

# Bioinformatics approach through SNPs for drought tolerance in rice

PRASHANT VIKRAM, ALOK KUMAR SINGH AND S.P. SINGH

Accepted : December, 2009

## SUMMARY

Rice is global staple food crop grown mainly in Asia. Drought hampers yield of rice drastically in rainfed areas (Khush 1997). Sequence of whole rice genome is available in database and Oryza SNPs (single nucleotide polymorphism) are already available for 20 varieties (oryzasnp.org). A small region on distal arm of chromosome 1 was annotated using the SNP (single nucleotide polymorphism) data to work out putative candidate genes. Interestingly there were some SNPs inside exons including DUF protein, F-box protein interaction domain, kinase domain protein, TPR-like domain containing protein, pectinacetyltransferase family protein and conserved hypothetical protein in exons. There was no strong clue from the *sdl* gene revealing the fact that other proteins in this region are equally important.

**Key words :** Rice, Swarna, N22, Single nucleotide polymorphism, Drought

**D**rought may simply be defined as reduction in yield due to shortage of water (Bernier *et al.*, 2008). Drought in rice crop can be classified mainly on basis of stage of crop falling under drought stress. There may be three kinds of drought (i) vegetative stage drought, (ii) intermittent drought and (iii) reproductive stage drought or terminal drought. Drought at reproductive stage is the most devastating one in terms of reduction of yield (Kamoshita *et al.*, 2008). So far breeding for drought tolerance is concerned; it has been concentrated on either drought avoidance or resistance. Various physio-molecular approaches have been employed for breeding of drought tolerance in rice. Numerous QTLs have been identified in rice for drought tolerance. So far more than 15 populations have been used for it (plantstress.com; Kamoshita *et al.*, 2008). Most of drought QTLs were found clustered on chromosome 1, 4, 8 and 9 (Kamoshita *et al.*, 2008). Distal arm of chromosome 1 has been reported by many workers as most important locus for stress tolerance and yield related traits. Comparative analysis of SNPs in this locus could be quite useful in way to identify candidate genes for drought tolerance and yield as well.

## MATERIALS AND METHODS

### Comparative analysis of drought tolerance, height and yield:

Data pertaining to height, yield and drought tolerance

#### Correspondence to:

S.P. SINGH, Department of Crop Physiology, N.D. University of Agriculture and Technology, Kumarganj, FAIZABAD (U.P.) INDIA

#### Authors' affiliations:

PRASHANT VIKRAM AND ALOK KUMAR SINGH, Department of Genetics and Plant Breeding, T.D.P.G. College, JAUNPUR (U.P.) INDIA

related traits of released rice varieties of India was analyzed. More than 500 rice varieties have been released in India. Comparative analysis of varieties of different rice-ecosystems was done along with their respective plant height data. Similarly plant height of drought tolerant varieties was compared (<http://dacnet.nic.in/Rice/Rice%20Varieties%20-%202001.htm>).

### Single nucleotide polymorphism data analysis on distal arm of chromosome 1 :

SNP data of N22, IR64 and Swarna were downloaded from the oryzasnp consortium website. All the QTLs identified so far on distal arm of chromosome 1 were compiled to know exactly the consensus marker associated with yield and drought related traits. There after sequences of rice microsatellite markers RM315 and RM431 were downloaded from Gramene database. Forward sequences were BLAST with whole rice genome to know the coordinates. Pseudomolecule build v4 was taken as reference. To intensify our study we annotated a small region only *i.e.* 39609051 bp and 40648577 bp. SNP polymorphism data of N22/ IR64/ Swarna/ Nipponbare was downloaded. Comparative analysis of SNP polymorphism was done. SNPs within genes were worked out.

Marker name	Position (Co ordinates)
RM315	38609051 bp
RM431	40648577 bp

### Comparative analysis of SNPs within the genes:

Single nucleotide polymorphism survey among the genic-regions of N22 and other three varieties *e.g.* Swarna, IR64 and Nipponbare was done. Exons as well