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Data in Brief

Computational analysis of miRNA-target community network reveals cross talk among different metabolisms

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ABSTRACT

To date, only a few conserved miRNAs have been predicted in hexaploid (AABBDD) bread wheat and till now community behavior among miRNA is still in dark. Analysis of publically available 1287279 ESTs from NCBI resulted 262 putative pre-miRNAs and 39 novel mature miRNAs. A total 22,468 targets were identified on 21 chromosomes. MiRNA target community was identified for genomes with different levels of cross talks. Gene ontology of these community targets suggests their differential involvement in different metabolisms along with common and stringent involvement in nitrogen metabolism.

Specifications	
Organism/cell line/tissue	*Triticum aestivum*
Sex	N/A
Sequencer or array type	N/A
Data format	Raw ESTs (Fasta files), CAP3 assembled contigs (Fasta files)
Experimental factors	Pooled ESTs from multiple experiments majorly belongs to biotic and abiotic stress
Experimental features	Novel miRNAs were identified from assembled ESTs and targets were identified on the draft genome sequence of wheat.
Consent	N/A
Sample source location	NCBI EST database

1. Direct link to deposited data

http://www.ncbi.nlm.nih.gov/nucest.

2. Introduction

MicroRNAs (miRNAs) play important roles in plant growth regulations, development and adaptation to abiotic stresses [1–3]. It is an important class of small RNAs, a non-protein coding segment of genome, originates from fold back precursors and functions as negative regulators of gene expression in plant [1,4,5]. A large number of miRNAs have been discovered and functionally identified in plant kingdom. Currently, 8496 mature miRNAs have been identified from *Viridiplantae* and deposited in a publicly available database (miRbase, Release 21, June 2014) [6]. In agriculturally important monocot species, miRNAs have been reported in large number for fully sequenced genome but fewer in partially or incomplete sequenced genomes. Though, wheat (*Triticum aestivum*) is one of the most extensively cultivated crop among monocots but only 115 mature miRNAs have been reported [7]. Whereas in other monocots viz. *Oryza sativa*, *Zea mays*, *Sorghum bicolor* and *Hordeum vulgare*, 713, 321, 241 and 71 mature miRNAs have been reported respectively. The regulatory role of many of these miRNAs under drought, salinity and low temperature stress has been demonstrated [8–10]. Moreover, the homeostasis of the nutrients such as sulfur, copper and phosphate, which are critical for growth and development, has been found to be regulated by miRNAs [11–13]. A number of putative miRNAs in wheat have been identified [14–17] yet the association of miRNA with different metabolic processes is still in dark. Therefore, identification of novel miRNAs as well as their association with metabolic pathways in wheat may facilitate its improvement and production.

The most challenging problem in understanding plant miRNAs is the identification of novel miRNAs. EST based computational analysis is a powerful technique for identifying conserved miRNAs, especially for plants with partially or un-sequenced genomes [18]. Thus in the present study, EST based computational technique was employed in search of potential miRNA in wheat. Available miRNAs in miRBase and downloaded wheat EST dataset were used for detection of potential miRNAs. Altogether 39 novel miRNAs were detected and 22,468 target genes were identified in wheat. Further, the mechanism of miRNA-target crosstalk was deciphered by employing a meta-analysis for

Abbreviations: miRNAs, microRNAs; GRN, Gene Regulatory Network; FDR, false discovery rate.

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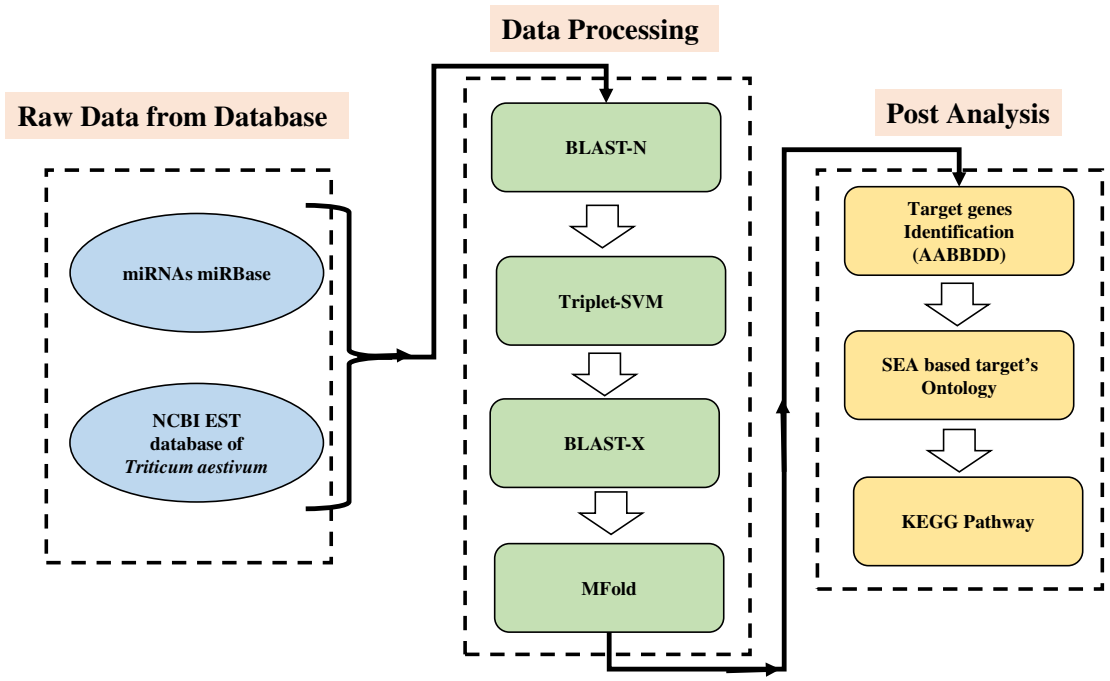

Fig. 1. Workflow for the identification of miRNAs and their targets in *Triticum aestivum* (AABBDD).

chromosomal mapping, gene ontology, and miRNA-target community network. It was observed that most of these miRNAs in wheat were primarily involved in regulating nitrogen metabolism that needs to be further validate.

3. Materials and methods

3.1. MiRNA reference set

For prediction of potential miRNAs, previously known miRNAs (8496) of whole *Viridiplantae* were obtained from miRNA Registry database (Release 21, June 2014). To avoid the overlap of miRNAs, the redundant miRNA sequences were removed using an in-house Perl script and the remaining sequences were used as a reference set.

3.2. Software used

Initially, software BLAST-2.2.14 was used from NCBI GenBank. CAP3 was used for assembly in the form of contigs and singlets. Triplet SVM classifier was used to predict potential miRNA precursor [19]. These precursor sequences were used for BLASTx analysis for removing the protein-coding sequences and retained only non-protein encoding sequences. RNAfold was used online to analyze secondary structure of RNAs. BLASTn from NCBI (http://www.ncbi.nlm.nih.gov) was used to

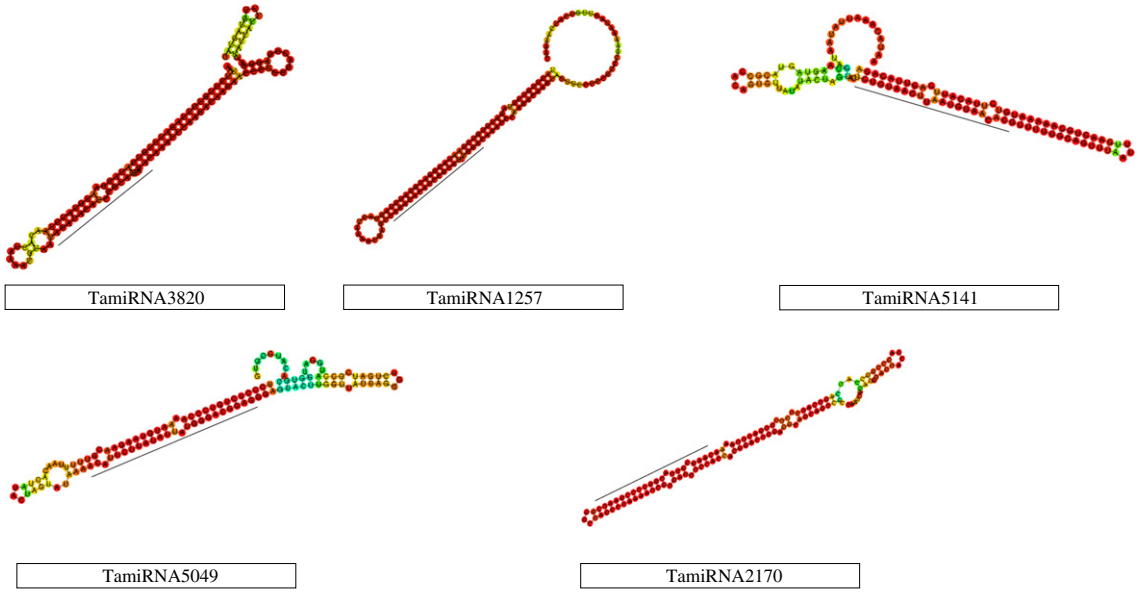

Fig. 2. Stable secondary structures of top five novel miRNAs of *Triticum aestivum*.