

Rice genetics*

Rice, from being a poor cousin to maize and wheat in terms of genetic information, has catapulted to the centre stage to become the model cereal in the past two decades and is heading for a grand amalgamation with the plant geneticists' Cinderella, the *Arabidopsis*. This was the message, conveyed loud and clear, at the just concluded Fifth International Rice Genetics Symposium (IRGS). This event, held once in five years attracted a total of 710 delegates from 46 countries and had 64 platform presentations under six thematic plenary sessions, eight concurrent sessions and four evening workshops. Besides, 378 posters were presented in 15 sections.

The Fifth IRGS, which was combined with the Third Annual International Rice Functional Genomics Symposium (IRFGS), focused mainly on the just completed rice genome sequence representing a major milestone in the history of rice genetics and the march from structural genomics to functional genomics. The symposia provided a forum for reviewing the latest advances in rice genetics and for in-depth discussions and exchange of information on classical genetics and genomics.

In the inaugural session, the lead paper by Ron Phillips (USA) highlighted the centrality of rice as a reference genome while Takuji Sasaki (Japan), who is heading the International Rice Genome Sequencing Project, explained the progress of rice genome sequencing efforts and highlighted the benefits expected to accrue due to the availability of complete genome sequence of the japonica rice cultivar, Nipponbare. The completed quality sequence covers 95% of the 389 Mbp genome, including virtually all of the euchromatin and two complete centromeres. A total of 37,544 non-transposable element-related protein coding genes have been identified in rice. Complete genome sequence information will facilitate easy identification of many important genes

by both forward and reverse genetic strategies and clarify the relationship between sequence variation and phenotypes.

Wild species of rice contain largely untapped reservoir of agriculturally important genes. The genus *Oryza* contains two cultivated and 22 wild species that represent ten distinct genome types. Rod Wing (USA) explained a new resource '*Oryza* map alignment project (OMAP)', which has been established to generate a comprehensive set of genomics resources to investigate genome evolution and enhance positional cloning efforts in the genus *Oryza*. Xing Wang Deng (China) gave an account of 'Genome wide transcription analyses in rice using tiling microarrays'. Studies by his group using high-density oligonucleotide tiling microarrays has revealed the presence of 35,970 annotated gene models and 5464 additional unique intergenic regions representing novel transcripts. Robin Buell (USA) spoke on the rice genome annotation database called Osa1, publicly available at <http://rice.tigr.org>, according to which gene density of rice is estimated to be one gene per 5.7 kb. Jun Yu (China) presented a paper highlighting the completion of sequencing of 93-11 and PA64S (parental lines of the Chinese two-line super hybrid LYP9). The study has yielded useful genetic markers and candidate genes for further investigations into molecular and functional basis of heterosis, a critical area for hybrid rice research. Gynheung An (Korea) presented the progress on 'T-DNA tagging for developmental biology', covering 47,932 T-DNA tagged lines. More than 40% of these had tag insertions in genic regions, distributed non-uniformly on each chromosome with higher insertions at distal ends. These mutant lines form a valuable resource for study of gene function.

John Bennett (IRRI, Manila) explained the progress of research at his institute on molecular basis of spikelet sterility caused by drought stress-induced defects in anther dehiscence, pollen germination and panicle exertion. K. Shinozaki (Japan) spoke about a number of genes and transcription factors associated with drought response and tolerance. *SRK2C*, a member of the SNF1-related phospho-

kinase family group of proteins, is a good candidate gene for inducing drought tolerance. Makato Matsuoka (Japan) spoke on 'Isolation of a QTL gene controlling grain number and QTL number, and QTL pyramiding to combine loci for grain number and plant height'. 'Gn1', a QTL that increases grain productivity in rice is actually a gene for cytokinin oxidase/dehydrogenase (OsCKX2), which causes cytokinin accumulation in inflorescence meristems and increases the number of reproductive organs. E. Guiderdoni (France) presented on 'Novel insights in rice root adaptive development'.

D. J. Mackill (IRRI) highlighted the role of QTLs in rice breeding, with specific emphasis on mapping and understanding of the major QTLs associated with submergence tolerance called 'Sub1'. Susan McCouch (USA) presented a paper on the efforts towards identification, functional characterization and utilization of yield-related QTLs from wild relatives of rice. Preliminary analyses suggested that the yield-related QTLs might be actually transcription factors which activate downstream genes. China has ventured into a comprehensive programme towards development of eco-friendly 'green super rice' through the application of genomic tools targeting traits like resistance to diseases and insects, efficiency in utilization of nitrogenous and phosphorus nutrients, drought resistance and water-use efficiency. The blueprint of this programme was explained by Qifa Zhang.

David Tuan-hua Ho (Taiwan) dealt with the use of 'tissue specific/ABA inducible promoters' for controlled transgene expression which is critical for maximizing the benefits of genetic engineering in rice and also to address environmental and biosafety concerns. The major pairing locus in wheat, *Ph1* stabilizes the pairing of the multiple related chromosomes at meiosis in polyploid crops like wheat. Graham Moore (UK) has identified *Ph1* homologues in rice. A. K. Tyagi (India) presented a paper on 'Expression and functional analysis of rice genes involved in reproductive development and stress response'. More than 7000 genes encoding transcription factors and signal transduction components, belonging to about 110

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classes have been used to prepare a database. Jan Leach (USA) gave an insight into 'Understanding broad-spectrum, durable resistance (BSDR) in rice'. Using varieties that show durable resistance historically, rice genes that are candidates for contributing to BSDR have been identified through co-localization with disease-resistance QTL in mapping studies.

A study on 'Multilocus analysis of nucleotide diversity of *O. sativa* complex' by Song Ge (China) indicated that the individuals of *O. rufipogon* and *O. nivara* were entirely mixed together in genealogical trees, indicating no distinct genetic differentiation between the two species. The study also revealed that the nucleotide diversity in cultivated rice was only 30–50% of that in the wild species and thus significant loss of genetic diversity occurred during the domestication process. Ken McNally (IRRI) dealt with 'Adding value to *Oryza* germplasm through biosystematic research: series latifoliae in focus'.

Shoshi Kikuchi (Japan) presented a talk on mapping of >580,000 ESTs from full-length cDNA clones of japonica rice. This study has resulted in the identification of 29,875 unique transcription units on the rice genome. F. Quetier (France) made a presentation on 'Chloroplast and mitochondrial DNA insertions in the rice nuclear chromosomes'. There is significant insertion of chloroplast genomic component in the nuclear genome (5.6 genome equivalent of chloroplast). More than 2000 gene products are targeted from nuclear genome into the organelles.

Since its inception a few decades ago in China, hybrid rice is slowly but steadily spreading to many rice cultivating countries, including India. Sant Virmani (IRRI) traced various developments in the history of hybrid rice and exhorted that large-scale adoption of hybrid rice is the key to meeting the emerging food demand in India. Hybrid rice is not only profitable to farmers who cultivate it, but also to seed producers. Cheng Shi-Hua (China) recalled the historical and scientific developments related to hybrid rice in China. The current focus of Chinese hybrid rice breeding efforts is towards utilization of innovative breeding techniques like application of marker-assisted selection and wide hybridization. Basavaraj Viraktamath (India) summarized the Indian efforts towards development of superior rice hybrids. The total area under hybrid rice cultivation in India during the wet season in 2005 has increased to

~750,000 ha. Similarly, during the same year hybrid rice seed production was taken up in more than 6000 ha, with a target production of ~12000 tons of hybrid seed. A major chunk of this effort (95%) is being undertaken by the private sector. Current research efforts aim at the development of hybrids with better grain quality and introgression of pest and disease resistance with the help of biotechnological tools. Ish Kumar (India) presented the perspectives of private sector on hybrid rice.

One of the major challenges facing breeders is the simultaneous improvement of both drought tolerance and yield, considering the complexity of inheritance of both these traits. Zhikang Li (China) has undertaken a massive backcross breeding effort using three elite lines, IR64, Teqing and a new plant type (NPT) line as recipients, and a diverse set of over 260 germplasm from 15 countries worldwide as donors. Several QTL groups associated with significantly improved yield potential and drought tolerance have been identified and introgressed through marker-assisted pyramiding. An important aspect of research on abiotic stress tolerance is the discovery of genes associated with salt stress response and salt tolerance. Arjula Reddy (India) presented the progress of research work on gene expression profiling under field drought stress. A novel cDNA chip consisting of 15,552 features has been developed from the EST collections derived from the drought-tolerant Indica rice variety, N22. Julia Bailey Sorres (USA) has completed the functional characterization of a major QTL associated with submergence tolerance, *Sub1*. *Sub1* encodes two to three ethylene responsive factor (ERF) genes that are induced at the level of mRNA accumulation in response to complete inundation. Plants possessing *Sub1* have significantly higher enzymatic activities of pyruvate decarboxylase and alcohol dehydrogenase. Matthias Wissuwa (Japan) reported the fine mapping of a major QTL associated with P uptake from soil called Pup1 on chromosome 12 of rice.

Durable disease resistance is a long-standing goal for crop improvement. One of the approaches for durable disease resistance is the introduction of disease resistance genes from related cereals into rice. Scot Hulbert (USA) presented an interesting lecture on the efforts of his research group to induce durable resistance in rice using an analogous gene from

maize called *Rxo1*, which conditions a hypersensitive reaction (HR) after infiltration with the rice bacterial streak pathogen, *Xanthomonas oryzae* pv. *oryzicola* (*Xoo*). The gene is a typical cereal *NBS-LRR* gene but it controls HR in all *Xoo* strains tested and also confers resistance to the unrelated maize pathogen, *Burkholderia andropogonis*. When transferred to rice, *Rxo1* provides bacterial streak resistance, demonstrating the feasibility of non-host resistance gene transfer between cereals. Shiping Wang (China) has identified that the popular bacterial blight resistance gene, *xa13* has evolved due to mutation in the promotor region, indicating that the *xa13* gene product is a negative regulator of disease resistance.

Grain quality is the sum total of various genetic and environmental factors. Apichart Vanavichit (Thailand) presented the progress of research work on 'Positional cloning of *Os2AP*, the aromatic gene controlling the biosynthetic switch of 2-acetyl-1-pyrroline and gamma aminobutyric acid (GABA) in rice'. The gene has been fine-mapped to a region on chromosome 8 of rice and characterized to possess 15 exons encoding a 503 amino acid peptide highly homologous to betaine-aldehyde dehydrogenase. Rhian Howell (UK) made a presentation on a new version of Golden rice called Syngenta Golden rice 2 (SGR2), which possesses high levels of beta carotene in its endosperm (~37 µg/g), and this line is expected to provide a child's recommended dietary allowance (RDA) in just two portions of rice. The uptake and translocation of mineral nutrients in plants is essential for plant growth and also for human nutrition. Naoko Nishikawa (Japan) presented an interesting lecture on identification and characterization of rice metal-nicotianamine and iron-phytosiderophore transporter proteins involved in the uptake and translocation, and accumulation of iron and zinc in rice grains. Similar efforts by Sam Sun (Hong Kong) have resulted in improvement of rice grain protein quality through introduction of lysine-rich proteins from winged bean.

In addition to the plenary and concurrent sessions, late evening workshops were also organized on the following topics: (a) Temperate rice; (b) Reproductive biology; (c) *Oryza* map alignment and alien introgression; and (d) Genetics of insect resistance.

In the workshop on insect resistance brief status presentations included a re-

port of tagging and mapping of a major QTL for BPH resistance introgressed from *O. rufipogon* on chromosome 7 by Chen Jie (China); evaluation of a gene pyramided line, with *Bph1* and *bph2* genes, against two populations of the pest by Naeemullah (Japan), and a new gene (*Bph18t*) isolated from *O. officinalis* by Jeung (Korea). While Yolanda Chen (IRRI) observed that yeast-like endosymbionts in BPH gut could influence virulence status of the insect, Yasui reviewed work on four resistance genes, *GRH1* to *GRH4*, conferring resistance against green rice leafhopper and map-based cloning of *GRH2* gene. Jagadish Bentur (India) reviewed the work on gene pyramiding for durable gall midge resistance. Gurdev Khush, who chaired the session, summed up the progress made on the genetics of insect resistance in rice and emphasized the need to establish allelic relationship of any new gene being reported with those of earlier ones.

Besides the above platform presentations, 378 posters organized into 15 sections were on display. Novel breeding objectives and approaches, focused in one of the sections, involved enhancement of iron content in rice in Vietnam, high-yielding doubled haploids in India and generating polyploid rice targeting two-fold heterosis in China. Extensive use of molecular markers for diverse breeding targets was evident in another section, while the targets ranged from pyramiding

blight and blast resistance genes, selection for BPH resistance, transfer of beta carotene loci, analysis of QTL X E interaction for yield and improving drought or submergence tolerance. Great pace of progress in gene mapping for agronomic traits, heterosis, biotic and abiotic stresses was evident in over 70 posters, and targeted genes ranged from those determining grain size, number, dormancy, storability, aroma to heading time, internode elongation and the entire range of biotic and abiotic stresses. Posters covering genetic diversity, evolution and alien introgression had a gamut of interests spanning from varietal classification, gene flow, reproductive isolation to genetic diversity in blast pathogen, *Magnaporthe grisea* and sibling species of BPH. A range of posters on analysis of rice mutant lines effectively conveyed the immense potential of this genetic resource in identification of useful mutants to understanding gene action of specific genes through loss-of-function mutants. Posters on gene identification and function reported cloning of an array of genes responsible for seed shattering, seed length, tiller bud growth, rice aroma and phosphorus-deficiency tolerance. These also uncovered the molecular interactions between plant resistance gene and blast pathogen avirulence gene products.

Studies on gene expression highlighted available tools like enhancer traps, SAGE-microarray analysis, suppression subtrac-

tive hybridization, PCR-based subtraction method, RNAi and others, and their application to study specific genes related to stress and pest resistance genes. There were representative posters covering organelle genome, analysis of rice genome, novel molecular markers, including SNPs, genomic databases and transgenics for rice improvement.

The symposium concluded with an overview by Khush. A discernable thread woven all along the proceedings was the commonality in genome structure and organization among the major cereal crops like rice, maize and barley. Also evident was the similarity between the genomes of rice and *Arabidopsis*. While functions of all the genes in the latter will be known in a few months time, leading participating rice geneticists responded positively to commit to unravel functions of all the rice genes possibly by 2010. This will be a unique gift to mankind on the 50th anniversary of foundation of the International Rice Research Institute in Manila, the Philippines.

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MEETING REPORT

Biotechnology and insect pest management*

Biotechnology has contributed much to the field of insect pest management so far, through development of transgenic plants and other novel ecofriendly products to control insects. Recognition of the value and relevance of biotechnological applications in insect control is gaining momentum. There is also increased interest among scientists in developing novel strategies for insect pest manage-

ment. Realizing the potential benefits and constraints in the use of biotechnology in insect pest management, a national symposium on 'Biotechnology and Insect Pest Management' was organized recently. Deliberations during the symposium covered various aspects such as insect resistant transgenic crops, microbial pesticides – process and development, botanical pesticides – process and development, hybridization techniques in the production of potential natural enemies, insect and animal vectors of diseases and biosafety concerns, etc.

Sixty-one papers were presented at the symposium. Inaugurating the symposium,

M. S. Swaminathan (Chairman, National Commission on Farmers, and Chairman, M. S. Swaminathan Research Foundation, Chennai) said that the theme had two important areas, namely core molecular biology for development of transgenic crops and processes for producing and using biopesticides. He emphasized that these are urgently required in order to reduce the use of hazardous chemical pesticides. B. Jeyaraj (Loyola College, Chennai) talked about non-chemical methods of pest management, including the use of insect sex pheromones.

S. Jayaraj (S. Jayaraj Research Foundation, Chennai) spoke on 'Host plant

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