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The *Brassica* and *Arabidopsis* lineages diverged ~20 MYA with comparative late and so their genome is syntenic and collinear. Based on comparative sequence analysis of 91,179 BAC end sequences (BES), we have allocated a total of 4,317 *Brassica* BAC clones (9.5%) on the counterpart region of *Arabidopsis* chromosomes that span 92 Mb of unique sequence of *Arabidopsis* chromosome. Furthermore, we selected 629 *Brassica* BAC clones that compose the minimum tiling path on *Arabidopsis* chromosome (http://www.brassica-rapa.org). The comparative tiled BACs evenly distributed in the *Brassica* genome had been sequenced in 2005. The actual location of each BAC clone of *B. rapa* can be identified by FISH or sequence based genetic mapping. Up to date, around 210 among 629 sequenced BACs have been mapped through development of SSR marker in each BAC. Totally 1500 SSRs primer pairs(1 to 3 every 629 BAC clones) were designed and among these, around 500(30%) have shown polymorphism between parental lines of two mapping populations (Jangwon $F_{2:3}$ family and Chiifu X Kenshin Double haploid). Using these SSR markers, 210(33 %) BAC clones were mapped to linkage groups of Jangwon F3 population and their actual location in *Brassica* were identified. As the same previous comparative study, BACs selected from a collinear segment on *Arabidopsis* were localized to three parts and it proves again that *Brassica* genome occurred triplication after divergence with *Arabidopsis*. Sequence based and genome widely well distributed DNA markers can be a valuable resource to provide unlimited information for breeding and genome evolution study as well as genome sequencing of the genus *Brassica*.

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(O5-05)

In Silico identification of *Brassica rapa* BAC clones containing harboring genes related to circadian associated factors

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In *Arabidopsis thaliana*, a number of circadian associated factors have been identified TOC1 (TIMING OF CAB EXPRESSION 1) is a member of a small family of proteins, designated as *ARABIDOPSIS* PSEUDO-RESPONSE REGULATORS (APRR1/TOC1, APRR3, APRR5, APRR7, and APRR9). These APRR1/TOC1 quintet members are crucial for a better understanding of the molecular links between circadian rhythms, control of flowering time through photoperiodic pathways, and also photosensory signal transduction. In this respect, other plants might share the evolutionarily conserved molecular mechanism underlying the circadian rhythm. Based on such an assumption, we asked the question of whether *Brassica rapa* also has a set of pseudo-response regulators, and if so, whether or not they are associated with the circadian rhythm. To identify and characterize these circadian response genes in the *B. rapa*, we have tried a novel method for in silico identification of BAC clones containing these genes based on comparative genomics information with *Arabidopsis* because *Brassica* genome is syntenic and co-linear with the *Arabidopsis* genome. We have compared 91,179 BAC end sequences (BES) with the *Arabidopsis* genome sequence and allocated each BAC on the specific counterpart region of *Arabidopsis* chromosome. A total of 4,317 BAC clones (9.5%) are allocated on the counterpart region of *Arabidopsis* chromosomes (http://www.brassica-rapa.org). Based on these information we have selected *Brassica rapa* BAC clones spanning the locus of the quintet circadian rhythm factors. By subsequent fingerprinting, southern hybridization, and PCR. we can identify have identified BAC clone sets containing five circadian related genes. By shotgun sequencing of the selected BAC clones, we characterized and cloned each gene which is orthologous to *Arabidopsis* quintet.

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