Genomics Data 3 (2015) 1–3

Contents lists available at ScienceDirect

Genomics Data

journal homepage: http://www.journals.elsevier.com/genomics-data/

Data in Brief

The high-throughput sequencing of small RNAs profiling in wide hybridisation and allopolyploidisation between *Brassica rapa* and *Brassica nigra*

Muhammad Awais Ghani, Junxing Li, Linli Rao, Muhammad Ammar Raza, Liwen Cao, Ningning Yu, Xiaoxia Zou, Liping Chen *

Department of Horticulture, College of Agriculture and Biotechnology, Zhejiang University, Yuhangtang Road No. 866, Hangzhou 310058, Zhejiang Province, PR China
Key Laboratory of Horticultural Plant Growth, Development, and Biotechnology, Agricultural Ministry of China, Hangzhou 310058, PR China

ARTICLE INFO

Article history:
Received 25 October 2014
Accepted 30 October 2014
Available online 8 November 2014

Keywords:
Wide hybridisation
Allopolyploidisation
Small RNAs

ABSTRACT

Small RNAs play an important role in maintaining the genome reconstruction and stability in the plant. However, little is known regarding the role of small RNAs during the process of wide hybridisation and chromosome doubling. Therefore, the changes in the small RNAs were assessed during the formation of an allodiploid (genome: AB) and its allotetraploid (genome: AABB) between *Brassica rapa* (♀) and *Brassica nigra* (♂) in the present study. Here, the experimental methods described in details, RNA-seq data (available at Gene Expression Omnibus database under GSE61872) and analysis published by Ghani et al. [1]. The study showed that small RNAs play an important role in maintaining the genome stability, and regulate gene expression which induces the phenotype variation in the formation of an allotetraploid. This may play an important role in the occurrence of heterosis in the allotetraploid.

Specifications	
Organism/cell line/tissue	*Brassica rapa* and *Brassica nigra*
Sex	*Brassica rapa* as female and *Brassica nigra* as male
Sequencer or array type	Illumina HiSeq 2000
Data format	Raw data: FASTQ files, analysed data: txt files
Experimental factors	Tissues/organs
Experimental features	RNA-seq dataset for small RNAs profiling in wide hybridisation and allopolyploidisation between *B. rapa* and *B. nigra*
Sample source location	Zhejiang University, Hangzhou, China

Direct link to deposited data

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE61872.

Experimental design, materials and methods

Sample collection and RNA isolation

Wide hybridisation between *B. rapa* (♀, genome: AA) and *B. nigra* (♂, genome: BB) was performed to produce allodiploids (F_1, genome: AB), and subsequently allotetraploids (F_1, genome: AABB) were obtained by treating the allodiploids with 0.2% colchicine for 16 h, as described in our pervious study reported by Ghani et al., [1,2]. After self-crossing of the allotetraploids, F_2 allotetraploids were obtained (Fig. 1). All of the plants were grown in vermiculite mixed with 30% soil in a growth chamber under growth conditions of 22/18 °C (day/night) and 16 h of illumination per day. The leaves from three plants of each type were collected 45 days after sowing in the vegetative stage for the analyses of small RNAs.

High-throughput sequencing of small RNAs

To determine small RNA populations in *B. rapa*, *B. nigra* and their progenitors (both the allodiploid and the allotetraploid), small RNA libraries were generated from the leaves of the four genotypes, i.e., *B. rapa* (AA), *B. nigra* (BB), the allodiploid (AB), and the allotetraploid (AABB). The total RNA was isolated using the Trizol reagent (Invitrogen, Carlsbad, CA, USA) according to the manufacturer's instructions and was sent to Beijing Genomics Institute (BGI) for sequencing. After treatment of the raw data, the clean sequences were subjected to further analyses as previously described [3]. The clean reads were analysed by length distribution and common sequences. The sequences were then matched to the genome of all of the plants to identify the repeat-associated sRNAs and to assess the expression of sRNAs. We identified known miRNAs using miRBase. To reveal the differential expression of miRNAs, the abundance of miRNAs in all of the libraries

* Corresponding author at: Department of Horticulture, College of Agriculture and Biotechnology, Zhejiang University, Yuhangtang Road No.866, Hangzhou 310058, Zhejiang Province, PR China.

http://dx.doi.org/10.1016/j.gdata.2014.10.021

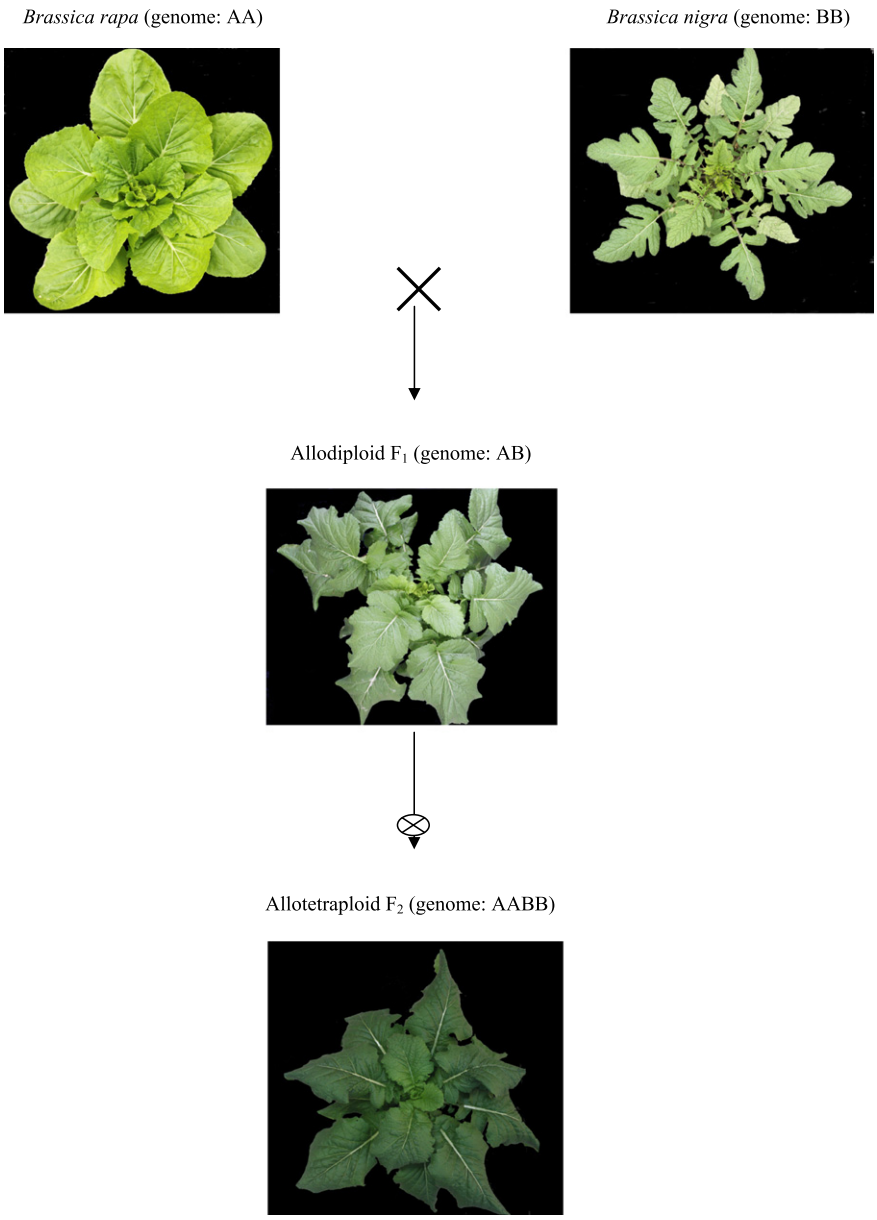

Fig. 1. The layout of the experiment plants; the parents and their allodiploid and allotetraploid.

was normalised. The normalisation values were compared between the two libraries and were calculated in the form of fold-changes (fold-change = log2 (treatment/control)). Moreover, the *p*-value was obtained using a previously described formula [4]. For the prediction of targets, the gene function, including the biological process, cellular component localisation, and molecular function of the genes were analysed (Fig. 2).

Conclusion

This result showed that siRNAs play key roles in maintaining the genomic stability through the regulation of small RNA levels. Moreover, most miRNAs were highly overexpressed in the allotetraploid, which might be induced by the heterosis, such as miR159, miR169, and miR164, miR165, and miR166, which have a major role in flower and leaf development in the allotetraploid. Taken together, the findings of this study demonstrated that siRNAs and miRNAs maintain the genomic and phenotypic stability in the allotetraploid.

Conflict of interest

Authors declare no conflict of interest.

Acknowledgments

This work was supported by the National Natural Science Foundation of China (No. 31272159), the Zhejiang Provincial Natural Science Foundation of China (No. LZ12C15001) and the Specialized Research Fund for the Doctoral Program of Higher Education (20110101110089). We thank Mrs. Zhang Fenglan, the Beijing Vegetable Research Centre (BVRC), and the Beijing Academy of Agriculture and Forestry Science (BAAFS), Beijing, China for providing the seeds (*Brassica rapa*).

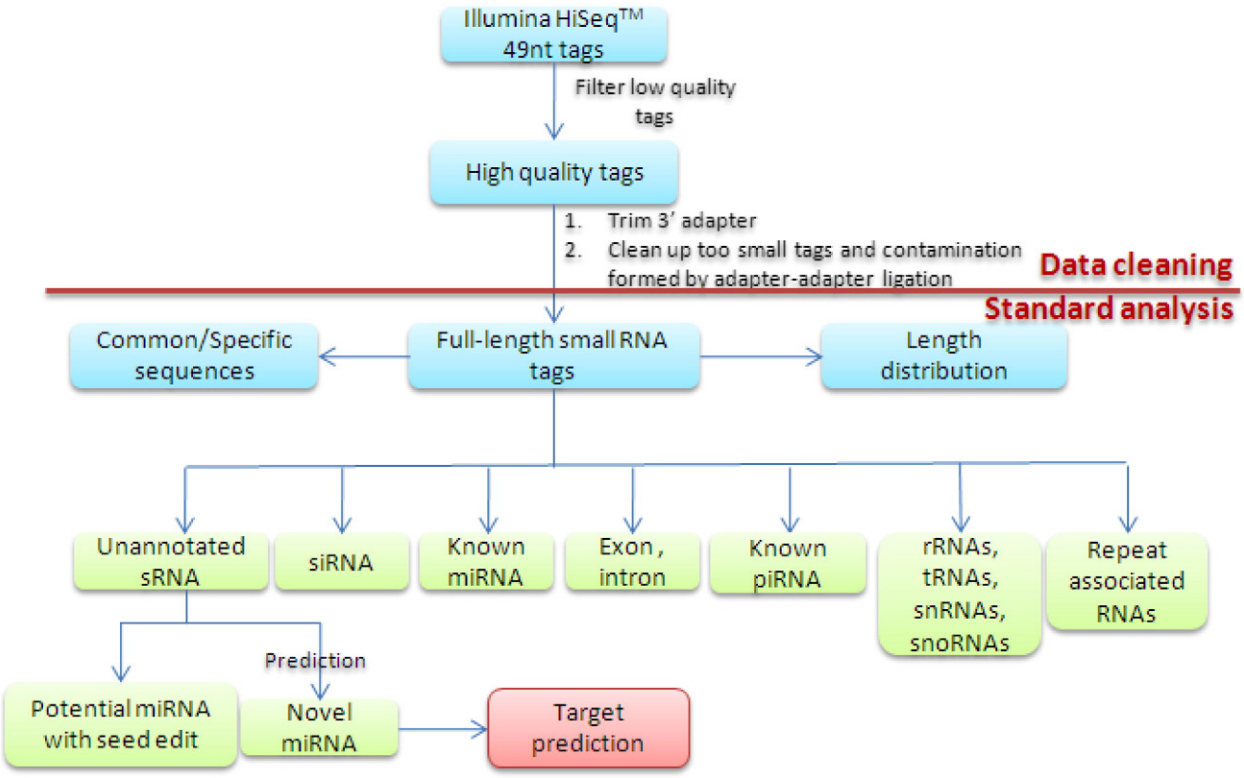

Fig. 2. Workflow for RNA-seq experiments conducted in the study.

References

[1] M.A. Ghani, J. Li, L. Rao, M.A. Raza, L. Cao, Y. Ningning, X. Zou, L. Chen, The role of small RNAs in wide hybridisation and allopolyploidisation between *Brassica rapa* and *Brassica nigra*. BMC Plant Biol. 14 (2014) 272.

[2] M.A. Ghani, S. Qian, J. Li, L. Cao, L. Rao, X. Zou, L. Chen, Phenotypic and genetic variation occurred during in wide hybridisation and alloploypoidisation between *Brassica rapa* and *Brassica nigra*. Sci. Hort. 176 (2014) 22–31.

[3] R. Sunkar, X. Zhou, Y. Zheng, W. Zhang, J.K. Zhu, Identification of novel and candidate miRNAs in rice by high throughput sequencing. BMC Plant Biol. 8 (2008) 25.

[4] Z.H. Gao, T. Shi, X.Y. Luo, Z. Zhang, W.B. Zhuang, L.J. Wang, High-throughput sequencing of small RNAs and analysis of differentially expressed microRNAs associated with pistil development in Japanese apricot. BMC Genomics 13 (2012) 371–384.