

Rice Genetics: Progress and Applications

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Five years have passed since the publication of the gold standard of rice genome sequence in 2005. During this time, much progress has been made towards understanding the rice plant. We have learned more about rice genome structure and diversity, its evolution, and how the rice plant copes with changing environments. Importantly, we have seen an accelerated discovery of gene function and genetic regulation of agronomic traits. Such progress has led to applications in breeding, and in some cases realized impact in the farmer's field. These advances were captured in the joint meeting of the 6th International Rice Genetics Symposium and the 7th International Symposium of Rice Functional Genomics that was held in November 16–19, 2009 in Manila, The Philippines.

Looking back 25 years, the First International Rice Genetics Symposium was held at the International Rice Research Institute (IRRI), Los Baños, Philippines, in 1985. This meeting was attended by 200 scientists. Subsequent meetings were held under the auspices of the Rice Genetics Cooperative and IRRI at 5-year intervals. We have seen rice emerge as a model plant for genetic research and a growing interest for the study of rice genetics. Indeed, progress was considered sufficiently fast that the Rice Genetics Symposium is now being held at 4-year intervals beginning 2005. In 2009, the joint symposia of Rice Genetics and Rice Functional Genomics were attended by 777 participants from 34 countries—breaking the previous record of attendance in 2005.

Opened by Her Royal Highness Princess Maha Chakri Sirindhorn of Thailand, the meeting featured 77 oral and

400 poster presentations. Among the highlights was the presentation of a special award from IRRI to Dr. Takuji Sasaki for his achievements in the field of rice genetics and his service to the international rice research community.

This issue of RICE features a selection from the papers presented at the meeting. They represent studies spanning genomics, molecular biology, stress tolerance, breeding, and applications in rice production.

Two papers provided a glimpse of the exciting advances in using second generation sequencing to gain a deeper understanding of the genomes of wild and domesticated rice. Goicoechea et al. reviewed progress of the on-going *Oryza* Map Alignment Project with the goal of decoding the major wild rice genomes, and called for international collaboration to functionally characterize all rice genes for translational genomics in rice. Zhao et al. described an analytical pipeline for analyzing data from next-generation sequencing.

Zhou and Hu provided an up-to-date review of histone modifications in rice and how this process affects gene expression and phenotypes without heritable changes in DNA sequence—under the little known phenomenon of epigenetics. The potential role of epigenetics in regulating agronomic traits will certainly attract much attention in rice research in the future.

Two papers demonstrated the application of cellular and molecular techniques in unraveling the regulatory mechanisms of disease resistance and iron transport. Kawano et al. described current work on plant innate immunity, focusing on the role of Rac GTPase as a molecular switch for expression of innate immunity in rice. Bashir et al. reviewed the progress in understanding iron transport, and how this knowledge can be used to increase level of iron in rice grain. It suggests hope for rice biofortification to reduce the hidden hunger caused by iron deficiency in preponderant rice consumers.

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For practical breeding, Fukuoka et al. offered insights on the integration of QTL studies and genomics and genetic resources for rice breeding. The paper emphasizes the importance of developing specialized genetic resources if we are to take advantage of the wealth of sequence information. Bailey-Serres et al. provided a historical perspective for the identification, cloning, and functional analysis of *SUB1*, the ethylene responsive factor (ERF) gene that confers submergence tolerance in rice, and summarized the progress made in its use in breeding. Thomson et al. discussed the current status of QTL mapping for salinity tolerance in rice, underlining *Saltol* as a major QTL associated with tolerance, and highlighting the progress made so far for its use in rice improvement. With continuing efforts to improve salt stress

tolerance in rice, it appears that promising varieties can reach farmers' fields soon. Jena and Kim provided an overview of the current status of the genetics of resistance to brown planthopper, a serious insect problem plaguing many regions in Asia. The paper highlighted the needs as well as opportunities for delivering impact through developing insect tolerant rice.

The well-attended series of the International Rice Genetic Symposium and the International Symposium for Rice Functional Genomics were reflections of the collective research power of a striving rice research community. We hope this Special Issue serves to show the fertile ground of rice genetic and genomics research, and help promote further advances in rice science.