



BioResource now!

February 2005



BioResource now! No.2 is here

Ongoing monthly periodical

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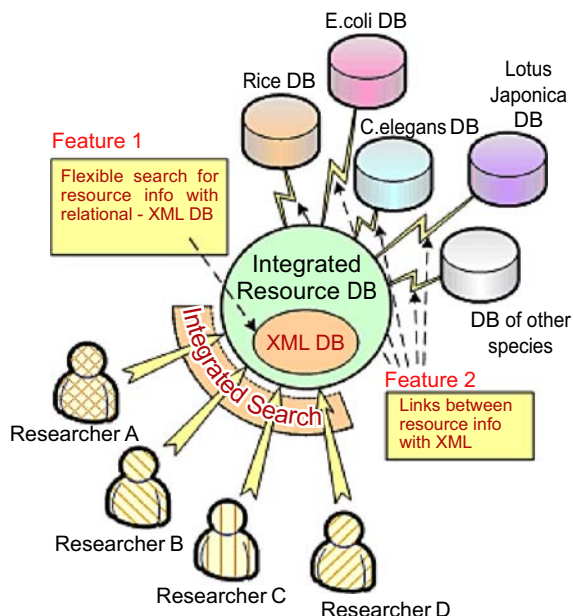
News from the Resource Center No.2

Database Integration Trial

1. Test Version of an Integrated Search System for Bioresource Was Released

As part of the National BioResource Project (NBRP), we released a test version of an integrated search system for bioresource called BioResource World (BRW) in July, 2004. Out of a total of 23 species maintained under NBRP, this system allows a comprehensive search for resource information on 19 species.

Previously, users looking for resource information had to search the resource database of each species separately but with this new system, one can carry out a comprehensive search from a single website, speeding up the time needed to obtain necessary resource information. This system has two distinctive features.



Structure of BRW System

Distinctive Features of this System

- 1** Flexible search for resource information made possible by relational - xml database

Research information with discrepancy between species is stored in XML format which enables flexible data structure. Meanwhile, common information carried by all species such as preservation information and availability for distribution, is stored as collections of tables. By storing data in formats tailored to the structure of the data, this system is flexible and is able to perform highly efficient searches.
- 2** Use of XML to link resource information between the integrated DB and the DB of each species

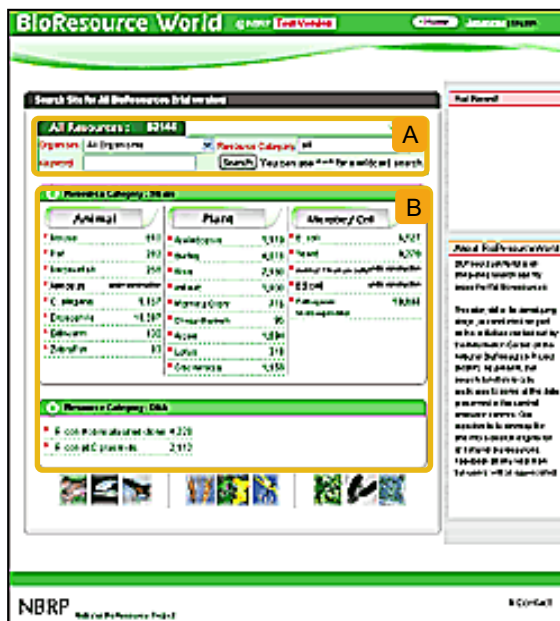
We implemented data association functions in XML format so that any updates performed on the resource information of any species in their respective databases will also be reflected in the integrated database.

We hope to develop a system that will be fully utilized by the users.

BRW (BioResource World)
<http://resourcedb.nbrp.jp/>

BRW (BioResource World)

- A** Integrated resource search system
- B** Types of resources and total count (strains/ DNA)



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<http://www.shigen.nig.ac.jp/shigen/news/news.jsp>



Resource Feature (Rice) No.1

Japan is one of the leading countries in the world in rice studies. Japanese researchers have long been conducting various studies in all matters concerning rice from fundamental researches such as biology and genetics, to breeding researches in attempts to produce rice that tastes good and is resistant to harsh weather. Moreover, the International Rice Genome Sequencing Project (IRGSP), an international effort that recently mapped the entire rice genome was based in Japan and lead by the Japanese team. Resources used in rice researches such as those mentioned are accumulated, preserved and managed by NBRP (National BioResource Project) rice resource institutions, the Rice Genome Resource Center (RGRC) and the NIAS (Ministry of Agriculture, Forestry and Fisheries) Genebank. Wild rice resources and experimental strains are accumulated, preserved and provided mainly by NBRP Rice; cultivated strains by NIAS Genebank; and cDNA clones, Tos17 lines and other genome resources are provided by the Rice Genome Resource Center. Table 1 shows the latest information about rice resources available in Japan and their corresponding resource centers.



● Wild rice cultivation in a greenhouse (NIG)

Table 1 : Rice resources and their centers

<p>● Wild Rice :</p> <ul style="list-style-type: none"> ◆ 1708 strains : NBRP Rice (National Institute of Genetics) ◆ Related Wild Rice : 1435 strains : NBRP Rice (Shizuoka University)
<p>● Rice Cultivars :</p> <ul style="list-style-type: none"> ◆ Native Rice Cultivars : 1963 strains : NBRP Rice (Shizuoka University) ◆ Rice Cultivars : 9083 strains : NIAS Genebank
<p>● Induced Mutation Lines :</p> <ul style="list-style-type: none"> ◆ MNU Induced Mutants : 471 strains : NBRP Rice (Kyushu University) ◆ Tos17 Mutant Line: approx.50000 strains : Rice Genome Resource Center
<p>● Experimental Strains Group :</p> <ul style="list-style-type: none"> ◆ Chromosome Substitution Lines, Reciprocal Translocation Lines, Recombinant Inbred Lines : 1608 strains : NBRP Rice (Kyushu University) ◆ Backcross Inbred Lines, Chromosome Segment Substitution Lines, etc : 668 lines : Rice Genome Resource Center
<p>● Full-length cDNA clones :</p> <ul style="list-style-type: none"> ◆ Full-length cDNA : approx.30000 clones : Rice Genome Resource Center

NBRP Rice <http://shigen.lab.nig.ac.jp/rice/oryzabase/>
 RGRC <http://www.rgrc.dna.affrc.go.jp/>
 NIAS Genebank <http://www.gene.affrc.go.jp/plant/>



● Controlling sunlight exposure with mobile short-day treatment devices (NIG)



● Distribution seeds kept in a freezer (NIG)

Information on rice resource related international websites and other miscellaneous information concerning rice is available at **WGR** (<http://shigen.lab.nig.ac.jp/wgr/>). At present, 54 rice related websites are registered with WGR. An online registration system is also available.



Information Technology

Vol. 2



“Contents of an Access Log”

In the previous issue entitled “What is an Access Log?”, I have mentioned that lots of information can be derived from an access log. In this issue, I will focus on the actual contents of an access log.

Although I am sure that most of you would have heard of “Apache” by now, let me explain briefly what it is. Apache is an open source WWW server software that runs on UNIX based servers. On the other hand, Microsoft’s “IIS” is commonly used as the web server for Windows platforms.

These WWW servers are equipped to store access information in the log whenever the website is accessed. Let us have a look at the actual contents of an access log.

```

1- 133.39.xx.xx - [01/Feb/2005:00:04:07 +0900] -- 2
3- "GET /shigen/grc/grc.jsp HTTP/1.1" 200 33639 "-"
4- "Mozilla/4.0 (compatible; MSIE 5.22;Mac_PowerPC)"
  
```

The illustration above shows the information recorded by the server in an access log when a particular webpage is accessed. This information is stored in a text file and can be viewed on editor programs. This is what the information stands for.



- 1 User's IP address
- 2 The time of access
- 3 The name of the file that was accessed
- 4 The type of web browser used

Based on this information, we can perform many tasks, for example increasing the popularity of a certain webpage or analyzing the usage of WWW browsers by users.

However, multiple logs are produced per access by a user resulting in a massive amount of data that would be difficult for the human eye to analyze. Therefore, a tool is needed to analyze this massive amount of access information and graphically display the analysis result.

In the next issue, I will introduce the tools used to analyze these access log information.

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Editor's notes: Similar to food which has its in season and off season, the demands of experimental bioresource will change with time. However, unlike food, even when a resource is in season, it isn't always released extensively. From the point of view of a resource center, I sometimes find this frustrating.

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