Genomics Data 10 (2016) 153–154

Contents lists available at ScienceDirect

Genomics Data

journal homepage: www.elsevier.com/locate/gdata

Data in Brief

De novo transcriptome assembly of *Schisandra chinensis* Turcz. (Baill.)

Zhang qing-tian, Fan shu-tian, Yang yi-ming, Xu pei-lei, Ai jun *

Institute of Special Wild Economic Animals and Plants, Chinese Academy of Agricultural Sciences, Changchun, China

ARTICLE INFO

Article history:
Received 27 October 2016
Accepted 9 November 2016
Available online 10 November 2016

ABSTRACT

The fruit of *Schisandra chinensis* Turcz. (Baill.), namely "Wuweizi" in China, is a well-known herbal medicine and health food. At present, research focused on the extraction of effective chemical component and function identification. Little known about the secondary metabolism gene pathway of chemical composition. Its fruit color usually red, however, the white fruit color variation has been found. It made us interested in exploring which gene change lead to this result. In order to understand the genetic background of *S. chinensis*, we performed a transcriptome analysis of *S. chinensis*, including red fruit and skin of 'Yanhong' cultivar and white fruit and skin of 'Jinwuwei'. We obtained 26.4 GB raw data (NCBI accession number: SSR4449123). De novo transcriptome assembly using Trinity revealed 92,415 transcripts and generated 71,443 unigenes. All unigenes were annotated in database.

This study provides transcriptome of *S. chinensis*, which might be useful for comparative transcriptome analyses and understand gene expression of secondary metabolites.

Specifications [standardized info for the reader]	
Organism/cell line/tissue	*Schisandra chinensis*/white fruit and skin and red fruit and skin
Sex	N/A
Sequencer or array type	Illumina HiSeq2500
Data format	Raw data: Fastaq file
Experimental factors	De novo transcriptome assembly of *Schisandra chinensis* Turcz. (Baill.)
Experimental features	RNAs were isolated from the red fruit and with white fruit and skin, respectively.
Consent	N/A
Sample source location	Zuojia Town, Jilin City, Jilin Province, China (44°06′47″ N 126°07′18″ E)

1. Direct link to deposited data [provide URL below]

http://www.ncbi.nlm.nih.gov/sra/SRR4449123 for *Schisandra chinensis*.

2. Introduction

Schisandra chinensis Turcz. (Baill.) is a source plant of traditional Chinese medicine. The *S. chinensis* fruit (SF), which has five-flavored fruits (salty, pungent, bitter, sweet and sour), is called "Wuweizi" in China. It naturally distribute in China, Russian, Korea and Japan [1] and was used in treatment of diseases including liver injury [2], tumor inhibition [3], urinary tract disorders [4], insomnia and palpitation [5], even inhibit both HIV-1 RT-associated DNA polymerase activity and virus replication [6]. In addition to its application as a Chinese herbal medicine. It is also used for making beverages, tea, wine, health food industries and cosmetics [7]. Therefore, recent research has been focused on extracting active ingredients and identifying function. Despite of the importance of *S. chinensis*, the availability of genetic information is scare. The next generation sequencing technology has dramatically improved the efficiency and speed of gene discovery. It helps us further clarify the mechanisms of active ingredient biosynthesis pathway.

3. Experimental design, materials, and methods

3.1. Plant material

Two cultivars 'Yanhong' (red skin) and 'Jinwuwei' (white skin) were grown in orchard located in Zuojia Town, Jilin City, Jilin Province, China

* Corresponding author.
E-mail address: aijun1005@163.com (A. jun).

http://dx.doi.org/10.1016/j.gdata.2016.11.008

Table 1
Quality of sequencing.

Sample	Raw reads	Clean reads	Error (%)	Q20 (%)	Q30 (%)	GC (%)
R_fruit	72,479,628	67,859,218	0.035	94.47	89.54	46.41
W_fruit	55,069,062	48,352,042	0.035	94.79	89.97	48.61
R_skin	68,011,506	63,851,434	0.035	95.20	90.92	46.08
W_skin	69,345,058	59,975,984	0.035	95.16	90.85	47.06
Summary	264,905,254	240,038,678	0.035	94.91	90.32	47.04

(44°06′47″ N 126°07′18″ E) that belong to the Plant resources nursery of Institute of Special Wild Economic Animal and Plant Science, Chinese Academy of Agricultural Sciences. Fours samples, including fruits and skins, were harvested and immediately frozen in liquid nitrogen for further experiments.

3.2. RNA extraction, library construction and deep sequencing

Total RNA was extracted using modified CTAB method [8], Library construction and high-throughput sequencing for each sample was performed at a contract sequencing company (Novogene, China). The cDNA library was sequenced using an Illumina HiSeq2500 platform.

3.3. De novo transcriptome assembly and annotation

With the purpose of determining the red fruit, white fruit, red skin of red fruit and white skin of white fruit of *S. chinensis*.

We obtained a total of 72.5 million, 55.1 million, 68 million and 69.3 million raw data reads from four sequencing libraries prepared, respectively (Table 1), >94.9% bases has a Q value ≥20 (an error probability of 0.035%). After cleaning and quality checks, the de novo assembly of all sequencing data using the Trinity method. It generated 92,415 all-transcripts with an average length of 496 bp and an N50 of 1466 bp; and 71,443 all-unigenes were achieved. Of these, 46,461 (65.0%) were 200–500 bp, 11,322 were 500–1000 bp, 8612 were 1–2 kb and the remaining 5078 were >2 kb (Table 2). All 71,443 unigenes were annotated.

Some unigenes highly present association with secondary metabolic pathways. The results provides us useful information for further explorer the gene synthesis pathways of active ingredients.

Conflict of interest

All the authors have approved submission and there are no conflicts of interest.

Table 2
Length distribution of assembled transcripts and unigenes.

Nucleotides length (bp)	Transcripts	Unigenes
200–500 bp	53,323	46,431
500–1 kbp	16,269	11,322
1 k–2 kbp	14,025	8612
>2 kbp	8798	5078
Total	92,415	71,443
Minimal length (bp)	201	201
Maximal length (bp)	15,989	15,989
N50 (bp)	1466	1299
N90 (bp)	292	260
Mean length (bp)	796	682

Acknowledgments

This work was carried out with the support of 'Science and technology innovation project of Chinese Academy of Agricultural Sciences'.

References

[1] A. Szopa, R. Ekiert, H. Ekiert, Current knowledge of *Schisandra chinensis* (Turcz.) Baill. (Chinese magnolia vine) as a medicinal plant species: a review on the bioactive components, pharmacological properties, analytical and biotechnological studies. Phytochem. Rev. (2016).
[2] M.-K. Jang, J.S. Nam, J.H. Kim, Y.-R. Yun, C.W. Han, B.J. Kim, H.-S. Jeong, K.-T. Ha, M.H. Jung, *Schisandra chinensis* extract ameliorates nonalcoholic fatty liver via inhibition of endoplasmic reticulum stress. J. Ethnopharmacol. 185 (2016) 96–104.
[3] H.M. Qu, S.J. Liu, C.Y. Zhang, Antitumor and antiangiogenic activity of *Schisandra chinensis* polysaccharide in a renal cell carcinoma model. Int. J. Biol. Macromol. 66 (2014) 52–56.
[4] S.H. Choo, H.H. Sung, M.R. Chae, S.J. Kang, D.H. Han, J.K. Park, I. So, S.W. Lee, Effects of *Schisandra chinensis* extract on the relaxation of isolated human prostate tissue and smooth muscle cell. J. Ethnopharmacol. 156 (2014) 271–276.
[5] B. Wei, Q. Li, D. Su, R. Fan, L. Zhao, L. Geng, B. He, X. Chen, Y. Jia, K. Bi, Development of a UFLC-MS/MS method for simultaneous determination of six lignans of *Schisandra chinensis* (Turcz.) Baill. in rat plasma and its application to a comparative pharmacokinetic study in normal and insomnic rats. J. Pharm. Biomed. Anal. 77 (2013) 120–127.
[6] L. Xu, N. Grandi, C. Del Vecchio, D. Mandas, A. Corona, D. Piano, F. Esposito, C. Parolin, E. Tramontano, From the traditional Chinese medicine plant *Schisandra chinensis* new scaffolds effective on HIV-1 reverse transcriptase resistant to non-nucleoside inhibitors. J. Microbiol. 53 (4) (2015) 288–293.
[7] J.L. Yang, Y.D. Niu, C.P. Yang, G.F. Liu, C.H. Li, Induction of somatic embryogenesis from female flower buds of elite *Schisandra chinensis*. Plant Cell Tissue and Organ Cult. (PCTOC) 106 (3) (2011) 391–399.
[8] F.F. Rosas-Cárdenas, N. Durán-Figueroa, J.-P. Vielle-Calzada, A. Cruz-Hernández, N. Marsch-Martínez, S. de Folter, A simple and efficient method for isolating small RNAs from different plant species. Plant Methods 7 (2011) 4.