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Data in Brief

RNA-Seq analysis of urea nutrition responsive transcriptome of *Oryza sativa* elite indica cultivar RP Bio 226

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ABSTRACT

Rice yield is greatly influenced by the nitrogen and rice varieties show variation in yield. For understanding the role of urea nutrition in the yield of elite indica rice cultivar RPBio-226, the urea responsive transcriptome was sequenced and analyzed. The raw reads and the Transcriptome Shotgun Assembly project has been deposited at DDBJ/EMBL/GenBank under the accession GDKM00000000. The version described in this paper is the first version, GDKM01000000.

Specifications	
Organism/cell line/tissue	*Oryza sativa* indica RP Bio-226
Sequencer or array type	Illumina_Next seq500
Data format	Processed
Experimental factors	Laboratory grown plant
Experimental features	Transcriptome sequencing
Consent	Not applicable

1. Direct link to deposited data

This Transcriptome Shotgun Assembly project has been deposited at DDBJ/EMBL/GenBank under the accession GDKM00000000. The version described in this paper is the first version, GDKM01000000.

2. Experimental design, materials and methods

High yielding rice cultivars need high quantities of nitrogen which is usually supplied in the form of urea fertilizers. Rice cultivars show diversity in their nitrogen use efficiency which influences the yield of particular cultivars [1]. Nitrogen use efficiency is influenced by nitrogen uptake, transport, vacuolar storage, utilization and remobilization. So, it is necessary to understand the molecular basis of nitrogen use efficiency of high yielding rice cultivars for understanding the basis of their high yield [2]. The high throughput Rna-Seq analysis enables understanding of the functioning of all genes at a particular time and location. In this work RNA-Seq analysis is employed for understanding the genomic basis behind nitrogen use efficiency of the high yielding indica rice cultivar RPBio-226.

RP Bio-226 seeds were surface sterilized with 0.1% $HgCl_2$ for 30 min, rinsed thoroughly with distilled water and germinated on Murashige and Skoog medium that lacked a nitrogen source. Ten day old seedlings were transferred to 0.1 mM urea containing Murashige and Skoog medium. After three days the leaves were harvested and used for transcriptome analysis. Total RNA was isolated from the leaves and RNA concentration and purity were estimated with a Nanodrop spectrophotometer. The integrity of the RNA sample was checked with RNA Bioanalyzer chip. mRNA was purified and fragmented at elevated temperature (94 °C) in the presence of divalent cations. First strand cDNA synthesis was carried out by fragmented mRNA and reverse transcribed with Superscript III Reverse transcriptase by using random hexamers. Second strand cDNA was synthesized in the presence of DNA polymerase I and RnaseH. The cDNA was cleaned up using High Prep PCR. Illumina Adapters were ligated to the cDNA molecules after end repair and addition of 'A' base. The library was amplified using 8 cycles of PCR for enrichment of adapter ligated fragments. The prepared library was quantified using Qubit and validated for quality by running an aliquot on high sensitivity Bioanalyzer Chip. The library showed peak at the

Table 1
Oryza sativa indica RP Bio 226 transcriptome statistics.

Attributes	Value
Number of reads	65,167,570
Coverage	20×
Number of contigs	68,026
Number of transcripts	24,837
SNP	12,640
Indels	5013

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range of 250–700 bp. The effective sequencing insert size is 130–580; the inserts are flanked by adapters whose combined size is 120 bp.

Transcriptome sequencing was carried out with the Illumina_Nextseq500 system (Illumina, San Diego, CA). The preprocessing of the reads was performed with FastQC and the adapters were removed with Fastx toolkit [3,4]. Samtools (ver 0.1.18) and SnpEff (ver 4.1) were used for creation of variation report with a mapping quality of >30 and read depth of >20 as cutoffs [5,6]. *De novo* transcriptome assembly was performed with Velvet and Oases softwares [7,8] (Table 1).

We have planned to analyze the transcriptome of RP Bio 226 in comparison with other rice cultivars for understanding the variation in nitrogen use efficiency of rice.

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