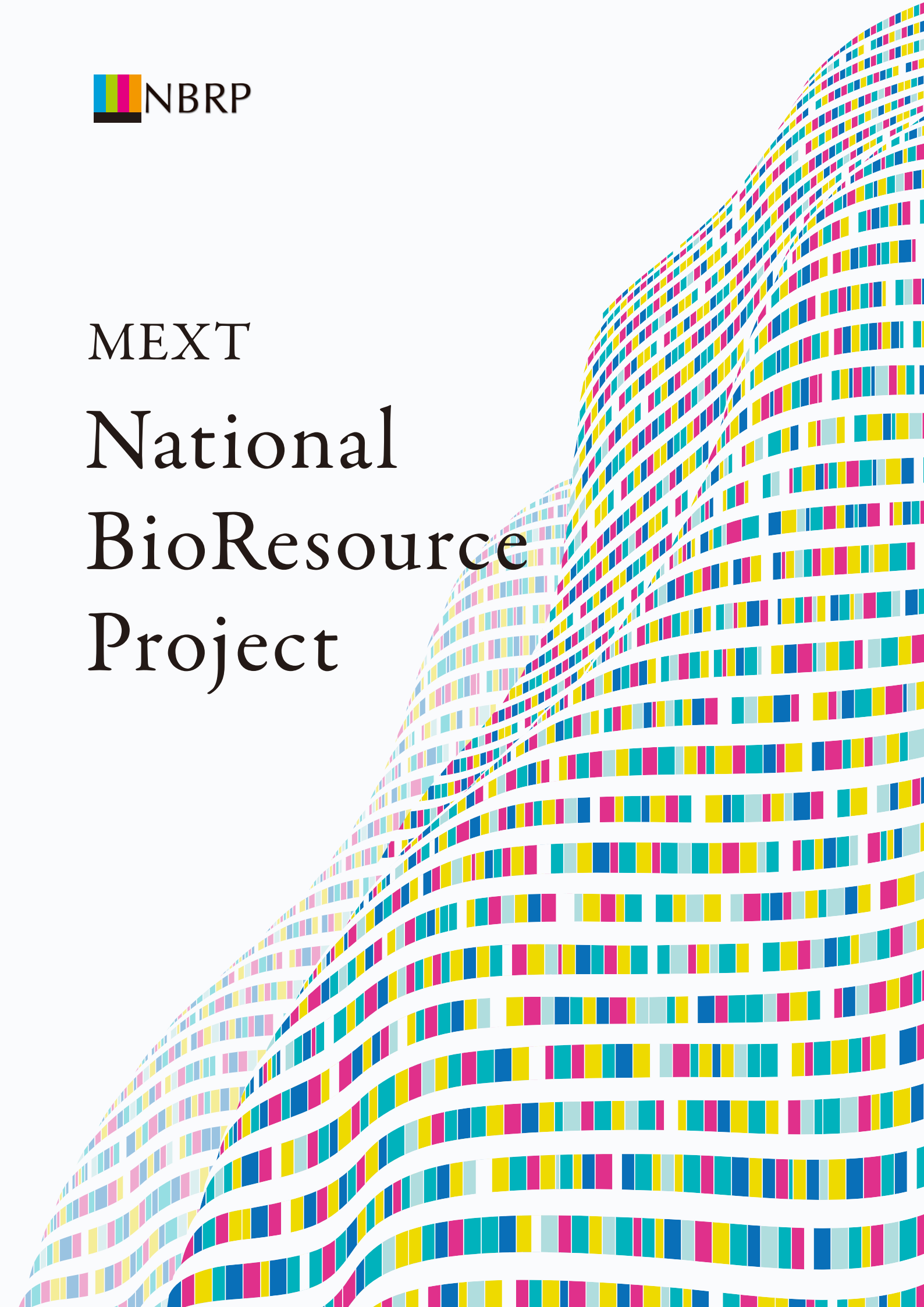




MEXT

National
BioResource
Project



Message from the Program Director

Bioresources—the strains, populations, tissues, cells and genes of animals, plants and microorganisms used for research and development, and the information associated with these materials—represent essential infrastructure for life sciences. Bioresources are developed over many years of painstaking work and form the foundation of future research. Sharing them among researchers is vital for advancing research and development. In addition, providing a common set of bioresources for use within the scientific community makes it possible to compare research results across studies and will ultimately enhance reproducibility. Developing outstanding collections of bioresources will therefore give Japan an internationally competitive edge in life sciences.

In accordance with the Japanese Government's Science and Technology Basic Plans, in FY2002, the Ministry of Education, Culture, Sports, Science and Technology (MEXT) established the National BioResource Project (NBRP) to construct a framework for the systematic collection, preservation, and distribution of bioresources, with a special focus on resources that require strategic development by the national government. The importance of bioresources continues to be stipulated in the Basic Plans, with the current Sixth Plan (FY2021–FY2025) outlining the need to strategically and systematically establish and upgrade the bioresources and intellectual infrastructure necessary for data-driven research.

The NBRP is revised every five years. The fifth phase of the NBRP, which started in FY2022, has so far seen the addition of the “aged mice” and “mushrooms” categories. At its core, the current NBRP consists of 33 categories

of bioresources and one center that provides information on these resources. The importance and value of the bioresources established under this project are continuously being elevated by the addition of genomic resources and development of preservation technologies. In fact, several of our bioresource centers have been recognized as meeting the highest global standards. Currently, the Program Director (PD) and Program Officers (PO) are responsible for promoting the activities of the NBRP according to current trends in life sciences.

Finally, I would like to emphasize a lesson we learned from the Great East Japan Earthquake: bioresources cannot be restored once they are lost. Since the 2011 disaster, we have developed a backup system that includes long-term cryopreservation of bioresources. However, the emergence of COVID-19 in 2020 necessitated restrictions to staff attendance, which put the maintenance and provision of bioresources at risk. To solve this problem, we are promoting a labor-saving approach to bioresource maintenance and the adoption of remote monitoring systems. We will continue to strive to maintain and provide bioresources even in the face of crises such as the current pandemic. Your cooperation and support of this project is greatly appreciated.

April 2022

Yuji Kohara, Ph.D.

Program Director, NBRP

Director, Database Center for Life Science,
Research Organization of Information and Systems,
Inter-University Research Institute Corporation

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About the NBRP

Overview

MEXT first established the NBRP in FY2002 as a comprehensive approach to promote life sciences. The project involves the systematic collection, preservation, and distribution of bioresources—the strains, populations, tissues, cells, and genetic materials of animals, plants, and microbes and their associated information—that require strategic development by the national government.

In the Sixth Science and Technology and Innovation Basic Plan (FY2021–FY2025), the government stipulated the need to strategically and systematically provide intellectual infrastructure and biological and genetic resources, such as genetic data, that form the foundation of data-driven research. The NBRP therefore plans to build on its existing intellectual infrastructure by improving the quality of available resources based on the diverse needs of researchers and promote the strategic collection and utilization of these bioresources.

Details

The NBRP is made up of two programs, (1) the resource center program and (2) the information center program, which together aim to facilitate the collection, preservation, and provision of bioresources and develop related technologies.

1. Resource center program

This program aims to establish core centers that will collect, preserve and provide bioresources that are unique to Japan and form the foundation of life science research. The program consists of two subprograms: the first aims to improve the quality and value of the bioresources, and second aims to develop new technologies, such as those that will enable the long-term preservation of bioresources.

Value addition subprogram

Recipients of funds awarded under this subprogram will analyze the genomic, metabolomic, proteomic, metabolomic, and other characteristics of bioresources and biologically-derived components with beneficial physiological effects.

Technology development subprogram

Recipients of funds awarded under this subprogram will develop new technologies related to the collection, proliferation, preservation and provision (including transportation) of bioresources. The goal of this program is to elevate the quality control, preservation technologies, value and, in turn, quality of the resources.

2. Information center program

This program aims to construct and make available databases containing such information as the location and genetic and other characteristics of the bioresources collected at the core and sub-core centers. This program will also raise the profile and visibility of the NBRP through various public relations activities.

Placing an order and supporting the NBRP

Steps for requesting bioresources from NBRP

Anyone who intends to use our bioresources for his or her own research can purchase them by following the steps below. We ask recipients to pay a fee that covers the actual cost of supplying the bioresources. Note that NBRP bioresources can be used for commercial purposes.

1. Searching for a bioresource

Each bioresource has its own website. To access the website of your desired bioresource, select the biological or genetic resource (bioresource) from the list on the “Resource Search” page of the NBRP website. Navigate to the resource list or use the search function to find your desired bioresource.

2. Placing an order

To place your order, use the web-order system (if available), complete an order form (if available), or send an inquiry by email.

All orders must be accompanied by a completed Material Transfer Agreement (MTA). In addition, the following documents may also need to be submitted depending on the regulations of the core or sub-core center supplying the resource:

- Order form
- Approval form (if the depository has additional terms of use)
- Written acceptance to receive animals carrying recombinant DNA (in the case of genetically modified organisms (GMOs)).

Formal orders will be placed after the required documents, such as the MTA, have been received and confirmed.

We are currently working to digitize the MTA agreement process to shorten the ordering process.

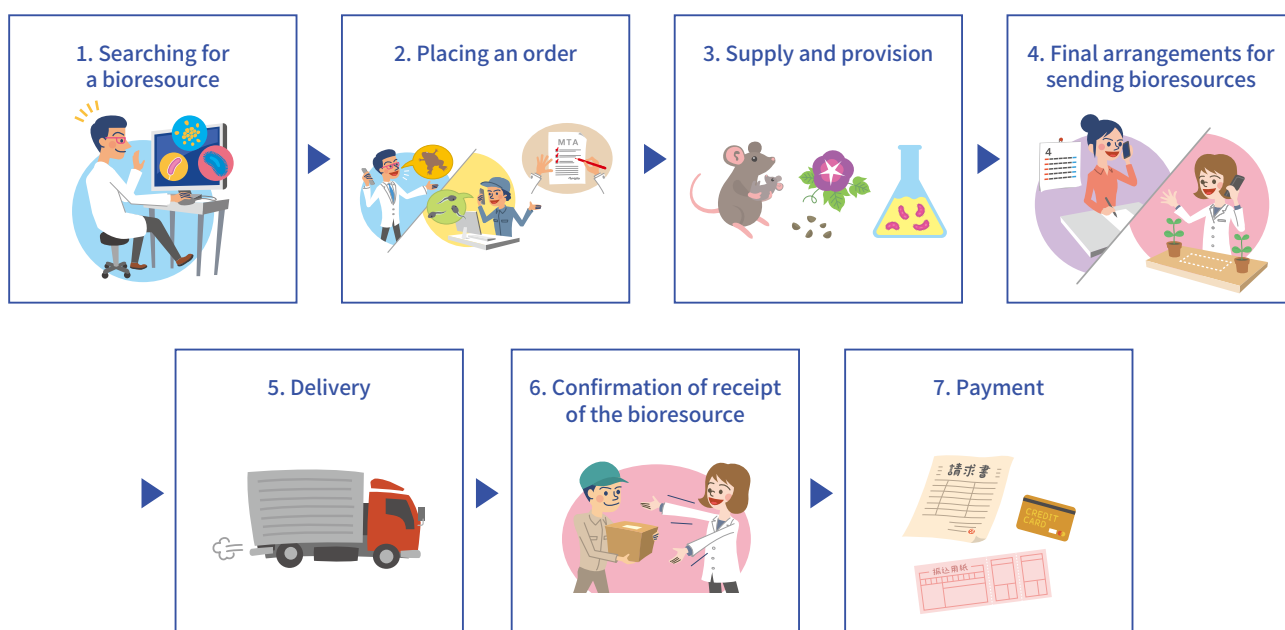
3. Factors to consider for supply and provision

Organisms that have a long life-cycle will require more time before they can be sent to the recipient. Additionally, the time required to provide the bioresource will vary greatly depending on the strain or line’s proliferation capacity and storage needs (e.g., factors for animals: live or frozen (embryo or germ cell), season).

When requesting bioresources, we suggest that you contact the core or sub-core center supplying the resource as soon as possible to agree on a realistic plan.

4. Final arrangements for sending bioresources

When the bioresources are ready, we will contact you to coordinate the delivery date and make final arrangements



to confirm the delivery address and recipient.

5. Delivery / 6. Confirmation of receipt of the bioresource

7. Payment

The payment method will differ depending on the institution (core or sub-core center) providing the resource and the delivery destination (Japan or overseas). Payment can be made by bank transfer or credit card, or both. Please check the website of the facility from which you have or will make your purchase.

In addition to providing bioresources, the NBRP core and sub-core centers also make experiment and breeding protocols available on their website and organize technical training seminars. These resources and events will be particularly informative and useful for first-time users of NBRP bioresources.

Supporting the NBRP

We ask the research community to support the NBRP in the following two ways:

1. Submit details of academic publications

We ask that bioresource users

- 1) name the bioresource and its provider in the Materials and Methods section or the Acknowledgements section of any academic publication that made use of an NBRP resource, and

- 2) send the details of the publication to the NBRP core center or sub-core center from which they purchased the bioresource, upon publication.

Details of academic publications can also be registered at the “Research Resource Circulation website”.

The NBRP collects research outcomes, including academic publications that make use of NBRP resources, and adds this information to the NBRP resource database. The generation of databases on the resources and related publications will further enhance the value of our bioresources.

2. Deposit bioresources

We welcome any requests to deposit bioresources to institutions funded under the “Resource Center Program”. Once a deposit is made, the institution will reproduce, send, and document the resources on your behalf.

Depositors can stipulate various conditions for third-party-use of the deposited bioresources. These conditions can include citation of certain publications, restrictions on the purpose of use, and requirement for a separate license agreement for commercial use. If you are considering making a deposit, please contact the core or sub-core center most relevant to your bioresource.

You can support the development of life science research in Japan by making your deposited bioresource(s) continuously available to the research community through the NBRP. We thank you for your support.

History

1996	July	The Cabinet decides the first Science and Technology Basic Plan.
2002	April	The National BioResource Project (NBRP) led by the Japanese Ministry of Education, Culture, Sports, Science and Technology (MEXT), as a part of the Research Revolution 2002 (RR2002) begins. The first phase of the NBRP starts off with 22 bioresource categories. The NBRP is made up of the Resource Center Program and the Information Center Program.
2003	April	Two bioresource categories are added to the Resource Center Program.
2007	April	The second phase of the NBRP begins with 27 bioresource categories. The Value Addition Program and the Technology Development Program begin.
2012	April	The third phase of the NBRP begins with 29 bioresource categories.
2015	April	The Japan Agency for Medical Research and Development (AMED) becomes responsible for the operation of the NBRP.
2017	April	The fourth phase of the NBRP begins with 30 bioresource categories.
2021	March	One bioresource category is added to the Resource Center Program.
	April	MEXT becomes responsible for the operation of the NBRP for the second time.
2022	April	The fifth phase of the NBRP begins with 33 bioresource categories.
		The Value Addition Program and the Technology Development Program are reorganized as subprograms of the Resource Center Program.



Overview

Mice are widely used as animal models in life science research to understand higher order biological phenomena, identify approaches to promote human health and conquer diseases. Numerous genetically-uniform inbred mouse strains and their genomic information are available for research purposes. Additionally, gene-modified mice are being actively generated using gene-targeting in embryonic stem cells and genome-editing in fertilized eggs using CRISPR/Cas9 technology.

Stock

The RIKEN BioResource Research Center (BRC) has about 10,000 mouse strains predominantly gene-modified strains (e.g., Tg, KO, cKO, KI mice), including:

- Human disease models: about 220 strains
- Cre/Flip driver mice: about 230 strains
- Fluorescent and luminescent reporter mice: about 1,000 strains

Unique Features

RIKEN BRC has a collection of mouse strains developed mainly in Japan that have been reported in academic publications. The collection focuses on human disease models and gene function analysis tools. We stock highly unique mouse resources that cannot be obtained from repositories overseas.

Update and Maintenance Activities

Core Center

RIKEN BRC will continue to add value to the collection by providing related genomic and phenotypic information.

Popular Strains and Applications

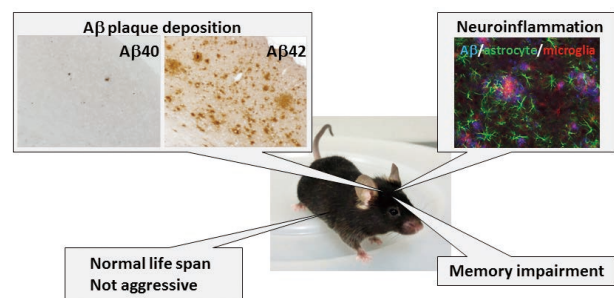
Alzheimer's disease (AD) model

The second generation AD model (RBRC06344) has been used around the world as a standard model on which to test potential preventive and therapeutic treatments for AD. The model carries triple mutations in

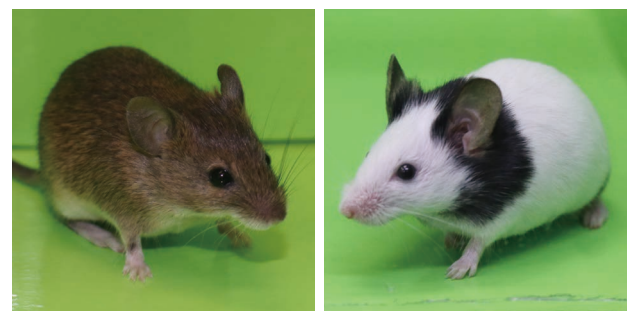
the *App* gene that have been identified in AD patients. We also provide the third generation AD model (RBRC11518), which has mutations in both the *App* and *Psen1* gene.

Wild-derived inbred strains

We also provide Japanese subspecies inbred strains such as MSM/MsRbrc (RBRC00209) and JF1/MsRbrc (RBRC00639) together with their genomic information. The enormous number of genomic polymorphisms present between these subspecies and common inbred strains is useful for understanding genomic function and diverse biological phenotypes in humans.



The second generation Alzheimer's disease model C57BL/6-*App*^{tm3(NL-G-F)Tcs} (RBRC06344) recapitulates the amyloid pathology observed in patients.



The Japanese wild-derived strain MSM/MsRbrc (RBRC00209) (left) and Japanese fancy strain JF1/MsRbrc (RBRC00639) (right).

Contact

Core Center: Experimental Animal Division,
RIKEN BioResource Research Center

Principal Investigator: Atsushi Yoshiki

Email/URL: animal.brc@riken.jp



ANIMALS

Aged mice

Overview

It is often difficult for research institutions, including universities, to rear mice for long periods and transfer them between institutions. Since environmental conditions and long-term rearing can affect the phenotype of aged mice, breeding these mice in a uniform environment is crucial. The aged mice supplied by the NBRP are bred for approximately two years in a uniform environment that is strictly controlled for microbes. Our aged mice are therefore microbially safe and can be used in aging research.

Stock

- Standard mouse strains (C57BL/6J, C57BL/6N, BALB/cA): 3 strains
- Rearing conditions (single bred, group bred): 2 conditions

Unique Features

The aged mice supplied by the NBRP are housed for long periods in a uniform environment that is strictly controlled for microbiota. Apart from the National Institute on Aging, which systematically supplies aged mice to researchers in the United States, we are the only organization in Japan that distributes aged mice.

Update and Maintenance Activities

Core Center

The Foundation for Biomedical Research and Innovation at Kobe started supplying aged mice as part of the NBRP in 2022. We hope to contribute to the wide use of

standardized aged mice and lay the foundations for aging research in Japan.

Popular Strains and Applications

C57BL/6 aged mice

C57BL/6 is the standard mouse strain used in experimental research. Many prior studies have investigated various aspects of the aging process and age-related diseases using this mouse strain.



Aged C57BL/6J mouse at 102 weeks.

Contact

Core Center: Department of Animal Experimentation, Foundation for Biomedical Research and Innovation at Kobe

Principal Investigator: Shigeharu Wakana

Email/URL: info-nbr-agedmouse@fbri.org

ANIMALS

PLANTS

MICROBES

CELLS, DNA MATERIALS

INFORMATION



Overview

Rats exhibit behaviors and metabolic systems that resemble those of humans, and their moderate size facilitates experimental procedures. Rats are also amenable to strict control of genetic and environmental factors. Because of these superior properties, various rat disease models have been developed and used in medicine, pharmacology, life science, nutrition, neuroscience, genetics and other fields. Recent developments in genome editing technology have enabled the development of complex genetically modified rats, further increasing their value as a bioresource.

Stock

- Number of strains available: about 820 strains
- Information on 109 physiological characteristics: about 200 strains
- Genomic DNA and frozen sperm from ENU mutagenesis: about 10,000 rats
- Recombinant inbred lines between LE/Stm and F344/Stm: 34 lines
- Genome sequencing information on F344/Stm lines and more.

Unique Features

The NBRP is home to the world's largest rat resource center in terms of quality and quantity. We provide various models of human disease such as hypertension, diabetes and epilepsy that have been bred and developed in Japan. We also have severely immunodeficient rats produced by genome editing.

Update and Maintenance Activities

Core Center

Kyoto University will develop and make available rat reproductive technologies and expand our Cre rat collection.

Sub-Core Center

The University of Tokyo will add characterization data on Cre driver and reporter rats to enhance the value of our high-quality rat resource.

Popular Strains and Applications

Severely immunodeficient rats

We have three immunodeficient strains: Il2rg KO (NBRP Rat No. 0883), Rag2 KO (NBRP Rat No. 0894) and Il2rg, Rag2 double KO (NBRP Rat No. 0895). Human iPS cells and cancer cells can be transplanted into these strains for *in vivo* functional analysis.

Cre driver rats

We have a growing line-up of Cre driver rats which are predominantly neuronal lineages, including VGAT-cre (NBRP Rat No. 0839) and Drd2-cre (NBRP Rat No. 0843). These Cre rats can be crossed with a Cre reporter rat (NBRP Rat No. 0734) for visualization of specific cells and tissues.



A rat expressing EGFP throughout its body. Many other reporter rats are available, including those that express luciferase and cell-specific fluorescence markers.



Rats that express photosensitive ion channels in a neuronal and Cre-dependent manner can be used for optogenetic experiments.

Contact

Core Center: Institute of Laboratory Animals, Graduate School of Medicine, Kyoto University

Principal Investigator: Masahide Asano

Email/URL: <http://www.anim.med.kyoto-u.ac.jp/NBR/contact.aspx>



Japanese macaque

Overview

The Japanese macaque is a species of macaque monkey that is closely related to humans. It is often used as an experimental animal model and is indispensable in various life science fields, including neurophysiology, infectious disease/immunology, and regenerative medicine. Japanese neuroscientists have produced crucial research findings on higher brain functions using Japanese macaques. Furthermore, Japanese macaques exhibit specific susceptibility and immune response to tropical and subtropical pathogens because they were isolated from the Eurasian continent several hundreds of thousands of years ago. Such characteristics are advantageous for comparative infectious disease studies.

Stock

- Japanese macaque: 1 line

Unique Features

Japanese macaques are a species native to Japan. The NBRP is the only organization that maintains a large purpose-bred colony to provide macaques for research purposes. Global supply of macaques has become unreliable due to the COVID-19 pandemic, which has increased their value as a bioresource.

Update and Maintenance Activities

Core Center

Kyoto University's Center for the Evolutionary Origins of Human Behavior will conduct whole genome sequencing of breeding individuals to make available genetic characteristics that differ across habitats.

Sub-Core Center

The National Institute for Physiological Sciences will continue to work with Kyoto University's Center for the Evolutionary Origins of Human Behavior to improve the efficiency and ensure smooth operation of the project.

Popular Strains and Applications

Compared to other Southeast-Asian macaque species,

such as rhesus and cynomolgus, Japanese macaques have a curious and calmer temperament, and highly-developed cognitive and learning abilities, which make them suitable for research into higher brain functions. They have contributed to a variety of basic research studies, including explorations of the onset mechanism and pathology of neurological disorders such as dementia and Parkinson's disease, and the development of treatments to restore function.



Japanese macaques are seasonal breeders that produce one offspring every other year. It also takes time to raise them to the age needed for supply.



Group-reared in a semi-wild habitat, the monkeys we provide exhibit well-developed motor skills and cognitive function.

Contact

Core Center: Center for the Evolutionary Origins of Human Behavior, Kyoto University

Principal Investigator: Katsuki Nakamura

Email/URL: https://www.nbr-macaque.pri.kyoto-u.ac.jp/?page_id=13



Overview

Among the approximately 9,600 bird species in existence, chickens and quails are most widely used in various research fields. For example, chickens are often used in embryology because their embryos are easy to manipulate for live-tracing of developmental processes. Although commercially available chickens and quails with extremely high heterogeneity are most commonly used in research today, use of the NBRP's genetically controlled strains, such as inbred strains, will improve the reproducibility of experimental results.

Stock

- Standard strains, mutant/disease model strains: 39 chicken strains, 23 quail strains
- Genetically modified strains: 3 chicken strains, 1 quail strain (to be expanded)

The above strains can be supplied in the form of fertilized eggs, blood, genomic DNA, live animals (chicks, adults) and more.

- Primordial germ cell lines (including genetically manipulated lines): 29 lines, available from 2022

Unique Features

Restrictions exist in the international transportation of live avian resources to prevent epidemic expansion of influenza. The NBRP provides strains that cannot be obtained elsewhere, such as inbred strains and genetically-modified strains.

Update and Maintenance Activities

Core Center

Avian Bioscience Research Center at Nagoya University will soon provide chicken primordial germ cell (PGC) lines, which are suitable for genetic engineering including genome editing.

Sub-Core Center

Hiroshima University is preparing to provide several Japanese chicken strains for research purposes.

Popular Strains and Applications

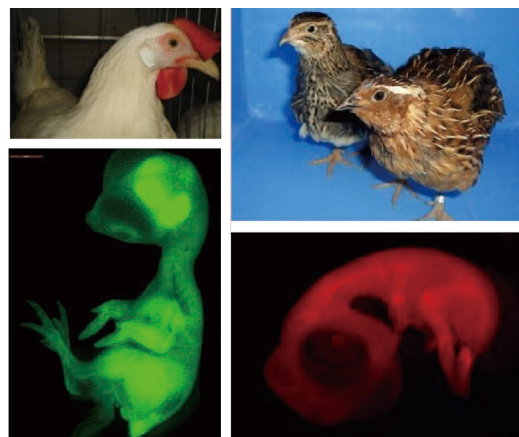
Reporter-expressing transgenic lines (pLSi/ Δ AeGFP-TG chicken, PGK:H2B-chFP-TG quail)

Chickens and quails that express EGFP and mCherry,

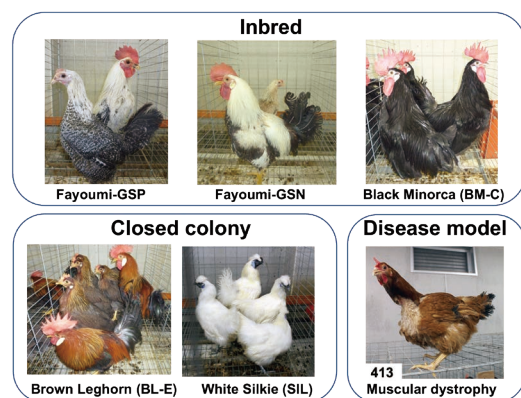
respectively, are frequently used for live-imaging of developmental processes.

Quail WE strain, chicken M/O strain

These are widely used as standard strains for various purposes including chemical safety tests, physiology, and anatomy.



Transgenic chickens and quails are suitable for live-imaging. Chickens and quails expressing EGFP and mCherry, respectively.



Chicken resources available from the Avian Bioscience Research Center at Nagoya University.

Contact

Core Center: Avian Bioscience Research Center,
Graduate School of Bioagricultural Sciences,
Nagoya University

Principal Investigator: Ken-ichi Nishijima

Email/URL: abrc@agr.nagoya-u.ac.jp

Clawed frogs & Newts



Overview

The short generation time of clawed frogs and newts makes them suitable for a variety of biological studies. *Xenopus tropicalis* has a generation time of 4-6 months, making it suitable for genetic studies. Although *Xenopus laevis* has a slightly longer generation time (1-2 years), it is suitable for developmental biology studies due to the ease with which embryos can be manipulated. Whole genome sequencing information is available for both species. Finally, *Pleurodeles waltl* has a short generation time similar to that of *Xenopus tropicalis*, and is especially suitable for regeneration studies.

Stock

- *X. tropicalis* (inbred, transgenic or mutant): about 90 strains/lines
- *X. laevis* ("): about 10 strains/lines
- *P. waltl* ("): about 10 strains/lines
- Genomic DNA, cDNA clones, *in situ* hybridization kits, CRISPR/Cas9-positive control kits: about 500 samples/clones/kits

Unique Features

The highly inbred *X. tropicalis*, *X. laevis*, and *P. waltl* strains were developed in Japan and are unique in the world, making the NBRP home to a core international stock center for these model amphibians.

Update and Maintenance Activities

Core Center

The Amphibian Research Center at Hiroshima University will begin providing *X. laevis* and *P. waltl* from 2022. These species are often used together with *X. tropicalis*.

Sub-Core Centers

Yamagata University and Waseda University will continue to maintain backup storage of seed parents and frozen sperm of valuable strains.

Popular Strains and Applications

X. tropicalis inbred strains (NA, NH, NBH, IC)

NA is a direct descendant of Nigerian, the classic inbred strain

used in the first whole genome sequencing study. NH and NBH are derived from the same colony from which Nigerian was developed, while IC is genetically distant from Nigerian-related strains at the subspecies level. These strains are used for developmental, genetic, evolutionary, and physiological studies. The *X. tropicalis* inbred strain (NBH) is often used in genome editing research because of its robust eggs and embryos.

X. laevis inbred strain (J)

This strain is widely used for developmental and evolutionary studies.

P. waltl inbred strains (Y, T)

These strains are widely used for regeneration studies.



Wild-type *X. tropicalis* (left: adult female, right: adult male).



Top: Wild-type *X. laevis* (left: adult female, right: adult male).
Bottom: Wild-type *P. waltl*.

Contact

Core Center: Amphibian Research Center, Hiroshima University

Principal Investigator: Hajime Ogino

Email/URL: nbrpfrog@hiroshima-u.ac.jp



Overview

Zebrafish are vertebrates that remain transparent throughout embryogenesis. They are also easy to breed, have a short life cycle, and are amenable to mutation and genetic modification. As a result of these characteristics, zebrafish are used to study biological regulatory processes such as those involved in development and regeneration using molecular genetics and imaging technology. Use of zebrafish as a substitute for mammalian models has increased in recent years, reflecting the rise in awareness of animal welfare issues.

Stock

- Wild-type: 1 strain
- Mutant lines: about 400 strains
- Transgenic lines: about 1,800 strains

Unique Features

By using the efficient sperm cryopreservation method developed under the NBRP, we are able to supply strains that were developed uniquely in Japan to researchers in Japan and around the world.

Update and Maintenance Activities

Core Center

RIKEN Center for Brain Science will continue to collect, preserve, and distribute zebrafish strains produced in Japan.

Sub-Core Centers

The National Institute of Genetics and National Institute for Basic Biology will continue to preserve and distribute gene and enhancer trap lines and nervous system cell-manipulated lines.

Popular Strains and Applications

dao:cre-mCherry; vglut2a:loxP-DsRed-loxP-GFP (RIKEN)

This strain has been used to study the habenulo-raphé pathway, a conserved neural circuit among vertebrates

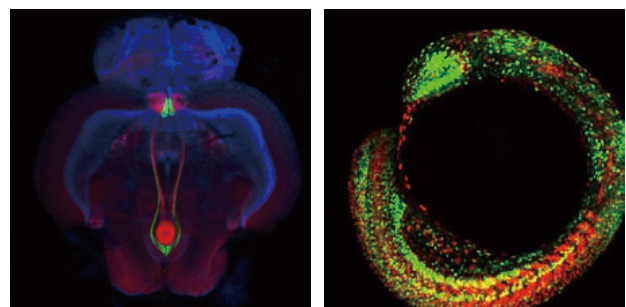
that encodes the expected level of aversiveness for learning the appropriate behavior to avoid danger.

Fucci fish (Depositor: Dr. Atsushi Miyawaki, RIKEN)

In Fucci fish, the nuclei of cells in S/G2/M phase fluoresce green while the nuclei of cells in G1 phase fluoresce orange using the Fucci method invented by Dr. Atsushi Miyawaki. The phase of cell division can thus be observed from the fluorescent color.



Adult zebrafish, one cell-stage embryo, and 16-hour post-fertilization embryo.



Left: The brain of a transgenic fish in which the output pathway from the habenula is fluorescently labeled. Right: Fucci fish embryo.

Contact

Core Center: RIKEN Center for Brain Science

Principal Investigator: Hitoshi Okamoto

Email/URL: hitoshi.okamoto@riken.jp



Medaka

Overview

Medaka is a small freshwater fish with a relatively short life cycle (3 months) and small genome size (800 Mbp). Medaka can adapt to low temperatures (4°C) in the winter and high temperatures (40°C) in the summer, as well as to relatively high salinity environments. In addition to medaka, the NBRP also provides medaka-related species and hatching enzymes essential for embryonic manipulation, along with high quality genome sequence information and genome annotations.

Stock

- Standard strains and wild-derived strains from Japan, China, and Korea: about 100 strains
- Mutant and transgenic lines: about 730 strains
- Related species: about 10 strains
- Genome resources (cDNA, BAC, Fosmid clones): about 730,000 clones
- Hatching enzymes

Unique Features

The NBRP is home to the only Medaka biological and genetic resource center in the world. We provide biological resources, genome resources, hatching enzymes, and various related databases.

Update and Maintenance Activities

Core Center

In collaboration with Tohoku University, the National Institute of Basic Biology and Utsunomiya University, will sequence the genomes of 100 wild-derived strains and construct a more accurate reference genome using PacBio Hi-Fi reads.

Sub-Core Center

The National Institute of Genetics and other facilities will develop user-friendly web tools to integrate medaka genome information and omics data.

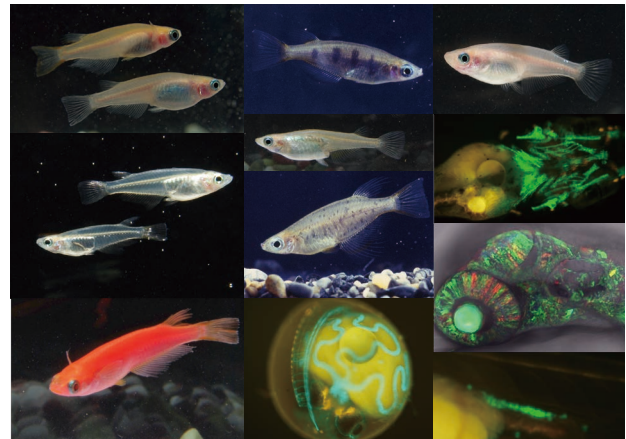
Popular Strains and Applications

HdrR-II1 inbred line

This inbred line is derived from d-rR/Nagoya, which was established by Dr. Toki-o Yamamoto. The HdrR-II1 line was used to determine the sequence of the medaka genome, and genome annotation was subsequently performed based on the HdrR-II1 genome sequence. Genome sequences of other inbred lines, including HNI-II, which is derived from wild medaka in Niigata, and HSOK, which is derived from medaka in Sokcho, Korea, are also available. HNI-II is a sister clade to HdrR-II1, and HSOK can be used as an outgroup.

OK-Cab strain

OK-cab is a strain derived from medaka provided by Carolina Biological Supply in the USA. It can be bred in many laboratories around the world because of its high fecundity and ease of breeding.



The National Institute for Basic Biology and Utsunomiya University offer a variety of resources including standard strains, inbred strains, medaka-related species, and transgenic strains.

Contact

Core Center: Lab of Bioresources, National Institute for Basic Biology

Principal Investigator: Kiyoshi Naruse

Email/URL: nbrp.medaka@bioresource.jp

Ciona intestinalis



Overview

Ciona intestinalis belongs to the marine invertebrate chordate, ascidian. Ascidian is the closest living relative of vertebrates. Elucidating the molecular mechanisms of ascidians is necessary for understanding the evolution of chordates. The simple body structures and genome of *Ciona* make it well-suited for molecular studies. Its genome sequence has been well-annotated and gene resources comprehensively prepared. It has a generation time of only 3 months and inland culture systems have been established.

Stock

- Mutants and transgenic lines: about 150 lines
- Wild-type (closed colonies established from wild populations): 2 populations
- Expression vectors: about 400 clones

Unique Features

The NBRP cultivates wild-type populations to ensure that they are available throughout most of the year. Our collection of transgenic lines covers nearly the entire set of tissue/organ visual markers. We are the only center that strategically provides live *Ciona* material.

Update and Maintenance Activities

Core Center

The University of Tsukuba's Shimoda Marine Research Center is working to improve the quality of our transgenic collections.

Sub-Core Centers

Kyoto University (Graduate School of Science and Maizuru Fisheries Research Station) and the University of Tokyo (Misaki Marine Biological Station) will continue to cultivate wild-type populations and conduct genomic analyses of wild-types to provide high quality material to researchers.

Popular Strains and Applications

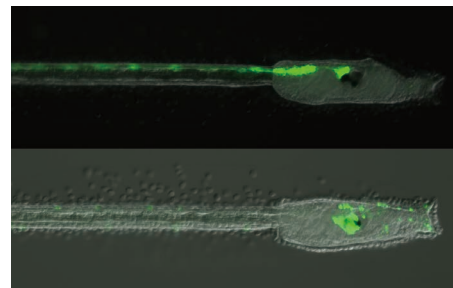
Neuron marker transgenic lines (such as Tg [MiCiVACHTK] 5)

Despite having a limited number of neurons, *Ciona* can

produce various responses to stimuli in its environment. Together with the connectome of the larval nervous system, transgenic lines that mark specific neuronal populations are a useful tool in neurobiology. We have collected various neuronal marker lines, which have been used to characterize the specific mechanism of terminal differentiation of neurons, to identify the neurons that respond to stimuli, and to trace cells during metamorphosis and regeneration.

Wild-type

We cultivate wild-type *Ciona* as closed colony populations so that we can provide this resource throughout most of the year. Although *Ciona* has frequent genetic variations in its genome, closed colonies can limit these variations. Our sequenced genomes of wild-type populations are useful for identifying genetic variations.



Larva of transgenic lines expressing the Kaede reporter in acetylcholine-positive (top) and glutamate-positive (bottom) neurons.



Wild-type *Ciona intestinalis* cultivated in the ocean.

Contact

Core Center: Shimoda Marine Research Center,
University of Tsukuba

Principal Investigator: Yasunori Sasakura

Email/URL: sasakura@shimoda.tsukuba.ac.jp



Drosophila

Overview

Drosophila is a small insect that is widely used as a model organism in both basic biological research and medical science because it shares 70% or more of its genes with humans. It has a short generation time of only 2 weeks and is easy to cultivate. Moreover, the *Drosophila* genome has been sequenced and precisely annotated. The last 20 years has seen significant growth and advancement of *Drosophila* resources, and the pace of advancement is continuing to increase in Japan.

Stock

- RNAi strains: about 14,000 strains
- FlyCas9 strains: about 30 strains
- Basic strains: about 3,700 strains
- NP strains: about 4,200 strains
- Regional wild/mutant strains: about 1,500 strains

Unique Features

The NBRP has developed unique strains such as FlyCas9 strains. We are the only comprehensive *Drosophila* resource consortium in Asia and have the largest scale of *Drosophila* species.

Update and Maintenance Activities

Core Center

The National Institute of Genetics is working on revamping our catalog database to improve international visibility and user experience. We provide systematic genome-edited strains that are unique around the world.

Sub-Core Centers

Kyoto Institute of Technology will continue to provide basic strains and human ORF strains, and cryopreserve primordial germ cells. Kyorin University will continue to act as a global *Drosophila* species stock center.

Popular Strains and Applications

FlyCas9 strains (CAS-0001–CAS-0004)

By crossing this strain with a guide RNA strain,

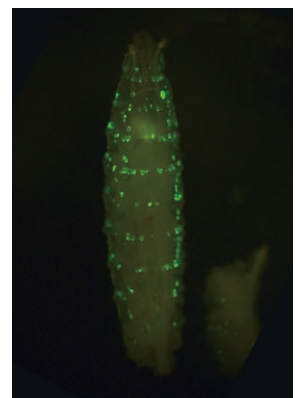
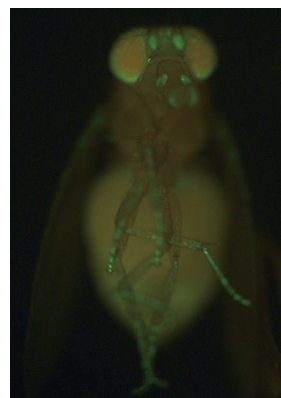
researchers can efficiently produce gene knockout flies. These gene knockout flies can then be used for screening purposes, which will help advance basic biological research.

NP strains

This is a collection of GAL4 enhancer trap insertion strains produced by the NP consortium in Japan that has been widely used both domestically and internationally for tissue-specific expression and knockdown using the GAL4/UAS system.



Drosophila.



EGFP-expressing strain driven by a tissue-specific promoter (left: adult, right: pupa).

Contact

Core Center: Department of Chromosome Science,
National Institute of Genetics

Principal Investigator: Kuniaki Saito

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Overview

Silkworms are easy to rear, have a short generation time of approximately 50 days and are amenable to genome editing. Females can lay 500 eggs in one night, all of which are genetically uniform. The NBRP is home to the world's most diverse selection of silkworm mutations. We have also developed cryopreservation techniques for ovaries and sperm to facilitate the preservation of genome-edited lines.

Stock

- Genetic mutation lines (mostly spontaneous mutations): about 500 lines
- Consomic and congenic lines with *Bombyx mandarina* chromosomes: about 200 lines
- Genome-engineered lines: about 150 lines
- Wild silkworm species: 11 species
- Cultured cell lines: 5 strains

Unique Features

The NBRP is home to the world's most diverse silkworm mutants. The majority were generated through spontaneous mutations and allow us to explore the diversity of life and the mysteries of nature and chance.

Update and Maintenance Activities

Core Center

Kyushu University will continue to add genomic information on frequently-requested representative strains and enhance the maintenance of cultured cells to elevate the value of our resource.

Sub-Core Center

Shinshu University will develop an efficient and reliable distribution system for wild silkworm resources which are closely related to silkworms.

Popular Strains and Applications

Silkworm p50 line (a consomic line between silkworm and silkworm)

The p50 strain is the standard strain used to analyze the

silkworm genome and is widely used because of its resistance to disease. This consomic line was developed by replacing each chromosome of the ancestral silkworm species, *Bombyx mori*, with that of the p50 lines. We expect the number of requests for this consomic line to increase because it allows researchers to explore the domestication process of silkworms.

Silkworm strains (NB1, NB2, NB3)

These three strains are easy to raise and suitable for beginners. NB2 can be easily identified as male or female by its appearance in the larval stage. NB3 is large and can be inoculated with drugs and pathogens by injection, and is widely used in the fields of medicine and pharmaceuticals.



Diverse silkworm cocoons. The variation in cocoon shape is due to differences in larval cocooning behavior, and is useful for behavioral analysis.



Silkworm larval mutants. There was a time when 40 billion silkworm larvae were reared annually in Japan, which led to the discovery of unique spontaneous mutations.

Contact

Core Center: Institute of Genetic Resources,
Graduate School of Bioresources and
Bioenvironmental Science, Kyushu University

Principal Investigator: Tsuguru Fujii

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Caenorhabditis elegans



Overview

C. elegans is a useful animal model for human diseases because around 40% of its genes are orthologous to those of humans. It has a short life cycle of about 3 days at 20°C and is amenable to culture with *E. coli*. Further, *C. elegans* has only about 1,000 somatic cells, the cell lineages of which have been comprehensively described. Thanks to serial electron microscopic images, detailed descriptions of its morphology have also been produced, and it was the first multicellular organism to have its whole genome sequenced. Thus, *C. elegans* is suitable for genetic analyses, and its mutants are useful for exploring gene function.

Stock

- Deletion mutant lines: about 13,400 lines
- High function balancers: 69 lines
- Cre transgenic lines: 43 lines

Unique Features

The NBRP has about half the number of deletion mutants as there are genes in wild-type *C. elegans*. We also have high function balancers that do not exhibit aneuploidy.

Update and Maintenance Activities

Core Center

Tokyo Women's Medical University will continue to collect and distribute deletion mutants, high function balancers, and Cre-transgenic *C. elegans* strains.

Popular Strains and Applications

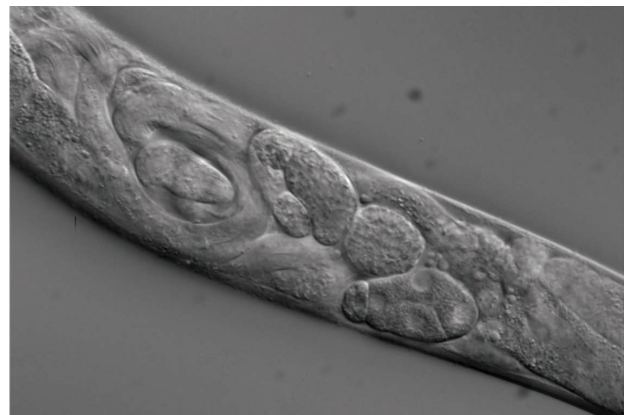
lrk-1 (*tm1898*) deletion mutant

Because the *C. elegans lrk-1* gene is homologous to a familial Parkinson's disease gene in humans, a mutant lacking the *lrk-1* gene (*tm1898*) is an important animal model for understanding the disease. Further, elucidating

the function of protein kinase LRK-1 in *C. elegans* may facilitate the development of new treatments for Parkinson's disease.



C. elegans balancer *tmC6[dpy-2(tm15189)]*. Pharyngeal fluorescence is used as an indicator that the balancer is present.



Deletion mutant *egl-26(tm1244)*. This strain shows the egg-laying defective (*egl*) phenotype. The mutant has eggs and L1 larvae in its uterus.

Contact

Core Center: Department of Physiology, School of Medicine,
Tokyo Women's Medical University

Principal Investigator: Sawako Yoshina

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Overview

Arabidopsis is a recognized representative model plant used in various research fields. It is a small plant with a short life cycle of only 3 months. Under laboratory conditions, each *Arabidopsis* plant produces thousands of seeds. In addition, it requires a simple procedure for transformation, and the plant's entire genome sequence has been annotated. Japan is a leader in the field of cultured plant cells, which have been widely used in studies on cell biology and the production of useful substances.

Stock

- Mutants and transformed lines: 508 lines
- Ecotypes: 1,018 lines
- Gene-knockout lines: about 20,000 lines
- *Arabidopsis* cDNA clones: about 240,000 clones
- Cultured plant cell lines: 80 lines

Unique Features

The RIKEN BioResource Research Center (BRC) is home to a unique resource center in Asia that distributes *Arabidopsis*-related materials developed in Japan. In addition, we are the only institution in the world that distributes plant-cultured cells to the international research community.

Update and Maintenance Activities

Core Center

The Experimental Plant Division at RIKEN BRC is characterizing the phenotypes of Japanese accessions using the RIKEN Integrated Plant Phenotyping System (RIPPS). The data will be made available together with the genome sequences.

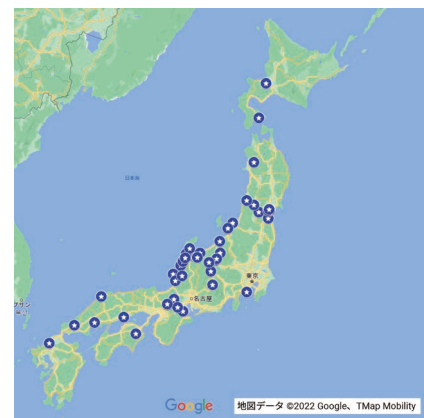
Popular Strains and Applications

Natural accessions that grow under various environmental conditions harbor polymorphisms in both genotype and phenotype. We distribute natural accessions collected from various regions around the world. In addition, based on single-nucleotide polymorphism data, we have selected

100 representative lines from our collection to establish a set of natural accessions which we will provide as a new resource named psw00001. Each line in this set was crossed with the standard lines Col and Ler, and the progeny seeds of the F2 generation are available for quantitative trait locus analysis. Furthermore, a set of seed pools is available for screening purposes. Together with the availability of genotyping services, we expect that these resources will accelerate the study of quantitative traits.



Japanese accessions.



Sampling locations of Japanese accessions.

Contact

Core Center: Experimental Plant Division,
RIKEN BioResource Research Center

Principal Investigator: Masatomo Kobayashi

Email/URL: plant.brc@riken.jp



Overview

Rice is an essential and major calorie source required to feed the large population on Earth, and rice plants have co-evolved with humanity. *Oryza* genus-related genetic resources, including wild progenitor species, are used in various fields of research, including breeding science and basic research in genetics and biology. We provide wild *Oryza* accessions and mutation lines derived from cultivated species.

Stock

- Wild *Oryza* accessions: about 1,700 accessions
- MNU-induced mutation lines
(derived from Kinmaze, TC65, Kitaake & Yukihikari)
- Chromosome segment substitution lines (CSSLs) and others
(chromosomes of *Oryza glaberrima*, *O. meridionalis*, *O. glumaepatula*, *O. sativa indica* and *O. sativa japonica* are introduced into cultivated rice and more.)

Unique Features

NBRP Rice is home to one of few facilities to preserve and provide an eclectic collection of wild *Oryza* accessions in the world. Wild *Oryza* species are valuable genetic resources as their habitats are in decline due to urban development and environmental changes.

Update and Maintenance Activities

Core Center

The National Institute of Genetics will continue to provide wild *Oryza* accessions and their genetic/genomic information through Oryzabase.

Sub-Core Center

Kyushu University will continue to provide experimental lines, such as mutation lines of cultivars and CSSLs of wild *Oryza* species.

Popular Strains and Applications

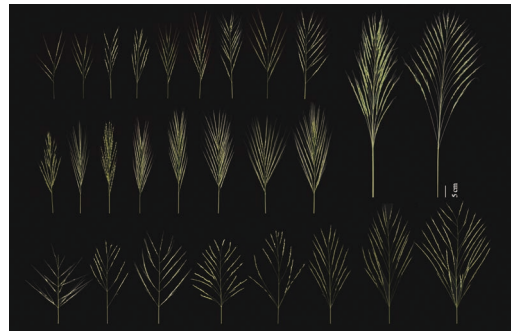
Wild *Oryza* accessions

We offer about 1,700 accessions of wild *Oryza* species covering 21 species in the *Oryza* genus, some of which

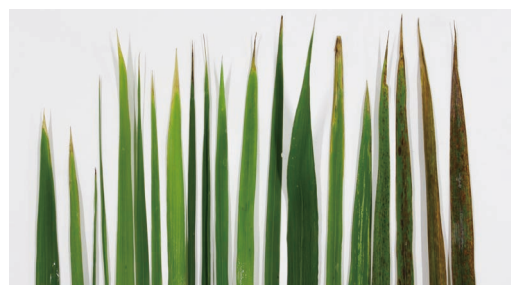
are capable of transformation. Wild *Oryza* accessions are suitable for studies aimed at identifying valuable genes for use in breeding and studies on genome evolution using species that have adapted to diverse environments. Closely related wild species such as *O. rufipogon* are also used to study the rice domestication process.

MNU-induced mutation lines

We also offer mutation lines derived from rice cultivars (e.g., Kinmaze, Taichung 65, Kitaake, Yukihikari). These mutation lines were produced by treating fertilized eggs with MNU. These lines are used in basic research such as morphological and physiological studies of rice, and research on agronomically important traits such as disease resistance and grain quality.



Diverse panicle shapes of wild *Oryza* accessions. The size of the panicle and the length and number of branches differ among accessions.



Variation in leaf morphology among MNU-induced mutation lines.

Contact

Core Center: Department of Genomics and Evolutionary Biology, National Institute of Genetics

Principal Investigator: Yutaka Sato

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Overview

Wheat, one of the world's three major cereals, has a complex genome structure that can be diploid ($2n = 14$; Einkorn wheat), tetraploid ($2n = 28$; Emmer wheat), or hexaploid ($2n = 42$; common wheat). Recent scientific advances have made whole genome sequence information and transformation available, opening new doors for wheat science research^{1), 2), 3)}. Wheat research can contribute to everything from basic biological science to global food issues.

Stock

- Landraces/Cultivars: about 10,800 lines
- Wild species: about 4,800 strains
- Experimental lines: about 1,600 strains
- NAM population of common wheat: about 4,900 lines

Unique Features

While most genebank collections around the world focus on cultivars, the NBRP provides an extensive number of landraces, wild relatives, and experimental lines.

Update and Maintenance Activities

Core Center

Kyoto University is developing large-scale recombinant inbred lines in the two types of wheat that have played a significant role in the polyploidy evolution of wheat: tetraploid wheat and the diploid wild relative, *Ae. tauschii*.

Popular Strains and Applications

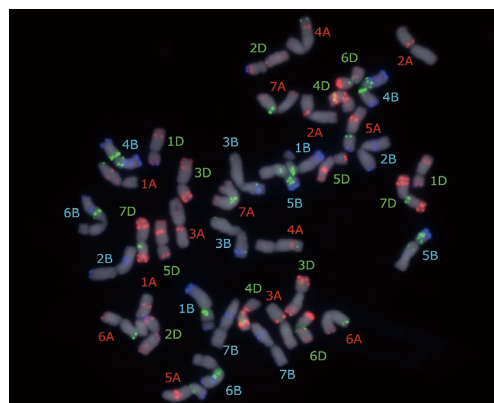
'Norin 61' (LPGKU2305)

Wheat in the West is genetically highly differentiated from that in Asia⁴⁾. As Asian genetic resources have generally been under-utilized in the world of wheat breeding⁵⁾, there

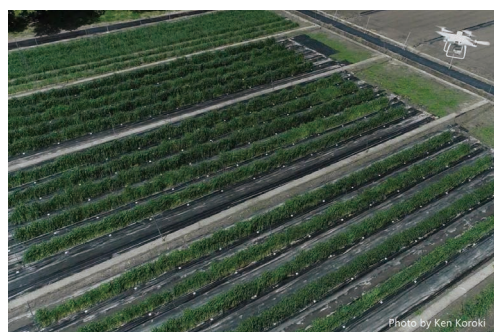
is a high likelihood of discovering unknown alleles among Asian varieties. This line is a representative Asian wheat variety, and its genomic sequence has been determined⁵⁾. It has been used for gene isolation of agronomic traits. We have developed experimental lines derived from crosses between this line and 24 Asian wheat lines.

'Fielder' (LPGKU2330)

While wheat is often difficult to transform, this line is one of the standard varieties used for transformation. Given that its genome sequence has already been determined, reverse genetics is possible using this line.



ND-FISH of 'Norin 61' the representative bread wheat variety in Asia.



A field photo of a NAM population of common wheat, derived using bread wheat 'Norin 61' as the fixed parent.

Contact

Core Center: Graduate School of Agriculture,
Kyoto University

Principal Investigator: Ryohei Terauchi

Email/URL: nbrpkmg.ku@gmail.com

1) International Wheat Genome Sequencing Consortium (IWGSC), *Science* 361: eaar7191, 2018

2) Abe et al. 2019

3) Sato et al. 2021

4) Balfourier et al. 2019

5) Walkowiak et al. 2020



Barley

Overview

Barley is used for brewing, food, and feed. It exists as a variety of wild and cultivated species with high adaptability and resistance to environmental changes such as drought, salt, and moisture damage. Due to its diploid genome structure, mutations are easy to detect in cultivated species. A high-quality genome assembly has also been completed. Therefore, barley is used as a model in plant science and practical applications, including the identification of useful genes.

Stock

- Cultivated and wild strains collected from around the world: about 11,000 lines
- Genetic experimental stocks: about 9,000 lines
- Genome-modified lines: 3 lines
- Full-length cDNA clones (to be expanded in 2022): about 220,000 clones
- Genomic DNA: about 3,300 samples

Unique Features

The NBRP is one of the world's five best barley resource centers located in East Asia. We preserve barley strains that have been independently collected and developed, and provide the genome assemblies of key strains.

Update and Maintenance Activities

Core Center

Okayama University is working to provide high-quality genome DNA, trait information and genome information on barley strains.

Popular Strains and Applications

Haruna Nijo (J247)

Haruna Nijo is a key Japanese strain that has been used to develop a BAC library, full-length cDNAs and a molecular genetic map. The chromosome-scale genome assembly of this strain has been released and used for gene isolation and genetic analysis of useful traits.

Barley Standard Varieties (274 lines)

These varieties are a core collection selected from NBRP strains with reliable collection-site information. Single-nucleotide polymorphism information on these varieties is available from our online database. This collection has been used to represent the world barley diversity, particularly in molecular evolution studies of genes and genome-wide association studies.



Barley seeds.



Diverse barley spike patterns.

Contact

Core Center: Institute of Plant Science and Resources,
Okayama University

Principal Investigator: Hiroshi Hisano

Email/URL: barley@okayama-u.ac.jp

Lotus japonicus & Glycine max



Overview

Lotus japonicus is a wild legume that grows naturally in Japan and is widely used as a model legume in basic research. This is because the plant is easy to grow and has a short life cycle (about 3 months) and small genome, the sequence of which has been determined and made publicly available. *Glycine max* is widely used around the world as food, feed, and a high-value cash crop, because its seeds contain many functional components such as isoflavones and saponins, in addition to proteins and lipids.

Stock

- Experimental lines of *L. japonicus*: 3 lines
- Japanese wild accessions: about 1,000 lines
- Recombinant inbred lines and taglines: about 1,600 lines
- DNA clones (including *Rhizobium*): about 240,000 clones
- *Rhizobium* STM mutant strains: about 7,000 lines

Unique Features

The NBRP provides a unique collection of wild strains and *Rhizobium* for both *L. japonicus* and *G. max*. We are the only organization that provides these resources in Asia and the only distributor of wild strains and *Rhizobium* STM mutant strains in the world.

Update and Maintenance Activities

Core Center

University of Miyazaki will collect *L. japonicus* LORE1 taglines, *Rhizobium* STM mutants, and develop a core collection for *G. soja*.

Sub-Core Center

Tohoku University will select LORE1 core lines and provide information on mutation insertion sites in *Rhizobium* STM mutants.

Popular Strains and Applications

Miyakojima MG-20 and Gifu B-129

These lines were recently used to isolate new

symbiosis-related genes. This was a globally acclaimed achievement because there are only a small fraction of potentially discoverable genes left; many genes related to symbiosis between plants and microorganisms have already been isolated (*Nat Commun* 9:499 2018, *PLoS Genet* 15(1): e1007966 2019).

Wild *L. japonicus* line (MG line)

Genome analysis of 136 MG lines collected throughout Japan and cultivation experiments on these strains in a wide range of environments have revealed that *L. japonicus* was first established in Kyushu approximately 20,000 years ago and subsequently expanded throughout Japan. Furthermore, genes related to overwintering and flowering regulation were found to be crucial for adaptation of *L. japonicus* to northern Japan (*Nat Commun* 11:253 2020).



Wild *Lotus japonicus* growing near the mouths of rivers in Miyazaki city. It grows in open areas, including riverbanks.



Various soybean seeds. More than 5,000 varieties of soybeans and wild soybean (*Glycine soja*) grow naturally in Japan.

Contact

Core Center: Faculty of Regional Innovation,
University of Miyazaki

Principal Investigator: Masatsugu Hashiguchi

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Overview

Studies on gene function, cultivation characteristics, and fruit chemistry of tomatoes attract much interest from scientists because tomatoes have one of the largest cultivation areas among all fruits and vegetables. In addition, tomatoes have the potential to become the next model plant for both basic and applied research. Tomato research contributes to the understanding of fruit development and light-independent flowering, both of which are unexplorable physiological events in traditional model plants. Additionally, metabolites in tomatoes are highly sought after target molecules in industrial research.

Stock

- Cultivars, wild species, and crossed lines: about 100 lines
- Individual mutant collections: about 2,700 lines
- EMS-treated bulked M₃ seed set:
originated from about 5,500 lines
- T-DNA insertion lines: about 500 lines
- cDNA and full-length cDNA clones: about 270,000 clones

Unique Features

The NBRP is home to the only center in the world that collects and makes available large mutant collections of Micro-Tom cultivars and a T-DNA insertion line series (simple T-DNA insertion, activation-tagging, and FOX hunting).

Upgrade and Maintenance Activities

Core Center

The University of Tsukuba will collect more detailed phenotypic/genetic information on individual mutants to increase their value to users and improve the TOMATOMA database to add value to our resources.

Popular Strains and Applications

Micro-Tom (TOMJPF00001)

Micro-Tom is a dwarf tomato cultivar with excellent phenotypes, including small plant size, short life cycle, and a complete life cycle in indoor growth rooms, making them suitable experimental model plants compared to standard

tomato cultivars, which require cultivation in greenhouses. Micro-Tom is used for various types of research including fruit development, metabolic regulation, hormone response, and stress responses.

Micro-Tom mutants (TOMJPE/M/W series)

Because this collection is one of the largest mutant tomato resources in the world, we receive many international requests to use phenotypic mutants. For instance, the *pro-2* mutant (TOMJPE2753-1), which harbors a mutation in the *DELLA* gene, has contributed to research on parthenocarpy, the phenomenon of fruit development without pollination.



Micro-Tom cultivation: Micro-Tom is amenable to high-density cultivation because of its small size.



Micro-Tom mutants: (clockwise from top left) flower-color, fruit-shape, vegetative-shape, fruit-shape, bud-formation, leaf-shape, leaf-color, and variegation.

Contact

Core Center: Institute of Life and Environmental Sciences/Tsukuba-Plant Innovation Research Center, University of Tsukuba

Principal Investigator: Hiroshi Ezura

Email/URL: requestomato@t-pirc.tsukuba.ac.jp



Overview

The *Chrysanthemum* genus, including cultivated chrysanthemum, has interesting characteristics that model plants do not have. However, the majority of the *Chrysanthemum* species are autopolyploid and self-incompatible, which makes genetic analysis difficult. NBRP facilities contribute to molecular genetic studies of the *Chrysanthemum* genus by offering a variety of interesting *Chrysanthemum* species and developing unique resources based on a pure line of *Chrysanthemum seticuspse*, a diploid wild chrysanthemum, whose whole genome sequence information is available.

Stock

- Wild strains of *Chrysanthemum sensu lato* (Anthemideae) mostly native to Japan: about 500 strains
- Experimental lines including the model strain, mutants, and interspecific hybrid lines: about 100 strains
- A BAC library of *Chrysanthemum seticuspe*: about 100,000 clones

Unique Features

The NBRP is home to the only center that publicly distributes one of the world's largest wild chrysanthemum collections. We offer the chrysanthemum model strain and mutants developed at our center.

Update and Maintenance Activities

Core Center

Hiroshima University will preserve the chrysanthemum collections, expand available mutants and update their genetic information in reference to the Gojo-0 strain.

Sub-Core Center

Kochi University will collect wild strains and preserve *Chrysanthemum* plants for backup purposes.

Popular Strains and Applications

Gojo-0 strain

The Gojo-0 strain was developed from *Chrysanthemum seticuspe*, a diploid species native to Japan. It is a pure

line generated by repeated selfing of a self-compatible mutant of *Chrysanthemum seticuspe*. In contrast to the majority of the *Chrysanthemum* genus, including cultivated chrysanthemum, which are autopolyploid and self-incompatible, Gojo-0 is diploid and self-compatible, making it suitable for genetic analysis and manipulation, such as isolation of recessive mutants. Gojo-0 is used as a platform to study the *Chrysanthemum* genus because of the availability of whole genome sequencing information, transcriptome data, and DNA marker information for this strain.



Wild-type and mutant *Chrysanthemum seticuspe*. Inflorescences of the model strain Gojo-0 (left) and the *shiboridama* mutant (right).



Chrysanthemum repestre, a diploid *Chrysanthemum* species lacking ray florets that grows on highlands in Japan.

Contact

Core Center: Laboratory of Plant Chromosome and Gene Stock, Graduate School of Integrated Sciences for Life, Hiroshima University

Principal Investigator: Makoto Kusaba

Email/URL: akusaba@hiroshima-u.ac.jp



Morning glories

Overview

The Japanese morning glory (*Ipomoea nil*) is useful for research purposes because its generation time is less than 3 months and its size can be controlled by manipulating the daylength. Research on this plant is increasing to take advantage of the fact that it is a short-day plant, has vining capabilities and short one-day flowering time. The genome of *I. nil* is also uniform among lines, making it easy to identify the gene responsible for a mutation. We maintain a variety of *I. nil* mutants originating in the Edo period, and new mutations can be induced using endogenous transposons.

Stock

- Mutant and wild-type lines: about 3,000 lines
- Sibling species lines: about 450 lines
- cDNA clones: about 61,100 clones
- BAC clones: about 115,200 clones
- Petal-specific expression vectors and more

Unique Features

The NBRP is the only resource distributor in the world that provides morning glory mutant lines originating in the Edo period, wild-type lines from around the world, mutant and wild-type lines of closely related species, and various DNA resources.

Update and Maintenance Activities

Core Center

Kyushu University will publish detailed information about our resources and their outstanding features to increase the number of users.

Sub-Core Center

The National Institute for Basic Biology will add the genome sequences of our mutant lines to elevate the genome database.

Popular Strains and Applications

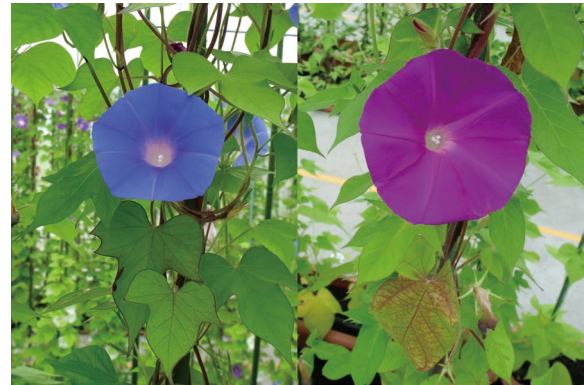
Tokyo Kokei Standard (TKS)

This is a wild-type line selected by Dr. Yo Takenaka of the National Institute of Genetics that was used as the

reference genome sample. The DNA clones we provide were produced from this line. Because the transpositions of endogenous transposons are suppressed in the line, the genome sequence has remained homogeneous.

Violet (Japanese: *Murasaki*)

This is the most requested line because it is a widely used standard line in various fields of plant research, including plant physiology. It has large-size organs and shows acute sensitivity to daylength.



Standard Japanese morning glory lines. Tokyo Kokei Standard (TKS, left) and Violet (right).



Some of the morning glory lines with available whole genome sequencing information. Sequence comparisons have revealed the genes responsible for the mutations carried by these lines.

Contact

Core Center: Department of Biological Science,
Graduate School of Science, Kyushu University

Principal Investigator: Eiji Nitasaka

Email/URL: asagao@kyushu-u.org



Overview

Algae are an evolutionarily phylogenetically diverse group and are important primary producers in a variety of aquatic environments, including oceans, coasts, terrestrial waters and even extreme environments. The National Institute for Environmental Studies (NIES) provides diverse algae and protists covering 21 phyla and 77 classes, while Kobe University provides the major taxa of seaweeds. Our algal resources have been used as model organisms in photosynthesis research and a wide range of research fields such as environmental research, biomass utilization and the development of medicines.

Stock

- Microalgae and protists closely related to algae: about 2,800 strains
- Freshwater macroalgae, such as charophytes and more: about 300 strains
- Seaweed strains comprising red, brown and green algae: about 1,100 strains

Unique Features

NIES provides diverse groups of algal resources, most of which originate from Japan. The NIES collection also includes model organisms such as *Chlamydomonas*. Kobe University has the only culture collection in the world that specializes in seaweed.

Update and Maintenance Activities

Core and Sub-Core Centers

NIES, as a core center, and Kobe University, as a sub-core center, are working to cryopreserve the algal resources and share useful information related to these resources through international databases and social media.

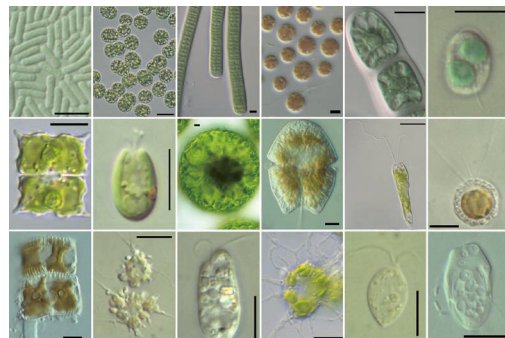
Hokkaido University, as a sub-core center, will continue to back up the core resources.

Popular Strains and Applications

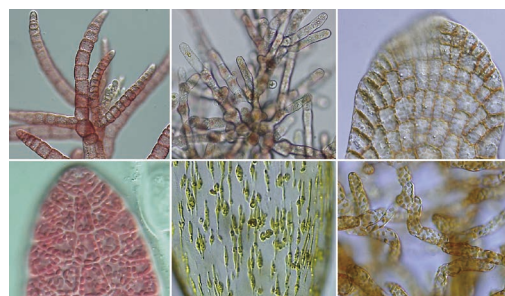
Well-known algal resources such as *Chlamydomonas* (NIES-2235), *Chlorella* (NIES-227), *Euglena* (NIES-48), and

Ectocarpus (KU-1372) have been used in various research fields because they have stable and good growth potential and are easy to handle experimentally. Many diversified algal resources have been used for many years in specific fields, such as research on algae-related environmental issues, ecotoxicology, and biomass research.

Successful whole-genome sequencing of some algae species has led to the wide use of these resources. Some examples are *Klebsormidium* (NIES-2285), which has plant hormones in common with land plants, and *Cyanidioschyzon* (NIES-3377), a hot-spring alga. We have recently seen a steady increase in the use of our resources, not only for algal biomass research, but also in more applied fields such as instrumentation and the development of medicines.



Light micrographs of various microalgal resources preserved and provided by NIES. Scale bars represent 10 μm .



Light micrographs of various seaweed resources preserved and provided by Kobe University.

Contact

Core Center: Biodiversity Division,
National Institute for Environmental Studies

Principal Investigator: Masanobu Kawachi

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Overview

Paramecium is one of the world's largest unicellular organisms. It is easy to culture and micromanipulate, making it a useful model organism of eukaryotic cells in a range of basic research studies, including those examining endosymbiosis, the natural host of pathogens, aging, motility, division, sexual cell recognition, learning, and water purification. In addition, the genome sequences of the macronucleus (vegetative nucleus) have been annotated for several species, and the range of genetic approaches available for *Paramecium* is increasing.

Stock

- 24 out of 33 species that can be collected in the field
- Standard strains: 3 species, 6 strains
- Strains recommended for use: 24 species, 63 strains
- Representative strains of syngens and mating types of *P. caudatum*: 15 strains

Unique Features

The NBRP is home to the only center in Asia that preserves and provides *Paramecium* resources. Our collection is one of the largest in the world and includes 24 species of *Paramecium* spp., syngens and mating types of *P. caudatum*.

Update and Maintenance Activities

Core Center

Yamaguchi University will continue to work on planned collection and progeny production, and the development and improvement of cryopreservation methods to sustain and add value to our resource.

Popular Strains and Applications

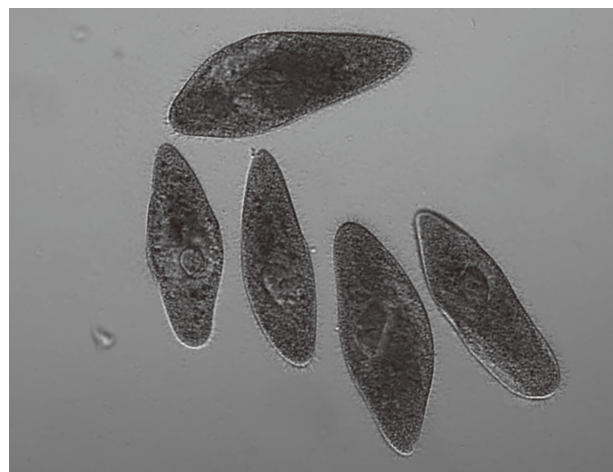
P. caudatum dKNZ-12E (PC122029A)

P. caudatum is used as a representative *Paramecium* strain because of its stable growth and phagocytic ability. It has been used in conjugation studies with the same syngen mating type O strain dKNZ-12O (PC121031A). This

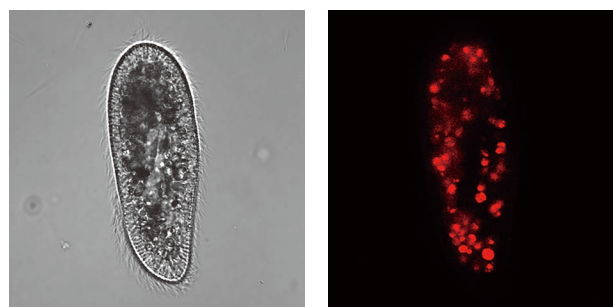
strain is also used as a natural host model for *Legionella*, an intracellular bacterium.

P. bursaria Yad1g1N (PB031010B)

P. bursaria harbors symbiotic *Chlorella* inside its cells (secondary symbiosis: intracellular symbiosis between eukaryotic cells). A comparative analysis of the genes expressed between the *Chlorella* symbiotic strain Yad1g1N and the alga-free strain led to the identification of multiple genes involved in secondary symbiosis.



Standard *Paramecium* (*Paramecium caudatum*).



Paramecium bursaria. Symbiotic *Chlorella* autofluoresce as red granules.

Contact

Core Center: Joint Faculty of Veterinary Medicine,
Yamaguchi University

Principal Investigator: Masahisa Watarai

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Cellular slime molds



Overview

Cellular slime molds are eukaryotic unicellular soil amoebae that feed on bacteria and, upon starvation, aggregate to become multicellular and form fruiting bodies composed of a spore mass and a stalk. They have been used as a model organism in cytology, embryology, and mathematical biology, and are also attracting attention as a novel drug discovery resource. Genome-edited strains can be easily produced, and a wide variety of expression vectors are available.

Stock

- Genetically mutated or transformed lines: about 1,600 strains
- Wild strains collected from around the world: about 450 strains
- Gene disruption vectors, expression vectors: about 980 vectors

Unique Features

The NBRP is home to one of only two cellular slime mold resource centers in the world and the only one based in Asia. We are the only institution that stores and provides genome-edited vectors and genome-edited strains.

Update and Maintenance Activities

Core Center

The University of Tsukuba will endeavor to improve our training courses and expand our collection to raise international recognition, improve user experience, and the number of users.

Popular Strains and Applications

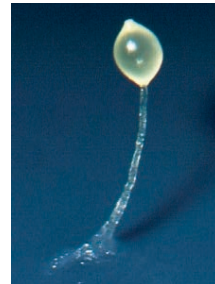
Strains AX2, KAX3, and AX4 of *Dictyostelium discoideum*

Dictyostelium discoideum is the most commonly used standard species for cellular slime mold research worldwide. The standard strains AX2, KAX3, and AX4 can be cultured without bacteria and have whole genome data available. Research studies focusing on

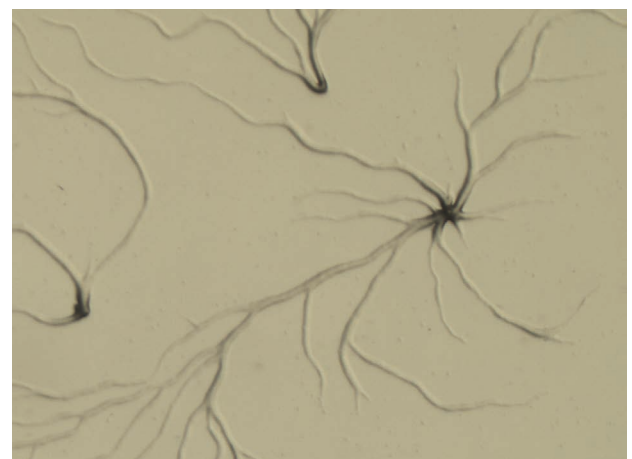
the functional analysis of genes at the genome level have been conducted on all of these standard strains.

Genome Editing Vectors (pTM Vector Series)

As cellular slime molds are hemizygotes, analysis of gene function using genome modification is straightforward in these organisms. In addition, the high efficiency of gene transfer also makes it feasible to produce the desired genome-edited strains. Studies have used these genome editing vectors to examine the molecular functions of various genes.



The fruiting body of *Dictyostelium discoideum*. After 24 hours under starvation conditions, the cellular slime molds form a fruiting body.



Cellular slime mold (*Dictyostelium discoideum*) in the aggregation phase. Cells form aggregates about 10 hours after being starved.

Contact

Core Center: Institute of Life and Environmental Sciences, University of Tsukuba

Principal Investigator: Hidekazu Kuwayama

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MICROBES

Mushrooms

Overview

Mushrooms are used in a variety of fields. For example, they are widely used as traditional herbal medicines and as bioremediation agents to exploit their specific decomposing enzymes. Mushrooms are promising resources for medicines, pesticides, and other products, and may be a source of novel bioactive compounds that differ from those produced by molds and other microbes.

Stock

Our strains belong to diverse ecological groups including wood decomposing, mycorrhizal, edible, and poisonous mushrooms.

- Wild mushrooms collected mainly in Japan:
8,579 strains of 1,768 species belonging to 586 genera (as of March 2024)

Unique Features

NBRP's Tottori University Fungal Culture Collection (TUFC) is one of the largest mushroom culture collections in the world. We have several strains of wood decomposers including agaricoids, corticioids, polyporoids, and auriculoids. We also have various rare mycorrhizal strains, whose isolation, cultivation, and preservation are difficult.

Update and Maintenance Activities

Core Center

Tottori University hopes to raise the profile of its resource center and improve user experience. The university will also engage in publicity activities and continue to update its strain database.

Popular Strains and Applications

TUFC contains wild strains of edible mushrooms, such as "Shiitake" and "Matsutake", and industrially useful strains that produce lignin or cellulose decomposing enzymes, ecologically important or rare species and taxonomically important ex-type strains. The use of these strains in both basic and applied research has generated many patents and scientific papers in the fields of medical and

agricultural sciences. Some examples are listed below.

Neolentinus lepideus "Matsuouji" (TUFC 31432)

Culture extracts of this strain contain novel tyrosinase inhibitors that are a useful skin whitening agent (Patent number: JP7054156).

Phlebia tremellosa "Siwatake" (TUFC 11737)

Culture extracts of this strain contain novel tyrosinase inhibitors that are a useful skin whitening agent (Patent number: JP7054156).

Daedalea dickinsii "Hourokutake" (TUFC 31876)

Culture extracts of this strain contain growth inhibitors against *Helicobacter pylori* and *Campylobacter jejuni* (Patent application number: 2019-208982).



Preparation of cryotubes containing mycelial samples.



Cultivation of *Gymnopilus junonius*.

Contact

Core Center: Fungus/Mushroom Resource and Research Center, Faculty of Agriculture, Tottori University

Principal Investigator: Tsuyoshi Ichiyanagi

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Overview

Yeast is a major model organism in life sciences. Various experimental methods and research resources have been developed for yeast for genetic, biochemical, and molecular biology studies, including recombinant DNA technology. Yeast research has contributed to our understanding of many molecular mechanisms important for life, including those involved in the cell cycle and autophagy. Because of the availability of a comprehensive range of genomic, transcriptomic, proteomic, and other -omic information, yeast research is expected to play a leading role in post-genome research.

Stock

- Fission yeast strains: about 18,000 strains
- Fission yeast plasmids: about 60,000 clones
- Budding yeast strains: about 20,000 strains
- Budding yeast plasmids: about 7,000 clones

Unique Features

The NBRP is the only resource center in the world to have large-scale fission yeast resources and original budding yeast resources created mainly by Japanese researchers.

Update and Maintenance Activities

Core Center

Osaka Metropolitan University will continue to collect, preserve, and provide fission yeast.

Sub-Core Centers

Hiroshima Institute of Technology will continue to collect, preserve, and provide budding yeast. Hiroshima University will continue to preserve the resource for backup purposes.

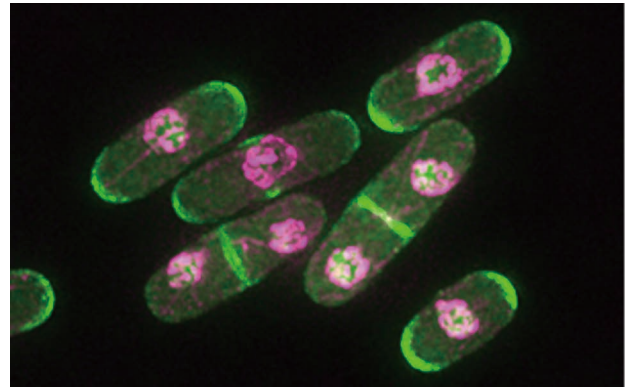
Popular Strains and Applications

Fission yeast GFP-fusion gene expression strains

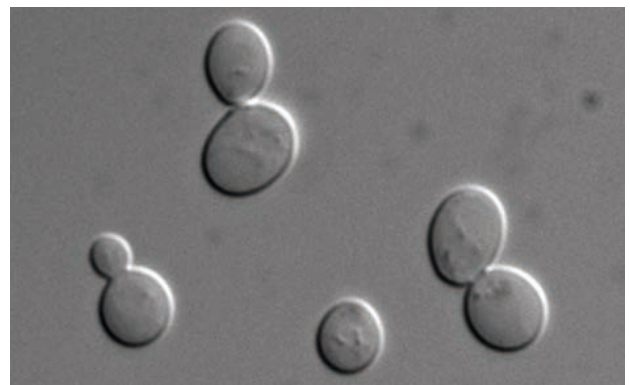
This is a set of fission yeast strains (about 1,000 strains) in which each gene is chromosomally tagged with GFP. These strains can be used to observe the subcellular localization of a protein of interest and is very useful for analyzing protein function. We receive many requests for these strains.

Auxin-inducible degron system (about 100 resources)

Auxin-inducible degron (AID) technology, which was originally developed by Japanese researchers, is a unique protein knockdown system that enables a protein of interest to be depleted in a half-life of less than 30 minutes simply by adding auxin to the culture medium. Since the AID system is the most effective tool for *in vivo* protein knockdown, AID is an in-demand technology for studying the function of essential genes and in drug discovery research.



Fluorescence micrograph of the fission yeast *Schizosaccharomyces pombe* (Image courtesy of Dr. Masashi Yukawa, Hiroshima University).



A differential interference contrast image of the budding yeast *Saccharomyces cerevisiae*.

Contact

Core Center: Yeast Genetic Resource Center, Graduate School of Science, Osaka Metropolitan University

Principal Investigator: Taro Nakamura

Email/URL: contactus-yeast@shigen.info



Overview

The Japan Collection of Microorganisms (JCM) provides diverse microbial strains of bacteria, archaea, yeast, and filamentous fungi. Our operations are certified by the quality management ISO 9001 system, and we will continue to ensure the high credibility of our resources and services. We also provide highly valuable microbial strains that have been reported in scientific publications. JCM strains are widely used and contribute to a variety of research fields related to environmental and health science as well as general microbiology.

Stock

- Bacteria: about 22,000 strains
- Archaea: about 1,100 strains
- Fungi: about 9,100 strains
- Type or type-derived strains: about 10,500 strains

Unique Features

JCM has one of the world's largest number of prokaryotic and yeast type strains. All available type strains are well characterized. We receive deposits of a large number of strains corresponding to novel species annually from both domestic and overseas researchers.

Update and Maintenance Activities

Core Center

JCM will maintain reliable quality of our microbial strains and will continue to update genome sequencing data to add value to our strains.

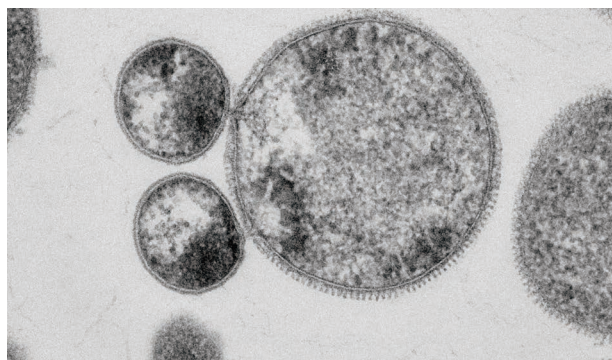
Popular Strains and Applications

Archaea and extremophile strains

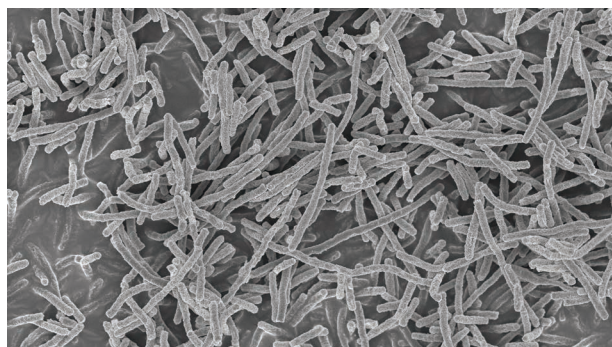
These strains inhabit various environments on Earth and are actively used in studies to understand specific environments, the evolution of life, their unique metabolism, and in applied science, such as investigations of thermophilic enzymes. We have one of the world's largest number of archaeal and extremophile strains, including those that are very difficult to cultivate and not available from other resource centers.

Commensal bacterial strains of humans and other animals

Commensal bacteria in the gut, oral cavity, and skin, and lactic acid bacteria and/or bifidobacteria have a significant impact on our health. The strains we provide are used for a variety of studies, such as the investigation of their effects on immune function, prevention of disease, obesity, and beauty. Many of these strains are anaerobes and a large number are unique commensal strains available only in JCM.



The nanoarchaeal strain *Nanobdella aerobiophila* JCM 33616 (left, two small cells) associated with the cell surface of the host archaeal strain *Metallosphaera sedula* JCM 33617 (middle, large cell).



Legionella pneumophila subsp. *pneumophila* JCM 7571, an isolate from human lung.

Contact

Core Center: Microbe Division/Japan Collection of Microorganisms, RIKEN BioResource Research Center

Principal Investigator: Moriya Ohkuma

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Prokaryotes

(*Escherichia coli*, *Bacillus subtilis*)



Overview

There is a wealth of available biological knowledge on and experimental methods for *E. coli* and *B. subtilis*. As a result, a number of extremely important *E. coli* and *B. subtilis* resources exist. Among these is the KEIO collection, a set of single gene knockout mutants of *E. coli*, and the BKE library of *B. subtilis*, the contents of which are recognized as international standards for genetic analyses of Gram-positive and Gram-negative bacteria. Bioresources for both *E. coli* and *B. subtilis* are important for advancing science and technology in both medical and industrial fields.

Stock

- Original collection of mutant strains
- Single gene knockout collection (*E. coli* KEIO and *B. subtilis* BKE collections)
- Large-scale chromosomal deletion mutants (KHK collection)
- Gene clone collection (ASKA strains)
- Cloning and expression vectors (467 vectors)

Unique Features

The NBRP provides *E. coli* K12 derivatives and *B. subtilis* 168 derivatives to researchers worldwide who work in the life science field. Collections of single gene knockouts of *E. coli* and *B. subtilis* are also available. Each collection comprises approximately 4,000 strains.

Update and Maintenance Activities

Core Center

The National Institute of Genetics will continue to collect, preserve, and provide *E. coli* and *B. subtilis* strains, and perform whole genome sequencing of these strains to validate their genotype.

Sub-Core Center

Kyushu University will continue to preserve bioresources for backup purposes.

Popular Strains and Applications

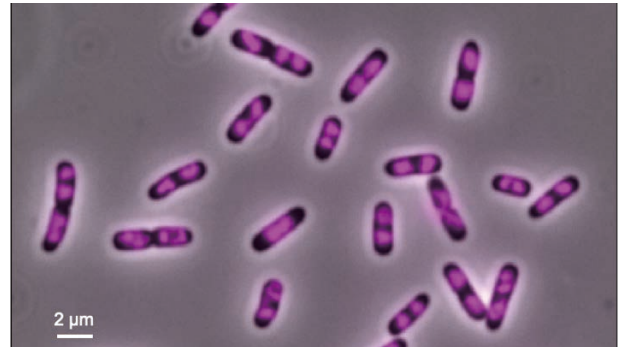
iVEC strains (ME9806)

The *E. coli* iVEC strain is amenable to seamless cloning, a

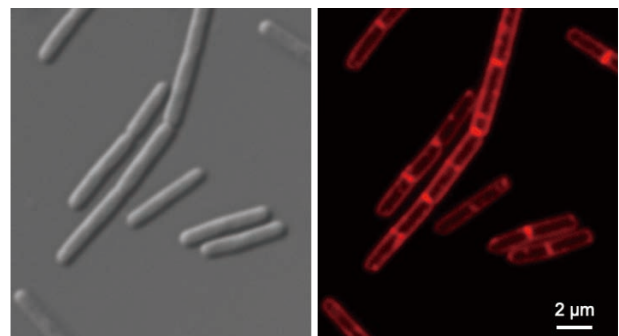
recent technology that has become popular because it is inexpensive, easy to use, and convenient. This resource contributes to prokaryote research and also to various life science fields.

KEIO collection and BKE library

These are collections of single gene knockouts of *E. coli* and *B. subtilis*, respectively. We offer individual strains or the whole set. These resources can be used for comprehensive screening, functional analysis of a gene of interest, or to produce functional biomaterials.



E. coli cells. A phase contrast image showing nucleoids stained with DAPI (magenta).



B. subtilis cells. (Left) Differential interference image. (Right) Cell membrane stained with FM4-64.

Contact

Core Center: Department of Gene Function and Phenomics, National Institute of Genetics

Principal Investigator: Hironori Niki

Email/URL: genkaku@nig.ac.jp

Pathogenic eukaryotic microbes



Overview

The pathogenic eukaryotic microbe collection at the NBRP consists mainly of reference strains for major pathogenic fungi and actinomycetes and clinical strains. These strains are widely used to evaluate new drugs, to elucidate antifungal resistance mechanisms, and to discover useful substances. We also provide more than 40 pathogenic protozoa species. These are used to establish infectious animal models, evaluate the quality, safety and effectiveness of drugs, study parasitic mechanisms and as positive controls in clinical tests.

Stock

- Fresh clinical isolates of fungi, highly pathogenic fungi species and major mycosis-causing fungi: about 16,000 strains
- Standard and clinical strains of pathogenic actinomycetes, mainly of the *Nocardia* genus: about 2,800 strains
- Pathogenic protozoa: about 380 strains

Unique Features

The NBRP has the highest quality and largest number of clinical isolates of pathogenic fungi and actinomycetes among the bioresource centers around the world. We have also preserved more than 40 protozoan species. In particular, we boast the largest number of *Trypanosoma cruzi* strains in the world.

Update and Maintenance Activities

Core Center

Chiba University will continue to collect and provide clinical strains and drug-resistant information.

Sub-Core Center

Nagasaki University will continue to collect transgenic protozoa and hybridoma cells that produce anti-pathogenic protozoan antibodies.

Popular Strains and Applications

Azole drug-resistant *Aspergillus fumigatus* and terbinafine-resistant *Trichophyton* spp.

The emergence of drug-resistant fungi has become a

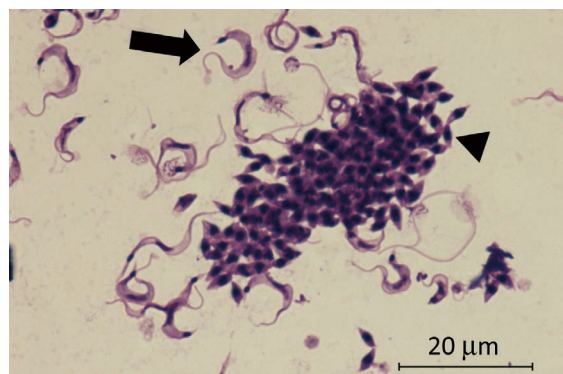
major problem in recent years. These resistant strains are used to elucidate the genes involved in resistance and the mechanisms of resistance by comparing resistant and susceptible strains isolated from clinical isolates.

Luciferase-expressing strains of *Trypanosoma cruzi* (Tc143–Tc147)

We provide five luciferase-expressing strains generated from different origins. *Trypanosoma cruzi* is a protozoan parasite that causes Chagas disease. It is difficult to detect at the intracellular parasitism stage in the host. Luciferase-expressing strains can be detected through luciferase activity.



Aspergillus fumigatus. Typical fungal species that causes mycoses.



Trypanosoma cruzi. Giemsa staining of trypomastigotes (arrow) and amastigotes (arrowhead) cultured *in vitro*.

Contact

Core Center: Medical Mycology Research Center, Chiba University

Principal Investigator: Takashi Yaguchi

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protozoa@tm.nagasaki-u.ac.jp

Pathogenic bacteria



Overview

There is no end to humankind's fight against infectious diseases, which can be life-threatening and significantly reduce quality of life in later life. However, it can be difficult for university researchers and companies to obtain pathogenic bacteria to study pathogenic mechanisms, develop therapeutic and diagnostic agents, and examine the pathogenic bacteria themselves. The NBRP conserves and provides a wide variety of pathogenic bacteria for research purposes.

Stock

- Pathogenic bacteria that cause opportunistic infection; biosafety level 3; class II, III, and IV pathogens under the Infectious Diseases Control Law; non-pathogenic bacteria related to these pathogens: about 6,700 strains
- Human enteropathogenic bacteria including *Vibrio parahaemolyticus*, *V. cholerae*, and Shiga toxin-producing *Escherichia coli* (about 12,000 strains in total): 1,286 strains

Unique Features

NBRP Pathogenic Bacteria is home to the only resource center in Japan with about 350 genera of bacteria, including specific pathogens and pathogens of rare infectious diseases. We also have a rich collection of wild strains of respiratory infectious and enteropathogenic bacteria.

Update and Maintenance Activities

Core Center

Gifu University will revamp the resource website and catalog database to improve visibility and user experience.

Sub-Core Center

Osaka University will continue to analyze the genomes of the strains in our culture collection.

Popular Strains and Applications

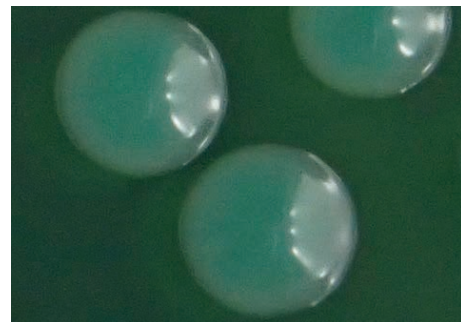
Human enteropathogenic bacteria

Vibrio parahaemolyticus and enterohemorrhagic *Escherichia coli* isolated from outbreaks of foodborne diseases in Japan are frequently requested and used for

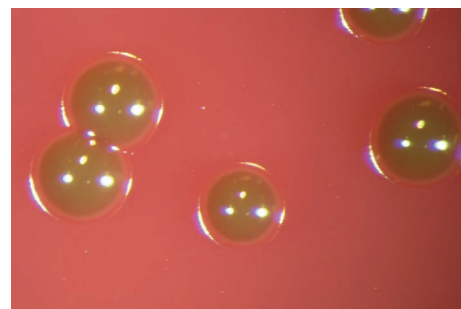
research into pathogenic mechanisms and gene marker and antigen analysis for pathogen detection. High-impact papers have been published using these strains.

Respiratory pathogens such as *Legionella* and mycobacteria, enteric infectious disease pathogens

Target bacterial species, species requiring discrimination from target bacterial species, and their related species are used to develop diagnostic methods and to test and verify new methods during the development of diagnostic agents and identification kits. These species are particularly essential for assessing the performance of methods for diagnosing infectious diseases that involve many pathogens and require prompt diagnosis.



Vibrio parahaemolyticus. This pathogen causes seafood-associated acute gastroenteritis.



Porphyromonas gingivalis. A red-complex bacteria that causes periodontitis also known to be associated with various chronic diseases.

Contact

Core Center: Center for Conservation of Microbial Genetic Resource, Institute for Advanced Study, Gifu University

Principal Investigator: Kaori Tanaka

Email/URL: g_cmr@gifu-u.ac.jp

Human pathogenic viruses



Overview

A few hundred virus species are thought to be pathogenic to humans. In addition, many novel viruses have been identified in the 21st century. Each species has a variety of strains that target different animal hosts, organs, tissues, and have different cell specificity, pathogenicity and antigenicity. A variety of these virus strains have been used to analyze virus pathogenicity, antigenicity and epidemiology, and to develop diagnostics and antivirals.

Stock

- Number of species: 31 species
- Wild and mutant strains: 1,642 strains
- cDNA clones: 27 clones

Unique Features

The NBRP has one of the largest number of influenza viruses, herpes simplex viruses, gastroenteritis viruses and arboviruses. We are the only facility that distributes human pathogenic virus strains in Japan.

Update and Maintenance Activities

Core Center

Nagasaki University will expand its collection and database, and engage in promotional activities to increase the number of requests for resources.

Sub-Core Centers

The University of Tokyo, Hokkaido University, Osaka University, and RIKEN will continue to diversify the collection and increase the number of requests for resources.

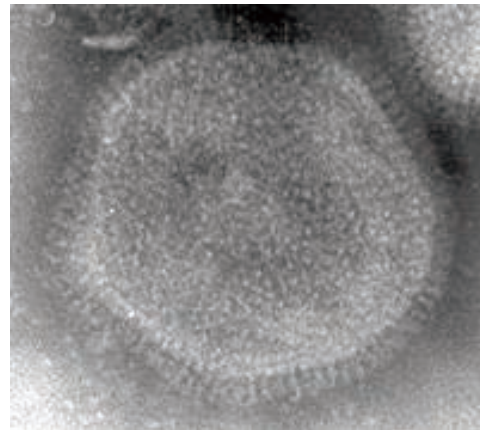
Popular Strains and Applications

SARS-CoV-2 strains

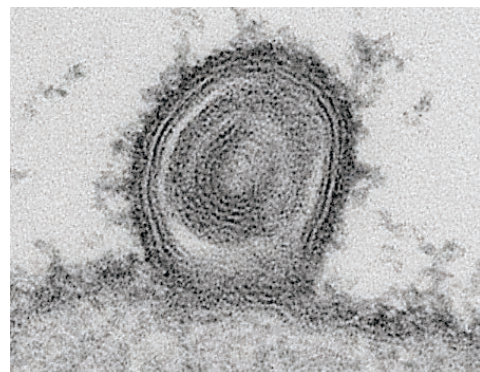
SARS-CoV-2 is the virus that causes COVID-19. We have isolated many SARS-CoV-2 strains from clinical specimens. Whole genome sequencing has been performed on most of these isolates. These resources have been used to analyze mechanisms involved in virus growth and pathogenicity, to study viral epidemiology, and to develop diagnostics and antivirals.

Influenza A virus strains

Influenza A virus is one of the most popular zoonotic viruses and is responsible for causing seasonal influenza each year. A new type of influenza virus emerges every few decades and causes an influenza pandemic. Our resources have been used to analyze the mechanisms involved in virus growth and pathogenicity, to study viral epidemiology, and to develop diagnostics and antivirals.



Influenza A virus. Two viral glycoproteins, HA and NA, can be seen on the virion surface.



Herpes simplex virus. Progeny virus can be seen budding from an infected cell.

Contact

Core Center: National Research Center for the Control and Prevention of Infectious Diseases,
Nagasaki University

Principal Investigator: Jiro Yasuda

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Overview

Cord blood (CB) contains an abundance of the most immature hematopoietic stem cells, and is widely used in medical and biological studies, including regenerative medicine, drug discovery, immunology, infection, and genetics research involving iPS cells. The NBRP provides researchers with quality-assured human CB samples that will contribute to the advancement of life science and medical research. The collected CB is processed into several frozen samples at The University of Tokyo's Cell Resource Center (IMSUT-CRC) and made available to researchers upon request.

Stock

- Frozen CB mononuclear cells (Small volume > 1×10^7 /tube)
- Frozen CB mononuclear cells (Large volume > 1×10^8 /bag)
- Frozen CB nucleated cells (> 3×10^8 /bag)
- Frozen CB CD34 positive cells (> 1×10^5 /tube)

Unique Features

CB contains the youngest human somatic stem cells of fetal origin. Frozen living cells, DNA, RNA, proteins, miRNA, exosomes and mitochondria can be extracted from CB.

Update and Maintenance Activities

Core Center

The University of Tokyo IMSUT Hospital will continue to collect CB from gynecology hospitals and process it into several types of frozen samples using aseptic techniques.

Sub-Core Center

The RIKEN BioResource Research Center will continue to provide various frozen CB materials collected by the University of Tokyo.

Popular Strains and Applications

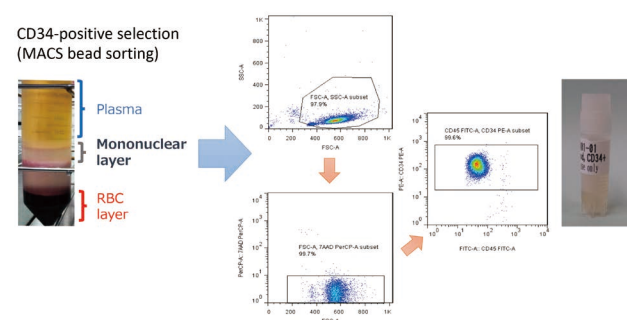
Frozen CB CD34-positive cells (CD34) (> 1×10^5 /tube)

These frozen CD34-positive cells were collected using magnetic beads (MACS) within 48 hours after delivery

of a baby. After thawing, one tube usually contains approximately 1×10^5 cells and more than 90% of the cells are CD34-positive. The CD34+ CB cells can be used for hematopoietic stem cell transplantation research and also regenerative research where the cells act as a source of iPS cells.

Frozen CB mononuclear cells (MNC) (Small volume > 1×10^7 /tube)

MNCs are the most experimentally accessible cells for researchers. These cells are useful for studies of immune cells such as T/B cells, macrophages, NK cells, Tregs, mast cells, and dendritic cells. MNCs can also be used to extract mitochondria, exosomes, and nucleic acids such as RNA under various conditions, and for genomic and proteomics research.



Frozen CD34-positive cord blood cells purified with magnetic beads (MACS). Cord blood cells are processed into mononuclear cells and sorted by selecting for CD34-positive cells (Purity >90%) and then frozen.

Contact

Core Center: IMSUT Hospital, The Institute of Medical Science, University of Tokyo

Principal Investigator: Tokiko Nagamura-Inoue

Email/URL: cellqa.brc@riken.jp



Human and animal cells

Overview

Cultured cells, particularly immortalized cell lines, are a common resource used by many researchers around the world. They can be cryopreserved and expanded, and can thus be used whenever necessary. They have been used in many basic and medical science applications, including as factories to produce proteins. Furthermore, somatic stem cells, embryonic stem (ES) cells, and induced pluripotent stem (iPS) cells are increasingly being used in the field of regenerative medicine as cell transplantation therapy.

Stock

- Human cell lines (e.g., cancer cell lines): about 4,600 lines
- Animal cell lines (e.g., mouse, rat): about 3,800 lines
- Human and animal ES cell lines: about 4,200 lines
- Human and animal iPS cell lines: about 1,500 lines
- Human disease-specific iPS cell lines: about 4,200 lines

Unique Features

Because iPS cell technology was developed in Japan by Dr. Shinya Yamanaka, many national projects in Japan provide financial support for research using iPS cells. As a result, the human disease-specific iPS cell bank at the RIKEN BioResource Research Center (BRC) is now the world's largest of its kind.

Update and Maintenance Activities

Core Center

The Cell Engineering Division at RIKEN BRC is planning to establish a "patient blood cell bank" that will contain a collection of blood cells from patients with various diseases.

Popular Strains and Applications

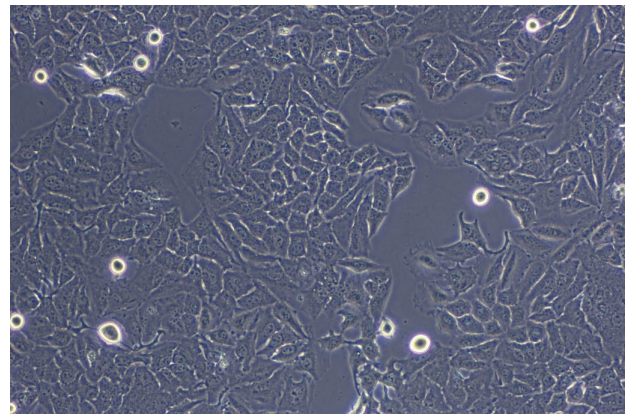
Human disease-specific iPS cells

It is impossible to extract brain cells from patients suffering from brain diseases. However, thanks to iPS technology, disease-specific iPS cells can be generated from a patient's blood cells and subsequently induced to differentiate into brain cells for use in basic research on the disease and drug discovery. iPS technology is driving

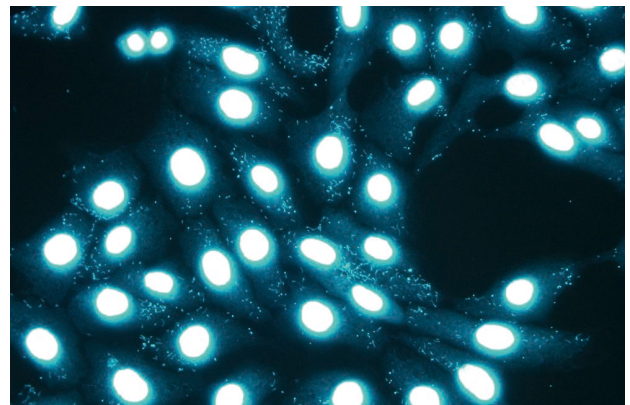
innovation in the field of disease research.

Human cancer cell lines

The HeLa cell line was generated in 1952 from cervical cancer cells, and is still used in many research studies today. Since HeLa, many other cancer cell lines have been generated around the world. Those cancer cell lines have contributed enormously to the basic sciences and medical sciences.



HeLa cells: the world's first cancer cell line. The line was derived from cervical cancer cells in 1952 and is still widely used in research today.



Mycoplasma test. Mycoplasma in infected cells is visualized as spots in the cytoplasmic area.

Contact

Core Center: Cell Engineering Division,
RIKEN BioResource Research Center

Principal Investigator: Yukio Nakamura

Email/URL: cellbank.brc@riken.jp



Overview

Genetic material such as plasmids, expression and reporter vectors and comprehensive clone sets of cDNAs and genomic DNAs are one of the most important and fundamental bioresources for life science research. Genetic material is now widely used in a variety of life science fields ranging from basic research aiming to analyze gene function and the mechanisms involved in regulating gene expression, to applied research studies to develop therapies and drugs and produce materials.

Stock

- Research tools for imaging and genome editing: about 3,400 items
- Human cDNA and genomic DNA clones: about 600,000 items
- Mouse cDNA and genomic DNA clones: about 350,000 items
- Animal cDNA and genomic DNA clones: about 1,030,000 items
- Genomic DNA of microorganisms and mouse strains from RIKEN BRC and more.

Unique Features

The RIKEN BioResource Research Center (BRC) is the only organization in Asia that actively collects, preserves and provides genetic material developed by researchers. We also provide large-scale clone sets produced by national projects.

Update and Maintenance Activities

Core Center

In response to rapid advancements in research methods, RIKEN BRC's Gene Engineering Division is planning to build a system that can quickly collect and provide new genetic material.

Popular Strains and Applications

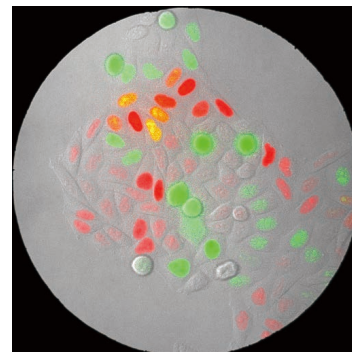
Imaging resources (fluorescence and luminescence)

We collect fluorescent proteins and luminescent enzymes from various organisms, and biological imaging resources developed based on these molecules with desirable properties such as high brightness and multicolored emissions. These resources are useful for studying

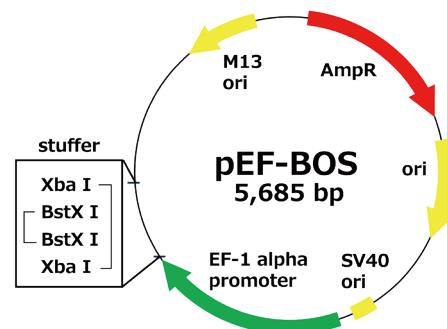
cellular responses to external stimuli because they enable the visualization of vital phenomena such as cell cycle phase and organelle behavior in real time.

Recombinant lentivirus vector plasmids

We have collected a large number of plasmids developed by the late Dr. Hiroyuki Miyoshi and related modified plasmids. These plasmids can be efficiently transferred into the genes of cultured cells and individual animals, and are used to study cancer and animal development. More than 420 papers have been published using the plasmids we supply.



Fucci-transfected cells. Fucci can be used in living cells to visualize cells that are in the G1 phase of the cell cycle in red, the G1/S phase in yellow, and the S/G2/M phase in green (Photo provided by Dr. Asako Sakaue-Sawano, RIKEN CBS).



The pEF-BOS vector. This is one of the plasmid vectors available from our institution. Regardless of the type of mammalian cell, this vector can strongly express the inserted gene in the host cell.

Contact

Core Center: Gene Engineering Division,
RIKEN BioResource Research Center

Principal Investigator: Yoshihiro Miwa

Email/URL: dnabank.brc@riken.jp



Overview

One of the biggest hurdles experienced by individuals who want to use biological/genetic resources is not knowing where and what kind of resources are available. The NBRP Information Center provides information on NBRP resources to researchers all over the world via the internet. We develop resource databases containing resource phenotype, genotype, and other related information, and search and order systems for these databases. We have also developed genome browsers for each resource and resource-related literature databases. Our aim is to create a comprehensive database of NBRP resources.

Services/Products

- Resource databases/websites: 25 organism species
- Organisms with publicly available genome information: about 10 species
- Comprehensive resource search: about 6.5 million items
- Resource-related literature database: about 50,000 items

Unique Features

The NBRP Information Center provides a one-stop service to locate and purchase desired bioresources. Based on open data and open access policies, we are making our databases and websites easy for anyone to access to ensure that all resource information is readily available.

Update and Maintenance Activities

The National Institute of Genetics plans to standardize all available information by converting all databases to RDF format to ensure the information can be used across organisms.

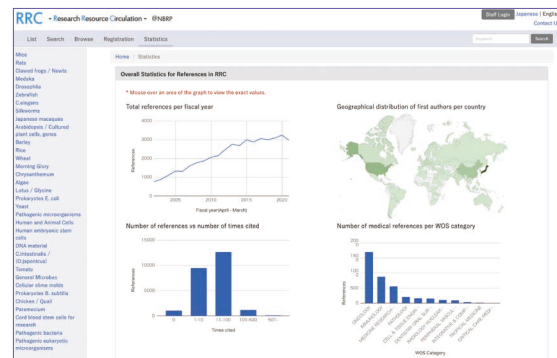
Popular Services/Products

Research Resource Circulation (RRC)

RRC is a database of published papers and patents that have used NBRP resources. Users can freely register the bibliographic information of any publications that have used NBRP resources.

Genome Information Service

In cooperation with the NBRP core and sub-core centers, we have developed a genome browser and homology/keyword search engine. The database that is linked to these tools contains the results of the NBRP Value Addition Program, including those for the following bioresources: Medaka (*Oryzias latipes*), *Xenopus*, mice, quails, rice, wheat, barley, morning glory, *Lotus japonicus*, *Escherichia coli* and *Bacillus subtilis*. We hope to expand on the genomic and other omics information in this database in the coming years.



RRC: a database of published papers that have used NBRP bioresources. The figure shows that NBRP bioresources have been used in a variety of research studies around the world.



Information Center Server System. Our server stores data on approximately 6.5 million bioresources.

Contact

Core Center: Department of Informatics,
National Institute of Genetics

Person in Charge: Shoko Kawamoto

Email/URL: <https://forms.gle/DKwethuRZFCfu77p6>

INFORMATION

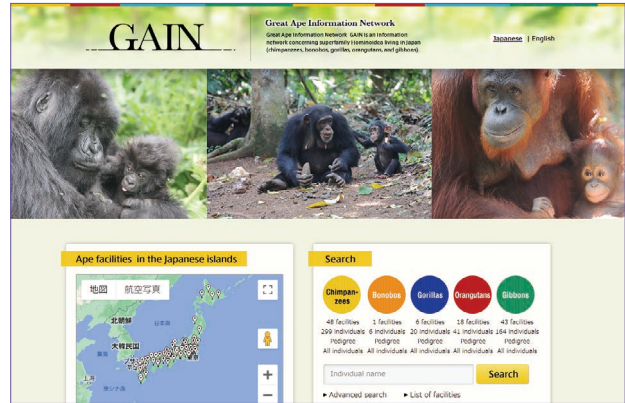
Great Ape Information Network (GAIN)



Overview

Apes, the most closely related animals to humans, are critical for academic research. However, all species of apes are endangered and research into these animals requires a variety of considerations. GAIN is building a database of all great and small apes (chimpanzees, bonobos, gorillas, orangutans and gibbons) kept in Japan. We collect and manage available information on non-invasive samples (such as those derived from dead bodies) and information on their background, family history, and genome, among other data, and make them available for shared use by researchers to promote academic research.

- Collect information on individual apes kept in zoos
- Manage real-time databases of information on individual apes
- Provide information on the availability of non-invasive samples
- Provide support for various procedures during sample collection



Contact

Core Center: Wildlife Research Center, Kyoto University
Person in Charge: Satoshi Hirata
Email/URL: gain-core@wrc.kyoto-u.ac.jp

Website: <https://gbif.jp/en>

INFORMATION

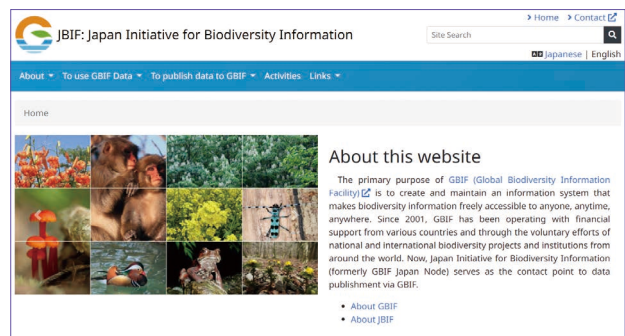
Japan Initiative for Biodiversity Information (JBIF)



Overview

Humans benefit from biodiversity in many aspects of our lives on Earth, ranging from our food, clothing, and shelter to economic activities. To maintain biodiversity, we need to know how it works and how to conserve it. JBIF (formerly GBIF Japan Node) is working to consolidate and disseminate information on biodiversity in Japan both domestically and internationally, to ensure that the information can be shared with the world and freely viewed and used by anyone.

- Release specimens/observation data through the GBIF/JBIF website
- Promote the use of biodiversity information
- Collaborate with museums and ecosystem observation networks
- Provide information on species names and promote DNA barcoding



Contact

Core Center/Sub-Core Center: National Museum of Nature and Science and National Institute for Environmental Studies
People in Charge: Utsugi Jinbo and Hiroya Yamano
Email/URL: <https://gbif.jp/en/contact>

INFORMATION

Access and Benefit-Sharing (ABS)



Overview

To access and use foreign genetic resources for research, it is important to abide by the relevant laws and regulations of the country providing the resources. Based on the Convention on Biological Diversity, the Nagoya Protocol on Access and Benefit-Sharing took effect in 2014 to regulate the sharing of benefits arising from the use of genetic resources between a provider country and a user country. The ABS support team provides a range of services to help researchers navigate the different laws and regulations among provider countries.

- Provide advice on ABS-related inquiries from researchers
- Provide ABS-related information and learning tools
- Organize workshops on ABS and other relevant rules
- Participate in relevant international conferences



Contact

Core Center: ABS Support Office, Research & Innovation Bridge Center, National Institute of Genetics
Person in Charge: Mutsuaki Suzuki
Email/URL: abs@nig.ac.jp

Website: <https://nbrp.jp/en>

INFORMATION

Public relations



Overview

The Public Relations team coordinates events and campaigns to encourage life science researchers to use the bioresources collected, preserved, and provided by the NBRP core and sub-core centers. We are also committed to raising awareness of the project among the general public, including students and young people. In doing so, we strive to connect the NBRP core and sub-core centers with our stakeholders.

- Coordinate exhibits
- Manage the NBRP website
- Create posters and brochures
- Organize events



Contact

Core Center: NBRP Public Relations Office, National Institute of Genetics
Person in Charge: Ayumi Koso
Email/URL: <https://forms.gle/DKwethuRZFCfu77p6>

Human resource development for promoting external verification of animal experimentation



Overview

The Fundamental Guidelines for the Conduct of Animal Experiments set forth by the Ministry of Education, Culture, Sports, Science and Technology (MEXT) requires that research institutions be socially transparent by undergoing external verification of animal experiments. To this end, the Human Resource Development for Promoting External Verification of Animal Experimentation project aims to promote and raise awareness of the external verification system for animal experiments. The NBRP is working to improve the verification system, increase the rate of external verification, and develop related educational materials.

Achievements

- Number of external verifier experts trained: 22 (in 2015) to 101 (in 2020)
- Total number of institutions that have undergone external verification: 111 (in 2015) to 237 (in 2020, including 14 institutions outside the jurisdiction of MEXT)
- Total number of external verifier participants: about 108

Unique Features

The NBRP holds briefing sessions and individual consultations for institutions that conduct animal experiments to support them through external verification inspections. By the 2020 academic year, a total of 704 institutions (1,286 individuals) had participated in our briefing sessions and 141 institutions had received individual consultations.

Update and Maintenance Activities

We will continue to support qualified external verification specialists and diversify our educational materials for institutions that conduct animal experiments.

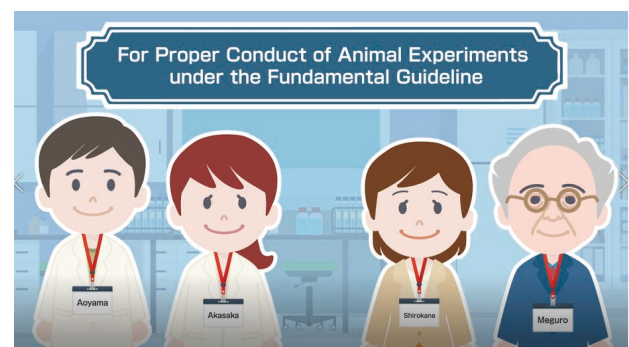
management take a course comprising our educational materials, and two mock written and on-site exams that use multiple simulation materials. We evaluate the reports and grant provisional qualification only to those who meet certain achievement criteria. After gaining additional work experience in external verification, the candidates are officially certified as verification specialists.

Educational support

We also support internal animal committee activities and education and training activities for institutions by, for example, distributing the free educational video "Animal Experiments are Managed by Institutions" in Japanese, English, and Chinese.



Participants receiving individual consultation for external verification.



The opening frame of the Animal Experiments are Managed by Institutions educational video in English.

Popular Services/Products

Hands-on training program for external verification specialists

Potential specialists with a wide range of experiences in animal experimentation and laboratory animal

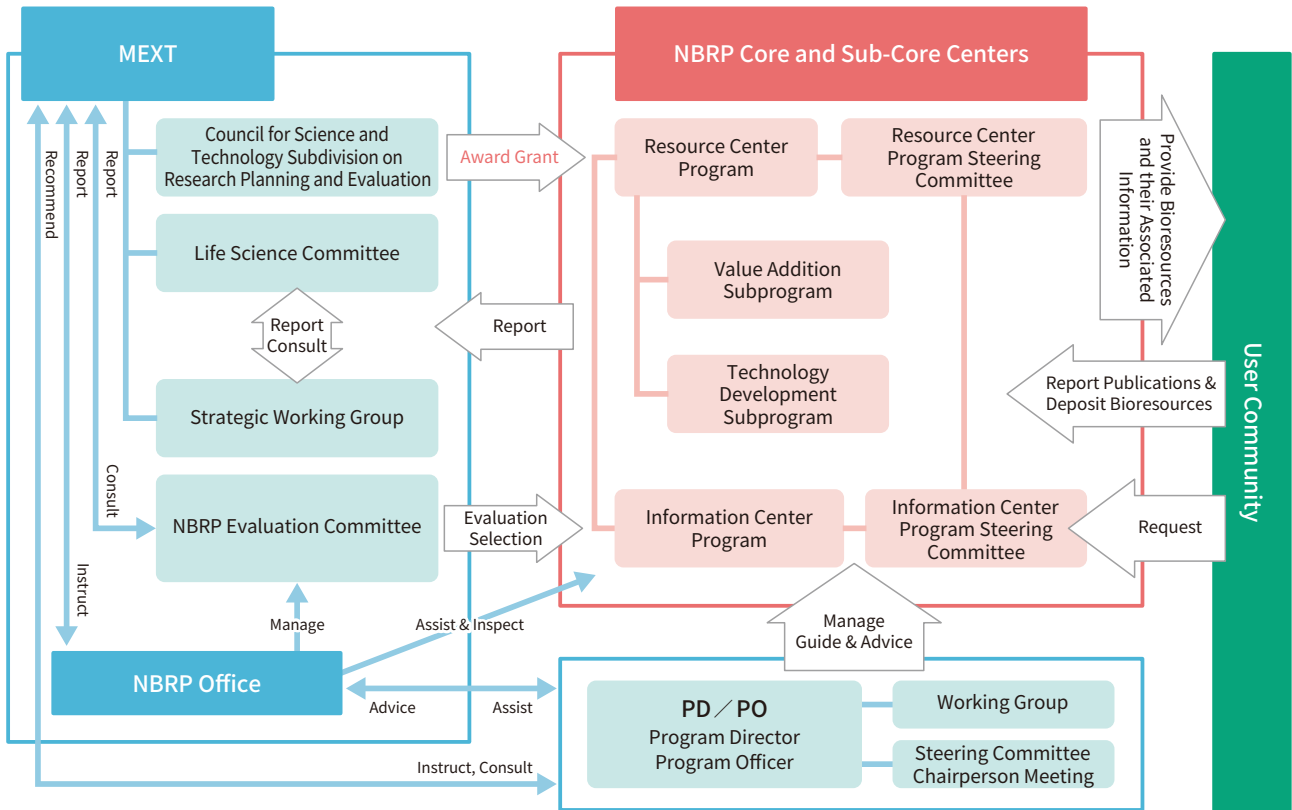
Contact

Core Center: Japanese Association for Laboratory Animal Science

Person in Charge: Chihiro Koshimoto

Email/URL: jinzaiikusei@jalas.jp

NBRP scheme



NBRP Program Director (PD)

The PD coordinates the operation of the project and facilitates the collaboration between the programs.

Name	Affiliation
Yuji Kohara	Director, Database Center for Life Science, Research Organization of Information and Systems

NBRP Program Officer (PO)

The POs assist the PD and facilitate the operation of the programs.

Name	Affiliation
Yuichi Obata	Honorary Scientist, RIKEN
Satoshi Tabata	Vice President / Director, Kazusa DNA Research Institute
Tetsuya Hayashi	Professor Emeritus, Kyushu University

List of NBRP organizations

Resource Center Program

Bioresource category	*	Principal Investigator	Organization name
Mice	○	Atsushi Yoshiki	Experimental Animal Division, RIKEN BioResource Research Center
Aged mice	○	Shigeharu Wakana	Department of Animal Experimentation, Foundation for Biomedical Research and Innovation at Kobe
Rats	○	Masahide Asano Tomoji Mashimo	Institute of Laboratory Animals, Graduate School of Medicine, Kyoto University The Institute of Medical Science, The University of Tokyo
	B	Atsushi Yoshiki	Experimental Animal Division, RIKEN BioResource Research Center
Japanese macaque	○	Katsuki Nakamura Masaki Isoda	Center for the Evolutionary Origins of Human Behavior, Kyoto University National Institute for Physiological Sciences, National Institutes of Natural Sciences
	○	Ken-ichi Nishijima Hiroyuki Horiuchi	Avian Bioscience Research Center, Graduate School of Bioagricultural Sciences, Nagoya University, Tokai National Higher Education and Research System Graduate School of Integrated Sciences for Life, Hiroshima University
Clawed frogs & Newts	○	Hajime Ogino Takashi Kato Haruki Ochi	Amphibian Research Center, Hiroshima University Faculty of Education and Integrated Arts and Sciences, Waseda University Institute for Promotion of Medical Science Research, School of Medicine, Yamagata University
	○	Hitoshi Okamoto Koichi Kawakami Shin-ichi Higashijima	RIKEN Center for Brain Science Department of Gene Function and Phenomics, National Institute of Genetics, Research Organization of Information and Systems National Institute for Basic Biology, National Institutes of Natural Sciences
	○	Kiyoshi Naruse Masaru Matsuda Shigehiro Kuraku Masatsugu Hashiguchi	Lab of Bioresources, National Institute for Basic Biology, National Institutes of Natural Sciences Center for Bioscience Research and Education, Utsunomiya University Department of Genomics and Evolutionary Biology, National Institute of Genetics, Research Organization of Information and Systems Faculty of Regional Innovation, University of Miyazaki
<i>Ciona intestinalis</i>	○	Yasunori Sasakura Yutaka Satou Manabu Yoshida	Shimoda Marine Research Center, University of Tsukuba Graduate School of Science, Kyoto University Misaki Marine Biological Station, Graduate School of Science, The University of Tokyo
	○	Kuniaki Saito Toshiyuki Takano Takeshi Awasaki	Department of Chromosome Science, National Institute of Genetics, Research Organization of Information and Systems Applied Biology, Kyoto Institute of Technology School of Medicine, Kyorin University
Silkworms	○	Tsuguru Fujii Zenta Kajiura	Institute of Genetic Resources, Graduate School of Bioresources and Bioenvironmental Science, Kyushu University Faculty of Textile Science and Technology, Shinshu University
	○	Sawako Yoshina	School of Medicine, Tokyo Women's Medical University
<i>Arabidopsis</i>	○	Masatomo Kobayashi	Experimental Plant Division, RIKEN BioResource Research Center
Rice	○	Yutaka Sato Takahiko Kubo	Department of Genomics and Evolutionary Biology, National Institute of Genetics, Research Organization of Information and Systems Faculty of Agriculture, Kyushu University
	○	Ryohei Terauchi	Graduate School of Agriculture, Kyoto University
Barley	○	Hiroshi Hisano	Institute of Plant Science and Resources, Okayama University
<i>Lotus japonicus & Glycine max</i>	○	Masatsugu Hashiguchi Shusei Sato	Faculty of Regional Innovation, University of Miyazaki Graduate School of Life Sciences, Tohoku University
	○	Hiroshi Ezura	Institute of Life and Environmental Sciences, University of Tsukuba
Tomatoes	○	Makoto Kusaba Michiharu Nakano	Graduate School of Integrated Sciences for Life, Hiroshima University Research and Education Faculty, Natural Sciences Cluster, Agriculture Unit, Kochi University

Bioresource category	*	Principal Investigator	Organization name
Morning glories	○	Eiji Nitasaka Atsushi Hoshino	Graduate School of Science, Kyushu University National Institute for Basic Biology, National Institutes of Natural Sciences
Algae	○	Masanobu Kawachi Shinya Uwai	Biodiversity Division, National Institute for Environmental Studies Kobe University Research Center for Inland Seas
	B	Kazuhiro Kogame	Faculty of Science, Hokkaido University
<i>Paramecium</i>	○	Masahisa Watarai	Joint Faculty of Veterinary Medicine, Yamaguchi University
Cellular slime molds	○	Hidekazu Kuwayama	Institute of Life and Environmental Sciences, University of Tsukuba
Mushrooms	○	Tsuyoshi Ichiyanagi	Fungus/Mushroom Resource and Research Center, Faculty of Agriculture, Tottori University
Yeast	○	Taro Nakamura Minetaka Sugiyama	Graduate School of Science, Osaka Metropolitan University Faculty of Life Sciences, Hiroshima Institute of Technology
	B	Kenji Kitamura	Natural Science Center for Basic Research and Development, Hiroshima University
General microbes	○	Moriya Ohkuma	Microbe Division/Japan Collection of Microorganisms, RIKEN BioResource Research Center
Prokaryotes (<i>E.coli</i> , <i>B. subtilis</i>)	○	Hironori Niki	Department of Gene Function and Phenomics, National Institute of Genetics, Research Organization of Information and Systems
	B	Tsutomu Katayama	Graduate School of Pharmaceutical Sciences, Kyushu University
Pathogenic eukaryotic microbes	○	Takashi Yaguchi Osamu Kaneko	Medical Mycology Research Center, Chiba University Institute of Tropical Medicine (NEKKEN), Nagasaki University
	○	Kaori Tanaka Tetsuya Iida	Center for Conservation of Microbial Genetic Resource, Institute for Advanced Study, Gifu University, Tokai National Higher Education and Research System Research Institute for Microbial Diseases, Osaka University
Pathogenic bacteria	B	Haruyoshi Tomita	Graduate School of Medicine, Gunma University
	○	Jiro Yasuda Keita Matsuno Yasushi Kawaguchi Takeshi Kobayashi Yoshihiro Miwa	National Research Center for the Control and Prevention of Infectious Diseases, Nagasaki University Research Center for Zoonosis Control, Hokkaido University Institute of Medical Science, The University of Tokyo Research Institute for Microbial Diseases, Osaka University Gene Engineering Division, RIKEN BioResource Research Center
Human pathogenic viruses	○	Tokiko Nagamura-Inoue Yukio Nakamura	Department of Cell Processing and Transfusion, IMUST Hospital, The Institute of Medical Science, The University of Tokyo Cell Engineering Division, RIKEN BioResource Research Center
	○	Yukio Nakamura	Cell Engineering Division, RIKEN BioResource Research Center
Human and animal cells	○	Yoshihiro Miwa	Gene Engineering Division, RIKEN BioResource Research Center

* ○ : Core Center None : Sub-Core Center B : Backup Facility (Sub-Core Center with backup purpose)

Information Center Program

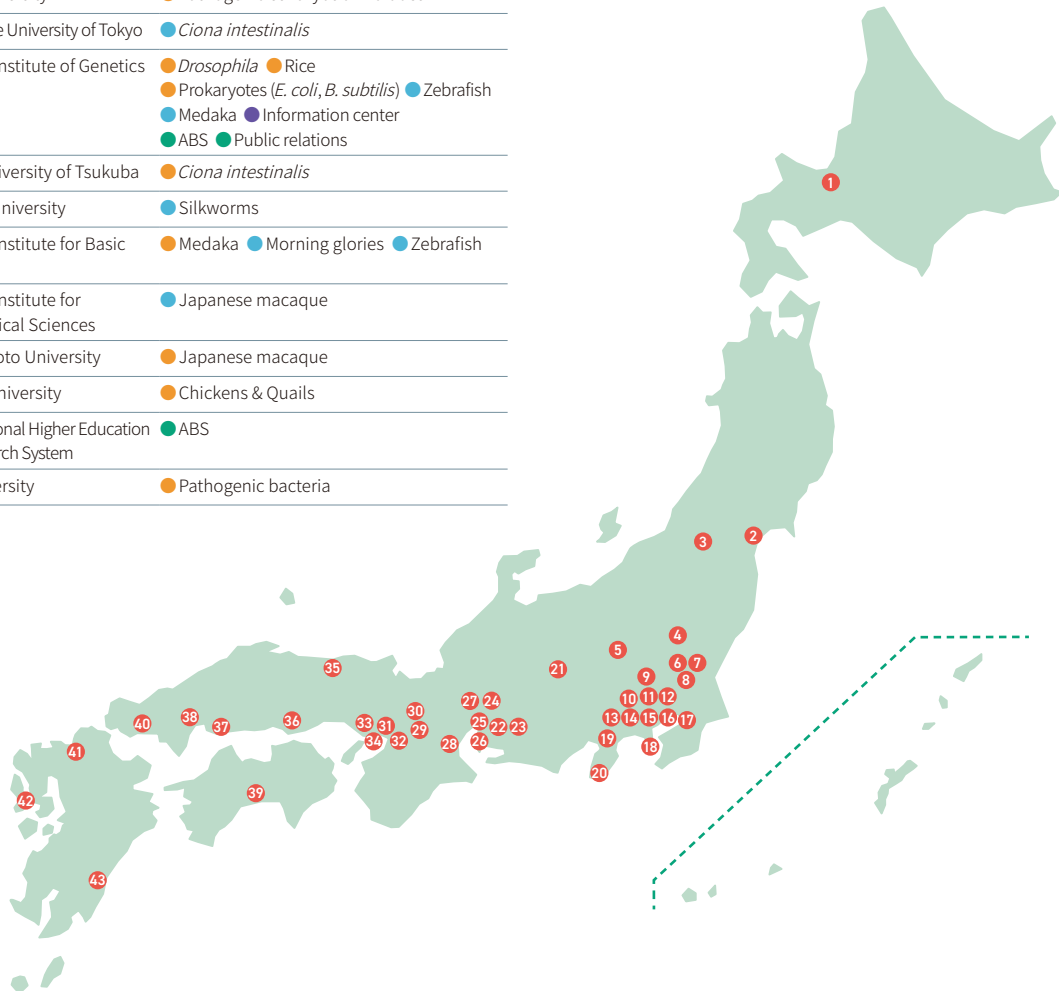
Category	*	Sub-category	Person in Charge	Organization name
Information	○	Information Center	Shoko Kawamoto	Department of Informatics, National Institute of Genetics, Research Organization of Information and Systems
		GAIN	Satoshi Hirata	Wildlife Research Center, Kyoto University
		JBIF	Utsugi Jinbo	Center for Collections, National Museum of Nature and Science
			Hiroya Yamano	Biodiversity Division, National Institute for Environmental Studies
		ABS	Mutsuaki Suzuki	ABS Support Office, Research & Innovation Bridge Center, National Institute of Genetics, Research Organization of Information and Systems
			Katsuyuki Eguchi	Graduate School of Science, Tokyo Metropolitan University
Ayako Ishikawa	Academic-Collaboration Risk Management Department, Academic Research & Industry-Academia-Government Collaboration Office, Tokai National Higher Education and Research System			
Mikihito Kanou Hiroya Yamano	Head Office for Research & Social Collaboration, Mie University Biodiversity Division, National Institute for Environmental Studies			
Public relations	Ayumi Koso	NBRP Public Relations Office, National Institute of Genetics, Research Organization of Information and Systems		
Human resource development for external verification of animal experiments	○		Chihiro Koshimoto	Japanese Association for Laboratory Animal Science

* ○ : Core Center None : Sub-Core Center

NBRP network of Japan (5th Phase)

1 Hokkaido University	Algae Human pathogenic viruses
2 Tohoku University	<i>Lotus japonicus</i> & <i>Glycine max</i>
3 Yamagata University	Clawed frogs & Newts
4 Utsunomiya University	Medaka
5 Gunma University	Pathogenic bacteria
6 University of Tsukuba	Tomatoes Cellular slime molds
7 NIES	Algae ABS JBIF
8 RIKEN BRC	Mice <i>Arabidopsis</i> General microbes Human and animal cells DNA-related materials Rats Human pathogenic viruses Human cord blood cells
9 RIKEN CBS	Zebrafish
10 Tokyo Metropolitan University	ABS
11 The University of Tokyo	Human cord blood cells Rats Human pathogenic viruses
12 Waseda University	Clawed frogs & Newts
13 Kyorin University	<i>Drosophila</i>
14 Tokyo Women's Medical University School of Medicine	<i>Caenorhabditis elegans</i>
15 JALAS	Human resource development for external verification of animal experiments
16 National Museum of Nature and Science	JBIF
17 Chiba University	Pathogenic eukaryotic microbes
18 MMBS, The University of Tokyo	<i>Ciona intestinalis</i>
19 National Institute of Genetics	<i>Drosophila</i> Rice Prokaryotes (<i>E. coli</i> , <i>B. subtilis</i>) Zebrafish Medaka Information center ABS Public relations
20 SMRC, University of Tsukuba	<i>Ciona intestinalis</i>
21 Shinshu University	Silkworms
22 National Institute for Basic Biology	Medaka Morning glories Zebrafish
23 National Institute for Physiological Sciences	Japanese macaque
24 EHUB, Kyoto University	Japanese macaque
25 Nagoya University	Chickens & Quails
26 Tokai National Higher Education and Research System	ABS
27 Gifu University	Pathogenic bacteria

Resource Center Program: ● Core Center ● Sub-Core Center	
Information Center Program: ● Core Center ● Sub-Core Center	
28 Mie University	ABS
29 Kyoto University	Rats Wheat <i>Ciona intestinalis</i> GAIN
30 Kyoto Institute of Technology	<i>Drosophila</i>
31 Osaka Metropolitan University	Yeast
32 Osaka University	Pathogenic bacteria Human pathogenic viruses
33 Kobe University	Algae
34 Foundation for Biomedical Research and Innovation at Kobe	Aged mice
35 Tottori University	Mushrooms
36 Okayama University	Barley
37 Hiroshima University	Clawed frogs & Newts Chrysanthemums Chickens & Quails Yeast
38 Hiroshima Institute of Technology	Yeast
39 Kochi University	Chrysanthemums
40 Yamaguchi University	<i>Paramecium</i>
41 Kyushu University	Silkworms Morning glories Rice Prokaryotes (<i>E. coli</i> , <i>B. subtilis</i>)
42 Nagasaki University	Human pathogenic viruses Pathogenic eukaryotic microbes
43 University of Miyazaki	<i>Lotus japonicus</i> & <i>Glycine max</i> Medaka



Contact

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