

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

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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

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