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BIOKEYS – AN INTEGRATED SYSTEM FOR WORKING WITH DATABASE AND POLYCLAVE IDENTIFICATION KEYS OF VARIOUS TAXONOMIC LEVELS

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ABSTRACT

Unlike the other currently available identification software, BioKeys allows the users to create and use own polyclave identification keys of various taxonomic levels. The information of dedicated taxonomic level is stored in the head line of the key file so that BioKeys can understand and search in the right field of the database for the records of matched taxa. The results of database referencing or specimen identification will be displayed in a form of web page. Besides, utilities are available for creating and managing the database, for analyzing the polyclave identification key. An example of using BioKeys is provided with polyclave key of plant families of Magnoliophyta that has been created based on the punched-card system of Betel Hansen and Knud Rahn (1969).

Keywords: polyclave key, identification, database, key analysis.

1. INTRODUCTION

Currently available identification systems allow the user only to use integrated keys to identify organisms at one taxonomic level [1, 2] or to create own keys but without automatic recognition of taxonomic level by the software (Ch. Oliver Coleman, James K. Lowry, Terry Macfarlane 2010 [3]). BioKeys is an integrated tool that allows the user to create and manage biological database, and to use and create own polyclave identification keys of various taxonomic levels. The result of an identification process is illustrated by displaying the records of matched taxa from the database in the form of a web page. BioKeys provides also several statistics of the database and of the polyclave identification key.

2. MATERIAL AND METHODS

Delphi XE Professional Workstation ESD (item number: 2010111885211109) of the Embarcadero Technologies company [4] has been used to create BioKeys. The Installation

package of BioKeys is available at the web site of the Institute of Ecology and Biological Resources, Vietnam Academy of Science and Technology [5].

3. DESCRIPTION OF BIOKEYS

3.1. BioKeys User Interface

BioKeys main window (Fig. 1) is a multiple document interface that can display an image component, a web browser component or a key file child window. BioKeys main window has a toolbar and a menu bar. Image component is dedicated for browsing database records. Web browser displays the results of database referencing or of specimen identification in a form of webpage that allows to use the links to open pictures or information of the taxa. Key file child window serves as device for editing polyclave identification key. It can also display the BioKeys simple stream files that contain results of the key analysis.

Dialog boxes of BioKeys are the utilities for interactive working. The 'Reference /Specimen Identification' dialog box (Fig. 2) is dedicated for selecting characters in case of database referencing or specimen identification.



Figure 1. BioKeys main window.

BioKeys-Identifying FAMILY of ANGIOSPERMAE (MAG	GNOLIOPHYTA)	×
Remaining characters: 168		
African		^
Anther 1, fertile		
Anthers 1-locular at anthesis		
Anthers 10, fertile		
Anthers 2, fertile		
Anthers 3, fertile		
Anthers 4, fertile		
Anthers 5, fertile		
Anthers 6, fertile		
Anthers 7, fertile		
Anthers 8, fertue		
Anthers 9, refuie		~
Selected characters: 4		
Leaves or leaflets lobed or divided		
Leaves or leaflets with entire margin. Without any lobes or teeth		
Q V w Gr Det-Illerer V w Detaile		
Open Key me: Dementarisen Knudikann. oki	Extract from selected data	
	OK Cancel C	tivate

Figure 2. Dialog box for database referencing or specimen identification.

'Create/Edit key file' (Fig. 3) is the dialog box for creating template of a new polyclave identification key file or editing an existing one. The 'Key analysis' dialog box (Fig. 4) is

dedicated for key analysis. In this dialog box we can let BioKeys calculate statistics to answer several questions: What is the size of the key (total number of characters)? How many characters each taxon owns in this key? In how many taxa each character is available? For a certain size of character set: How many total possible successful character sets and how many possible successful character sets of each taxon or character.

BioKeys - Create/Edit key file			
Remaining taxa: 405	Taxa to be treated: 6		
ACANTHACEAE ACERACEAE ACHARIACEAE ACHARIACEAE ACTINIDIACEAE ADOXACEAE AEGICERATACEAE AEGICERATACEAE AGAVACEAE AGDESTIDACEAE APIACEAE APONOGETONACEAE APONOGETONACEAE APONOGETONACEAE	ALANGIACEAE ANCISTROCLADACEAE ANNONACEAE OLACACEAE OLEACEAE OLINIACEAE		
Character to be treated: \\NewKey\\			
Options C Create new key file from family list	Add character O Remove character Process		
Open Key file: BertelHansen <u>K</u> nudRahn.bki	Close		



	BioKeys - Key a	inalysis					
Key file							
BertelHansen&KnudRahn.bki					Ope	n key file	,
Total number of characters:172		Character duplication check		check			
Character analysis:	List and numb	er of taxa of	f each char	acter			
CharacterBasedAnalysis-BertelHansen&Ki	nudRahn.bks						
Character analysis: L	ist and number	r of characte	ers of each	taxon			
Taxon Pacod Analysis Portal Honson & Kundl	Rahn.bks						
Maximal character number of one taxon:139(CA Character-set analysis 2 Hair stellate (alco 2 amed branched and tuffed)	PPARACEAE)	30.1.11.14.0	FAF				
Attaching association of the second secon	PPARACEAE)	30-LILLAC 3-RESTIO 32-EUPHO 4-CYPERA 23-MIMOS 1-CHENOS 6-MELAS 3-ASCLEP	EAE NACEAE RBIACEAE CEAE SACEAE PODIACEAE IOMATACE IADACEAE	AE			~
Maximal character number of one taxon:139(CA Character-set analysis 2 2-Hairs stellate (also 2-armed, branched and tufted) 36-Bulb present (monocots only) 25-Leaves with a ligule 2-Hairs stufted, non-glandular 33-Hairs stufted, non-glandular 33-Hairs stufted, non-glandular 31-Perianth segments 1 46-Pollen coherent into pollinia or wax-like masses 10-Hairs vesicular or bladder-like 6-Corona present, or scales in the throat 12-Tendnls present	PPARACEAE)	30-LILLAC 3-RESTIO 32-EUPHO 4-CYPERA 23-MIMOO 1-CHENOI 6-MELAS 3-ASCLEP 4-CYNOC 2-SAPIND 3-POACE/	EAE NACEAE RBIACEAE CEAE SACEAE PODIACEAE INDACEAE IADACEAE AAMBACEAE ACEAE	AE E			<
Maximal character number of one taxon:139(CA Character-set analysis 2 2-Hairs stellate (also 2-armed, branched and tufted) 36-Bulb present (monocots only) 25-Leaves with a ligule 2-Hairs stufted, non-glandular 33-Hairs stinging 11-Perianth segments 1 46-Pollen coherent into pollinia or wax-like masses 10-Hairs vesicular or bladder-like 6-Corona present, or scales in the throat 12-Tendrils present 16-Style gynobasic Possible number of successful character sets of ea	PPARACEAE)	30-LILIAC 3-RESTIO 32-EUPHO 4-CYPERA 23-MIMOO 1-CHENOF 6-MELAS: 3-ASCLEP 4-CYNOCI 2-SAPIND 3-POACE/ Possible n	EAE NACEAE RBIACEAE CEAE SACEAE PODIACEAE IADACEAE RAMBACEAE ACEAE LE Univer of su	AE E ccessful cha	aracter s	ets of eac	

Figure 4. Dialog box for key analysis.



Figure 5. Declared own file formats of BioKey.

3.2. BioKeys' Declared File Formats

BioKeys declared three own file formats (Fig. 5):

- Database file (the file extention is '*.bkd').
- Polyclave identification key file (the file extention is '*.bki').
- Simple stream file (the file extention is '*.bks').

Because being declared, once the BioKeys has been installed with installation package, double clicking on these files will cause BioKeys to be started with opening the clicked file.

3.3. Create and Manage Database

Database in BioKeys is image oriented. One species can be represented in the database by one or more images. The database file consists of the records that contain information of images with following fields: 1) Division/Phylum, 2) Class, 3) Order, 4) Family, 5) Genus, 6) Species, 7) Name of image file.

To create a new database, we click on the "Create new database" submenu and set the name of the automatically created one record template in the appeared save dialogbox to save it. After that we can open the newly created database and edit, add, delete records as needed. To view the opened database in web page form (Fig. 6), we click on the 'Create and show html' submenu. If we have text files with information on taxa (the file must be named after scientific name of the corresponding taxon with '_E' suffix, e.g., 'scientific name_E.txt' file for the 'species scientific name' taxon), we can click on the 'Info' link beside this taxon name in the web page to load and view this file.



Figure 6. Database view in web page form.

When we add a record to the database, the picture will be copied to the folder of BioKeys with original file name. We can change the various file names of the pictures to standard file names of BioKeys by clicking on the submenu item 'Change name of picture file'. After changing, the name of a picture file of a database record will have following formula:

 BioKeys - Database structure 	□ ×
Division/Phylum Class Order Family Genus Species	
SAURURACEAE - DIÉP CÁ	
PIPERACEAE - HẠT TIEU	
Selected taxon PIPERACEAE - HẠT TIÊU	Display
Search:	
In the field: Division/Phylum Class Order Family Genus Species	Close

's' + record number + '.jpg'

Figure 7. Displaying the database structure in tab view mode.

Drivision/Phytum Class Order Family Genus Species MAGNOLIOPHYTA - MộC L/ MAGNOLIOPSIDA - MỘC LA MAGNOLIALES - MỘC LAN ANNONACEAE - NA ANNONACEAE - NA BHDOPHYTA - RONG ĐỒ MAGNOLIOPSIDA - HÀNH MAGNOLIALES - MỘC LAN MAGNOLIALES - MỘC LAN MAGNOLIACEAE - MỘC LAN AnnonACEAE - NA Ann	•	BioKeys - D	atabase structure		- 🗆 ×
POLYGONALES - RAU RÅ PI LIMBA GINALES - DI TÔ V	Division/Phytum MAGNOLIOPHYTA - MÓC L: RHODOPHYTA - RONG ĐÓ PHAEDOPHYTA - RONG NÁU PHAEDOPHYTA - THÒNG MAGNOLIOPHYTA - MOC L	Class Order OPSIDA - MÓC LA MAGNOLIALES - MÓC LA (OPSIDA - MÓC LA A - HÀNH A - HÀNH CASUARISE - LONG NÃO PAPA VIERA LES - A PHIE HAMAMELIDALES - AÓ EUCOMMALES - DAN EUCOMALES - CANI CÓ MURICALES - CANI CÓ MURICALES - THANH M. TUGI ANDALES - MÓR EBETULALES - CÂN LÓ MURICALES - CANI CÓ MURICALES - CANI CÓ MU	Family N ANNONACEAE - NA ANNONACEAE - MÔC LA: ANNONACEAE - MÔC LA: ANNONACEAE - NA ANNONACEAE - NA	Genus Alphonsea Anaxagorea Cyathostemma Dasymaschalon Desmos Drepananthus Enicosanthellum Frisstötlesa Goniothalamus Meiogyne v	Species

Figure 8. Displaying the database structure in column view mode.

To explore a database, we need just to click on the "Display database structure" menu. In the appeared dialogbox we can choose to display the database structure in tab view mode (Fig. 7) or in column view mode (Fig. 8). In these views, the next lower ordered taxa will be displayed when any taxon is clicked. Once a taxon is clicked, we can display all the lower ordered taxa in a web page form by clicking on the "Display" button (in tab view mode) or on the button above the recently chosen taxon (in column view mode).

During exploring the database, when we came to the species list of a genus, we can change to the picture browsing mode by double clicking on the name of the species. In this mode, we can use the 'Change picture of species' button to view all the pictures of the species. During viewing a picture, we can use the 'Change picture size' up-down bar in order to change the size of the picture, and we can keep the mouse down on the picture and move it in order to move the picture. To browse the records of the database, we use the 'Switch between web/database browsing' button to change to the database browsing mode. In this mode, we use the 'Browse database' button to go through database. When the record number is changed, BioKeys loads the picture of the current record and displays it on the main window, the taxonomic information of the will be displayed in title bar. Here we can also change the size of the picture and move it around the screen.

BioKeys allows user to search in the fields of the database. In the tab view, we type the search string in the edit field after label 'Search', then click on a button in the line below that indicates a taxon level field of the database, where the searching should be conducted. In the column view, we type the search string directly into the edit field under the button with name of a taxon level field where the searching should be conducted. After searching, BioKeys displays the results in a web page form.

Finally, BioKeys can calculate and give statistics on taxa number of each taxonomic level of the database or of the selected records (Fig. 9). To get these statistics we click on the 'The whole database' or 'Selected items' submenu.

-	BioK	eys - Statistics	-	×
	Division/Phylum	11		
	Class	19		
	Order	121		
	Family	360		
	Genus	2330		
	Species	4219		
		Close	1	
			-	

Figure 9. Statistics of the database or of the selected records.

3.4. Working with Polyclave Identification Key

3.4.1. Format of polyclave identification key file

BioKeys supports working with polyclave identification keys. A polyclave identification key file consist of a head line and key content. The head line has the following format:

[WORD FOR TAXONOMIC LEVEL] OF [higher ordered taxon]

The word in the first square brackets must be capital and can be one of the following: DIVISION or PHYLUM, CLASS, ORDER, FAMILY, GENUS, SPECIES. For example, the head line of a polyclave identification key for identifying family of specimen of the Magnoliophyta plant division will be:

[FAMILY] OF [Magnoliophyta]

Thus the content of the first square brackets is the name of the taxonomic level, the taxa of which should be identified by this key. The content of the second square brackets describes the higher ordered taxon for which the current polyclave identification key is dedicated.

Each line of the key content consists of the taxon name and the characteristics of taxon (character list) and has following format:

 $TaxonName = \Character1 \Character2 \.... \CharacterN \$

Thus, each character is bound by two double backslash from the sides. In the case of a polyclave identification key for identifying family of specimen of the Magnoliophyta plant division, the TaxonName will be a name of plant family of this plant division: Magnoliace, Annonaceae,... and hence one line of the key content will be of following form:

Magnoliaceae=\\Character1\\Character2\\...

3.4.2. Create and edit polyclave identification key file

The first way to create and edit polyclave identification key file is to use the key file child window (Fig. 10). To open the key file child window we click on the 'Create key file child window' submenu item under the 'Key file' menu item. In the appeared child window we just type in a new key or open a saved key file to edit.





The other way for creating and editing polyclave identification key file is to use the 'Create/Edit key file' dialog box. To open this dialog box we click on the 'Create/Edit key file' submenu item under the menu 'Key file' item. In the appeared dialog box, after we open the saved polyclave identification key file, the taxa from the key will be listed in the left list box. To create a new, empty polyclave identification key file with the same taxa as these of the opened key, we choose the 'Create new key file from family list' item in the options box, then click on the 'Process' button. To add or remove a character from character list of any taxa of the opened key, we move these taxa from the left list box to the right list box (Taxa to be treated) by marking them and clicking on the appropriate arrow. Then we type the character in the 'Character to be treated' edit field, choose the appropriate option ('Add character' or 'Remove character'), and click on the 'Process' button.

3.4.3. Analysis of a polyclave identification key

The interface for analysis of a polyclave identification key that is saved in a file is the 'Key analysis' dialog box. To open this dialog box we click on the 'Key analysis' submenu. In the appeared dialog box we click on the 'Open key file' button to open a polyclave identification key, before any analysis can be conducted. Results of analysis will be saved in files of 'BioKeys simple stream file' format with '*.bks' extention. After analysis we can use the key file child window to open the file with analysis results.

To check, if any character is duplicated in the character list of one taxon, we click on the 'Character duplication check' button. BioKeys will check the character list of all the taxa of the key. If a character is represented more than once, BioKeys will make needed correction.

To create a file with information on how many and which taxa have a defined character (Fig. 11), we click on the 'Character analysis: List and number of taxa of each character' button. A save dialog box will appear with an automatic provided file name that consist of the 'CharacterBasedAnalysis-' prefix and the name of the opened key file. We just need to click on save button to save the results.

🐐 🛛 BioKeys - [BioKeys - Key file child window - CharacterBasedAnalysis-Polypodiophyta.bks] 💦 – 🗖 💌
Set Detabase Key file Html Info Opened database: None - ♂ 🗙
🛅 🛤 🔳 🚀 A 🍡 🕬 🎭 🛤 🕰 🤳
Results of character analysis: List and number of taxa of each character
Cỏ nổi// <nr of="" taxa="1">//azollaceae</nr>
Cây có thân to hoặc dạng như dừa// <nr of="" taxa="3">//dicksoniaceae//cyatheaceae//blechnaceae</nr>
Bao mô 2 månh// <nr of="" taxa="1">//dicksoniaceae</nr>
Lá kép, leo quần, dạng như thân dài// <nr of="" taxa="1">//schizeaceae</nr>
Lá không leo quấn// <nr of="" taxa="38">//ophioglossaceae//angiopteridaceae//marattiaceae//osmundace</nr>
Lá non không uốn cong như đuôi mèo// <nr of="" taxa="1">//ophioglossaceae</nr>
Lá non uốn như đuôi mèo// <nr of="" taxa="37">//angiopteridaceae//marattiaceae//osmundaceae//parkeri</nr>
Bào từ nang không cong// <nr of="" taxa="2">//angiopteridaceae//marattiaceae</nr>
Bào từ nang không vòng// <nr of="" taxa="1">//angiopteridaceae</nr>
Bào tử nang có vòng sơ sinh, do một nhóm tế bào// <nr of="" taxa="1">//marattiaceae</nr>



To create a file with information on how many and what characters each taxon of the key has, we click on the 'Character analysis: List and number of characters of each taxon' button. A save dialog box will appear with an automatic provided file name that consists of the 'TaxonBasedAnalysis-' prefix and the name of the opened key file. We just need to click on save button to save the results (Fig. 12).



Figure 12. Results of the taxon based analysis.

BioKeys allows us also to analyse the key in different aspects of identification capability – called Character-Set-Analysis. For this analysis we set at first a size of character set by entering a number in the edit field (next to the 'Character-set analysis' button on the 'Key analysis'

dialog box. Then we click on the 'Character-set analysis' to begin the analysis. A save dialog box will appear with an automatic provided file name that consist of the 'CharacterSetBasedAnalysis-' prefix and the name of the opened key file. We just need to click on save button to accept the file name. During analysis, BioKeys will inform us through message boxes on the total character number of the key, the maximal possible number of character sets (calculated based on total character number of the key and the size of character set), the number of successful sets of each character (based on the trial identification with using all possible character sets). After the analysis has been completed, we can open the file to see the results (Figs. 13-14).

👒 BioKeys - [BioKeys - Key file child window - CharacterSetBasedAnalysis-Polypodiophyta.bks] 🚽 🗖	×
Database Key file Html Info Opened database: None	ъ×
🛅 🐏 🔳 🚀 A 📭 🕬 🎭 🛤 🕰 🍠	
Number of all possible sets of 5 characters of the key:91962520	^
Number of successful sets of 5 characters:117	
Character related results: Number of successful sets of 5 characters with this character included	
16-Vòng đầy đủ	
15-Bào tử nang chín rời rạc hay từ đáy	
6-Vòng xéo, liên tục	
10-Nang quần dọc theo gân phụ hay thành cọng nang quần	
9-Phụ sinh	
0-I á đơn dài	~

Figure 13. Character set based analysis – Character related results.

🝓 🛛 BioKeys - [BioKeys - Key file child window - CharacterSetBasedAnalysis-Polypodiophyta.bks]	- 🗆 🗙
Database Key file Html Info Opened database: None	_ 8 ×
逝 🛤 🛲 🅢 A 📭 😪 🎭 🦊 🎘 💆	
12-Bao ur nang mio mọc ulann năng quan ở mặt dưới là này Đia là	~
12-Lá không leo quân	
12-Lá non uốn như đuôi mèo	
12-Bào từ nang có cong	
1-Nang quần tròn	
10-thelypteridaceae	
9-dipteridaceae	
27-dennstaedtiaceae	
23-aspleniaceae	
14-dryopteridaceae	
	~

Figure 14. Character set based analysis - Taxon related results.

3.4.4. Reference/Specimen identification in BioKeys

Because after the identification process BioKeys will search all matched records in the database and display them on the main window in the form of a web page, before we begin with identification, we need to open the database. After clicking on the 'Reference/Specimen

identification' submenu under the 'Key file' menu, a dialog box will appear. To open a polyclave identification key file, just click on 'Open' button on this dialog box. After the key has been opened, BioKeys extracts all the characters of the key and list them in the first list box.

To reference on what taxa have some defined characters, we choose these characters from the first list box (of source characters) and move them to the second list box (of selected characters) by using arrow keys, then click on the 'OK' button, the BioKeys will identify what taxa have all these characters then search the records of these taxa in the database and display them in a form of web page. BioKeys will also list the taxa that are not represented in the database by any records at the end of the resulted web page.

To identify a specimen, we read the characters of the specimen and choose these, if available, in the list box of source characters and move them to the list box of selected characters. Then we click on the 'OK' button and the same procedure will be done as in the case above of referencing database.

4. AN EXAMPLE OF USING BIOKEYS

4.1. The Polyclave Identification Key for the Families of Magnoliophyta Plant Division

The polyclave identification key for the families of Magnoliophyta plant division is built based on the punched-card system of Hansen and Rahn (1969) [6]. There are 411 families from Hutchinson (1959), Engler Syllabus (1964), Bentham & Hooker (1867-1880), and Engler Pflanzenfamilien ed. 1. The polyclave key therfore consists of a headline and the key content that consists of 411 lines (Bertel Hansen and Knud Rahn 1969). The key is saved to the file named 'BertelHansen&KnudRahn.bki'.

4.2. Reference/Specimen Identification

To use these utilities, we first open the plant database ('367.bkd'). Then we open the 'Reference/Specimen identification' dialog box by using the submenu of the same name under the 'Key file' menu. In this dialog box, we open the key file named 'BertelHansen&KnudRahn.bki'. After opening the file, BioKeys will list all the characters (172 characters) in the upper list box of the dialog box.

To reference, for example, which families from Magnoliophyta plant division have contorted petals, we select this character from the upper list box and move it to the lower one by using arrow key. After clicking on the 'OK' button, BioKeys will define the taxa that have this character by using the opened key file (matched taxa). Then BioKeys will search in the opened database for the records of the matched taxa, create for them the '_BioKeys.htm' file and open this file in the integrated web browser. A list of 27 families that are not represented in this database will also be attached.

4.3. Key Analysis

To analyze the polyclave identification key for the families of the Magnoliophyta plant division, we open the 'Key analysis' dialog box (Fig. 4). In the appeared dialog box we open the key from the 'BertelHansen&KnudRahn.bki' file. There are 172 characters used in the key. The results of taxon based analysis has shown that character lists of the Capparaceae and

Euphorbaceae plant families are largest and consist of 139 characters, while the character list of the Hydrostachyaceae plant family is smallest and consists of only 32 characters. The character based analysis has shown that there are 3 characters that are most rare characters and are presented each only in 4 taxa. These characters are 'Pollen coherent into pollinia or wax-like masses', 'Hairs stinging', and 'Bulb present (monocots only)'. The most common character is 'Filaments not connate' and is presented in 395 of 411 families.

Identification is based on the character sets. The bigger character set is, the larger the number of maximal possible character sets becomes. When the size of character set is 2 characters, the number of maximal possible character sets is 14706, and the possible successful character sets is 251. When the size of character set is 3 characters, the number of maximal possible character sets became 833340, and the possible successful character sets is 1554. But when the size of character set is 7 characters, the number of maximal possible character sets became 780842580024, and the possible successful character sets became 2487.

5. CONCLUSIONS

BioKeys is a fully functioned tool that allows the users to create and manage database and polyclave key, to reference database and to identify specimen. The current version of BioKeys can provide certain statistics of a database and polyclave key. In the future, it is desired to develop criteria or indices for quantitative evaluation of polyclave keys.

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TÓM TẮT

BIOKEYS - MỘT HỆ THỐNG LIÊN KẾT CHO PHÉP LÀM VIỆC VỚI CƠ SỞ DỮ LIỆU VÀ KHÓA ĐỊNH LOẠI ĐA TRUY Ở CÁC BẬC PHÂN LOẠI KHÁC NHAU

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Khác với các phần mềm phân loại hiện có, BIOKEYS cho phép người dùng tạo và sử dụng khóa định loại đa truy của riêng mình ở các bậc phân loại khác nhau. Thông tin về bậc phân loại của khóa được lưu tại dòng đầu của tệp khóa nên BIOKEYS có thể hiểu và tìm ở đúng trường cần thiết của cơ sở dữ liệu để lọc các bản ghi của các taxon phù hợp. Kết quả tra cứu cơ sở dữ liệu hoặc định loại được hiển thị dưới dạng web. Ngoài ra, còn có các tiện ích để tạo và quản lý cơ sở dữ liệu, phân tích khóa định loại đa truy. Một ví dụ về sử dụng BIOKEYS được cung cấp với khóa đa truy định họ thực vật ngành Mộc lan (Magnoliophyta) là khóa được xây dựng dựa trên hệ thống khóa đục lỗ của Betel Hansen và Knud Rahn (1969).

Từ khóa: khóa đa truy, định loại, cơ sở dữ liệu, phân tích khóa.