

Functional genomics of rice

ABSTRACT

Rice functional genomic research at the post-genomic era has been accelerated by the developmental of technical and resource platforms, focusing on construction of mutant libraries, isolation of full-length cDNAs, global gene expression, data mining and rice bioinformatics. Taking advantage of the high quality genome sequence and global gene expression profiles available in the public domain, our group have predicted: 1) biologically significant cis-acting regulatory elements (CREs), which help to prioritize candidate rice CREs for genetic and biochemical analyses; and 2) protein-protein interactions that extend known pathways and improve functional annotation of many unknown rice proteins and networks in rice. In addition, we studied the global gene expression profiles of two Malaysian rice cultivars, MR219 and MR84 of indica subspecies, which have different percentage of filled grains using the NSF 20 K rice oligonucleotide array developed from the rice sequences of japonica subspecies. Direct comparison of the transcriptomes of MR219 and MR84 during rapid grain-filling period at 5 and 10 days after fertilization (DAF) enhanced our understanding on poor grain filling (partially filled and empty rice grains) which affects the final yield of MR219. Following that, we also elucidated the functions of unknown rice genes by overexpressing or silencing them in MR219. Meanwhile, we used rice as a model for functional genomic research for other plant species such as mangrove and oil palm.