Plant Institute for Plant Breeding Research, Koln) presented the results on natural variation in potato by linking candidate gene variation to complex traits. Ilan Paran (Institute of Plant Sciences, Bet Dagan) talked about the variation in pigment content in pepper fruit associated with plastid compartment size.

The fourth day of the conference was devoted to a variety of topics, including: (i) Informatics and computational biology, (ii) Tools and emerging technologies, (iii) Tomato, (iv) Potato, and (v) Other Solanaceae species. In the morning session, Björn Usadel (Max-Plant Institute of Molecular Plant Physiology, Golm) talked about sequencing the *Solanum pennellii* genome as an approach to study diversity in the tomato clade. Maria Ercolano (University of Naples 'Federico II', Portici) discussed a combined approach for tagging R-gene candidate loci in the tomato genome. For identification of R-genes in the tomato genome, Ercolano and her group have developed a specific R-gene prediction tool based on HMM profiling and Interpro database scanning. Using this tool, they have predicted 867 R-genes with the mean coding sequence of 2256 bp and mapped them either at chromosomal regions previously shown to contain R-genes or at positions not yet identified as R-gene regions. David Martin (University of Dundee, Dundee) presented results on developing informatics resources for end-users of the potato genome sequence project data. John P. Hamilton (Michigan State University) talked about SNP identification from potato and tomato short read transcriptome sequences. Using Illumina GAI sequencing technology, Hamilton and his group have generated 2.82 Gb and >2.5 Gb of total

sequence for each potato and tomato cultivar respectively. A total of 20,828 putative SNPs were identified: 66% of these were *Solanum pimpinellifolium*-specific. Dan Bolser (University of Dundee) described how *in silico* approaches can be used for anchoring the potato genome. The parallel session under 'Tools and emerging technologies' mainly focused on RNA-seq analysis of the shade avoidance in tomato and its wild relatives (Jose M. Jimenez-Gomez, University of California, California), plant transformation using DNA minicircles without vector backbone sequences (Tony Conner, New Zealand Institute for Plant and Food Research Ltd, Christchurch) and Eco-TILLING in tomato to unravell the hidden gifts of nature (R. P. Sharma, University of Hyderabad, Hyderabad). Cornelius Barry (Michigan State University), talked on tomato trichomes as a model system for exploring diversity within specialized secondary metabolism. He presented data on metabolite profiling of trichomes from a set of chromosome substitution lines created from a cross between *Solanum lycopersicum* and the wild relative *S. pennellii*, which revealed considerable diversity in both acylsugar and terpene production. He concluded mentioning that chemical diversity makes the tomato trichome an excellent model system for elucidating the biosynthesis of these specialized metabolites. Romyana Karlova (Wageningen University, Wageningen) talked on *APETALA2* functions in fruit development and in a ripening regulatory network together with *CNR*. She described how *CNR* directly binds to the promoter of *AP2* and positively controls its expression in tomato fruits. She further showed that the two proteins were also able to interact with each other in plant cells *in vivo*. Yellamaraju Sreelakshmi (University of Hyderabad) talked on phototropin1, a new player in regulating the shelf-life of tomato fruits. Tools for gene function analysis, primarily based on *Agrobacterium*-mediated transient expression (fruit agroinjection), which allow limited but fast transgene expression in fruit tissues were discussed by Diego Orzaez (Instituto de Biología Molecular Celular de Plantas, Valencia). He described how agroinjection opened the way for in-fruit delivery of viral infective clones and consequently led to the development of fast virus-induced gene silencing methodologies

for fruit reverse genetics. Bjorn Kloosterman (Wageningen University) presented an integrative-omics approach for studying potato tuber quality traits. He showed that network reconstruction after data integration can be used to visualize pathways of individual components associated with a trait of interest. Raymond Campbell (SCRI) spoke about the understanding of carotenoid accumulation in potato tubers. His group has developed transgenic potato plants by silencing the best candidate gene, a carotenoid cleavage dioxygenase (CCD4), resulting in increased levels of tuber carotenoids and unexpected effects on tuber morphology that mimic a heat-sprouting phenotype. Heejin Jeong (Seoul National University) described how high resolution melting method can detect natural variation and EMS-induced mutation in *Capsicum*. He showed that this strategy can be used for

the identification of molecular diversity of agriculturally important genes.

Other presentations focused on metabolomics, proteomics, functional genomics and systems biology. Asaph Aharoni (The Weizmann Institute of Science, Rehovot) mentioned how silencing of the *TOMATO AGAMOUSLIKE 1 (TAGL1)* MADS-box gene results in altered fruit pigmentation. Ryan P. McQuinn (Cornell University) showed that apricot is not solely a carotenoid-specific mutation, rather a mutation in a more general regulator of tomato fruit ripening. Mireille Faurobert (National Institute for Agricultural Research, Montfavet Cédex) discussed the proteomic database (SOLstIS: <http://w3.avignon.inra.fr/solstis>). Wilco Ligterink (Wageningen University) talked on unravelling the complex trait of seed quality in tomato by genetic genomics approach. Tamas Dalmay (University of

East Anglia, Norwich) discussed the role of short RNAs in fruit development and ripening. He described how his group has identified targets of miRNAs at a genomic scale using the 'degradome' approach and then compared the expression profiles of miRNAs and their targets following mRNA expression analysis at the same time-points using Affymetrix arrays. He concluded by saying that some miRNA/target pairs showed the expected negative correlation, but surprisingly a high percentage showed mixed or positive correlation. During the closing session, it was announced that the next conference in this series will be held at Tsukuba, Japan in 2011.

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## New hopes from new minister

In January 2011, the Prime Minister of India, Dr Manmohan Singh reshuffled portfolios of his ministers. Shri Ashwani Kumar took charge as Minister of State for Science and Technology, and Earth Sciences. While taking charge of his ministry, he gave a lot of new hopes in the form of, The Biotechnology Regulatory Authority of India Bill, the DNA Profiling Bill, Public Funded Research and Development (Protection, Utilization and Regulation of Intellectual Property) Bill, and the Regional Centre for Biotechnology Bill.

He also stated that the scientific temper needs to be inculcated among more and more students in the country. In a brief media interaction, he underlined the

need to make the benefits of research available to the masses, particularly to the farmers. He further stated that the research and development in biotechnology must help farmers to get more yield and that the Meteorological Department must help them to get timely information to deal with the vagaries of drought or heavy rains.

The Minister stressed on the need to work for reverse brain-drain and ensure that the best Indian talent gets the right atmosphere to work in the country. 'We need to provide them a positive atmosphere and work-place for technical and scientific research,' he added.

The Academy of Scientific and Innovative Research Bill 2010 is pending in

Parliament. Ashwani Kumar said it would be the endeavour of the ministry to introduce four bills in Parliament in the Budget session.

'The Biotechnology Regulatory Authority of India Bill, the DNA Profiling Bill, Public Funded Research and Development (Protection, Utilization and Regulation of Intellectual Property) Bill, and the Regional Centre for Biotechnology Bill are in the pipeline,' he said.

To a question on commercial introduction of GM crops, the minister said the Government would take a 'collective and correct decision'.

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