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The activity and integrated service for microbial resources at the Korean agricultural culture collection

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The Korean agricultural culture collection (KACC) has developed a web-based system to provide an integrated database about microbial resources containing 12,924 registered cultures of microorganisms. This system- service platform consists of three major functions, namely microorganism search, ordering and deposit. In 2009, we newly registered 3,039 microbial resources and distributed the 3,992 strains using this system. This system services a function to secure on the registration and distribution, and analysis platform to provide information for curated microbial resources by KACC.

Key words: Korean agricultural culture collection, microbial resources, integrated service, microorganism information.

INTRODUCTION

Microbial resources are often encountered in our daily lives. Microbes are also exploited in biotechnology, traditional food and beverage preparation, and genetic engineering. As a resource, the value of a central information service is dependent on the number of microorganisms represented in a database, as well as on the quality and accuracy of the information contained (Weinbauer et al., 2002). Microbial databases have been developed in various fields, including the IMG 2.3 (Markowitz et al., 2008), NMPDR (McNeil et al. 2007), and MBGD databases (Uchiyama et al., 2007). The Belgian Co-ordinated Collections of Micro-organisms (BCCM™, http://bccm.belspo.be/) database is divided into four collections consisting of well-documented and authenticated strains of bacteria, filamentous and yeast fungi, plasmids, and DNA libraries. The United Kingdom National Culture Collection (UKNCC, http://www.ukncc.co.uk/) enables users to search for numerous organisms, including actinomycetes, algae, animal cells, arthropods, bacteria, filamentous fungi, nematodes, protozoa, mycoplasma, and yeast, according to research method. The Japan Collection of Microorganisms (JCM, http://www.jcm.riken.go.jp/) holds information about various microorganisms, such as bacteria, archea, and fungi. MicrobesOnline (http://www.microbesonline.org) portal services information over 1,000 complete genomes of bacteria, archaea, and fungi, as well as thousands of expression microarrays from diverse organisms (Dehal et al., 2010). The Genomes Online Database (GOLD) is a repository for more than 5,800 sequencing projects, of which 1,100 are complete. In addition to these, there are 4,543 ongoing sequencing projects, of which 3,271 are bacterial, 110 are archaeal, and 1,162 are eukaryotic (Liolios et al., 2010). The Microbial Genome Database (MBGD) services a platform for microbial comparative genomics and contains nearly 1,000 genomes based on automated ortholog group identification (Uchiyama et al., 2010). In addition, microorganism collection centers have provided an integrated microbial database about collection strains of microorganisms. For instance, NITE Biological Research Center (NBRC, http://www.nbrc.nite.go.jp/), Centraalbureau voor Schimmelcultures (CBS, http://www.cbs.knaw.nl/), German Collection of Microorganisms and Cell Cultures (DSMZ, http://www.dsmz.de/), ARS Culture Collection

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(http://nrrl.ncaur.usda.gov/) and NIAS Genebank (http://www.gene.affrc.go.jp/) have provided integrated information about their collection strains of microorganisms.

The Korean Agricultural Culture Collection (KACC) maintains microbial resources and has provided a database of microbial resources since 1995 (Kim et al., 2009a, b). In 2010, we updated a web-based system that provides integrated information on microbial resources and services information about 12,924 microbial strains with registration and distribution process information.

MATERIALS AND METHODS

Dataset

The information in the database were collected from the microorganism project (http://www.genebank.go.kr/) of the National Academy of Agricultural Science (NAAS, http://www.naas.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, information were collected from several collaborating international institutes, such as the CBS in The Netherlands, the ARS culture collection in the United States, DSMZ in Germany, as well as the NIAS Genebank and NITE Biological Research Center in Japan. The total number of microbial strains registered in the KACC is 12,924, including 4,345 strains of bacteria; 966 actinomycetes; 5,399 fillamentous fungi; 64 yeasts; 1,425 mushrooms and; 725 other organisms. In 2009, a total of 3,039 strains of new microbial resources were registered at the KACC, including 1,049 isolates of bacteria; 581 isolates of fungus; 182 actinomycetes and; 1,204 mushrooms.

Database design

The various integrated databases have been designed to provide information on microbial resources with a bio-database management system (Tae et al., 2008), identification of phenotype and genotype (Esma et al., 2009) and biotechnology tools (Manal et al., 2009). Using the collected information, we developed a microbial resources database in the Oracle Relational Database Management System (RDBMS) using MYSQL and JAVA. The logical and physical schema of the database followed the standard principles of relational databases according to the ERWin Data Modeler Software (http://www.ca.com). The Entity Relation Diagram (ERD) of KACC database and a simplified view of the data model for registration of microorganisms are shown in Figure 1. A registration process of microorganism is designed specifically to get confidential data which constructs a verified database (Figure 1a). The schema consists of three major function categories (Figure 1b); (i) a general characterization table for the identification of microorganism by TCSP_INFO table; (ii) a registration table for microorganism, Korean virus, fungi and strains data of others by KFUNGI and VIRUS_VIRUS table and; (iii) an operating table which views an ordering and deposit process for microorganism. To improve accessibility and ease-of-use, an integrated database management system was developed. Data were distributed into numerous tables to establish hierarchical relationships between or among the datasets (Kim et al., 2009). Moreover, KACC developed a system which provides a service for order and deposit of microorganisms. In order to distribute our strains safety, this system has been verified by the three process steps. In the deposit, a user(s) must give a brief

description of the strain prior to sending the culture. When KACC finds the deposit acceptable, the depositor(s) will possibly asked to send the culture.

RESULTS AND DISCUSSION

Implementation and features

This new integrated resource service provides information on text record, morphological images, and DNA sequence data. The database platforms consist of three major functions, namely microorganism search, ordering and deposit. The search function enables searching by strain type according to genus and species names. This action can be performed using two methods. First, users can search using partial or complete species names from two classifications or six categories that are accessible by pull-down menus. To choose a specific classification or category menu, users may specify one submenu from the pull-down menu. Second, users can search an alphabetical listing of strains arranged according to their scientific names. Screenshots of results pages from the two different search methods are shown in Figure 2.

Following the query, a table is provided that displays detailed information, including the scientific name, synonym, media and temperature, literature, strains, the KACC number, the identifier number used in other collections, history, location and date of isolation, DNA sequence, and image record (Figure 2a). A user can obtain sequence information about a specific strain by clicking on the linked 'DNA sequence' object (Figure 2b). Furthermore, a user can access a detailed table of images by clicking on the thumbnail on the right (Figure 2c). In addition, by clicking on the 'Media' hyperlink, users can access information on the media composition required to culture a particular strain. When using the keyword or alphabetical search, users can query different identification names or historical classification fields by using the hierarchical tree web form. The query results are linked to each detailed table through their respective strain lists. The user can then view a report page and download the information, such as the DNA sequence and image of the microorganism. In addition, the KACC provides a function for ordering and depositing information about microorganisms, including patents or cloned genes.

Registration and distribution of microbial resources

The integrated database system of KACC provides a service for order and deposit of microorganisms. Anyone who wishes to make a request is expected to have a basic knowledge and proper facilities for culturing and preserving strains. However, individuals may not order cultures for personal purposes. Users can order a strain following these three steps: (i) search proper strain from
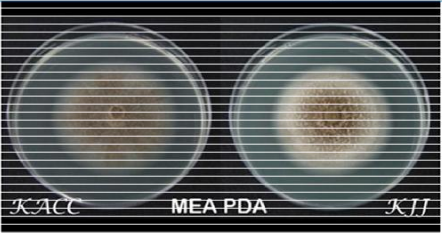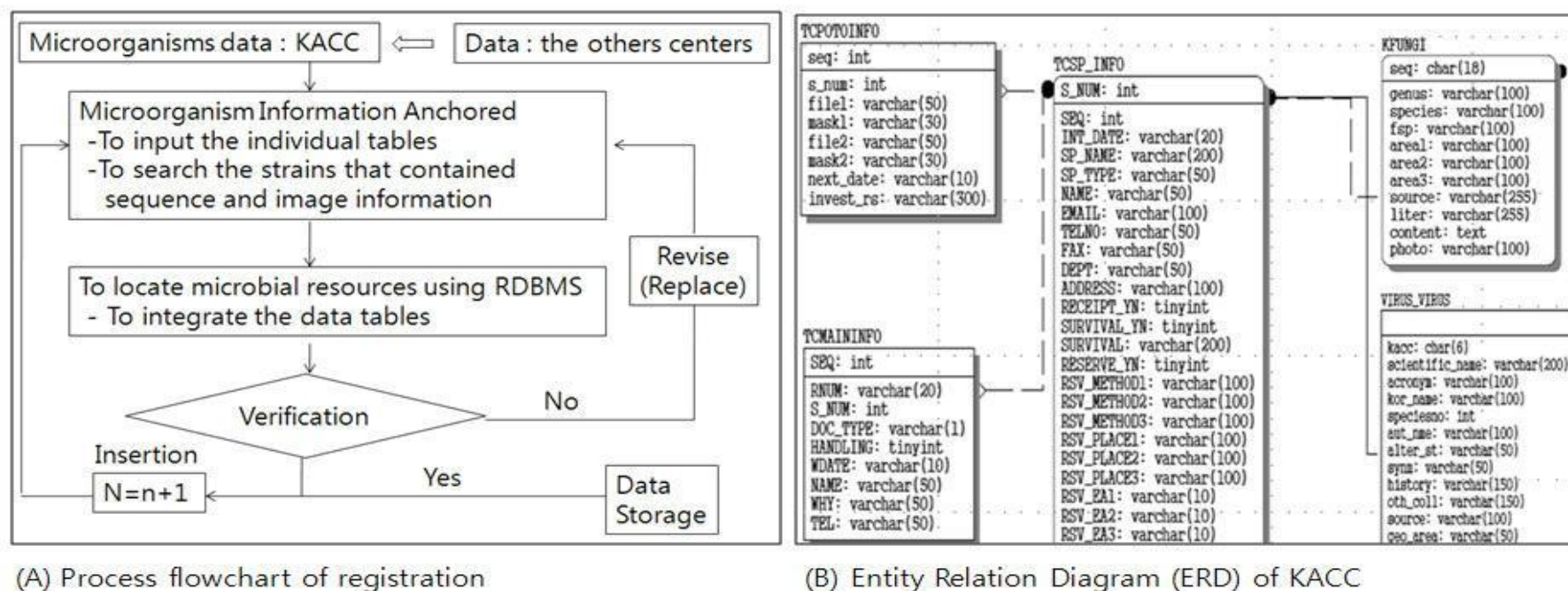
Figure 1. Overview of KACC database designs. (A) System process flowchart of registration microorganism information. Finally, data collected from users are stored in RDBMS of KACC. (B) Entity Relation Diagram (ERD) of KACC database. Each box represents a separate entity, implemented as a database table. Lines between entities indicate a relationship exists. Some tables and columns have been omitted to make the diagram more concise.

KACC microorganism database; (ii) fill an order form including 'Materials Transfer Agreement', and (iii) send your request form by postal mail (or by FAX). In the deposit, KACC deals with a wide range of strains generated from academic and industrial areas such as taxonomy, genetics, biochemistry, and medicine. If users wish to deposit microorganisms to KACC, give a brief description of the strain prior to sending the culture. When KACC finds the deposit acceptable, the depositor is requested to send the culture with the complete KACC 'Accession Form'. Although a lyophilized ampoule is preferred for a deposit, a live culture is also acceptable.

Registered microbial strains were preserved and maintained using various methods, such as lyophilization, cryopreservation by liquid nitrogen, temperature storage below -80°C, water storage, mineral oil storage, and other methodologies, according to the optimal preservation conditions. The registered strains were filed in the database to facilitate efficient utilization of microbial resources and to allow easy access through the internet. Anyone who wishes to make a request is expected to have the basic knowledge and proper facilities for culturing and preserving strains. For high quality microbial resources, all procedures (i.e., collection, preservation, and distribution) must

follow a formal protocol composed of 1 manual, 12 procedure guide, and 7 working instructions that are made on the basis of ISO (International Organization for Standardization) 9001 Standard. The total number of organisms registered and distributed by the KACC has increased rapidly each year. The newly registered microbial resources originate from domestic sources and were introduced from overseas culture collections by an exchange program. An accumulated microbial resource is distributed to the researchers involved in the development of microorganism -related industries (Figure 3). Currently, the KACC maintains 12,924 microbial cultures; including

Figure 2. Search results of the integrated database. The individual panels show samples of search results. (A) The type of information available in the database for a particular organism. (B) DNA sequence report page. (C) Image view with related general information.
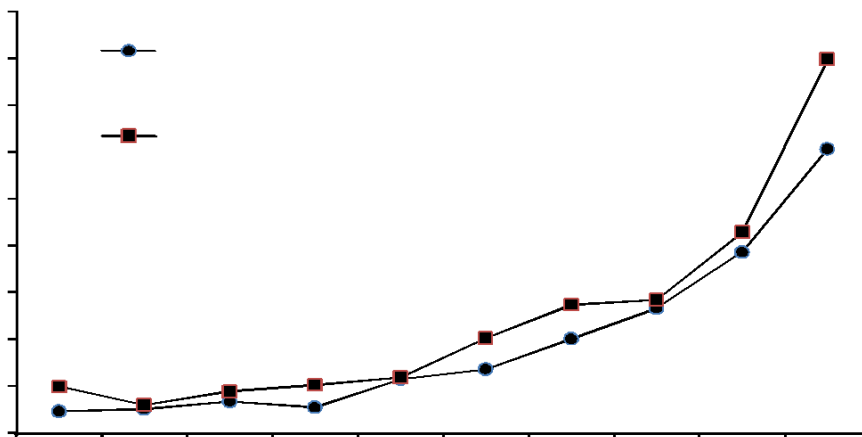

Figure 3. The number of microbial resources per year that were registered and distributed by the KACC from 2000 to 2009.

4,345 strains of bacteria; 5,399 fungi; 966 actinomycetes; 64 yeasts; 1,425 mushrooms and; 725 others. In 2009, the number of newly registered isolates totaled 3,039 including 1,049 strains of bacteria and 1204 mushrooms. This registration figure was 1.6-fold higher than that in 2008. From 1995 to 2009, the total number of distributed isolates totaled 12,861, including 4,832 strains of bacteria and 7,067 strains of fungi. The distributed strains were used in microbial research and development in universities and research institutes. In 2009, the number of distributed isolates was 3,992, including 1,973 strains of bacteria and 2,019 strains of fungi (Table 1). In 2009, the number of

Table 1. The accumulated number of registered microbial resources at the KACC from 1995 to 2009.

Year	Bacteria		Actinomycetes		Fungi		Yeast		Mushroom		Others	
	Reg.	Dis.	Reg.	Dis.	Reg.	Dis.	Reg.	Dis.	Reg.	Dis.	Reg.	Dis.
1995-2005	1587	951	386	120	2758	2661	64	58	155	132	589	17
2006	519	416	55	19	410	847	-	45	15	35	26	6
2007	574	639	54	51	700	660	-	20	27	43	14	5
2008	616	1006	289	89	950	982	-	25	24	41	73	1
2009	1049	1820	182	153	581	1917	-	49	1204	53	23	-
Total	4345	4832	966	432	5399	7067	64	197	1425	304	725	29
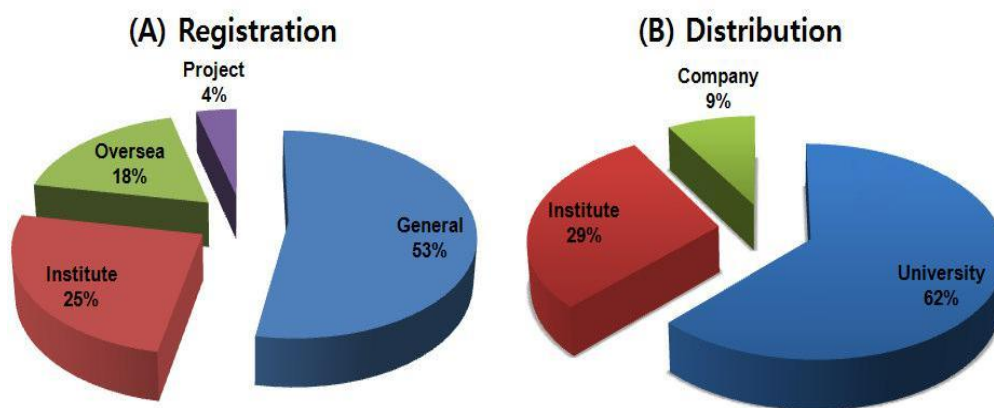
Figure 4. The allocation of microbial resources involved in: (A) registering new isolates and; (B) in receiving isolates distributed by the KACC in 2009.

registered isolates totaled 3,039 strains, of which 53, 25, 18 and 4% were collected in general laboratories, by research institutes, overseas collections, and specific projects, respectively. The number of isolates distributed by the KACC totaled 3,992 strains, which were used by laboratories in universities, research institutes and companies (Figure 4).

The KACC developed a web-based database system that provides integrated information on microbial resources and services information of about 12,924 microbial strains. In addition, we classify and preserve diverse Korean microbial resources and serve as an authorized organizer and official depository of microbial resources in Korea. This database system contains general information, such as identification numbers, culture media composition, images, and DNA sequence. This database also allows users to order and deposit microorganisms with the KACC. We especially provided the unique information with which KACC reported multiple species including 10 fungi in international journals such as the International Journal of Systematic and Evolutionary Microbiology (IJSEM, http://ijs.sgmjournals.org/). The novel species were isolated from the atmosphere (*Massilia niabensis*, *Massilia niastensis* and *Rubellimicrobium aerolatum*), soil (*Dyella soli*, *Dyella terrae*, *Niabella ginsengisoli*, *Chitinophaga niabensis*, *Solitalea koreensis*

and *Chitinophaga niastensis*), island (*Dokdonella soli*), wetland (*Aquitalea denitrificans*), sea sand (*Thalassobacter arenae*) etc.

In conclusion, the KACC has developed a Web-based system to provide an integrated database containing 12,924 registered cultures of microorganisms in 2010. This system services a function of securing the registration and distribution, and analyses platforms to provide information for curated microbial resources by KACC.

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