Data Article

Screening and Identification of putative long non-coding RNAs from transcriptome data of a high yielding blackgram (*Vigna mungo*), Cv. T9

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A B S T R A C T

Blackgram (*Vigna mungo*) is one of primary legumes cultivated throughout India, Cv.T9 being one of its common high yielding cultivar. This article reports RNA sequencing data and a pipeline for prediction of novel long non-coding RNAs from the sequenced data. The raw data generated during sequencing are available at Sequence Read Archive (SRA) of NCBI with accession number-SRX1558530

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Specifications Table

| Subject area       | Biology         |
|--------------------|-----------------|
| More specific sub- | *Plant molecular* |
| ject area           | biology         |
| Type of data       | *Sequence Data* |
| How data was       | *High throughput* |
| acquired            | *sequencing*    |
| Data format        | *Raw reads*     |
| Experimental factors | *High Yield* |
|                    | *Cultivar*      |

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Experimental features RNA sequencing from total isolated RNA, followed by computational prediction of long non-coding RNA
Data source location Kolkata, West Bengal, India
Data accessibility https://www.ncbi.nlm.nih.gov/sra/SRX1558530

Value of the data

- This is the first report of long non-coding RNAs in Vigna mungo.
- This study will enable researchers to identify lncRNAs of interest in a high protein yielding legume, Vigna mungo.
- This article also contains a pipeline for identification of long non-coding RNAs in Vigna mungo an in depth analysis with some adjustments which may pave the way for identification of lncRNAs in other non model plants as well.

1. Data

This works reports the long non-coding RNAs identified in common Indian cultivar of Vigna mungo (Blackgram) Cv. T9. This cultivar is widely cultivated in different states of India due to high agronomic yield; however, it is highly susceptible to Mungbean Yellow Mosaic India Virus (MYMIV) infection mediated by the vector whitefly (Bemisia tabaci).

2. Experimental design, materials and methods

2.1. RNA isolation and RNA sequencing

Sample preparation for RNA isolation was done as described by Kundu et al. [1]. Total RNA was extracted from prepared sample using Trizol reagent (Invitrogen, Carlsbad, CA) following the manufacturer’s instruction, followed by DNase-I treatment (Sigma-Aldrich, USA) and purification using a RNeasy Plant Mini Kit (Qiagen, USA). Qualitative and quantitative assessments of the extracted Total RNA were performed using Agilent 2100 Bioanalyzer (RNA Nano Chip, Agilent). RNA samples were transferred to Genotypic Technologies Pvt. Ltd. (Bangalore, India) for transcript library preparation and for performing high throughput sequencing using Illumina NextSeq. 500 platform. Data generated during this experiment was submitted to Sequence Read Archive (SRA) of National Centre for Biotechnology Information (NCBI) under accession no SRX1558530.

2.2. Bioinformatics analysis and long non-coding RNA prediction

The pipeline shown in Fig. 1 was followed to identify the long non coding RNAs. First raw reads were processed for removal of low quality reads using in house Perl scripts, followed by de-novo assembly of transcripts using Trinity [2]. De novo transcript statistics are provided in Table 1. Processed reads were aligned against assembled transcripts using Bowtie2 [3]. Further BLAST-n [4] was performed against CANTATAdb [5]. Annotated (305 RNAs, Supplementary file 1) and unannotated transcripts (8455 RNAs) were separated. Highest similarities were found with Glycine max (65%) (Fig. 2A). Unannotated transcripts were analyzed further, coding potential of transcripts was calculated using CPC Calculator tool [6] and transcripts having low coding potential were selected. Transcripts having length of over 300 bps were selected as suitable candidates for further analyses using TransDecoder. The retained transcripts were again subjected to BLAST nr-Db to establish their non coding character; reads were further searched for similarity against Vigna mungo cds (generated via transcriptome sequencing; results unpublished). Remaining 2874 (Supplementary file 2) reads are
being proposed as potential novel long non-coding RNAs. This entire pipeline for novel IncRNA prediction is illustrated in Fig. 1.

2.2.1. Prediction of SSR markers in novel IncRNAs

Simple sequence repeats were predicted using MISA-MicroSatellite identification tool [7]. Ten repeating units for mono nucleotide, 6 repeating units for di nucleotide and 5 repeating units for tri-, tetra-, penta- and hexa nucleotide were chosen as parameters for mining the SSR markers. Details of mined SSRs has been provided in Fig. 2B.
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Transparency document. Supplementary material

Supplementary data associated with this article can be found in the online version at http://dx.doi.org/10.1016/j.dib.2018.01.043.

Appendix A. Supplementary material

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