The Gene Engineering Division (RIKEN DNA Bank) is a non-profit resource center that provides genetic resources, technical services and educational program to qualified investigators of private industry, government and academic organizations around the world. RIKEN DNA Bank has been selected as a central facility to collect, preserve and deliver the DNAs of Animals and microorganisms by the National Bio-Resource Project funded by Ministry of Education, Culture, Sports, Science and Technology of Japan (MEXT). Our division undertakes research to ensure the authenticity of the genetic materials in the collection, and to improve and standardize the methods of characterization, maintenance, preservative and distribution of genetic materials. We distribute cloned DNAs, gene libraries (cDNA, phage, Cosmid, BAC, Phosmid, YAC library), vectors, hosts, recombinant viruses and ordered library-sets from human, mouse, microorganisms, viruses and other animal cells. Our division also performs and sponsors research to improve and standardizes for the advancement, validation and application of scientific knowledge.

RIKEN DNA Bank was established in June 1987 when a committee of scientists recognized a need for a central collection of recombinant DNA that would serve scientists in Asia. In 2001, RIKEN BioResource Center (RIKEN BRC) was established and then DNA Bank was reorganized to a Division of Gene Engineering.

1. Collection, preservation and distribution of genetic resources

The Gene Engineering Division (RIKEN DNA Bank) is divided into five sub-Banks:

(1) **Cloned-DNA Set Bank** handling cloned collection of full-length cDNAs which were assembled with the specific research areas like hormones, cytokines, apoptosis, cell cycle, signal cascades, transcription factors, replication factors, ubiquitination and so on. This Bank also authenticates the promoter genome fragments and is designated as “Promoter-Bank”. These representative cloned sets were isolated from cDNA libraries, phage libraries, cosmide, BAC, YAC, PAC, P1 and phosmid libraries.
(2) **Japanese-specific DNA Bank** handling human HLA class I clones which specified for the genetic character of Japanese and SEREX clones specific for Japanese and other clones for Japanese heredity.

(3) **Recombinant-virus Bank** handling the recombinant viruses which were constructed by inserting the full length cDNA into the viral vectors and generated the viral particles as the resources. The viruses are examined their qualities by methods developed in our division. The DNA fragments derived from human and mouse full length cDNA libraries were used as the donor of recombinant viruses.

(4) **Regular DNA Bank** handling cDNAs, genome DNA clones and vectors as well as host cells.

(5) **Bioinformatics section** handling the informatics of our genetic resources for DNA Banking.

We distributed the genetic resources to only qualified investigations who are associated with certain research, medical or educational organizations. We also reported the activities of our division by an annual report and qualified by the “**Resource Committee**” every year. We also discussed about a future plan of our mission. The “**Resource Ethics Committee**” ensured the banking activity of genetic resources of human, which was held every year. The “**Advisory Council**” is to be held to assess the activities of DNA-Bank every other year. We are evaluated not only the activities of DNA-Banking but also the research activities of developing technologies related to DNA-Banking.

2. Development of new technology to identify the mutation sites in the genetic materials.

The development and the improvement of methods for standardization and characterization of genetic resources are also conducted in our Division. Three technologies should be developed; 1) Identification of the mutation sites of the genetic resources; 2) Evaluation of the controlled expression system of the genes, and 3) Preparation of the novel adenovirus vectors for human gene therapy.
BRC Collaborative Researchers

BRC Technical Staffs
Kumiko INABE (2002.4 ~ )  Miho TERASHIMA (2003.1 ~ )
Takahito YAMASAKI (2003.4 ~ )

Visiting Members
Yukari KUJIME (Science Service Co., Inc.) (2001.4 ~ )
Miyuki YAMAMOTO ( " ) (2003.6 ~ )  Kazuko UENO ( " ) (2001.4 ~ )
Megumi KUNIFUDA ( " ) (2003.2 ~ )

Student Trainees
Kuniaki FUKUDA (Univ. of Tsukuba) (2001.4 ~ )
I. Collection, preparation and distribution of genetic materials.

1. Banking system
We have collected the following number of the genetic materials; host 76, vector 57, cloned DNA 1459, Nakamura-White RELF marker clone 123, human genomic YAC clone 35,712, mouse 15k cDNA clone 15,296, Mouse 7.4k cDNA clone 7,407, Mouse cDNA clones 45,216, Human cDNA library 15, mouse BAC cloned library 40,000, Human SEREX clone 190, Japanese HLA class I 25, Recombinant virus 219, and Primates BAC library 52,320.

II. Development of technology
We have performed the following research projects to develop a new technology for the DNA-Banking.

1. Detection of mutation of DNA of genetic resources
We have developed the novel techniques to detect the mutation of genetic resources with a higher sensitivity and reproducibilities. These techniques are used for the validation of quality of genetic resources.

2. Development of new gene-delivering system
(Antisense, Ribozyme, Antigene, siRNA and other methods).
To suppress the function of the target genes, we have introduced these methods to reduce the expression of genes.

3. Gene expression
We studied the key genes for commitment of cell differentiation or maintaining undifferentiation of embryonic stem cells or embryonic carcinoma cells.
4. Functional study of Adenovirus E1 genes and development of adenoviral vectors

In attempt to study the function of E1 genes of Adenoviruses, we have introduced the mutations into the E1 regions and generated these mutant viruses. The cells were infected with the mutants to know the function of E1 genes. We also develop the viral vectors for human gene therapy and viral transduction.

Operation of the automated machine for DNA-Extraction.

Reconfirmation of nucleotide sequences of the genetic samples.

Preparation of the ordered libraries for distribution.


Oral Presentations


