Physical mapping of the wheat chromosome arm 7D: a foundation for reference sequence assembly and position-cloning

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Bread wheat (Triticum aestivum L.) is one of the most important crops worldwide. Availability of its complete genome sequence holds the promise of meeting the challenges of increasing food demand and the changing global climate in the 21st century. However, wheat is an allohexaploid species (2n = 6x = 42) with the genome size of 17 × 10⁹ bp/1C and 90% repetitive sequences, making it a daunting task to sequence the wheat on the genome-based scale. The International Wheat Genome Sequencing Consortium (IWGSC) has proposed to map and sequence the wheat genome based on chromosome-by-chromosome approach. One prerequisite for generating a reference sequence of each chromosome is a high-density physical map to act as a scaffold for sequence assembly.

As part of the efforts of IWGSC, we constructed a physical map for the chromosome arm 7DL through fingerprinting 7DL-specific BAC clones using the high information content fingerprinting technique. A total of 50,304 clones (representing ca. 15x equivalent of the chromosome arm) were fingerprinted, of which 43,492 clone-fingerprints were suitable for assembly. An initial automated assembly with the FPC software resulted in 1,614 contigs and 6,125 clones remained as singletons. The size of contigs N50 was 361kb; L50 was equal to 353 contigs. And then, a total of 4,435 minimal tilling path (MTP) clones were selected from this assembled contigs. With the completion of Aegilops tauschii physical map, a new strategy was developed adopting the Ae. tauschii physical map as a template for anchoring contigs of individual chromosome/arm of wheat D genome thanks to the homology between Ae. tauschii and wheat D genome. Using this method, we have anchored 845 contigs of wheat 7DL chromosome according to the physical map of Ae. tauschii, the total length of anchored
contigs accounts for the 67.7% of the length of whole 7DL contigs. The contig N50 in size was 504kb, L50 = 204 contigs. These results suggested that using the physical map of *Ae. tauschii* to anchor contigs is an effective approach for construction of physical maps for wheat D genome. This approach also provides a valuable resource to studying the structural variations and molecular evolution between these two species. The 7DL physical map will be an essential tool for positional cloning and future assembly of a reference sequence.