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Perspective and Future of Chinese Genome Research

Jae Wook Bang, Yoon Kang Hur, Kwan Sam Choi, Ho Il Kim1 and Yong Pyo Lim
[1]Genomics Div., National Institute of Agricultural Biotechnology, RDA, Suweon, Korea and Genome Research Center, Chungnam National University, Daejeon, Korea

Chinese cabbage, which is the typical representative species of Brassica A genome. For genetic mapping of Chinese cabbage, several marker system including AFLP, RAPD, SSR, and PCR-RFLP has been developed with 89 DH lines from the F1 of \'Chiifu\' type x \'Kenshin\' type. We had also analyzed 33 morphological characteristics for QTL analysis. For construction of large mapping population, we are constructing the RI lines whose population is 249 F4 and 224 F5 lines by SSD methods. Chinese cabbage (550Mbp) BAC library was constructed with 56,592 clones, whose average size is 115kbp. This library is now using for genome reaserch. For physical mapping, 6,337 BAC clones were analyzed. The results generated the 406 contigs and 5,239 singletons. BAC FISH technology was also applied to confirm each chromosome. For efficient analysis and management of Brassica genome data, we have constructed the platform for genomics research with parallel computer of Beowulf-style. And Arabidopsis and Brassica genome database were constructed based on ACEDB and web site (http://www.brassicagenome.org) was constructed.

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Arabidopsis dwarf mutants define six genes involved in brassinosteroid biosynthesis and two in the signal transduction pathways

Sunghwa Choe
School of Biological Sciences, College of Natural Sciences, Seoul National University, Seoul 151-747, Korea

Physiological effects of brassinosteroids (BRs) include cell elongation, cell division, stress tolerance, and senescence acceleration. Arabidopsis mutants that carry genetic defects in BR biosynthesis or its signaling display characteristic phenotypes, such as short robust inflorescences, dark-green round leaves, and sterility. Currently more than 100 dwarf mutants representing 8 genetic loci in Arabidopsis have been isolated. Mutants of the 6 loci, dwf1/dim1/cbb1, cpd/dwf3, dwf4, dwf5, det2/dwf6, dwf7 are rescued by exogenous application of BRs, whereas bri1/dwf2 and dwf12/bin2/ucu1 share the dwarf phenotypes but are resistant to exogenously applied BRs. Biochemical analyses and molecular cloning of the genes revealed that dwf7, dwf5, and dwf1 are defective in the three consecutive steps of sterol biosynthesis, from episterol to campesterol via 5-dehydroepisterol. In addition, det2/dwf6, dwf4, and cpd/dwf3 are blocked in Ä4 reduction, 22á- hydroxylation, and 23á-hydroxylation, respectively. A signaling mutant bri1/dwf2 carries mutations in a leucine-rich repeat receptor kinase. A recently characterized semi-dominant gain-of-function mutant dwf12 was found to carry mutations in GSK3â-like kinase. To better understand the dynamic mechanisms coupling BR biosynthesis and signaling, it will be important to elucidate the signaling components that regulate DWF12, and to identify additional components downstream of DWF12 that lead to the transcription of BR biosynthetic and BR response genes.