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CONFERENCE REPORT

International Conference: Molecular Mapping and Marker Assisted Selection in Plants. Vienna 3^{rd}–6^{th} February 2008

A scientific program balanced by International Organizing Committee in chair with Prof. A. TOURAEV (Vienna University, Biocentrum) offered state-of-the-art information for basic and applied scientists as well as plant breeders. The dense three-day program was divided into six sessions covering relevant research fields: Plant genome organisation, Plant genome analysis and mapping, Molecular markers for genetic mapping of plant genome, Marker-assisted selection, Mapping of quantitative trait loci (QTL), Map-based cloning and chromosome mapping. Still longer was the list of plant species, starting from barley through pea to vine and wheat, which was presented by more than 350 scientists from 21 countries, from Australia to Norway, Malaysia to Mexico.

The theme of application of flourishing molecular technologies for facilitation and speeding up of the timely plant breeding process has received attention of geneticists and their practical fellows, breeders, for nearly two decades. There is no doubt that the current genomic knowledge of model species as well as emerging data for crop species offers enormous possibilities for speeding up and accuracy of the breeding process. However, a gap between breeders and academy-based research communities still exists. The former heavily rely on earned experience and often intuition of successful breeders, with inevitable extensive field performance testing and crude selection of best performers from a large number of crosses, having in mind the ultimate aim of their work – variety registration and use. While the latter community, often studying specific genes or processes, is driven largely by publication records. The conference also aimed to address these two aspects.

During the breeding process, numerous traits, including pest and disease resistances were introduced into modern varieties either from wild relatives or neglected old varieties. These traits were followed by genetic and phenotypic means such as heritable loci. Nowadays, in order to better understand, exploit and transfer them in crosses, there is an interest to map their positions genomically or at least to provide molecular markers sufficiently close to be usable in breeding process. The wild relatives and landraces are now coming back into focus, owing to genetic diversity richness carried in their genomes, often narrowed in high yield oriented modern varieties. This aspect of genetic diversity was documented at the conference from simple molecular diversity to complex linkage disequilibrium (LD) studies on various species. However, a large part of agronomical valuable traits is not governed by single genes but by several often interacting loci, well known as quantitative trait loci (QTLs). These are much more difficult to identify, moreover to map corresponding gene components. In this field, high-throughput genotyping technologies come to power, accompanied by laborious field phenotypic evaluation. I see this interaction as a good example of collaboration of breeding and academic communities, a niche where both parties can profit.

The impressive case how complex and large might be an experiment aiming to dissect gene versus environmental effects on wheat yield, resulting in "Meta-QTL analysis", was presented by J. SNAPE, head of Crop Genetics Department at JIC UK. From agronomical and physiological evaluation of numerous doubled haploid wheat lines over several years in several locations, through microsatellite (e.g. neutral markers) genotyping, culminating in the use of near-isogenic lines for fine mapping of candidate genes, the function of which was studied in mutants identified by modern TILLING approach. TILLING becomes a powerful and standard method of both genetic diversity studies and indentification of mutation, followed by a novel means of mutated gene allele identification. It is clear that to handle and find useful information in such an amount of generated data, appropriate statistical methods are essential, as demonstrated by J. Buntjer from KeyGene, Netherlands and J. White, London UK.

Another example is to use genomic synteny between model plants and crops. Such a gene specific approach was the exploitation of synteny in Cucurbits for the tagging of recessive Potyvirus resistances, given by M. Havey from Wisconsin USA. This is an example of recessive, e.g. difficult to select trait, moreover the manifestation of which requires careful glasshouse and laboratory examination. Thus, the identification of single nucleotide exchanges (SNPs) in respective gene, coding for eukaryotic translation factor (eIF4E) resulted in nice demonstration how "perfect marker" for breeding might look like. This is certainly where genomics and genetics will lead to in the nearest future, when sufficient knowledge of genes underlying respective traits is collected. Difficulties such as commonly exploited heterosis, epistasis, called the "hidden half" or even "the dark side" of QTL and frequent polyploidy of crop species were also mentioned.

One particular talk, considered as excellent by many participants, had a simple but mysterious title, Where Have All the QTL Gone?, given by Dani Zamir, a respected geneticist from Jerusalem, working on tomato QTL mapping. He guided us through a more than 15-year story of tomato introgression lines, being extensively studied for hundreds of QTLs, some of whose underlying genes were subsequently cloned, as exampled by invertase governing tomato sugar content. The major "take a home message" was the absence and urgent need of a database for recorded phenotypic data (Phenome Networks), since collected data are often lost, not being stored.

Currently, QTLs are map using linked molecular markers, such as SSRs, accuracy and usefulness of such derived markers is of great importance. As such, linked DNA markers undergo recombination, the frequency of which determines the effectivity and reliability of such marker. A. Price from Aberdeen, UK showed on dozens of published examples that critical distances for markers to be reliable are around and below 1 cM.

Although more and more genomic data are available for a broader spectrum of species, there are some species with extremely large genomes. The size complicates and even hinders effective sequence assembly. The final talk given by J. Dolezel from Olomouc, Czech Republic on chromosome genomics in such difficult crop as wheat, with genome surpassing nearly five times the human genome, demonstrated the power of flow cytometry for individual chromosomes and chromosome arms sorting and subsequent specific library construction. It is delighting that the Czech team is a world leader in this topic, making a landmark in cytogenetics and genomics. Such approach enables orientation in huge genomic space and identification of genes of interest for the world population feeding grasses.

Regarding the progress of genome sequencing, including rice, soybean, maize, potato, sugar beet, tomato etc., it is well anticipated that all this knowledge, when linked with agronomical, physiological and genetical data will permit better targeting of the breeding process and providing the speed required in today's dynamic world.

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