The genus *Brassica* L., phylogenetically related to *Arabidopsis thaliana*, includes many economically important food crops. This genus can serve as a botanical model of plant polyploidization and rapid phenotypic evolution. Recently, we established the Korea *Brassica* Genome Resource Bank (KBGRB), a *Brassica*-related seed and DNA stock center, to supply foundation plant materials for structural and functional genomics of *Brassica* species. The KBGRB has developed populations, including doubled haploid and recombinant inbred lines, and mutants of *Brassica rapa*, and has constructed genomic bacterial artificial chromosome (BAC) and cDNA libraries. Seeds and genomic DNA libraries of other *Brassica* species have also been collected. The germplasm held by KBGRB has been propagated and maintained. Information and other requests for genomic resources of *Brassica* are accessible at http://www.brassica-resource.org.

INTRODUCTION

Biological resources are essential for human life. Plant genetic resources, i.e. plant germplasm, are critical for the continuation and development of economically important food crops. The terms “germplasm” or “genetic resources” includes plant parts, seeds or, more precisely, the DNA of an organism. Worldwide, there are genebanks, or collections of plant, animal and bacterial germplasm, for use in breeding new crops or plants, and for the conservation of existent species.

Crop genetic resources are the basis of agricultural production, and significant economic benefits have resulted from their conservation and use. There are many genetic resource servers and databases, such as the System-wide Information Network for Genetic Resources (SINGER), which is the genetic resources information exchange network of the Centres of the Consultative Group on International Agricultural Research (CGIAR). SINGER provides access to information on the collections of genetic resources held by the CGIAR Centres. Chinese Crop Germplasm Information System (CGRIS) (http://icgr.caas.net.cn/cgris/english.html) is a central repository for genetic resources and information. These resources help biologists focus on specific genomic/proteomic regions or gene sets, providing functional annotations and visualization.

A number of European Central Crop Databases (ECCDBs) have been established through the initiative of individual institutes and of the European Cooperative Programme for Crop Genetic Resources Networks (ECP/GR) Working Groups. These crop databases centralize and hold information on germplasm accessions that are maintained by various European institutes.
Crops of the genus *Brassica*, which are in the same taxonomic family as *Arabidopsis thaliana*, are widely used in the cuisine of many cultures, due, in part, to the many choices of edible forms in the genus. The haploid genome equivalent of *B. rapa* is approximately 550 Mb and is closely related to the genome of *Arabidopsis* (125 Mb haploid genome equivalent) (Johnston et al., 2005). The genome of the latter species, considered the model plant, has been sequenced completely (The *Arabidopsis* Genome Initiative, 2000). The genus *Brassica* is one of the core genera in the subtribe Brassicinae and includes a number of crops with wide adaptation under varied agroclimatic conditions.

Of the six cultivated species of *Brassica*, *B. rapa* (AA, 2n = 20), *B. nigra* (BB, 2n = 16), and *B. oleracea* (CC, 2n = 18) are monogenetic diploids. The remaining three, namely *B. juncea* (AABB, 2n = 36), *B. napus* (AACC, 2n = 38), and *B. carinata* (BBCC, 2n = 34), are allopolyploids that have evolved by hybridization between the monogenic diploids. Economically, *Brassica* is loosely categorized into oilseed, vegetable, fodder and condiment crops (Paterson et al., 2001). *Brassica* species are a valuable source of dietary fiber, vitamin C, and other possible salubrious factors such as anticancer compounds (Fahey et al., 1995).

Genomic research in any organism encompasses understanding the structure of the target genome and genes, their function, and evolution. The availability of suitable genetic and genomic resources is a prerequisite to undertaking genomic research in *Brassica rapa*. Hence, we constructed the database of KBGRB to maintain and distribute resources for researchers throughout the world who study *Brassica rapa*. Furthermore, the user can search a variety of information regarding genetic and genomic resources using the database.

**THE ROLE AND RESPONSIBILITY OF KBGRB**

KBGRB (http://www.brassica-resource.org) has been established to provide basal materials for discovery of novel genes, their application to breeding, and finding new genetic interests via structural/functional genomics in *Brassica* species. To this end, KBGRB has developed mapping populations, inbred lines, and mutants of *Brassica* species, and constructed DNA stocks, bacterial artificial chromosome (BAC) and cDNA libraries. Moreover, species and/or cultivars showing wild-type and/or unusual characteristics have been collected and multiplied. These genetic resources have been used as the standard basal materials for the Multinational *Brassica* Genome Project (MBGP) and its subproject Multinational *Brassica rapa* Genome Sequencing Project (MBrGSP). Recently, by using those materials, genetic mapping, physical mapping and whole-genome sequencing of *B. rapa* have been performed by *Brassica* genomics teams.

**CURRENT STATUS OF KBGRB’S RESOURCES HOLDINGS**

We have developed reference mapping populations of Chinese cabbage (*B. rapa* ssp. *pekinesis*) comprising 86 double haploid lines derived from the anther culture of the *F*$_1$ generation of the Chinese cabbage inbred lines ‘Chifu’ and ‘Kenshim’. Using the same parents, we have also developed a recombinant inbred population comprised of over 257 lines in the *F*$_8$ generation. Using the population consisting of 78 DH lines, the reference genetic map of Chinese cabbage with a total of 557 markers, which includes 278 AFLP, 235 SSR, 25 RAPD and 18 ESTP markers, has been constructed for aligning and anchoring physical BAC contigs (Choi et al., unpublished). Currently, the linkage groups of the genetic map have been aligned with the chromosomes of the cytogenetic map using linkage group-specific genetic markers, which will give impetus to information on chromosome assignment.

The bacterial artificial chromosome (BAC) library is a valuable resource not only for physical mapping and the alignment of the genetic map, but also for DNA sequence analysis and gene cloning (e.g. map-based cloning). By isolating high molecular weight leaf DNA from the Chinese cabbage inbred line ‘Chifu’, we constructed two BAC libraries using the restriction enzymes, *Hind*III (KBrH) and *Bam*HI (KBrB); the BAC libraries were comprised of 56,592 and 50,688 clones, with an average insert size of 115 kb and 124 kb, respectively (Park et al., 2005; Lim et al., 2006).
The cDNA library and TILLING population is essential for functional genomic analysis. We have constructed four different cDNA libraries and analyzed the EST of 13,348 clones from cDNA library. TILLING population of B. rapa was established with the ‘Chiifu’ line of B. rapa in 2004, and we have since collected 864 M1 lines. We intend to expand the population to 10,000 lines.

Various kinds of mapping populations and BAC libraries are essential for structural and functional genomic research (Table 1).

**MANAGEMENT OF KBGRB**

The management of the seed and DNA stacks is the most important function of the KBGRB. The seeds must be kept in specific low temperature conditions and the seed activation must be tested to maintain the preserved generation. The required data include: species name, number of accessions, biological status of material held, e.g., wild species, landraces, and breeder’s material, an indication of the safety-duplication status, a summary of the geographical coverage of the material, and parameters on seed storage such as the type of container used and storage temperatures. A substantial part of these data has been published in the past in the *Directories of Germplasm Collections*. Presently there are more than twenty of these directories covering all major agricultural crops.

For the current protocol BAC clones are kept at -70°C. Three sets were made simultaneously for preservation in separate deep freezers. Each set and clone is assigned a specific number for management through the database. The cDNA libraries are also kept in the freezer and can be proliferated when needed. EST clones with complete sequence are kept at -70°C or -20°C and are also given a specific number. The libraries in 384 well plates are kept at -70°C, -20°C or 4°C.

KBGRB can be accessed freely using a web browser at www.brassica-resource.org. Summaries of all collecting missions undertaken from 1993 to the present are stored here. Users can search information from the database in this way. An accession is an entry in a germplasm bank for a seed collection from a particular inbred line from a particular plant, family or population. KBGRB gives a specific accession number to all of the seeds that are secured, along with BAC clones and cDNA clones. The database maintains coded names for each institute that receives the collected germplasm. We have also designed a mail delivery system for the researchers who order germplasm through the internet, giving information about the seeds, gene group, cDNA, and BAC clone on the web site (Fig. 1). KBGRB was appointed the Sub-genebank for Seed or Clonal Plant Germplasm Resources at National Agrobiodiversity Center, Genetic Resources Division, National Institute of Agricultural Biotechnology, Rural Development Administration.

**KBGRB DATABASE**

KBGRB was constructed using a Linux CentOS 4.2 system and maintained using My-SQL 5.0, a relational database management system. The database uses a series of PERL scripts, which act as wrappers for *Brassica* species, cultivar, annotation and management of My-SQL database. A web-based interface allows the researcher to interrogate and navigate the processed information on *Brassica*.

**EXPECTED CONTRIBUTION**

The establishment of Korea *Brassica* Genome Resource Bank (KBGRB) will provide an important base to support structural and functional genomic research, as well as the genetic and breeding project in *Brassica* species. KBGRB will provide the most efficient, well-organized and integrated services for *Brassica* research groups through systematic collection, conservation, and distribution of *Brassica* genomic and genetic resources in the world. We propose to adopt the Ensemble database and software environment as the main project data interface and for the data warehouse for the comparative data.
ACKNOWLEDGEMENT

This research was supported by grants from Korean Science and Engineering Foundation (KOSEF. R21-2004-000-10010-0), Korean BioInformation Center (KOBIC) Research Initiative Program and Genebank Management Fund & National Agrobiodiversity Center.

Literature Cited


Tables

Table 1. Current status of KBGRB resources.

<table>
<thead>
<tr>
<th>Resource</th>
<th>Source material</th>
<th>Number</th>
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<tbody>
<tr>
<td>Seed</td>
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<td>Brassica species</td>
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Fig. 1. KBGRB user interface.