

## Decoded Rice Genome for Decipherment of Origin, Domestication and Functional Attributes of Rice

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### ABSTRACT

Rice is inseparable part of Indian culture and life. It is also a staple not only for India but for major world population, especially in developing nations. Out of about 450 million tons of milled rice produced world-wide in 2015, more than 100 million tons has been produced in India. The sequence of its 12 chromosomes was decoded under the auspices of an International Rice Genome Sequencing Project (IRGSP), involving ten nations including India. Indian Initiative on Rice Genome Sequencing (IIRGS) supported by the Government of India related to chromosome 11 and was the first Indian effort on high-throughput genome-wide sequencing. The present day rice genome of about 400 Mb has resulted from whole genome, segmental and tandem duplications. Non-shattering seeds and white seed are some of the traits distinguishing domesticated from wild rice. Interestingly, these traits are due to the presence of certain alleles most likely selected by human beings long ago. Rice cultivation possibly began in South-central China near Yangtze river several thousands years ago. Other evidences suggest Ganges river valley as origin of rice cultivation. Some genetic evidences also suggest possibility of hybridization between *Japonica* and native wild rice. While global occurrence of certain alleles for domestication traits (shattering and pericarp colour) reflects on single domestication event, recent genome-wide analysis indicates multiple domestication events. Decoded rice genome has served as an invaluable resource for structural and functional annotation of about 32,000 genes in rice and, so far, function of over 2,000 genes has been unraveled by forward and reverse genetics approaches. By deploying, microarray-based transcriptome profiling, over-expression and knock-down transgenics, association and molecular mapping, and haplotyping approaches, we have defined evolution, phylogenetic relationship and composition of over 25 gene families along with biological function of several selected genes and regulatory elements related to seed development, male-sterility, hybrid vigour and stress tolerance. This is expected to help genetic enhancement of rice.

The Rice Genome representation included here is prepared by Dr. S. Parida, NIPGR.



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