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Sequencing of flow-sorted wheat chromosome 5D using 454-GSFLX

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Wheat chromosome 5DS-specific BAC library was fingerprinted and 25,429 good quality fingerprints were assembled into 164 contigs (including 44 short contigs <6 clones) using Linear Topological Contig (LTC) Software. The assembly covered ~177MB of 5DS, with an average contig size of 1,078kb and N50/L50 values of 89 MB/27 contigs. To date, 33 contigs have been anchored with at least one of 12 COS markers, 11 SSR markers, 2 gene-based markers and 22 ISBP markers. We have also sequenced flow-sorted short (S) and long (L) arms of chromosome 5D using GSFLX and obtained a total of 3,208,630 reads corresponding to 1.34x and 1.61x coverage for 5DS and 5DL, respectively. About 74% of the sequences were classified as known or novel wheat repetitive DNA elements. Non-repetitive sequences were blasted against protein sequences of reference grass genomes, revealing 1493 and 2843 conserved genes on 5DS and 5DL, respectively. We have identified 1812 and 4500 Triticeae-specific genes or gene fragments on 5DS and 5DL, respectively. Furthermore, a virtual gene order for 5D chromosome was constructed utilizing the order of syntenic genes in *Brachypodium* integrated with 518 EST and SSR marker positions mapped onto 5D shotgun sequences. Accordingly, a large-scale rearrangement was revealed in the peri-centromeric region of 5DL, and a high concentration of genes was observed in 5DS telomeric region. Data obtained in this study increase our understanding of the gene content and structure of the wheat genome.

Biography

Hikmet Budak has completed his PhD from University of Nebraska-Lincoln and led the grass genetics and breeding program at the same university. He is a full Professor at Sabanci University, Turkey and adjunct faculty member at the University of Nebraska-Lincoln. He has published more than 70 papers in reputed journals and serving as an editorial board member of Genomics, European Journal of Molecular Biology, International Journal of Plant Genomics.

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