

Meeting report

New pulses in plant research

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A report on the second International Conference on Legume Genomics and Genetics, organized jointly with the fifth AEP European Conference on Grain Legumes "Legumes for the benefit of agriculture, nutrition and the environment: their genomics, their products and their improvement", Dijon, France, 7-11 June 2004.

The development of sustainable agriculture is a major challenge for humanity: we could eradicate hunger from the earth but still preserve our planet for coming generations, for example by using less pesticides and chemical fertilizers, reducing the greenhouse effect, maintaining small farming communities, preserving biodiversity. It is clear that legumes can provide a solution: in terms of protein content they are amongst the richest plants in the world, and they contribute to feeding the majority of the inhabitants of developing countries. Thanks to symbiotic nitrogen fixation, legumes do not need nitrogenous fertilizers, production of which consumes petroleum and which contribute significantly to groundwater pollution as well as to the greenhouse effect. Last but not least, legumes are very rich in molecules that have potential pharmaceutical uses. As stated by Rodomiro Ortiz (International Institute of Tropical Agriculture, Kampala, Uganda) "food legumes are a gold-mine for the developing world", but their productivity remains limited by a lack of access to, and control of, water resources.

As a joint meeting, the conference brought together for the first time researchers working on improving grain-legume breeding and processing with those using modern genomic strategies on model plants. Jean-Jacques Drevon (INRA, Montpellier, France) identified the central theme of the conference as "how to link genomics and agronomy". Over five days, 450 participants from 45 countries tried to provide answer(s) to this question. It should be noted, however, that the attendance came essentially from developed

countries - fewer than 4% of participants came from Africa, for example. This report focuses on a few of the presentations that illustrate the multidisciplinary nature of current research into the genetics and genomics of legumes.

Genetics and molecular biology of model and other legumes

The large diversity of legume species initially encouraged researchers to develop two model legumes: *Medicago truncatula* and *Lotus japonicus*. It now appears that, contrary to early concerns, having two model legumes does not necessarily lead to a duplication of results but, in fact, often leads to an acceleration of research by creating complementary and synergistic approaches between the two research communities. Nevin Young (University of Minnesota, St. Paul, USA) presented persuasive evidence that the *M. truncatula* genome is organized into distinct regions of gene-rich euchromatin and repeat-rich pericentromeric heterochromatin. Thus, sequencing the gene-space of *M. truncatula* can be performed efficiently using a BAC-by-BAC strategy, making use of bacterial artificial chromosomes (BACs) anchored in the expressed genome. Young went on to describe the organization of the international sequencing consortium, which comprises groups from the USA and EU and is expected to finish sequencing the gene-space of *M. truncatula* by the end of 2006 (further details on this sequencing project can be found at [<http://www.medicago.org/genome>]).

Most plant species form symbiotic associations, known as mycorrhizae, between their roots and fungi. Helge Kuester (University of Bielefeld, Germany) reported studies using oligonucleotide microarrays to characterize the transcriptome of a particular type of mycorrhizal symbiosis - arbuscular mycorrhiza - formed by *M. truncatula* in response to two different species of *Glomus* fungi. A subset of 205 genes, including several novel transcriptional regulators, was found to be induced in both endosymbioses. Interestingly,

in addition to these co-induced genes, several hundred genes were activated only by one or the other species of symbiotic fungus, indicating that the plant transcriptome in arbuscular mycorrhiza roots is strongly dependent on the nature of the infecting microsymbiont. Root hairs are specialized outgrowths of epidermal cells of the root that represent an essential interface between the plant and the soil for nutrient and water uptake. Gary Stacey's group (University of Missouri, Columbia, USA) was able to isolate gram quantities of soybean root hairs, and therefore open the door to future DNA microarray and proteomic studies of legume root-hair infection by rhizobia.

Measurement and identification of the metabolome allows various issues to be addressed, such as the influence of genotype, genetic modifications and stress factors on a plant's behavior. Adrian Charlton (Central Science Laboratory, York, UK) uses nuclear magnetic resonance (NMR) spectroscopy to study the pea leaf metabolome and is able to discriminate between members of the germplasm collection maintained at the John Innes Centre (Norwich, UK) and between plants subjected to different watering regimes. Ole Søgaard Lund (Danish Institute of Agricultural Sciences, Slagelse, Denmark) described the transferal to legumes of another technology, virus induced gene silencing (VIGS). His group has inoculated pea plants with constructs combining the tobnavirus Pea early-browning virus (PEVB) with the *PHYTOENE DESATURASE* (*PDS*) or *UNIFOLIATA* (*UNI*) genes. As would be predicted, bleaching of leaves was observed with the *PDS* constructs and abnormal flowers with the *UNI* constructs, whereas plants inoculated with a control construct were unaffected.

Biotic and abiotic interactions

The nature of molecular recognition specificity was addressed by Tom Ashfield (Indiana University, Bloomington, USA) through a study of bacterial disease resistance mediated by so-called R-genes. The *RPM1* and *Rpg1-b* genes, from *Arabidopsis* and soybean respectively, confer resistance to *Pseudomonas syringae* strains expressing the effector protein *AvrB*. By comparing their sequences, Ashfield discovered that the genes were not orthologous, implying independent evolution of two functionally equivalent R-alleles ('convergent evolution').

Martin Crespi (CNRS, Gif-sur-Yvette, France) reported the characterization of the *M. truncatula* transcriptome during root-growth accompanying adaptation to salt stress, using microarrays, subtractive hybridization libraries (SSH) and homology searches. He has identified 320 genes, of which 52 were completely unknown and 72 appear to be legume-specific, suggesting novel pathways linked to environmental stress responses in *M. truncatula*. Several of these genes are potential regulators, for example, Crespi found 11 transcription factors.

Plant development and breeding

Christine Beveridge (University of Queensland, Brisbane, Australia) reported the integration of genetic and phenotypic data to test genetic models related to the control of pea bud outgrowth. One of seven *RAMOSUS* genes, *RMS1*, is auxin-responsive and encodes an enzyme of unknown function acting on the pathway for the biosynthesis or metabolism of a long-distance developmental signal involved in the inhibition of bud outgrowth. Moreover, *RMS1* is regulated by auxin-independent long-distance signal(s).

Hans Weber (Institute for Plant Genetics and Crop Plant Research, Gatersleben, Germany) showed that transgenic legumes that have incorporated metabolic pathway genes - either by expressing a bacterial phosphoenolpyruvate carboxylase gene or by the overexpression of a legume amino-acid transporter gene - have increased seed sink strength (the ability to accumulate metabolites) and protein content. These results reveal an enormous complexity and flexibility in seed development and metabolism because pleiotropic phenotypes are created even if the expression of a single gene has been altered.

A general conclusion to the conference was given by Marc Zabeau (European Plant Science Organisation, Ghent, Belgium) who developed the idea that there is an urgent need for a long-term global vision to integrate plant biotechnologies, genomics and agriculture in order to double agricultural productivity by the 2050s. Only an improved understanding of plant biology, coupled with concerted international efforts, will allow us to reach the objective of an economically and environmentally sustainable agriculture. Further details of the conference can be found at [<http://www.grainlegumes.com/>].