De novo transcriptome assembly of Sorghum bicolor variety Taejin

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ABSTRACT

Sorghum (Sorghum bicolor), also known as great millet, is one of the most popular cultivated grass species in the world. Sorghum is frequently consumed as food for humans and animals as well as used for ethanol production. In this study, we conducted de novo transcriptome assembly for sorghum variety Taejin by next-generation sequencing, obtaining 8.748 GB of raw data. The raw data in this study can be available in NCBI SRA database with accession number of SRX1715644. Using the Trinity program, we identified 222,161 transcripts from sorghum variety Taejin. We further predicted coding regions within the assembled transcripts by the TransDecoder program, resulting in a total of 148,531 proteins. We carried out BLASTP against the Swiss-Prot protein sequence database to annotate the functions of the identified proteins. To our knowledge, this is the first transcriptome data for a sorghum variety derived from Korea, and it can be usefully applied to the generation of genetic markers.

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Keywords: RNA-Seq
Sorghum bicolor
Transcriptome
Variety

Specifications

| Organism/cell line/tissue | Sorghum (Sorghum bicolor variety Taejin)/leaves |
|--------------------------|-----------------------------------------------|
| Sex                      | N.A.                                           |
| Seuqencer or array type  | HiSeq2000                                     |
| Data format              | Raw and processed                             |
| Experimental factors     | De novo transcriptome assembly of sorghum variety Taejin |
| Experimental features    | Leaves of five sorghum plants (variety Taejin) were harvested for total RNA extraction. A prepared library was paired-end sequenced using the HiSeq 2000 system. The obtained data were subjected to de novo transcriptome assembly using Trinity, and coding regions were predicted by TransDecoder. We performed BLASTP against the Swiss-Prot protein database to annotate the identified proteins. |
| Consent                  | N/A                                           |
| Sample source location   | Hoengseong, South Korea (37°28′49.6″N 127°58′34.3″E) |

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1. Direct link to deposited data

http://www.ncbi.nlm.nih.gov/sra/SRX1715644 for Sorghum bicolor variety Taejin.

2. Introduction

Sorghum (Sorghum bicolor)—also known as great millet, dura, jowar, or milo—is one of the most popular cultivated grass species in the world. Sorghum is frequently consumed as food for humans and animals as well as used in ethanol production [1]. Sorghum is the fifth most important cereal crop after rice, wheat, maize, and barley. The origin of sorghum is northern Africa; however, sorghum is currently cultivated in tropical and subtropical regions [2]. Because sorghum is native to tropical climates, researchers are developing new cultivars resistant to cold tolerance. In addition, the availability of the genome of sorghum facilitates sorghum research, such as breeding new cultivars and studies on drought-tolerance mechanisms [3]. Sorghum, along with Italian millet and hog millet, has long been cultivated in Korea, and it is currently consumed as a healthy food in Korea. In this study, we performed de novo transcriptome assembly for sorghum variety Taejin by next-generation sequencing.
3. Experimental design, materials, and methods

3.1. Plant materials

Plants for sorghum variety Taejin were grown in a field located in Gadam-ri, Hoengseong-up, South Korea. Leaves from five such plants were harvested and immediately frozen in liquid nitrogen for further experiments.

3.2. RNA isolation, library preparation, and sequencing

Ten leaves collected from five plants were pooled and used for total RNA extraction using the RNeasy Plant Mini Kit (Qiagen, Hilden, Germany). For mRNA library preparation, we used a TruSeq RNA Library Prep Kit v2 according to the manufacturer’s instructions (Illumina, San Diego, U.S.A.). In brief, the poly-A-containing mRNAs were isolated using poly-T oligo-attached magnetic beads. The first strand of cDNA, followed by a second strand of cDNA, was synthesized from purified mRNAs. End repair was performed followed by adenylation of 3’ ends. Adapters were ligated, and PCR was conducted to selectively enrich DNA fragments with adapters and to amplify the amount of DNA in the library, respectively. The quality control of generated libraries was conducted using a 2100 Bioanalyzer (Agilent, Santa Clara, U.S.A.). The libraries were paired-end sequenced by Macrogen Co. (Seoul, South Korea) using the HiSeq 2000 platform.

3.3. De novo transcriptome assembly, identification of protein coding regions, and annotation

We obtained 8.748 GB of raw data from sorghum variety Taejin by paired-end sequencing. We conducted de novo transcriptome assembly for sorghum variety Taejin using Trinity program ver. 2.0.6, which uses the de Bruijn graphs algorithm [4]. Detailed information on the de novo transcriptome assembly is summarized in Table 1. The numbers of total transcripts and components for sorghum variety Taejin were 222,161 and 95,030, respectively. The N50 value was 2374 bp, and the median contig length was 1100 bp. We further predicted coding regions within the assembled transcripts by the TransDecoder program implemented in the Trinity software distribution. As a result, we identified a total of 148,531 proteins. We carried out BLASTP against the Swiss-Prot protein sequence database to annotate the functions of the identified proteins. All but 37,653 proteins were matched to known proteins in Swiss-Prot. Many proteins were homologous to eukaryotes (9643 proteins) followed by bacteria (223 proteins) and viruses (73 proteins). To our knowledge, this is the first transcriptome data for a sorghum variety derived from Korea, and it can be usefully applied to the generation of genetic markers for sorghum species.

Conflict of interest

The authors declare that they have no competing interests.

Acknowledgments

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