

## MushBase: A Mushroom Information Database Application

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**A database application, namely MushBase, has been built based on Microsoft Access in order to store and manage different kinds of data about mushroom biological information of species, strains and their physiological characteristics such as geometries and growth condition(s). In addition, it is also designed to store another group of information that is experimental data about mushroom classification by Random Amplification of Polymorphic DNA (RAPD). These two groups of information are stored and managed in the way so that it is convenient to retrieve each group of data and to cross-refer between them as well.**

**KEYWORDS:** Access, Classification, Database, Mushroom, RAPD

Random Amplification of Polymorphic DNA (RAPD) is an efficient molecular biological method to differentiate various fungal species including mushrooms through the analysis of randomly amplified DNA fragments from unknown template DNAs (Zervakis *et al.*, 2001). Because there is no need to determine the nucleotide sequences, RAPD is a convenient tool for DNA fingerprinting of different strains, which share many common phenotypic properties, of the same species. This method is therefore popularly used in typing of fungal strains (Zhang and Molina, 1995) along with sequence analysis of known molecular markers such as ITS1-5.8S rDNA-ITS2, 18S rDNA etc.

We have currently worked on differentiation of an edible mushroom *Pleurotus eryngii* from Korean farm fields using RAPD (Ro *et al.*, 2007). One RAPD experiment produces several kinds of output format of data, including gel images, gel pattern in form of Excel file and phylogenetic tree images. Each classification experiment may also involve a number of mushroom strains which may be repeatedly detected in other experiments. By this way, with a large number of experiments, there will be complex relationships among different experiments, experimental data, species and strains. Therefore organizing information in an efficient and convenient way becomes a great demand. So far, there has been no available desktop or network applications for storing and retrieving data about mushroom.

Microsoft Access, which is a part of the ubiquitous Microsoft Office suite, is widely used to create and manage computer-based database applications on desktop computers and/or on connected computers (a network). It can be used for personal information management, in a

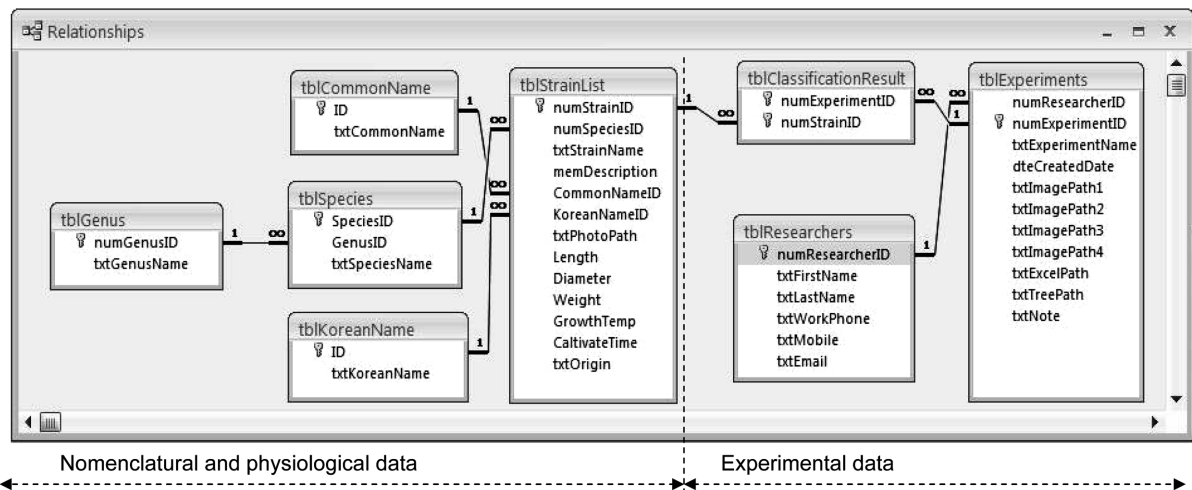
small business to organize and manage all data, or in an enterprise to communicate with servers. Furthermore, the convenience of developing graphic user interface (GUI) in combination with visual basic for application (VBA) which is an easy-to-use programming language, make Microsoft Access the software of choice to develop database applications that do not require many concurrent users. Some rare cases have shown Microsoft Access can be a powerful tool for biological database applications (Creighton and Hanash, 2003; Kokocinski *et al.*, 2003).

From above needs and Microsoft Access' capability, we have built a database application for mushroom information, which is so-called MushBase, based on Microsoft Access version 2003. Utilizing concepts of design database application in Microsoft Access (Swift, 2004), the cycle of building MushBase is divided into different stages including defining data entities, data table structures, table relationship, user interface design and user access control. Each stage and the whole cycle were revised many times to improve functionality and performance. Design tools in Microsoft Access were used to design tables' structure, GUI, whereas VBA was used to program behavior of GUI's elements and their interaction with user.

All entities of information that are necessary to be stored were listed out and put elegantly in tables based on their practical relationship (Fig. 1). Virtually the tables can be divided into two groups, nomenclatural and physiological data, and experimental data. Relationship among tables was defined to ensure desired flow of data in the application. By this way MushBase can be used for storing information about mushroom collections and for storing mushroom classification data at the same time.

MushBase's GUI was designed in task-oriented style which is the grouping of MushBase usage into five differ-

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**Fig. 1.** Data structure and relationship in MushBase: Relationships among data tables in MushBase are defined in relationships window of Microsoft Access. The key icon marks primary key of corresponding table. Tables in relationships view can be divided into two groups, (1) nomenclatural and physiological data and (2) experimental data. The two groups of tables can work independently and cooperatively with each other.

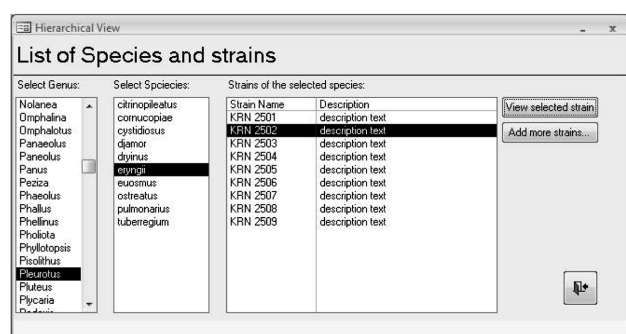
ent categories of activities: viewing/searching, adding, editing, and printing. Each of those groups, which is located in one tab of the main control form or in other word “switchboard” contains controls to access appropri-

ate functionalities (Fig. 2). With appropriate access rights, which are assigned by the administrator, a user can go to corresponding functions. With searching, viewing and printing rights, for example, a user can easily search in

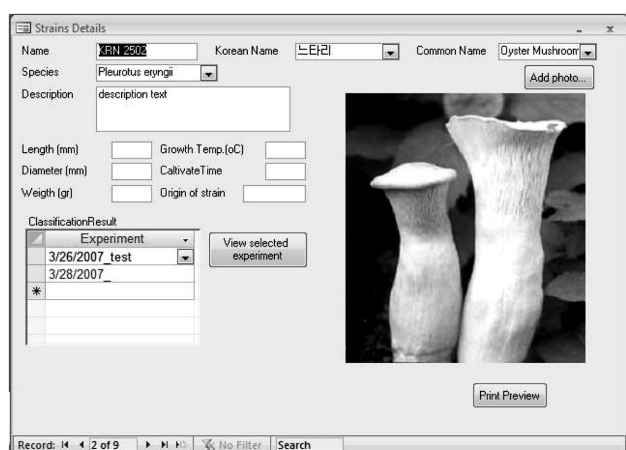
The Switchboard window displays the following elements:

- Title Bar:** Switchboard
- Header:** Mushroom Information Database
- Tabs:** Viewing/Searching (selected), Adding, Editing, Printing, Help
- Buttons and Search Fields:**
  - Relative View:** View genus, species and strains in their hierarchical relationship
  - View Strains...:** Genus: [dropdown], Speices: [dropdown], Strain: [dropdown]
  - View Experiments...:** Name: [input], Date: [dropdown]
  - View Researchers...:** Name: [dropdown]
- Footer:** View a specific record or open form in readonly mode, Exit Application

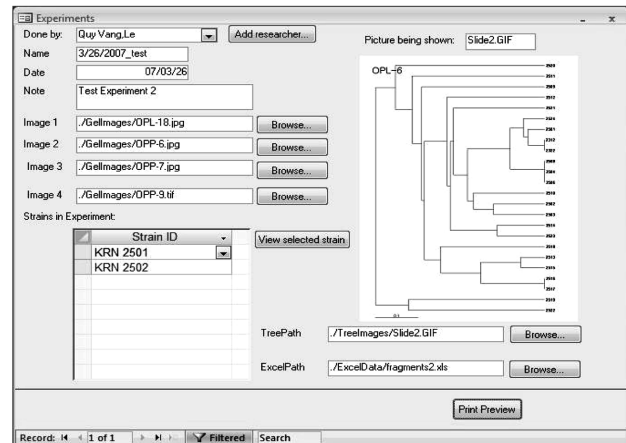
**Fig. 2.** MushBase’s main control board: All interactions with MushBase can be accessed from a main control board named “Switchboard”. Interactions are divided into five categories which are Searching, Adding, Editing, Printing and Help.



A



B



C

**Fig. 3.** Searching and browsing database was made easy and intuitive by cascading lists of genus, species and strains. (A) By selecting genus (i.e. *Pleurotus*) in genus list, species which belong to that genus are shown by selecting of species (i.e. *eryngii*), strains of that species are shown. A command button was provided for viewing strain details when clicked. (B) In strain-detail form view, there is a list of experiments in which the strain has involved; experiment details can be viewed by selecting experiment name and click “view experiment details” button. (C) Interactively, from experiment detail view, there is also a list which contains strains that have been classified.

different ways about stored information such as genus, species, strains, experiments, etc and then print them in printing format.

To ensure security and stability for database, a user-access-control system is implemented. To begin working with MushBase, a user must firstly log into her/his user account. Based on given access rights that user can do certain tasks such as viewing, adding, editing or printing. This is to avoid accidentally damage to the database. The logged in user will be presented the Switchboard to use the software within the permitted realm. The viewing workflow, for instance, enables user access to different viewing items, which include a form showing hierarchical views of genus, species and strains (Fig. 3). On the other hand, from the hierarchical view, users can search and view database in a very convenient way. At the same time, the adding, editing and printing let users add, edit and print data, respectively.

With current version and in desktop environment, MushBase may serve very well for the purpose of storing and retrieving both mushroom strains and related RAPD data. It can also be easily adapted for other kinds of database to which we may apply the same concept such as bacteria, plants, animals, etc. Further development of networking and multilingual user interface may enhance capability of MushBase and thereby expand its power.

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## References

- Creighton, C. and Hanash, S. 2003. Mining gene expression databases for association rules. *Bioinformatics* **19**: 79-86.
- Kokocinski, F., Wrobel, G., Hahn, M. and Lichter, P. 2003. QuickLIMS: facilitating the data management for DNA-microarray fabrication. *Bioinformatics* **19**: 283-284.
- Ro, H. S., Kim, S. S., Ryu, J. S., Jeon, C. O., Lee, T. S. and Lee, H. S. 2007. Comparative studies on the diversity of the edible mushroom *Pleurotus eryngii*: ITS sequence analysis, RAPD fingerprinting and morpho-physiological characteristics. *Mycol. Res.* In press.
- Swift, M. 2004. Access 2003 Essential Training. *Lynda.com*
- Zervakis, G. I., Venturella, G. and Papadopoulou, K. 2001. Genetic polymorphism and taxonomic infrastructure of the *Pleurotus eryngii* species-complex as determined by RAPD analysis, isozyme profiles and ecomorphological characters. *Microbiol.* **147**: 3183-3194.
- Zhang, Y. and Molina, F. I. 1995. Strain typing of *Lentinula edodes* by random amplified polymorphic DNA assay. *FEMS Microbiol. Lett.* **131**: 17-20.