

Molecular mapping and marker-assisted selection in plants*

During the last two decades, considerable progress has been made in the development of molecular markers and their use in mapping/tagging of genes/quantitative trait loci (QTLs) controlling important agronomic traits in all major crops. As a result, molecular markers closely associated with desirable traits are being utilized to increase the efficiency and effectiveness of conventional breeding by indirect selection of the desirable plants in segregating populations. An international conference was held recently to discuss the progress made and future challenges in molecular marker mapping and marker-assisted selection in plants. About 275 registered participants, including 44 speakers from different institutions belonging to 38 countries participated in this four-day event.

S. Briggs (University of California, USA), in his opening plenary lecture spoke on the progress made in the development of molecular markers, starting from protein-based iso-enzymes to restriction fragment length polymorphisms (RFLPs) and other DNA-based markers. He also outlined the progress made in the development of gene-based molecular markers with the sequencing of the rice genome, and the microarray-based molecular markers, which increased the density of markers and identification of expression QTLs (eQTLs). It was also emphasized that a revolutionary technology of mass spectrometry has raised the possibility that proteins may once again become important markers for breeding and genetics.

Among DNA-based markers, simple sequence repeat (SSR) markers are widely used in plants because of their abundance, hyper-variability, and suitability for high-throughput analysis. S. P. Kumpatla (Dow AgroSciences LLC, USA) highlighted the rapid and economical discovery of SSRs from expressed sequence tags (ESTs) available in public databases in a number of crop species and stated that among dicot species, dinucleotide repeats are most abundant.

K. Bilyeu (USDA-ARS, USA) suggested the use of candidate gene approach for developing useful, perfect markers for desirable traits in crop plants having complex genomes. For instance, in soybean multiple copies of candidate genes having probable involvement in the development of traits under improvement have been identified and characterized at the sequence and expression level between the wild and mutant lines. This led to the identification of mutant alleles in candidate genes, which were used to develop efficient molecular markers for distinguishing wild and mutant alleles. I. Matthies (IPK, Germany) highlighted the utility of the candidate gene approach in genetic association analysis for malting quality of barley. He identified the association between SNPs, InDels and haplotypes in a number of candidate genes and malting quality parameters by analysing the allelic diversity among 120 barley cultivars.

Molecular markers have a number of applications, including comparative and molecular mapping of desirable genes. In several plenary lectures, the role of molecular markers has been discussed for identification of the order and content of genes in individual chromosomes among related species. M. Freeling (University of California, USA) reported that although synteny is certainly a rule among species of the same family, there are some exceptions that cannot be explained due to the presence of multiple inversions, duplications and translocations. Using a flanking gene marker method, he evaluated authentic exceptions to synteny among *Arabidopsis*, papaya and grape, and stated that several non-transposon and non-tandem genes, which are not ancestral Brassicaceae genes, are present in *Arabidopsis*. Even the 5% genes representing the most ancestral gene families have been transposed into *Arabidopsis* and genes of some gene families have almost always new transpositions. He called these transposable genes as 'grey' genome and suggested that a new allele of interest may actually be a newly transposed gene that has been adapted rapidly after transposition. J. King (IGER, UK) stated that although a substantial component of the coding sequences is also localized

proximally in regions of very low recombination frequencies, a large proportion of this genetic variation could not be exploited during the domestication of monocot plants, because selection has been concentrated on genes located in the terminal regions of chromosomes within areas of high recombination frequency. T. Lelley (BOKU, Austria) also spoke on synteny and stated that two species of *Cucurbita* (*C. pepo* and *C. moschata*) have synteny at macro-level and do not have any major chromosomal rearrangement. M. Havey (USDA-ARS and UW, USA) and B. Hackauf (Julius-Kuhn Institut, Germany) highlighted the role of synteny in molecular tagging of useful genes in melon and rye respectively.

Genetic dissection of complex traits is still a challenge and efforts have been made for mapping genes/QTLs controlling yield and yield-contributing traits. J. Garcia-Mas (CSIC-IRTA-UAB, Spain), S. Vezzulli (IASMA Research Center, Italy) and H. Bagheri (WU, The Netherlands) discussed the development and use of molecular maps that also included functional markers in different crop species for this purpose. Vezzulli discussed a new freely available software (TMAP) that takes into account genotyping errors during map construction (<http://math.berkeley.edu/~dustin/tmap/>).

M. S. Roder (IPK, Germany) in her plenary lecture discussed fine mapping of a major QTL, explaining 84.7% phenotypic variation for grain weight on chromosome 7D of wheat and also reported identification of a novel gene for plant height on the same chromosome, which has strong correlation with grain weight either due to pleiotropic effect or due to tight linkage between the two genes. D. J. Somers (Agriculture & Agri-Food, Canada) highlighted genetic dissection of yield and yield-contributing traits using QTL analysis in spring wheat. He identified a number of QTLs on 12 chromosomes for nine traits and suggested the use of four validated grain-yield QTLs located on chromosomes 1A, 2D, 3B and 5A in marker-assisted breeding for improving yield of Canadian spring wheat. R. Kolliker (ARTRS, Switzerland) made successful efforts for

*A report on the International Conference on Molecular Mapping and Marker-Assisted Selection in Plants held during 3-6 February 2008 at Vienna, Austria.

QTL analysis in a cross-pollinated species of red clover, in which development and maintenance of mapping population is difficult, and identified the QTL for forage yield persistence and seed yield traits that are difficult to improve through phenotypic selection.

Molecular markers also allow us to dissect genomic regions interacting with environments for phenotypic expression of complex traits. J. W. Snape (John Innes Centre, UK) discussed the strategy of dissecting the gene \times environment interactions affecting wheat yield via QTL and physiological analysis. He used Meta-QTL analysis for yield and yield-contributing traits in a number of populations derived from genotypes adapted in different environments. This led to identification of useful allelic variations for these traits, which can be a focus in future for wheat improvement. Mapping and tagging of gene(s)/QTL(s) controlling root traits in maize, Fusarium head blight resistance in European wheat and nitrogen-use efficiency in sugarcane was discussed by R. Tuberosa (University of Bologna, Italy), H. Burstmayr (BOKU, Austria) and A. Whan (University of Queensland) respectively.

The main aim of molecular mapping is to identify markers that are closely associated with genes controlling desirable traits and are useful in breeding programmes for indirect selection of desirable recombinants in early segregating generations. O. Moullet (ACW, Switzerland) identified and evaluated plants ho-

mozygous at marker loci linked with a major QTL for FHB in wheat, but no significant increase in the level of FHB resistance was observed in these plants probably due to loss of QTL by double recombination, $G \times E$ interactions or epistasis interactions. Similarly, C. Thienpont (Louvaia-la-Neuve, Belgium) suggested the limitations of marker-assisted selection for root morphology in chicory due to strong environmental influence on this trait. However, Biradar obtained positive results when he evaluated several maize near-isogenic lines carrying a major QTL for chilling tolerance introgressed through marker-assisted backcrossing. D. Zamir (The Hebrew University of Jerusalem, Israel) pointed out that although QTL analysis has been widely conducted in plants and animals, its successful use in marker-assisted selection (MAS) is limited. He laid more emphasis on using the accurate phenotyping data in QTL analysis and also suggested development of an integrated phenomic database in each crop, which may unravel some unifying principles about the architecture of complex traits and pave the road for genomic assisted breeding. A. H. Price (University of Aberdeen, UK) discussed the utility of accurate QTL mapping by giving several examples of map-based cloning of major and minor QTL in plants. J. Dolezel (Institute of Experimental Botany, Czech Republic) highlighted the role of flow cytometry in separation of individual chromosomes and chromosome arms and their use in

preparation of chromosome-specific BAC libraries that can be useful in map-based cloning of genes/QTLs.

The applicability of molecular markers for other purposes, including analysis of genetic diversity using microsatellite markers in order to exploit the germplasm for improving the yield capacity of oats (I. Griffiths, IGER, UK) and understanding the molecular mechanism responsible for heterosis in maize (F. Hochholdinger, UT-ZMBP, Germany) was also discussed. Thus, considering the potential of the molecular marker technology for crop improvement, the conference provided a platform to understand the current bottlenecks and challenges in molecular mapping and MAS. The meeting also provided a feedback that mapping of genes/QTLs controlling agronomically important complex traits can be useful for crop improvement, if accurate phenotyping data are taken on mapping populations and used in QTL analysis. A major effort is also needed on molecular mapping of genes/QTLs for yield and yield-contributing traits, especially in major food crops and their exploitation in the development of new and improved genotypes through breeding programmes.

Jitendra Kumar, Molecular Biology Laboratory, Department of Genetics and Plant Breeding, Ch. Charan Singh University, Meerut 250 004, India.
e-mail: Jitendra_kumar-2k1@rediffmail.com

MEETING REPORT

Neutron Scattering 2008*

The International Symposium on Neutron Scattering 2008 (ISNS 2008) covered various aspects of neutron scattering research and applications in physics, chemistry, biology and materials science. More than 200 participants from 15 countries, including some pioneers of the neutron scattering activity in India, participated in the deliberations.

*A report on the International Symposium on Neutron Scattering 2008, held at the Bhabha Atomic Research Centre, Mumbai during 15-18 January 2008.

There were 48 invited talks out of which 40 were from abroad, including those from ORNL, ANL, LANL, UCSD, NIST, Chalk River, ISIS, PSI, ILL, LLB, HMI, FRM2, FZJ, FZK, JINR, Vienna, Copenhagen, Warwick, JAEA, J-PARC and ANSTO. The talks included topics on new experimental facilities, and studies involving diffraction, magnetism, biological systems, hydrogen and diffusion, dynamics, neutron optics, small-angle scattering, reflectometry, and other applications. Present-day mega-facilities, upcoming as well as proposed ones, were

presented. There were also 90 contributed papers put up as posters. Presentations covered the wide range of science that is being pursued all over the world.

In the first technical session there were four talks. The first talk was by Ian S. Anderson (Oak Ridge National Laboratory) entitled 'The spallation neutron source - New opportunities'. The existence of both SNS and HFIR reactor with new cold source and guide hall under a single umbrella at ORNL will provide an opportunity to develop science and instrumentation taking advantage of unique