An Integrated Database and Web Service for Microbial Resources at KACC

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Abstract
The Korean Agricultural Culture Collection (KACC) has developed a web-based system to provide an integrated database with information updates about microbial resources. This integrated database consists of 5 major functions and contains general information, which includes identification numbers, culture media composition, image information, DNA sequences, patent information, and general forms for ordering and depositing microorganisms. In 2008, KACC started providing characterization information. KACC maintains 9,801 cultures of microorganisms, including 3,296 strains of bacteria, 4,734 fungi, 784 actinomycetes, 64 yeasts, and 923 others.

Keywords: KACC, microbial resource, integrated database, microorganism information

Introduction
Microbial resources are closely associated with our daily life, and their collection and utilization are very important. In terms of microbial resources, the value of a microorganism database depends on the amount, quality, and accuracy of the information that it contains. Microbial databases have been developed in various fields, including the IMG 2.3 (Victor et al., 2008), NMPDR (McNeil et al., 2007), and MBGD databases (Uchiyama et al., 2007). In line with the increase in the number of databases for microbial resources, various integrated web service systems have been constructed. BCCMTM (http://bccm.belspo.be/) consists of 4 complementary research-based service culture collections. This database maintains over 53,500 well-documented and authenticated strains of bacteria, filamentous and yeast fungi, over 950 plasmids, and 18 DNA libraries. KCTC (http://kctc.kribb.re.kr/) has a wide and systematic collection of materials that comprise microorganisms, animal and plant cell lines, and patent strains from domestic and international sources. UKNCC (http://www.ukncc.co.uk/) offers identification by a range of techniques for many organisms, including actinomycetes, algae, animal cells, arthropods, bacteria, filamentous fungi, nematodes, protozoa, mycoplasma, and yeast. JCM (http://www.jcm.riken.go.jp/) supplies authentic microorganisms to researchers in the fields of life sciences and biotechnology. JCM preserves 6,800 strains of bacteria, including actinomycetes, 280 strains of archaea, and 4,000 strains of fungi, including yeast.

In Korea, the Korean Agricultural Culture Collection (KACC, http://kacc.rda.go.kr/) serves as an authorized organizer and the official depository (NIAB, 2008) of microbial resources. KACC maintains microbial resources, including bacteria, actinomycetes, yeast, and filamentous fungi, and has developed a database of microbial resources (Chang et al., 2009). In order to collect microbial resources from international centers, KACC joined the World Federation for Culture Collection (WFCC), the World Data Center for Microorganism (WDCM), and the Asian Consortium for the Conservation and Sustainable Use of Microbial Resources (ACM). In 2008, KACC developed a web-based system to provide an integrated database, which contains updated information on microbial resources.

Methodology
Dataset
The database information was collected from the microorganism project (http://kacc.rda.go.kr/), the National Agrobiodiversity Center (NAC, http://genebank.rda.go.kr/), the National Academy of Agricultural Science (NAAS, http://www.niast.go.kr/), the Bio-Green 21 project (http://biogreen21.rda.go.kr/), relevant microorganism divisions of universities, and various institutes in Korea. In most instances, the strains were isolated from Korean agricultural environments, but some strains were shared with other culture collections. In addition, the database information was accumulated and maintained through several collaborating international institutes, such as the Centraalbureau voor Schimmelcultures (CBS, http://www,
Database design

The integrated database is designed to provide information on Korean microbial resources with a bio-database management system (Tae et al., 2008). The Entity Relation Diagram (ERD) of the database is shown in Fig. 1. The schema consists of 4 major functional categories. In the first category, a general characterization table shows the identification of microorganisms by TCSP_INFO table. The MGDTD table shows the process of registration for microorganisms, including Korean viruses, fungi, and others. The operating table and management table show the ordering and management process for microorganisms, patent strains, and gene clones. Using the collected information, a microbial resources database system was developed. The platform was developed using MYSQL and JAVA languages, and the data were stored in an Oracle Relational Database Management System (RDBMS). The logical and the physical schema of the database followed the standard principles of relational databases using by ERWin Data Modeler software (http://www.ca.com), and the data were distributed into numerous tables to establish the hierarchical relationships (Chang et al., 2008) between or among the datasets.

Database contents

The integrated database now maintains 9801 cultures of microorganisms, including 3296 strains of bacteria, 4,734 fungi, 784 actinomycetes, 64 yeasts, and 923 others (mushrooms, gene clones, etc.). In 2008, a total of 1,855 strains of new microbial resources were registered, including 616 isolates of bacteria, 950 isolates of fungus (including Basidomycetes), and 289 actinomycetes. In most instances, microorganisms are industrial bacteria, such as Lactobacillus, Bacillus, and Burkholderia. The database contains rare fungi, such as Cercospora, Septoria, and Ramularia, Table 1 shows the number of registered microbial resources by year.

Implementation and features

The integrated database provides various information, including text record, morphological images, and DNA
An Integrated Database of Microbial Resources

Table 1. The accumulated number of registered microbial resources at KACC, 2005-2008

<table>
<thead>
<tr>
<th>Year</th>
<th>Bacteria</th>
<th>Fungi</th>
<th>Actin.</th>
<th>Yeast</th>
<th>Others</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>~2005</td>
<td>1,587</td>
<td>2,674</td>
<td>386</td>
<td>64</td>
<td>893</td>
<td>5,604</td>
</tr>
<tr>
<td>2006</td>
<td>519</td>
<td>410</td>
<td>55</td>
<td>-</td>
<td>26</td>
<td>1,010</td>
</tr>
<tr>
<td>2007</td>
<td>574</td>
<td>700</td>
<td>54</td>
<td>-</td>
<td>4</td>
<td>1,332</td>
</tr>
<tr>
<td>2008</td>
<td>616</td>
<td>950</td>
<td>289</td>
<td>-</td>
<td>-</td>
<td>1,855</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td><strong>3,296</strong></td>
<td><strong>4,734</strong></td>
<td><strong>784</strong></td>
<td><strong>64</strong></td>
<td><strong>923</strong></td>
<td><strong>9,801</strong></td>
</tr>
</tbody>
</table>

Fig. 2. Search windows of the integrated database. The individual panels show the windows for searching microorganisms. (A) Web interface for keyword search by genus and species, (B) Web interface for alphabetical search by scientific names, (C) Web interface for searching gene clone by classification, (D) A media search window and report page with detailed information on a specific element name.
In addition, KACC provides a function for the ordering and depositing of microorganisms, including patent microorganisms or gene clones. Anyone with the basic knowledge and the facilities for culturing may order and deposit microorganisms. However, orders for personal purposes may not be accommodated. A user can order a strain in 3 steps: (i) search for a strain from the database; (ii) fill-in the order form, including the ‘Materials Transfer Agreement;’ and (iii) send the request form by postal mail or email. The patent menu has 3 major functions, such as those related to ordering, depositing, and regulations. Users can view different classification tables or specific forms by using the corresponding web forms.

Discussion

KACC classifies and preserves diverse Korean microbial resources including bacteria, yeasts, filamentous fungi, and mushrooms and provides an integrated database.

Table 2. The total number of microbial resources distributed to researchers, 2006-2008

<table>
<thead>
<tr>
<th>Year</th>
<th>Bacteria</th>
<th>Fungi</th>
<th>Actin.</th>
<th>Yeast</th>
<th>Others</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>2006</td>
<td>416</td>
<td>847</td>
<td>19</td>
<td>45</td>
<td>41</td>
<td>1,368</td>
</tr>
<tr>
<td>2007</td>
<td>639</td>
<td>660</td>
<td>51</td>
<td>20</td>
<td>48</td>
<td>1,411</td>
</tr>
<tr>
<td>2008</td>
<td>1,006</td>
<td>982</td>
<td>89</td>
<td>25</td>
<td>42</td>
<td>2,144</td>
</tr>
</tbody>
</table>

This integrated database contains general information, such as identification numbers, culture media composition, image information, DNA sequence, and general forms for ordering and depositing microorganisms. In 2008, KACC, which maintains 9,801 cultures of microorganisms, started providing characterization information. With this, the number of isolates that were distributed to researchers who are involved in microorganism-related industries increased to more than 2,100 in 2008 (Table 2).
References


