

Conference Report

BRASSICA 2004

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In this article I briefly describe two aspects of this meeting that are relevant to researchers who study *Brassica napus*. The conference was a joint meeting comprising the 14th Crucifer Genetics workshop and the Fourth International Society for Horticultural Science Symposium on Brassicas. The scientific program is on the web (<http://www.brassica2004.org/>) and papers based on the oral presentations will be published as an issue of the journal, Acta Horticulturae, in 2005. About 200 delegates participated in an informative and enjoyable meeting which was extremely well run by a committee headed by Professor Pyo Yong Kim, Chungnam National University. There were four days of talks and more than 100 posters. Also participants enjoyed a fascinating technical tour that included visits to a Kimchi factory, a Korean temple, and a field of Chinese cabbage by moonlight.

The meeting focussed on vegetable brassicas, as well as breeding and genetics of crucifers. Many of the local talks and posters were on genetic improvement of Chinese cabbage (*Brassica rapa* subspecies *pekinensis*). This crop is an important part of the Korean diet consumed as chimki, a product that is fermented and processed with seasoning mixture of red pepper, garlic, ginger, radish. The meeting gave Koreans the opportunity to display their strong profile in international science and technology. Many of the presentations by locals were underpinned by applications of cutting edge technology, such as genomic analysis microarray analysis and understanding of global regulation.

This meeting was an opportunity for the Multinational Brassica Genome project to be presented to a broad gathering of Brassica scientists. This project is aimed at sequencing the genome *B. rapa* subspecies *pekinensis*, which has a genome size of 550 Mb (see http://brassica.bbsrc.ac.uk/brassica_genome_sequencing_concept.htm). An emphasis of the project is make all resources publicly available and to apply information to enhance genome analysis of other Brassica species. Accordingly physical maps, communal information resources, nomenclature, sequence databases and analytical tools are being developed and integrated between various laboratories. Activities based around these themes were described from research groups from countries including Australia, China, Korea, US, UK.

An afternoon was devoted to club root of Brassicas which is caused by *Plasmodiophora brassicae*. This fungus-like pathogen affects vegetable Brassicas

more than *B. napus*, although in Sweden it has been seen in *B. napus* crops for almost 100 years and often causes major yield losses. Club root is also a problem in Germany. Control is by breeding resistant cultivars and cultural practices such as soil fumigation, liming (for vegetable Brassicas). Genes conferring resistance in Brassicas including Chinese cabbage have been mapped and closely linked markers have been identified. *Arabidopsis thaliana* is susceptible to club root and this interaction has been analysed using microarrays where changes in transcription patterns of *Arabidopsis* genes have been determined. In contrast to the large amount of research on the plant, there have been very few studies of the pathogen, as it is not amenable to analysis being polyploid, obligate and not closely related to any other well characterised organism.

From the perspective of a canola pathologist, this meeting was a very valuable reminder of the importance of links between scientists studying Brassicas and of how technologies and findings applicable to the vegetable industry can also be often readily applied to the grains industry.