Development of High Density Integrated Reference Genetic Linkage Map for Multinational *Brassica rapa* Genome Sequencing Project

Xiao Nan Li *, Nirala Ramchiary *, Su Ryun Choi *, Dan Van Nguyen, Md. Jamil Hossain, Hyeon Kook Yang and Yong Pyo Lim§

Department of Horticulture, and Genome Research Center, Chungnam National University, Daejeon, 305-764, Korea

**Abstract**

A high density integrated map of *B. rapa* was constructed based on two mapping populations, ‘Chifu x Kenshin’ and ‘Chifu x RcBr’. The integrated map contains 1017 markers covering 1262.0 cM in length with an average of 1.24 cM between two loci. A total of 155 SSR anchoring 102 new BACs and 146 intron polymorphic markers were mapped in the integrated map which would be helpful in aligning the sequenced BACs in ongoing multinational *B. rapa* Genome sequencing project (MBrGP). Further, high degree of co-linearity between A genome linkage groups were observed by integration of *B. rapa* consensus map with that of 10 A genome linkage groups of *B. juncea*. It suggested conservation of chromosomal regions between *B. rapa* and *B. juncea* even though the two species evolved independently after their divergence. Thus, the sequencing information of *B. rapa* would be helpful for *B. juncea* breeding and the already identified gene blocks and known QTLs information in *B. juncea* could be transferred to *B. rapa* species.

**Introduction**

Chinese cabbage inbred line Chifu-401-42 was selected as the representative model for *Brassica* A genome sequencing by the Multinational Brassica Genome Project (MBrGP) in 2003 (Yang et al., 2005). As its ongoing, amounts of BAC specific SSR markers were developed and it gave an opportunity to develop integrated genetic, physical and sequence-based maps of *B. rapa*. Kim et al. (2009) updated the version I reference map of Choi et al. (2007) and could align 188 seed BACs in 10 *B. rapa* linkage groups using BAC anchored SSR markers. However, the number of BAC anchored SSRs markers were very less to cover the whole genome of *B. rapa* in all the maps for MBrGP.

In our study we have mapped additional BAC sequences derived SSR markers and constructed a high density integrated linkage map of *B. rapa* for MBrGP, using two populations with Chifu-401-42 as common parent.

**Materials and methods**

- **Mapping population**

  CKDH population consisting of 78 doubled haploid lines from F1 crossing by ‘Chifu-401-42’ and ‘Kenshin’.

  F1 population (190 individuals) derived from self-pollination of an F1 individual originated from a cross between ‘Chifu-401-42’ and ‘RcBr-IBM-218-DH1’.

- **Molecular markers**

  The SSR markers were developed based on BAC-end sequence of *B. rapa* ssp. *pekinesis* inbred lines, Chifu-401-42 and were used to construct reference map of CKDH and CKRI population before.

  IP (Intron polymorphic) markers developed by Panjabi et al. (2008) were also used to genotye CKDH population and CRF2 population.

- **Linkage map analysis:** Joinmap 4.0 was used to construct individual map and generate integration map by “Combine the Groups for Map Integration” function.

**References**

