Mycorrhiza (2002) 12:161–162

NEWSCORNER

The 10th MPMI conference: sparkling mycorrhiza research!

The 10th International Congress on Molecular Plant-Microbe Interactions (MPMI) was held 10–14 July, 2001 at the University of Wisconsin, Madison, Wisconsin, with over 1,000 participants from more than 40 countries. The overall organization of the conference was excellent. Together with the fabulous conference site on the shore of Lake Mendota and the pleasant summer weather, the conference was most satisfactory and unforgettable! On behalf of all in attendance, particularly the mycorrhizasts, I thank Sally Leong and the local organising committee for their efforts in making this meeting such a great success.

The scientific program covered the entire scope of plant-microbe interactions and topics: from the molecular level of 'gene-for-gene' interactions to the ecology and population level, from investigation of single genes to gene systems and the whole genome, and from theoretical to modern practical techniques. The program was arranged into eight plenary sessions and six concurrent sessions, and included about 70 speakers and nearly 700 posters. The proceedings can be accessed through the web site (http://www.plantpath.wisc.edu/mpmi). The plenary sessions were stimulating and gave participants a good opportunity to learn of recent advances across the field, and the concurrent sessions dealt with more specialised subjects. The posters were well organised according to topic and were displayed throughout the week, thus providing delegates with good opportunities to have face-to-face discussions with the researchers. The whole meeting went through with an interactive atmosphere for the whole of plant-microbe interactions.

Because the time of this conference clashed with ICOM3, the mycorrhizasts were sparse. Nevertheless, the mycorrhizal work presented at the meeting was sparkling, and reflected the latest achievements and trends in plant-fungal interactions (for AM fungi in particular). Maria Harrison (Noble Foundation, USA), the only speaker focusing on this area, presented work undertaken in her group and highlighted the major approaches and achievements.

Medicago truncatula and *Lotus japonicus* have been well developed as model legumes for analysis of nodulation and mycorrhizal symbioses, both of which are absent in *Arabidopsis thaliana*. More and more mutants affecting both nodulation and mycorrhizal associations are being identified in these legumes. The most exciting advances are the identification of two mutants in *M. truncatula* (by Maria Harrison's group). These mutants fail to form normal mycorrhizal associations but are not impaired in nodulation. The discovery of these mutants has confirmed a new and independent pathway of genetic control of AM associations in legumes. With modern molecular genetic studies, a clearer picture is being obtained of genes required for nodulation and/or mycorrhizal associations.

Two additional mycorrhizal mutants have also been identified in non-leguminous plant species, one in a monocotyledon species, maize (Thomas Boller's group, Basle, Switzerland) and the other in tomato (Yoram Kapulnik's group, Volcani Centre, Israel). Both mutants define novel genetically controlled steps in mycorrhizal colonisation. The maize mutant does not allow formation of fungal appressoria and the tomato mutant prohibits pre-infection growth of fungi. Mapping and cloning of the "mycorrhiza" genes in mycorrhiza-defective mutants is currently underway in a number of groups and will represent a breakthrough towards understanding the genetic and molecular biological mechanisms of mycorrhizal interactions.

As with other plant-microbe interactions, new technologies such as high-throughput EST sequencing and expression profiling have been introduced into the studies of plant-AM fungal interactions. A fungal EST sequencing program has been initiated in Maria Harrison's group and over 1,000 ESTs have been obtained in *Glomus intraradices* and *G. versiforme*. These sequences are valuable for studying regulation and functioning of fungal genes during the establishment of mycorrhizal symbioses. cDNA microarray and suppression subtractive hy-

---

Ling-Ling Gao
Adelaide University, Australia

bridisation techniques are being used by several groups (Maria Harrison's group; Vivienne Gianinazzi-Pearson's group, Dijon, France; and groups led by Franziska Krajinski, University of Hannover and Philipp Franken, Max Planck Institute for Terrestrial Microbiology, Germany). These techniques permit investigation of multiple genes or gene systems rather than single genes, and play an important role in the study of mutualistic mycorrhizal symbioses, which must involve a large number of genes.

As *A. thaliana* is naturally non-mycorrhizal and *M. truncatula* and *L. japonicus* involve interactions with rhizobia, it is important to establish model systems in non-legume plants, such as the tomato and maize mutants mentioned above and the tomato mutant being used by the groups led by Sally Smith (Adelaide University, South Australia) and Susan Barker (University of Western Australia). I hope that these model systems will facilitate a more cooperative and concentrated research approach into this exciting area of plant-mycorrhiza interactions. With the increased number of plant mutants identified and with the application of new techniques, I confidently expect to see great achievements in this area at the next International Congress on MPMI, which is scheduled to be in St. Petersburg, Russia, in 2003.