**Rice** (*Oryza sativa*, L.) is considered one of the most important crops in the world. Half of the world population depends largely on rice, including more than 60% of the undernourished people living in Asia, Africa, and the Pacific region where rice is considered a staple food (FAO-OECD, 2008). Although rice production has doubled in the last 30 to 40 years as a result of modern agricultural practices and introduction of new varieties, the current rate of rice production will no longer meet the expected increase in the world population, which is estimated to reach nine billion in the next 30 years (U.S. Census Bureau, 2008). The completion of the rice genome sequence by the international effort (IRGSP) in 2005 has opened new possibilities in rice research in terms of developing innovative strategies that can be used to increase rice production (International Rice Genome Sequencing Project, 2005). The high-quality sequence of a *japonica* cultivar (Nipponbare) is now considered as the “gold standard” for rice genomics to promote rice functional genomics, gene isolation, and marker-based breeding. This reference genome sequence of *japonica* rice was obtained by the “classical” Sanger technology, which required massive sequence production capacity. Because of the large amount of manpower and resources involved, the *japonica* rice genome sequence was brought to completion mainly due to collaboration of several research groups supported by governmental funding.

With the availability of a reference genome sequence, research in rice genomics has now shifted to functional and applied genomics strategies. A novel methodology called genomics-based breeding approach has also started to emerge (Tuberosa and Salvi, 2006). In this strategy, many agronomically important phenotypic traits are located on the rice genome in nucleotide-level resolution using the genome-wide DNA markers generated by sequence polymorphism such as SNPs and Indels. The DNA marker methodology has several advantages over classical phenotypic markers used in conventional breeding. Basically, genotyping could be performed even in the seedling stage, and confining the responsible portion within a narrow genomic region could reduce the chance of dragging totally unrelated genes.

Finding the genome-wide polymorphism for any rice variety is unrealistic and impractical because this virtually means re-sequencing entire genomes. The cost of sequencing entire genomes has remained a limiting factor. However, if the ongoing revolution of sequencing technology could reduce the cost of total genome sequencing to a few hundred dollars, or even few dollars, sequencing will not be limited to reference genomes. Instead, revealing the nucleotide sequences of specific genetic analysis materials such as recombinant lines and their parent cultivars for example, will become a reality. This will allow breeders or researchers to immediately recognize the origin of genomic segments anywhere in the genome for every recombinant plant. Eventually, this will contribute to accelerating many aspects of agricultural research, particularly in introducing specific chromosome regions from one cultivar to another. Such a target-specific approach in genetic modification will benefit many breeding goals to increase yield, incorporate resistance to biotic/abiotic stress, and develop cultivars that could grow well in adverse environmental conditions. In addition, sequencing rice varieties and wild rice accessions within the genus *Oryza* at a reasonable cost will accumulate polymorphisms for all the genes and non-genic regions. This knowledge will accelerate the acquisition of fundamental knowledge such as elucidating the history of both domestication and breeding (human selection) of rice, as

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