

Category	: International Rice Research Conference
Select Theme	: Genetic improvement
Endorsement email	:
Keyword 1	: Pre-breeding
Keyword 2	: Genomics-assisted breeding
Keyword 3	: Germplasm Enhancement
Title of Entry	: Hybridization to Broaden the Genetic Base of Local Rice Landrace Tulaipanji and Genome-wide Diversity Analysis by WGS
Presenting author	: Subhas Chandra Roy
Presenting author email	: subhascr@rediffmail.com
Co author 1	:
Co author 2	:
Affiliation presenting author	: Plant Genetics & Molecular Breeding Laboratory, Department of Botany, University of North Bengal, PO- NBU, Siliguri-734013, Dist-Darjeeling, WB, India.
Affiliation 1	:
Affiliation 2	:
Select only one type of presentation	: 3-5 minute flash talk
Abstract	: Tulaipanji is non-Basmati aromatic rice (<i>Oryza sativa</i> L.) of Uttar Dinajpur district, West Bengal, India famous for its fragrance, good grain quality and medicinal value (GI tagged). Tulaipanji is low yield efficient local rice landrace (1.8 -2 t/h). Reason may be that genetic architecture is not responsive to high input of resources due to narrow genetic base prevailed in this gene pool. Hybridization was made between Tulaipanji and HYV cultivars (Ranjit, IR64, PB1460), and with wild rice <i>Oryza rufipogon</i> (collected locally) to widen the genetic base of Tulaipanji. Whole genome sequencing of Tulaipanji rice was performed using Illumina HiSeq4000 platform for genome-wide diversity analysis. Sequencing reads were aligned with the three reference genomes (Nipponbare, indica 93-11, Kasalath) for genetic variation analysis. Two lines were selected from the cross between Tulaipanji x Ranjit. Progeny Awnless line is showing a new trait which is red pericarp for Rc/Rd gene recombination. Genetic marker (SNP and InDel) variations were studied in these rice lines using NGS based GBS technique and segregation distortion (SD) was observed. Four progeny lines were selected at F5 stage from the cross between Tulaipanji x IR64, among these two lines were showing high yield capacity. Crossing was made between Tulaipanji and <i>O. rufipogon</i> for the development of CSSL/BIL line in 2016 and BC1F1 and F2 lines were morphologically analyzed. In WGS, 245,261 variant (SNP/Indels) was detected while compared to Nipponbare, 787,560 while compared to indica 93-11 and 733,927 while compared to Kasalath. Total 232,407 SNPs was identified based on Nipponbare and SNP density was 62.68/100 kb. Synonymous and non-synonymous variant was identified 16616 and 25154 in the exonic CDS region respectively. Total 39 unique and novel

SNPs were identified. Functional analysis of genes containing SNPs was analyzed based on GO term. Seventy-seven alleles were analyzed -Gn1a, EP3, SCM3, Wx, ALK, Hd17, qGW8, SSIVa, SBE1, SSIIIb, SSIIc, OsMADS65, BAD2, BLB, etc for important agronomic traits and allele mining. Promising Tulaipanji lines were developed. Wide hybridization was made between Tulaipanji x O. rufipogon. WGS enabled to identify sequence diversity and detection of allelic variations in the genomic locations of heritable traits.

[Read Less»](#)

Uploaded Files »

No files found.