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Minimum Tiling Path BAC Clones of Mitochondria and Chloroplast Genome of *Brassica rapa*

Jee Young Park¹, Tae-Jin Yang¹, Ki-Byung Lim¹, Soo-Jin Kwon¹, Jungsun Kim¹, Jin-A Kim¹, Mina Jin¹, Myung-Ho Lim¹, Beom-Soon Choi¹, Hyo-Jin Lee¹, Ho-Il Kim¹, Seok-Hyoung Kim¹, Yong Pyo Lim², and Beom-Seok Park^{1*}

1. Brassica Genomics Team, National Institute of Agricultural Biotechnology (NIAB), RDA, Suwon, 441-707, Korea 2. Chungnam National University, Daejeon, 305-764 Korea

Objectives

We have constructed the minimum tiling path BAC clones contig representing whole sequence of cellular organelle genomes (mitochondria and chloroplast) by selection of BAC clones based on blast analysis of 80,292 BAC-end sequence of *Brassica rapa*.

Materials and Methods

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BAC libraries: *Brassica rapa* HindIII, BamHI, and Sau3AI (KBrH, KBrB, KBrS)

BLAST, shotgun sequencing, BAC-end sequencing, Fingerprinting

Results and Discussion

We have analyzed a total of 95,000 BAC end sequences from three BAC libraries (*HindIII*, *BamHI*, and *Sau3AI*) of *Brassica rapa*. Among them, 80,292 BAC-end sequences were used in this study. BLASTs to Arabidopsis chloroplast and mitochondria genome reveal that 3,958 BAC-end sequences (about 4.9%) and 1,414 BAC-end sequences (about 1.7%) show significant hits ($<E-6$) with chloroplast and Mitochondria genome, respectively. Among them, 1063 BACs (about 2.65%) and 57 BACs (about 0.14%) show significant hits with chloroplast and Mitochondria genome, respectively, by both ends. Based on the hit positions, we have selected BAC clones for representing each of genome, chloroplast and mitochondria. Fingerprinting of the selected BAC clones show same ordering with the hit positions. As the results, the whole mitochondria genome (370kb) is covered by three tiling BAC clones and the chloroplast genome (150kb) is covered by only one BAC clone. Full sequence of the organelle genome will be characterized soon by shotgun sequencing of the four BAC clones.