

**Sequencing and comparative analysis of *Aegilops tauschii* chromosome arm 3DS revealed rapid evolution of Triticeae genomes**

**2016**

Posted by : webmaster

Posted on : 2016/10/11 11:31:20

Jingzhong Xie, Naxin Huo, Shenghui Zhou, Yi Wang, Guanghao Guo, Karin R Deal, Shuhong Ouyang, Yong Liang, Zhenzhong Wang, Lichan Xiao, Tingting Zhu, Tiezhu Hu, Vijay Tiwari, Jianwei Zhang, Hongxia Li, Zhongfu Ni, Yingyin Yao, Huiru Peng, Shengli Zhang, Olin D Anderson, Patrick E McGuire, Jan Dvorak, Ming-Cheng Luo, Zhiyong Liu, Yong Q Gu, Qixin Sun

Journal of Genetics and Genomics

Received 19 August 2016, Revised 26 September 2016, Accepted 27 September 2016,

Available online 5 October 2016

Abstract

Bread wheat (*Triticum aestivum*, AABBDD) is an allohexaploid species derived from two rounds of interspecific hybridizations. A high-quality genome sequence assembly of diploid *Aegilops tauschii*, the donor of the wheat D genome, will provide a useful platform to study polyploid wheat evolution. A combined approach of BAC pooling and next-generation sequencing technology was employed to sequence the minimum tiling path (MTP) of 3176 BAC clones from the short arm of *Ae. tauschii* chromosome 3 (At3DS). The final assembly of 135 super-scaffolds with an N50 of 4.2 Mb was used to build a 247-Mb pseudomolecule with a total of 2222 predicted protein-coding genes. Compared with the orthologous regions of rice, *Brachypodium*, and sorghum, At3DS contains 38.67% more genes. In comparison to At3DS, the short arm sequence of wheat chromosome 3B (Ta3BS) is 95-Mb large in size, which is primarily due to the expansion of the non-centromeric region, suggesting that transposable element (TE) bursts in Ta3B likely occurred there. Also, the size increase is accompanied by a proportional increase in gene number in Ta3BS. We found that in the sequence of short arm of wheat chromosome 3D (Ta3DS), there was only less than 0.27% gene loss compared to At3DS. Our study reveals divergent evolution of grass genomes and provides new insights into sequence changes in the polyploid wheat genome.

Keywords

*Aegilops tauschii*; Genome sequencing; Sequence assembly; Comparative genomics; Grass evolution

<http://dx.doi.org/10.1016/j.jgg.2016.09.005>