BioResource now !

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BioResource now! Vol2.No.1 is here

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Download the PDF version of this newsletter at
http://www.shigen.nig.ac.jp/shigen/news/news.jsp

Bioresources information is available at the following URL:

NBRP (http://www.nbrp.jp/index.jsp)
SHIGEN (http://www.shigen.nig.ac.jp/indexja.htm)
WGR (http://shigen.lab.nig.ac.jp/wgr/)
JGR (http://shigen.lab.nig.ac.jp/wgr/jgr/jgrUrlList.jsp)

Information on Resource-related Events

- March 9 NBRP symposium at the Tokyo International Forum
- March 19–21 NBRP panel exhibitions, etc. being planned at the Annual Meeting of the Japanese Society of Plant Physiologists
- May 12–13 Panel exhibition at the Annual Meeting of the Japanese Association for Laboratory Animal Science "Bioresource of Laboratory Animals: Now and Future" being planned.
- May 12–13 FIMRe RIKEN BRC

Detailed information is available at
http://www.nbrp.jp/index.jsp

Introduction to Resource Center No.5

RIKEN Bioresource Center (RIKEN BRC)
Overview of DNA Bank Operations

Kazunari Yokoyama, Ph. D., General Manager,
Gene Engineering Division, RIKEN BioResource Center

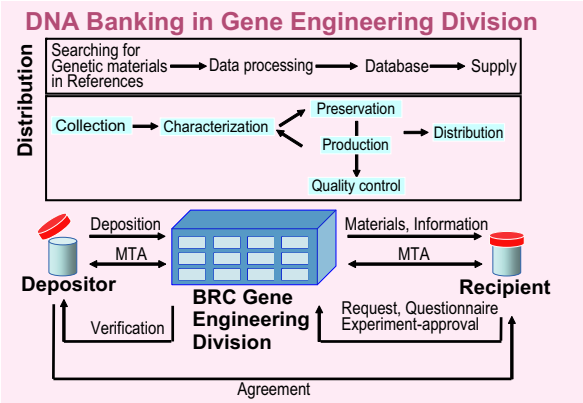
Genetic resources provided by RIKEN DNA bank

1) Host, Vector, DNA Clones
2) Japanese-specific cDNA Clones
   (Human HLA Clones, Human SEREX Clones)
3) Shuttle Vector for Sugano Full-Length cDNA Clones
4) Recombinant Virus
5) CEPH MEGA YAC Clone Library
6) NIA/NIH Mouse cDNA Clone Library
7) MSM/Ms Mouse BAC Clone Library
8) ERATO Mouse Early Embryo EST Clone Library
9) cDNA Library
10) Primate Genome Library
11) Promoter Reporter Clone
12) Cis-Element Reporter Mini Library

RIKEN BRC http://www.brc.riken.jp/lab/dna/

History and Overview

RIKEN founded a cell and gene repository (RIKEN gene bank) in June 1987 and established a system that facilitates the development of research fields related to life sciences. The Gene Engineering Division (formerly known as DNA bank) started to collect and provide multipurpose host vectors and cloned genes in 1993. Since 1995, this division has provided the CEPH Mega YAC clone library endowed by the Foundation Jean Dausset-CEPH, viruses (retrovirus, adenovirus, and adeno-associated virus) and recombinant DNA shuttle vectors for gene transfer contributed by Dr. Hirofumi Hamada of Sapporo Medical Univ. and Dr. Izumu Saito of the Institute of Medical Science, Univ. of Tokyo. The project "Establishment of Recombinant Virus-Core Bank and Its Advanced Applications," which was adopted for the development of intellectual fundamental for life science research, was funded by the Special Coordination Fund for the Promotion of Science and Technology of the Ministry of Education, Culture, Sports, Science and Technology (MEXT) in 1998. For this project, numerous cDNA clones deposited in the bank and the full-length cDNA clones provided by Dr. Sumio Sugano of the Univ. of Tokyo were inserted into recombinant virus vectors to set up the Recombinant Virus Section. Moreover, mouse cDNA clone sets that are specific to the early embryogenesis stage contributed by Dr. Minoru Ko of the NIA/NIH and Dr. Hirofumi Doi of the ERATO Bioasymmetry Project; a series of cDNA libraries provided by Dr. Hiroshi Nojima; an HLA series specific to Japanese people contributed by Dr. Akatsuka Yoshiki at the Aichi Cancer Center Research Institute; cancer antigen cDNA clones that were identified by the SEREX method from the Ludwig Institute for Cancer Research, the Aichi Cancer Center Research Institute, and the Department of Biological Systems at the RIKEN BioResource Center; a mouse BAC genome clone library provided by Dr. Kuniya Abe of RIKEN were deposited. Furthermore, large-scale genomes such as a cloned library of the human chromosome genome were recently contributed by Dr. Yoshiyuki Sakaki of the RIKEN Genomic Sciences Center (RIKEN GSC).



In 2001, in accordance to the domestic and international trends in life science research, the BioResource Center was established. This center aims to collect genetic resources, individuals and cell lines of plants and animals, and genetic information necessary for promoting researches, as well as developing novel resources and related technology and disseminating bioresources to domestic and international researchers. Aside from the Gene Engineering Division, the BioResource Center comprises divisions of animal, plant, cell, bacteria, information, and cooperative research groups (http://www.brc.riken.jp). Targeting the consolidation and the promotion of an intellectual foundation for life science research, we will expand the resource development and the consolidation project under the catchwords "trust," " sustainability," and "leadership."

When the BioResource Center was established in 2001, the importance of an intellectual foundation for life science research, including the development of biological genetic resources, was pointed out in the Basic Plan for Science and Technology put forth by the government (the plan received cabinet approval). Moreover, in the same year, the "Sectoral Promotion Strategy" drafted by the Council for Science and Technology Policy stated that long-term continuance for collecting, securing, maintaining, administrating, and supplying various bioresources was necessary and that such operations should be conducted nationwide. On the other hand, at the MEXT Council for Science and Technology, after taking into consideration that Japan lags behind the US and Europe in terms of the amount of biological genetic resources available, the "Establishment of Scientific and Intellectual Foundation" plan indicated that by the year 2010, Japan would achieve the highest international standards for bioresources that should be selectively and primarily developed.

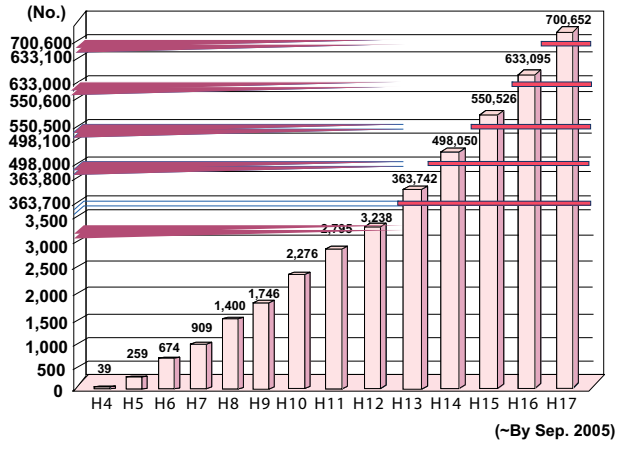
The MEXT established the National BioResource Project (NBRP) in 2002 and our division was designated as a core facility for collecting, preserving and providing animal and bacterial DNA. So far, we reexamined the material transfer agreement (MTA) and clarified that the intellectual property rights of a resource would not be transferred to the bank even if it was deposited but would remain with the resource provider. We have also accepted the deposition of BAC clones of the Japanese monkey that was developed by RIKEN GSC as a National BioResource Project. Furthermore, we have established a promoter bank for clones constructed based on journal articles and whose luciferase activity was confirmed. Numerous clones were provided and the assay data is published on the internet. In 2004, we officially initiated a project in collaboration with the Laboratory Animal Resource Center at the University of Tsukuba and the RIKEN BRC Experimental Animal Division to construct promoter-Cre mice. We have also constructed a reporter mini library in which the transcriptional cis elements are connected to the reporters. We have diversified the deposited resources from genes to recombinant viruses, recombinant cells, and recombinant mice. In future, we would like to construct, develop, collect and supply the next-generation resources that meet the needs of our users.

Overview of Genetic Resources

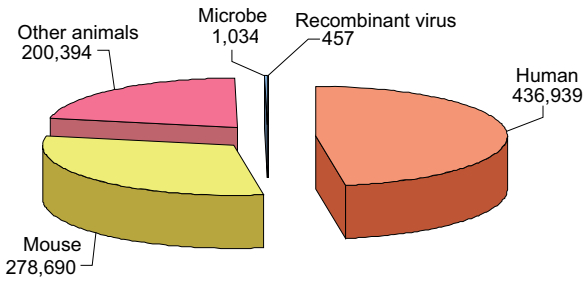
The DNA bank has been in operation since its initiation in 1987, focusing mainly on hosts, vectors, and gene clones. The number of cumulative collected gene clones exceeds 917,000 strains, and the collected number of genes from humans and mice accounts for more than 75% of all the collected genes. On the other hand, the number of distributed gene clones exceeds 700,000 strains and more than a quarter of it was distributed overseas. Our division is gaining recognition domestically and internationally. We would like to disseminate bioresources all over the world. However, our biggest problem as a gene bank is that a gene is used semipermanently once it is obtained. In other words, a resource is rarely requested repeatedly by the same researcher. As in the case of any other business, it is important for the gene bank to have researchers who request for bioresources repeatedly. In order to support the needs of researchers, we are trying to develop a bank that continuously develops novel technology, modifies genetic resources to meet the needs of researchers, and develops value-added genetic resources that are favored by the users. There is no future for a gene bank without self-advancement and fresh resources. We have subdivided the genetic resources into the following five divisions which operate as sub-banks.

[A] Basic Domain Type DNA Sub-bank
[B] Gene Transfer Sub-bank
[C] Japanese-specific DNA Sub-bank
[D] Library and Set Bank
1 NIA/NIH Mouse cDNA Clone Library
2 MSM/Ms Mouse BAC Library
3 Mouse Early Embryo EST Clone Library
4 CEPH Human MEGA YAC Clone Library
5 Wild Bird cDNA Library
6 Primate Genome Library
7 Promoter Bank
8 Cis-Element Reporter Clone
[E] Informatics Section

Annual Summary of Clones for Distribution



Total Number of Resource Collection (~By Sep. 2005)



[A] Basic Domain Type DNA Sub-bank

Since the establishment of the DNA bank, we have been pursuing activities based on collecting hosts, vectors, and gene clones. The DNA bank is public domain and is supported by the research community. Instead of specialized clones developed by large-scale projects, we focus on collecting and distributing clones developed by individual researchers which have been utilized in actual researches and have produced results.

[B] Recombinant Viruses and Shuttle Vectors (Gene Transfer Sub-bank)

In 1998, we were awarded a grant under the "Researches Related to the Establishment of Recombinant Virus Core-Bank and the Fundamental Technology for its Advanced Application" project funded by the Special Coordination Fund for the Promotion of Science and Technology of MEXT. We have developed vectors for gene transfer and gene therapy. We are currently integrating full-length cDNAs that were deposited in the RIKEN DNA Bank into vectors of adenoviruses, retroviruses, and adeno-associated viruses. Most of the recombinant virus strains deposited here were produced from Dr. Hirofumi Hamada's laboratory at the Sapporo Medical University. In addition, Dr. Izumu Saito of the Institute of Medical Science, University of Tokyo kindly guided us with the construction of recombinant adenovirus vectors. Moreover, the utilization of CA and CAG promoters was permitted by Dr. Junichi Miyazaki of Osaka University. Recently, we have prepared and distributed shuttle vectors of Sugano full-length human cDNA which contain 300 types of full-length cDNA provided by Dr. Sugano Sumio of the University of Tokyo. These virus strains and vectors are significantly valuable for gene transfer and basic research on gene therapy.

[C] Japanese-specific DNA Sub-bank

This sub-bank was developed with the purpose of promoting genetic, immunological, or comparative biological researches to elucidate the genetic characteristics of Japanese people because it is important for Japanese people to know their origin and their DNA. First, we focused on the HLA and SEREX antigens. The HLA are antigens related to immunological rejection during organ transplants and blood transfusion. Please refer to the website of the Japanese Society for Histocompatibility and Immunogenetics for details (http://square.umin.ac.jp/JSHI/frame.html). In particular, the cDNA series encoding the HLA class I antigens that are frequently observed among Japanese people were deposited by Dr. Yoshiki Akatsuka of the Aichi Cancer Center Research Institute (http://www.brc.riken.jp/lab/dna/en/GENESETBANK/HLA.html).
The cancer antigen cDNA series SEREX that was identified by the SEREX method was deposited by the Ludwig Institute for Cancer Research, Aichi Cancer Center and RIKEN BRC (http://www2.licr.org/CancerImmunomeDB/). Please refer to our website for further details on the library and clones (http://www.brc.riken.jp/lab/dna/ja/SEREXja.html).

[D-1] NIA/NIH Mouse cDNA Clone Library (Sub-bank)

NIA mouse 15K cDNA clone sets that are specific to each stage of the early development stages of the NIA/NIH mice were provided as a gratuitous bailment by Dr. Minoru Ko of NIA/NIH in the US. Under the sole condition that they would be distributed properly, these clones are distributed to both public and private sectors as a clone set or a single clone. These clones are well-known as the original clones used in the DNA microarray sold by Agilent Technologies, Inc. and the clones expressed in the mouse embryo during the initial stage of preimplantation are included as a set. These clones are included in a high-quality cDNA clone library and have an average insert size of 1.5–4.0 kb (http://lgsun.grc.nia.nih.gov/).

[D-2] MSM/Ms Mouse Bacterial Artificial Chromosome Library (Sub-bank)

A mouse genome BAC clone library of wild laboratory mouse strains (Mus musculus molossinus) was constructed by Kumamoto University and RIKEN BRC and provided by Dr. Kuniya Abe. This library comprises approximately 200,000 strains of BAC genome clones which have an average size of 150 to 300 kb. These clones are useful for Tg construction and positional cloning of BAC transgenes. Previously, the only mouse genome BAC library generally available was constructed from either C57BL/6 or 129/SVEvTAC, two kinds of inbred strains derived from Mus musculus domesticus. However, with the help of this library, efficient methods to search and identify genes that govern the QTL analysis and quantitative traits were developed. You can search for single clones on the MSM-B6 website (http://stt.gsc.riken.jp/msm/) and (http://shigen.lab.nig.ac.jp/mouse/polymorphism/top/top.jsp).

[D-3] Mouse Early Embryo EST Clone Library (Sub-bank)

A mouse early embryonic cDNA clone library was established by the ERATO Doi Bioasymmetry Project and comprises 45,216 strains of mouse cDNA clones (http://lgsun.grc.nis.nih.gov/cbi-bin/pro1).

[D-4] CEPH Human MEGA YAC Clone Library (Sub-bank)

The CEPH human MEGA YAC library was provided by the Foundation Jean Dausset-CEPH research institute. This human genome library comprises approximately 36,000 clones with human genes on yeast artificial chromosomes. You can search for single clones on the CEPH website (http://www.cephb.fr).

[D-5] Wild Bird cDNA Library (Sub-bank)

Forty series of high-quality cDNA libraries were deposited by Dr. Hiroshi Nojima at the Research Institute for Microbial Diseases, Osaka University. These libraries are used for screening target genes and as the substrate for PCR cloning. It is also useful for isolating full-length cDNA clones.

[D-6] Primate Genome Library (Sub-bank)

A large-sized BAC clone library containing primate genomes (human, monkey, chimpanzee, etc.) was provided by Dr. Yoshiyuki Sakaki of RIKEN GSC. The library was used for the shotgun-based sequence analysis of clones and is extremely useful.

[D-7] Promoter Bank (Sub-bank)

Transcription is the first stage of gene expression and is also a major regulatory checkpoint of gene expression which is why analysis at the transcription level is emphasized the most in the multistage process analyses of gene expression. Gene expression level analysis and regulatory mechanism analysis of genes involved in important biological functions and genes which act as markers of those functions are considered essential in cell biology researches such as those involving cell cycle, differentiation, proliferation, tumorigenesis and apoptosis and researches at the individual level which involves studying complex biological processes such as development, regeneration, morphogenesis, senescence, and disease. Moreover, control techniques are important to specifically express the introduced genes in appropriate tissues or cells at a specific time in application-oriented researches such as gene therapy and substance production using genetically engineered animal and cell lines. In addition, the demand for conditional knockout animals which possess certain genes that can be deleted in a tissue- and stage-specific manner is increasing and it is now possible to express Cre recombinase in a target tissue- and stage-specific manner and induce DNA recombination at the loxP sequence using the Cre/loxP system, a commonly used conditional targeting technique. For the induction of specific gene expression, control at the transcription level is the most general and effective strategy and the experimental selection of promoters that enable specific gene expression is crucial. Although promoters are indispensable genetic resources in various research fields such as those described above, the construction of promoters/reporter plasmids is a time and labor consuming task, even with the advanced DNA manipulation techniques and genome information technology available today. Promoters are non-coding regions of genomic DNA and often contain a bias in GC content and repeated sequences; thus, cloning is not a simple task.

Although, transcription start sites and promoter regions for the genes that are responsible for important functions in various biological phenomena have been analyzed, the results were obtained using different methods by numerous researchers. As a result, many articles show significant inconsistency among reports and in many cases, the promoter regions are not clearly defined. Therefore, there is a need to experimentally verify the functions of these promoters to ensure their reliability. Based on the above-mentioned issues, a promoter bank that constructs and collects promoters/reporter plasmids and releases them together with information on qualitative results to the public has great significance.

This promoter bank strives to guarantee the universality of analytical results, distribute qualified promoter resources to researchers, and, at the same time, continue to the promote life science researches related to both basic science as well as its application by selecting and developing promoters with high usability. The following is a detailed description of the undertakings of this promoter bank.

1. We will construct vectors that contain a reporter gene with high versatility and a restricted sequence (multicloning site) to the upstream of which promoter fragments are easily inserted. In addition, we will insert a restriction sequence in which a whole transcription unit from the promoter to the poly(A) signal site can be excised.
2. We will refer to literatures and databases and select promoters with a high usability. Regions considered to have promoter activity will be amplified from genomic DNA by PCR and will be inserted into the vectors described above.
3. Cell strains that are expected to show specific gene expression and inhibition will be used to verify the actual activity of each promoter.
4. Transgenic mice will be bred and the expression stage and tissue specificity of each promoter will be analyzed in collaboration with RIKEN BRC Experimental Animal Division and Laboratory Animal Resource Center, University of Tsukuba).
5. Adenovirus shuttle vectors that contain tissue-specific promoters and Cre genes will be constructed.

Promoters/reporter plasmids will be publicized and distributed based on the information above.

At present, the number of promoters that were constructed and assayed is 74 clones which contain upstream sequences derived from human genomic DNA. Hereafter, the clones in which luciferase activity has been confirmed will be sequentially added.

[D-8] Cis-Element Reporter Clone (Sub-bank)

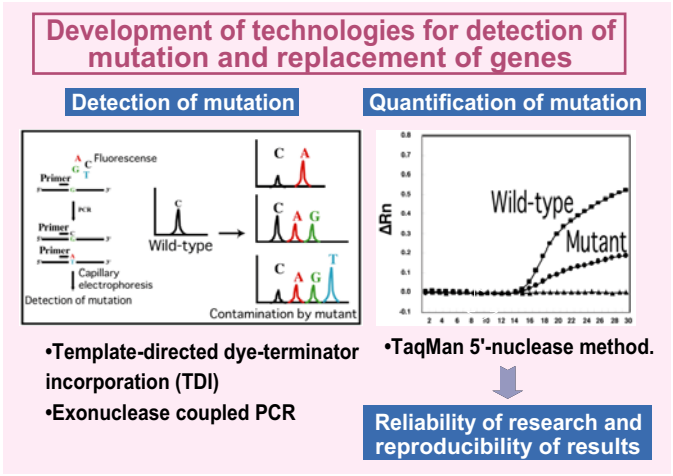
We connected synthetic cis element to the promoter for thymidine kinase gene and constructed animal cell expression vectors with the luciferase gene as a reporter. For each of the 38 elements, mutations in both forward and reverse directions and variations in point mutations were prepared. This is useful to measure promoter activity.

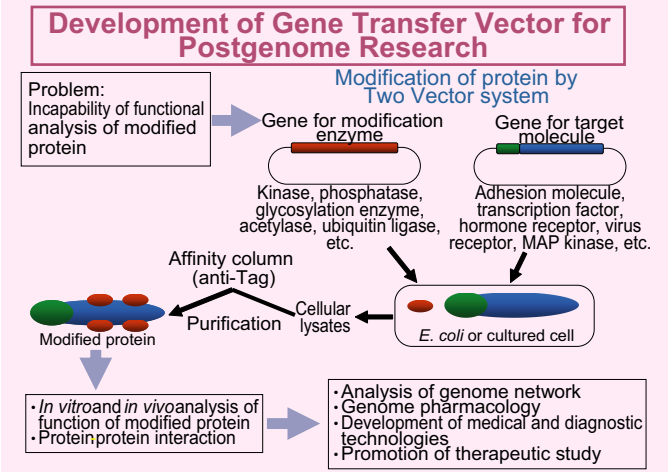
[E] Transmitting Information at the Gene Engineering Division (Informatics Section)

Irrespective of how useful a resource might be, if information on the resource is not plentiful, it will not be of any use. Information indicating only DNA base sequences will be nothing but dead storage. In order to provide information related to resources, our division actively gathers bibliographic retrieval systems for articles that indicate the use of sequences, restriction enzymes and clones, and compiles obtained information in a database as an online catalog. Moreover, instead of listing the clones by their gene names, we grouped them by the gene cascade or signal cascade and are developing a visual system to represent the relationship between genes as pattern diagrams. We also provide information on specific experiment methods which cannot be obtained through catalogs as well as information on problems that are faced during experiments and their solutions to the research community via email and also through the RIKEN Bioresource website. With regard to this, a section titled “A chat about DNA bank” is gaining popularity with every issue. Furthermore, we provide reports published by MEXT after the enforcement of the Law Concerning the Conservation and Sustainable Use of Biological Diversity through Regulations on the Use of Living Modified Organisms, and we focus our attention not only on research itself but also on gathering information and securing publicity for the BioResource center. Questions, opinions, or requests regarding the utilization of mailing news, the operations of our division, or genetic resources can be submitted by email (dnabank@brc.riken.jp).

Quality Control of Genetic Resources and Technology Development for the Development of Genetic Resources for the Next Generation

As DNA bank administrators, we should always consider improving the technology for quality control in supplying genetic resources. Research innovation in this field occurs at a very fast pace and it is often difficult just to keep up with it. However, we attend academic conferences annually and we incorporate new technology in order to advertise our DNA bank operations. We always consider the following questions: What are the current and future trends? Where should we apply new technology to develop novel resources? Currently, the emphasis is on developing qualitative and quantitative detection technology of unknown gene mutations and gene transfer technique for the functional analysis of modifier genes.
Please refer to our website stated below for other researches and developments related to gene expression
(http://www.brc.riken.jp/lab/dna/).



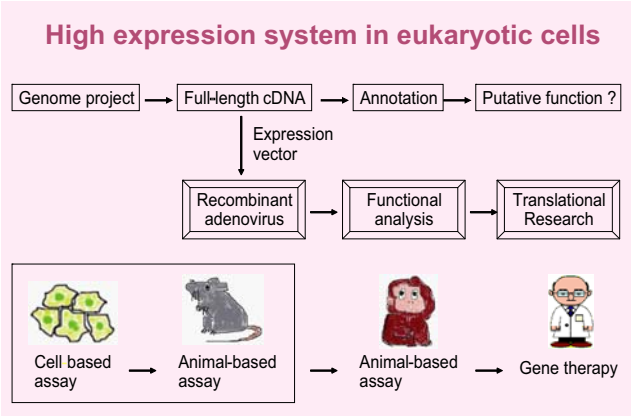


Training Program and Fostering DNA Bank Administrators

We, the RIKEN BRC Gene Engineering Division would like to contribute to the development of life sciences in Japan and are conducting training programs on novel technologies with the aim of increasing the utilization of bioresources and expanding our user base. In August 2005, a training program regarding the handling of recombinant adenovirus was conducted. We plan to enhance and popularize the training programs. We will also put effort into fostering DNA bank administrators to ensure the continuity of DNA bank operations (http://www.brc.riken.jp/lab/dna/).

The Continuity of DNA Bank Operations

Trust, sustainability, and leadership have been the guiding principles of RIKEN BRC in its resource activities. Among these three principles, affiliates of the NBRP and DNA bank administrators should be aware of the sustainability principle.



Looking at DNA Bank Operations Not 3 or 5 Years but 100 Years in the Future

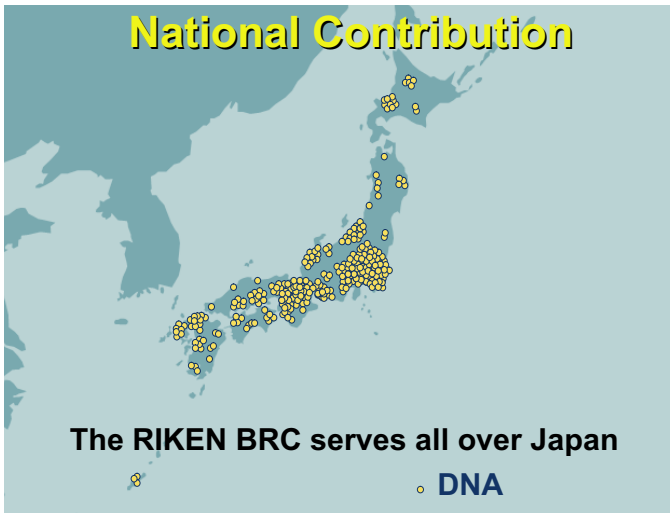
In order to resolve some of the most significant problems that mankind face in regard to health, food and the environment, several life science researches, starting with research on human genome and proteome, were launched as a national policy. It is clear that in addition to manpower and facilities, securing and controlling the quality of research materials (resources) is essential to provide support and promote biological science researches. Furthermore, achievements in life science research are now directly related to industrialization and not only advanced countries but also developing countries have started to exert claims over intellectual properties related to bioresources.

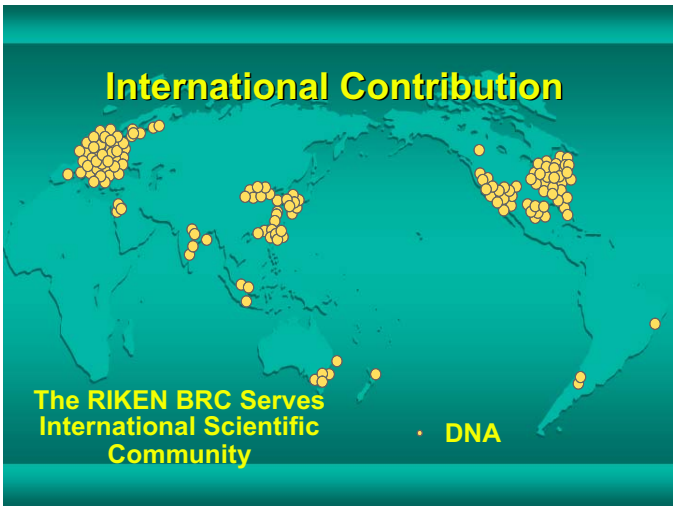
Under such circumstances, people are starting to acknowledge that the bioresources in Japan provide an intellectual foundation to promote scientific research and industries and that their consolidation should be considered an important national policy. However, there are also people who think that the goal has already been achieved because this bioresources project was initiated and established on par with the conventional 3- or 5-year long national projects. This misconception stems from the fact that people equate this project with a conventional scientific research-promoting project where success can be confirmed after 3 or 5 years. Are 5 or 10 years long enough a period to consolidate an intellectual foundation that would support future research in life science in our country? In order to establish our country as a nation of considerable scientific resources for the next 10 or 20 years, further enforcement of this intellectual foundation project should be predetermined, and further investment in life science researches for the next 100 years is necessary. Shouldn't we be apprehensive about the current situation where we are abandoning achievements and resources from large-scale projects which were funded by taxpayers and scientific research funds or sometimes allowing them to be taken away by other countries without being able to claim the intellectual property rights?

Resources, information and accomplishments achieved by our country should stay a property of our country even when transferred. We, the RIKEN BRC are recognized as a leading resource center in the world by both the domestic and international research communities for our work in building an intellection foundation such as quality controlling, collecting, conserving and providing resources. In addition, we are conducting training programs and educating the younger generation to take on the role of DNA bank administrators to ensure that the advanced technology related to the resources of our center is spread worldwide. We have to continue bioresource bank operations with this same enthusiasm in order to support Japan as a great nation of science for the next centuries.

We are determined to put our greatest efforts into making sure that we grow into a well respected and recognized institution which can provide an intellectual foundation to support life science researches in our country.

When it comes to building an intellectual foundation, look 100 years into the future and plan ahead for the next three generations. — You must sow before you can reap





Closing

Recently, with the accumulation of genetic information, there has been a shift in research trends such as using in silico cloning instead of the conventional method of isolating genes by hybridization from gene libraries. In keeping up with this trend, our division has been making the transition from a bank that simply supplies gene fragments to one that provides high-value added genetic resources. Moreover, during this year, not only the domestic utilization of genetic resources but also the international distribution requests of these resources have increased dramatically. Furthermore, introductory articles on our bank were published in Science (vol. 307, p. 1722, 2005), BioTechniques (vol. 38, p. 21, 2005), and J. Gene Med. (vol. 7, pp. 1148–1157, 2005), and we believe that our bank is being acknowledged all over the world.

We sincerely hope that the genetic resources provided by our division are useful to our users and their researches. Needless to say, these genetic resources are the research achievements of all the researchers affiliated to various research institutes; thus, we are sincerely grateful to all the researchers who deposited these extremely precious genetic resources. At the same time, all the staff members here will further put in their best efforts to continuously contribute to the development of life sciences research and we hope to receive your suggestions and opinions.

Hot news from abroad: No. 10

Plant and Animal Genome Conference XIV

We attended the Plant and Animal Genome Conference XIV (http://www.intl-pag.org/).

The Plant and Animal Genome XIV Conference (hereafter PAG) was convened in San Diego, CA for 5 days from 14th to 18th January.

As suggested by the name, the PAG is an international conference where researchers of various fields in animal and plant sciences get together. Approximately 2,000 people participated this year. Most of the participants were residents of the host country, the US. However there appeared to be many participants from Asian countries other than Japan such as China and India this year.

This time, I (Sakaniwa) presented a poster regarding Oryzabase (http://shigen.lab.nig.ac.jp/rice/oryzabase/), an integrated database of rice and introduced the physical map of all chromosomes which reflects the newest released version of base sequences, the online version of the Rice Genetics Newsletter, and the Multiple Ontology Browser (O3 Viewer).

PAG: http://www.intl-pag.org/

(Author : Shingo Sakaniwa)

Comments

On the database front, I noticed that new ontologies such as the Animal Trait Ontology were being developed and utilized but the use of Gene Ontology already appeared to be commonplace. Those who conduct research related to domestic livestock may find Animal Trait Ontology (http://www.intl-pag.org/14/abstracts/PAG14_P888.html) interesting. Various types of ontology have been emerging and therefore it will soon be necessary to integrate all of ontologies while taking their advantages into account.

Although various workshops were conducted at this time, personally I felt that the workshop on Gbrowse (http://www.gmod.org/?q=node/71), a genome browser was very easy to understand and I plan to install it in my computer.

Compared to last year, it seemed that more time and effort were invested into the commercial booths at the PAG this year. I also felt that the gap between researches in basic sciences and their practical application was being bridged. (Shingo Sakaniwa)

Although I was attending an international conference for the first time, I felt relaxed due to its informal atmosphere. I attended the conference with the aim of participating in the poster exhibition but I also attended various workshops. I found the workshop on ontology, a subject which I deal with on a regular basis, particularly impressive.

At a workshop which took up an entire day, it began with a discussion on a basic part of ontology such as the structural relationships and then while taking the current state of ontology into consideration, continued on to its future prospects. One of the goals is to promote collaboration with other research fields and that seems to be accomplished gradually. In addition, as a prospect, it appears that a wide range of biomedical ontology will be developed.

After attending each workshop, I was keenly aware of my limited knowledge. I would like to continue to try to bridge the gap that I felt at that time. (Tohru Watanabe)

Second Annual POC User's Meeting

The 2nd POC (Plant Ontology Consortium) Users Meeting was held during the PAG XIV. It was not a public meeting and was conducted separately from the official program of PAG. The meeting was held for PO developers and other potential users to discuss issues about the PO initial development stage and how to develop PO effectively so that many researchers can use it. The total number of participants at this meeting was a little more than 20, including individuals responsible for genomic databases of model plants such as SOL (Solanaceae), TAIR (Arabidopsis), NASC (Arabidopsis), Gramene (Rice, etc.), MaizeGDB, IRIS (Rice), SoyBase (Soybean) and Oryzabase (Rice) and developers of DAG-Edit and OBO-Edit. This year, discussions were focused on PATO (Phenotype And Trait Ontology), an ontology to systematically express mutant traits. At the same meeting last year, only IRIS and Oryzabase discussed PATO but surprisingly, only after a year, NASC for Arabidopsis has already started constructing PATO and is at a phase where the specifics are being discussed. The construction and utilization of PATO have already been initiated in zebrafish and killifish, and there is no doubt that it will also be used in plants in the future.

PATO: http://obo.sourceforge.net/cgi-bin/table.cgi

PO: http://www.plantontology.org/

In PATO, the parameters "Attribute" and "Value" are used, and to express a certain mutant trait by ontology, the combination of "Entity," "Attribute," and "Value" (EAV) is used. For example, the trait "the width of leaves is wide" is expressed with Entity = leaf, Attribute = relative width, and Value = wide. In addition, the trait "the color of seeds is yellow" can be expressed with Entity = seeds, Attribute = color, and Value = yellow. Entity represents a whole individual, organ, tissue, cell, gene, or developmental stage, and Ontology (Development Ontology, Anatomical Ontology, Cellular Ontology, Gene Ontology, Plant Ontology (PO)) can also be applied. In other words, a trait is expressed by the combination of ontologies ("the width of leaves is wide" = PO: 0009025, PATO: 0000086, PATO: 0000087).

However, I personally feel that the value parameter of PATO is too varied and I doubt if a value can be conceptually categorized, therefore making it not an applicable parameter for ontology. Taking color as an example, I mentioned that substituting the Japanese word "ai-iro" (the color of madder) with an English word might be a rather subjective matter. However, I learned that this problem can be resolved by digitizing the color. Considering the necessity of an international standard, I suppose that digitization will be the future direction. The MaizeGDB group has begun developing a system that extracts information from image data. Since ontology aims at analyzing the massive amount of information that will be generated in the future instead of organizing past data, I suppose that it will continue to undergo rapid development regardless of my personal reservations.

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Information Technology Vol.10

"Bioinformatics in 10 minutes"

"Constructing a Personal Database for BLAST Search and Executing BLAST"

In the November issue, I explained how to install BLAST and in this issue, assuming the path has already been set, we will execute it. However, it does not make sense to install something that is already provided as a service on many websites. Most web services allow you to select some or all of the sequences registered with the international DNA database as a subject of your BLAST search. Therefore, we will construct a personal database which will be subjected to a BLAST search and we will execute a BLAST search on it. (Windows)

1. Create a folder named "test" on your desktop. Obtain or construct a FASTA-format file of base sequences that will be the subject of your BLAST search and place it in the "test" folder (use the multi FASTA-format if you want to subject multiple sequences to the search). Here, the file name will be "target.fa."

2. Open a command prompt (Start→Program→Accessory→Command Prompt) and type "cd " (a half-size space following cd and the quotation marks are not necessary.) Drag and drop the " test" folder created in step 1 onto the black screen and press Enter. "target.fa" can be confirmed by typing "dir" and pressing Enter.

3. Type "formatdb .i target.fa .p F" in the command prompt window. A database file for your BLAST search will be constructed from "target.fa." Type "dir" and press Enter to confirm that three files, namely, "target.fa.nhr", "nin" and "nsq" are constructed.

4. Construct or obtain a fasta-format sequence file that you want to search for and place it in the "test" folder. Here, the file name will be "query.fa."

5. Finally, run BLAST. Type "blastall .p blastn .i query.fa .d target.fa" in the command prompt window and press Enter. If the result on your black screen is similar to the usual BLAST results, you have succeeded.

By typing "blastall .p blastn .i query.fa .d target.fa .o result.txt" and pressing Enter, your result can be written to a file, "result.txt" in the "test" folder.

Shingo Sakaniwa

Editor's Note : While there is a high demand for DNA resources, there is a tendency for certain resources to be used intensively for a short period of time. Therefore, the travail of the bank administrators is evident in every article. We would like to thank the general manager Dr. Yokoyama and the other staff members for their efforts.

As always, I am overwhelmed by the energy and passion exhibited at an international conference or meeting. (Y.Y.)

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