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## Introduction

The vast majority of germplasm collected for *ex situ* conservation in the 1970s and early 1980s was crop germplasm. However, since then, increasing attention has been focused on wild species, including crop relatives, forages, multipurpose trees and shrubs and forestry species. This has brought with it a special set of problems for collectors, not the least of which is the taxonomic identification of the plants. It is essential to obtain its correct scientific name if a specimen is to be connected to the wealth of information that may be known about the taxon to which it belongs. Germplasm that is not accurately identified in the field may remain uncollected, because its value is not recognized when encountered. Misidentification of any material that is collected will lead to spurious results when the germplasm is studied and used. The growing out and reidentification of several large germplasm collections (Maxted and Bisby, 1986, 1987; Maxted, 1989, 1992) have established that a significant proportion of the material was either wrongly identified or not identified at all. Material incorporated into gene banks as 'unknown legume species' or '*Eleusine* sp.' is of limited conservation value and is difficult to use.

Identification, or 'determination', of a plant specimen involves two steps. First, there is the choice of a taxon name to which the specimen may be referred, i.e. the act of recognizing or establishing the taxon to which a specimen belongs. Second, there is the decision as to what the correct name is, if in fact more than one name has been applied to the taxon. The correct name for a taxon is a legitimate name which is accepted according to the rules of the International Code of Botanical Nomenclature (ICBN) regarding the choice of names. Legitimate names are those which are in accordance with ICBN rules of publication and

are thus available for consideration as the acceptable name (Stace, 1989).

The second step requires a knowledge of the history of the taxon in the botanical literature, a subject which is introduced in Chapter 10. This chapter focuses on the mechanics of the first step in identification, i.e. attaching a name to the specimen. The difficulties encountered in doing this may be due to a number of factors (Abbott *et al.*, 1985). Some taxa are genuinely difficult to distinguish or show different features at different stages of their life history. However, it is undeniable that the available field identification aids are frequently poorly designed, and therefore difficult to use, particularly for those who lack formal taxonomic training and are unfamiliar with the terminology they employ. Some are also inaccurate. Collectors must learn to make the best use possible of what identification aids may already be available, but must also be occasionally ready to develop their own.

## Identification aids

Specimens are commonly identified to species, but if lower taxonomic entities have been described they could be named to subspecies, variety or form. The correct identification of the specimen is achieved by comparing its characteristics to the set of 'key' characteristics possessed by each species. If the specimen's characteristics fall within the range of key characteristics of a particular species, then the specimen is identified as a representative of that species. The range of the key characteristics for each species will have been previously determined by a detailed study of a broad range of specimens representing that species.

There are two approaches to identification, matching and elimination. Matching identification involves the comparison of the specimen to taxon descriptive data or some form of exemplar, such as a named herbarium sheet. Clearly, trying to match a specimen to one of a large number of possible taxa could be impossibly time-consuming. Some method is needed to narrow down the possibilities. Identification by elimination involves comparing a specimen to a set of mutually exclusive short descriptions, as in a printed key, and making a decision as to which fits the specimen best, repeating the process for another set of descriptions until only one taxon remains. Often, identification will begin by elimination, and proceed by matching when the range of possible taxa has been narrowed down to manageable proportions.

Four types of aids to identification are described below:

- single-access keys;
- multi-access keys;
- illustrations;
- computer-based aids.

### *Single-access keys*

A taxonomic key is a logical arrangement of the distinguishing features of all the members of a taxonomic group, designed to assist in the naming of unidentified members of that group. Keys are commonly based on gross morphological features, characteristics that are readily observable in the field, laboratory or herbarium. Traditional keys are commonly referred to as being:

- dichotomous, meaning that at each step the user is presented with two brief, diagnostic descriptions, only one of which should match the specimen being identified;
- single-access, meaning there is only one point of entry into the key, via the choice between the first pair of descriptions;
- sequential, meaning that once the first choice is made the user is faced with a second choice of alternative diagnostic information and then a third and so on, until by making the final choice the name of the specimen is obtained;
- diagnostic, meaning that the few characters used in the key distinguish the taxa included, but are not intended to provide a full description of the taxon.

The nature of the key design means that the process of identification thus follows a specific, structured sequence until the identification is finally made.

The two alternative descriptions provided in a dichotomous key are referred to together as a 'couplet'. Each individually is a 'lead'. The characters used for identification should be constant and stable for the particular species and the two leads in a couplet should be comparable and yet mutually exclusive without any overlap. Not all single-access keys are dichotomous: they can be polychotomous, presenting the user with more than two leads at any one point. For practical reasons, keys that use triplets or quadruplets are not commonly used, however. In a good key, the couplets will refer to easily observable (at most with the aid of a hand lens) characteristics that divide the taxa into two approximately equal groups. If the characters divide the initial set of taxa repeatedly into two in this way, the average number of questions one needs to answer to identify a specimen will be fewer, and thus the chances of making an error in identification are reduced and the speed of identification increased.

Single-access keys may be monothetic, if only one character is used in each lead, or polythetic, if several characters are used together. An example of a polythetic key to a group of vetches (the legume genus *Vicia*) is shown in Key 11.1.

There are two basic styles of single-access key, the parallel (or bracketed) and the yoked (or indented). The polythetic key provided in Key 11.1 illustrates the parallel style. The same key is shown in the yoked style in Key 11.2. The essential difference between the two styles of key is that in the parallel style all the components of a set of related

**Key 11.1****Parallel key to a group of vetches.**

1. Lower stipules subentire, 2–4 mm long; flowers 6–14 mm; seeds sculptured; tendrils mostly simple ..... **2**
  - Lower stipules distinctly toothed, > 4 mm long; flowers (10–)14–36 mm; seeds smooth; tendrils simple or branched ..... **3**
2. Flowers 5–12 mm; legume falcate, distal end beaked; seed surface ruminately-reticulate ..... *V. cuspidata*
  - Flowers 9–15 mm; legume not falcate, distal end unbeaked; seed surface tuberculate ..... *V. lathyroides*
3. Wings purplish; legume rounded in cross-section; hilum < third seed circumference ..... **4**
  - Wings cream or yellow; legume distinctly laterally flattened in cross-section; hilum > third seed circumference ..... **6**
4. Annual, stolons absent; standard cream, yellow or purple ..... **5**
  - Perennial, stoloniferous; standard purple ..... *V. pyrenaica*
5. Standard face purple; wings reddish purple ..... *V. sativa*
  - Standard face yellow; wings bluish purple ..... *V. barbazitae*
6. Aril present; flower (19–)24–36 mm ..... *V. grandiflora*
  - Aril absent; flower 20–21 mm ..... *V. qatmensis*

descriptions are printed together, whereas in the yoked style all the possibilities which depend on part of a description are set down and exhausted first, before other parts of a description are taken up. Neither style of key has a clear botanical advantage over the other, but parallel keys tend to take up less space because there is no need for indentation.

The single-access key is the traditional tool used for biological identification, but any biologist who has had to use one professionally will agree that it has many undesirable features. The user may not be able to proceed past the first couplet because neither of the leads provided fits the specimen or it may not be possible to score the characters. For example, the first lead may involve seed characters, and the specimen may still be only at the flowering stage. Also, users may not understand the technical terminology used. This may halt progress through the key or may result in errors when interpreting the specimen's character states, resulting in misidentification. A glossary should be used to check terms (see below) or the key should be annotated before use with definitions of all unfamiliar terms. When measurements are used in the key, several structures should ideally be looked at, but the specimen might have only one example, again causing uncertainty. One may also find that neither of the two alternative descriptions in a couplet appears to describe the specimen accurately. In this case one has to act pragmatically and follow the option that supplies the better fit, or try both choices and then compare full descriptions of the two answers with the specimen.

In fact, once an identification is achieved, the specimen should

**Key 11.2****Yoked key to a group of vetches.**

1. Lower stipules subentire, 2–4 mm long; flowers 6–14 mm; seeds sculptured; tendrils mostly simple ..... 2
2. Flowers 5–12 mm; legume falcate, distal end beaked; seed surface ruminant–reticulate ..... *V. cuspidata*
2. Flowers 9–15 mm; legume not falcate, distal end unbeaked; seed surface tuberculate ..... *V. lathyroides*
1. Lower stipules distinctly toothed, > 4 mm long; flowers (10–)14–36 mm; seeds smooth; tendrils simple or branched ..... 3
3. Wings purplish; legume rounded in cross-section; hilum < third seed circumference ..... 4
4. Annual, stolons absent; standard cream, yellow or purple ..... 5
  5. Standard face purple; wings reddish purple ..... *V. sativa*
  5. Standard face yellow; wings bluish purple ..... *V. barbazitae*
4. Perennial, stoloniferous; standard purple ..... *V. pyrenaica*
3. Wings cream or yellow; legume distinctly laterally flattened in cross-section; hilum > third seed circumference ..... 6
6. Aril present; flower (19–)24–36 mm ..... *V. grandiflora*
6. Aril absent; flower 20–21 mm ..... *V. qatmensis*

always be compared with a detailed botanical description of the taxon in order to check that no mistake has been made during the keying-out process. A botanical description is a logically laid-out statement, technically worded, of the characteristics of a taxon. If this checking is not done, then keying-out errors will remain undetected. If the description does not match the specimen or if, when using the key, neither of the leads seems appropriate, then it is possible that a mistake has been made in using the key. To attempt to locate the error the user must return to the first couplet and repeat the entire identification process, hoping that the error can be spotted and corrected.

Floras, monographs, revisions and other taxonomic works include keys and descriptions, sometimes supplemented by illustrations (see below). Collectors must know how to select the most appropriate aid to help identify their specimen. In attempting to identify a tree species from Zimbabwe, the collector might start out by using a key to angiosperm families. This key should enable identification of the specimen to the Ebenaceae, for example. A key to genera might then be used to identify the specimen as a *Diospyros* species. A key including all 500 *Diospyros* species will not be required for the final step if it is known that the specimen to be identified is native to Zimbabwe. Then the specimen is likely to be one of the 13 native Zimbabwean *Diospyros* species and so the key provided in *Flora Zambesiaca* (Brenan *et al.*, 1983) would be appropriate. A difficulty may arise when a Flora is not available for the region being visited or the species of interest is not

included in the Flora. The collector could then use identification aids for an adjoining area or those included in broader taxonomic treatments, if these are available. However, keys included in a Flora of a specific region are designed to work with the species found in that region and if used for an adjacent region may not provide an accurate identification, because the two regions are likely to have a similar but not identical range of taxa. Chapter 10 deals with finding the most appropriate taxonomic treatment for a given area or species. When using a key for the first time, it is important to read carefully any introductory comments on format details, abbreviations, etc. This will also reveal whether any special tools (in particular, a hand lens) will be necessary.

### *Multi-access keys*

Multi-access keys were developed to overcome some of the problems associated with single-access keys. A multi-access key does not force the user to go through the character set in a specific, preordained sequence. It allows the user to ignore particular characters and still obtain an identification. For example, if the specimen lacks fruit and seed, the identification can be based on vegetative and flower characters alone.

The early forms of multi-access or polyclave keys were produced using edge-punched cards. Each card, representing a taxon, has a series of labelled holes around its edges, each representing a particular character state. If the character state is absent, then the edge of the card is punched out at the appropriate point, making an indentation out of the hole. Depending on the character state of the specimen, the user selects a character and inserts a needle through the pack of taxon cards. When the needle is lifted, the cards (taxa) which do not match the specimen fall out of the pack, leaving those that possess the selected character state hanging from the needle. This process of selecting characters, projecting a needle through appropriate character state holes and excluding cards, is continued until only one card remains, the card for the taxon to which the specimen belongs (Stace, 1989).

One reason for the limited use to which punched-card keys have been put has been the practical difficulties in designing and producing the cards. Tabular keys are a more commonly used form of multi-access key and can take a variety of different forms. An example of a tabular key for the *Vicia* taxa of Keys 11.1 and 11.2 is provided in Table 11.1, with species in the columns and characters in the rows. The table is filled with coded character states for each taxon. For example, *V. pyrenaica* has the code P for the character 'life form', while the other taxa have the code A, indicating that *V. pyrenaica* is perennial and the other taxa are annuals. To identify a new specimen, the user records its characteristics using the same codes and row structure as the tabular key and then compares the specimen data with each column of the table. A match between the user's score card and a particular taxon provides the identification.

A refinement of the tabular format was proposed by Sinker (1975), who devised the lateral key. An example of a lateral key for the *Vicia*

Table 11.1. Tabular key to a group of vetches. For abbreviations see p. 189.

	<i>V. barbazitae</i>	<i>V. cuspidata</i>	<i>V. grandiflora</i>	<i>V. lathyroides</i>	<i>V. pyrenaica</i>	<i>V. qatmensis</i>	<i>V. sativa</i>
1. Life form	A	A	A	A	P	A	A
2. Stipule length (mm)	4-6.5	2.5-4	4-6.5	2-4	4-6	4-5.5	4-12
3. Number stipule teeth	H/D	H	H/D	H	H/D	D	H/D
4. Tendril form	S/B	S	S/B	S	S/B	B	S/B
5. Flower length (mm)	15-26	7-14	19-33	5-14	15-25	20-21	15-28
6. Standard colour	Y	L	Y	G	G	Y	G
7. Wing colour	G	L	Y	G	G	Y	G
8. Legume cross-section shape	R	R/C	C	R	R	C	R
9. Legume curvature	N	F	N	N	N	N	N
10. Legume shape	U	B	U	U	U	U	U
11. Seed surface	S	T	S	T	S	S	S
12. Hilum shape	O	R	E	R	O	E	O
13. Aril presence	-	-	+	-	-	-	-

taxa is provided in Table 11.2. The style is very similar to the tabular key, but in this variant there is a column for each character state. Characters are separated by a vertical line and each cell in the table is filled by a symbol which indicates if the character state is present or absent in that taxon. To identify a specimen the user constructs a one-row structure on paper similar to the structure of the lateral key. A description for the specimen is then prepared, recording the presence or absence of each character state in the table. Having completed the scoring, the score sheet is then slid down the table, keeping the columns of the lateral key and score sheet aligned, until a match is found, providing the identification.

The various printed forms of multi-access keys are now being superseded, at least in part, by computerized keys. It seems likely that in the future the use of printed multi-access keys will be restricted to identification guides designed for use in the field, where it may remain less convenient to use a computer.

### *Illustrations*

One of the problems non-specialists have in learning to use traditional keys is the amount of technical botanical terminology involved. Where is the calyx? What is a capitate style? Ideally, identification aids should either avoid such technical terms altogether or explain them. If illustrations (line drawings, photographs, paintings, etc.) of the key features of the species are provided, recourse to complex terminology may be avoided. Many botanical field guides now include illustrations as well as detailed text including scientific and vernacular names, diagnostic descriptions, distribution maps, phenology, ecological preferences, geographic distribution and conservation status. Information on whether illustrations are available for any particular plant group can be obtained from the relevant taxonomic revisions or monographs, where they should be cited, or from a survey of the appropriate catalogues in a good botanical library. *Index Londinensis* is a key to the botanical illustrations of flowering plants and ferns of the world up to 1935. After that date, *Index Kewensis* took up the task (Chapter 10).

The use of illustrations, when combined with technical terminology, can, in addition to facilitating identification, also help the user to learn and understand the meaning of botanical terms. Useful illustrated morphological glossaries are sometimes provided by Floras and field guides (e.g. Blundell, 1987) and may also be found in various botanical textbooks (e.g. Radford *et al.*, 1974; Radford, 1986). Bell (1991) is a specialized illustrated guide to morphological terminology as applied to flowering plants. Botanical dictionaries (e.g. Jackson, 1928; Stearn, 1983; Tootill, 1984) are also helpful in this context.

The relative efficacy of using line drawings, paintings or photographs to aid identification is a matter of subjective assessment and individual preference. However, one problem associated with using photographs for identification is that they can only show what is



**Table 11.2.** Lateral key to a group of vetches.

Character codes	A	P	<4	≥4	H	D	S	B	<14	≥14	Y	L	G	Y	L	G	R	C	N	F	U	B	S	T	R	O	E	+	-							
State numbers	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29							
<i>V. barbazitae</i>	■	○	○	■	■	○	○	■	○	■	■	○	○	○	○	■	○	○	■	○	○	○	○	○	○	■	○	○	○	■						
<i>V. cuspidata</i>	■	○	■	○	■	■	*	○	○	○	○	○	○	○	○	○	*	■	○	■	○	○	○	○	■	○	○	○	○	○	■					
<i>V. grandiflora</i>	■	○	○	○	■	○	*	■	○	■	■	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○				
<i>V. lathyroides</i>	■	○	○	○	■	○	*	■	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	■			
<i>V. pyrenaica</i>	○	■	○	○	■	■	*	■	○	■	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	■		
<i>V. qatmensis</i>	■	○	○	○	○	■	○	■	○	■	■	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	■	
<i>V. sativa</i>	■	○	○	○	■	■	*	■	○	■	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	■

Abbreviations used in Tables 11.1 and 11.2. A annual, P perennial; H hastate, D dentate; S simple, B branched; Y yellow, L lilac, G purple; C laterally compressed, R round; N not falcate, F falcate; U unbeaked, B beaked; S smooth, T tuberculate; O oval, E elongated; + present, - absent, / - or +; ■ state present, \* state rarely present, ○ state absent.

observed at a particular time in a two-dimensional image, whereas with a drawing or painting the illustrator can enhance the observed two-dimensional image to include features that may be less obvious on an individual specimen at that time or in that particular plane of view. For this reason, it is less likely that a specimen could be accurately identified by comparison with photographs. As a general rule drawn illustrations are preferable, to be used in conjunction with other aids.

### ***Computer-assisted identification***

Computers have been used by taxonomists in two main ways:

- to produce printed keys;
- for interactive identification.

### **Production of printed keys**

Several key-generating programs have been devised (Pankhurst, 1991). Perhaps the most user-friendly and widely used is KEY (Dallwitz, 1974). KEY is an integral part of the DELTA (Descriptive Language for Taxonomy) package (Dallwitz, 1980), a simple and versatile taxonomic coding system. The International Union of Biological Sciences Commission on Taxonomic Databases (TDWG) has endorsed the DELTA format for recording and exchanging descriptive data. The DELTA package (which is relatively inexpensive) comes with a set of programs which can be used to organize and manage taxonomic data. KEY generates bracketed and tabular keys from data coded into DELTA format (see Box 11.1 for case-study). There are a number of options which can be used to modify the basic key-generating algorithm, making it possible to experimentally produce numerous keys in a few minutes, compared with the several days which it might take to produce even just one key by hand. If the characters have been well structured and have been carefully chosen on the basis of the requirements of identification (rather than classification), good workable keys can be produced. Invariably, once a draft key has been generated by KEY, further editing with a word processor is likely to be required, but this extra work is minimal compared with the time saved in key construction.

### **Interactive identification programs**

There have been many attempts to produce computerized keys since the 1960s, one of the earliest being that of Boughey *et al.* (1968). Most of these efforts have not found an application outside their laboratory of origin, either because they have been experimental, have been tied to specific taxa or have used an inappropriate identification paradigm. Examples of contrasting approaches to interactive key generation and use are found in Wilson and Partridge (1986), Atkinson and Gammerman (1987), O'Shea (1988) and Colosimo *et al.* (1991).

The most successful systems seem to be those that employ a computerized multi-access key, or polyclave. In its simplest form, a polyclave

**Box 11.1****Case-study: use of identification software in a collecting project**

The International Centre for Research in Agroforestry (ICRAF), the International Board for Plant Genetic Resources (IBPGR), the International Livestock Center for Africa (ILCA), and national programmes in five Southern Africa Development Community (SADC) countries mounted a regional collecting programme for woody *Sesbania* spp. in 1993. To aid identification, software from two sources was used – the DELTA system (see text) and EXPLORE (an experimental program written by Richard Crust of the University of Zimbabwe). DELTA was used to put together a workable taxa/characters matrix from published sources, using CONFOR to help ensure consistency and accuracy. The DELTA program KEY was then used to generate a series of dichotomous keys. By using DOS batch files, it was possible to produce dozens of such keys in a very short time. The most plausible keys were then tested in the field, discovering in the process that the literature was occasionally somewhat inaccurate in the documentation of variation among taxa. The DELTA files were updated to take this into account, and another series of dichotomous keys produced. These included country-specific keys, keys based only on vegetative and/or fruit characters and keys biased towards common or important species (e.g. *S. sesban*) or particularly important characters. After further testing during the collecting missions, the original data files were again revised and corrected, and then used as input to EXPLORE, an interactive polyclave identification program intended for training plant collectors.

is a taxonomic data matrix stored in the computer's memory. For example, each row in the matrix might represent a taxon and each column a character. The program manipulates the matrix in response to input from the user. The choice of characters is decided by the user, but the program may assist by ranking the characters and presenting them in different ways, perhaps in a new sequence. A common method is to order the unused characters by separation coefficient (Gyllenburg, 1963), information function (Shannon and Weaver, 1949) or some similar parameter. These are dynamic values that indicate how evenly each remaining, unused character divides the residual set of candidate taxa. As each character is used, at least one column of the matrix is discarded. A variable number of rows may also be discarded as taxa are eliminated from the search. Discarded rows and columns may be restored, however, at the user's request. Thus, the active part of the matrix diminishes or expands until identification is complete, i.e. when only one taxon row remains, giving the identification of the unknown specimen.

The versatility of the computerized polyclave makes it easy to provide identification by simultaneous matching as well as sequential elimination. One of the most valuable benefits is that it is possible to allow the user to increase the accuracy of the identification. When a dichotomous key is used, many of the eliminated taxa may differ from the unknown specimen by just a single character but, because of the structure of the key, these taxa are excluded. The computer polyclave

user may set an arbitrary threshold for the minimum number of differences accepted before any taxon can be eliminated from the search.

A good example of a generalized computer polyclave is INTKEY, one of the programs in the DELTA package. INTKEY is a command-line driven program that can be used with any descriptive data set coded in DELTA. It demonstrates most of the functions described above, and can also be used for 'information retrieval', e.g. obtaining diagnostic descriptions. Watson *et al.* (1989) describe, with examples, how INTKEY has been used to disseminate information about the grass genera of southern Africa. Another example of a package that can be used with different descriptive data sets is CABIKEY (I. White, pers. comm.). This is a polyclave program which is perhaps most suitable for educational purposes. It is menu-driven, with displays appearing in windows. Information concerning the context in which identification takes place can be integrated into the data. At any time, the CABIKEY user can call up text descriptions, diagnoses and illustrations of both taxa and characters. CABIKEY data sets are entered by arrangement with the program author, and so, unlike INTKEY, it is not suitable for the casual or experimental user. The suite of programs described by Pankhurst (1986) allows the user to compare and match a specimen against data sets held in memory.

Current trends in database technology are moving towards what is generally known as 'multimedia', the integration of text with illustrations, video animation and sound. The Expert-centre for Taxonomic Identification (ETI) at the University of Amsterdam is developing sophisticated taxonomic software that uses multimedia concepts. Its identification software (IdentifyIt) is a computer polyclave that uses expert-system methods. It points to ways in which advanced technology may be used for more efficient taxonomic identification. The computer hardware required to use ETI's software and databases is likely to become more widely available in the near future.

## Future prospects

Current concerns about the rapid loss of biodiversity are imposing demands on the taxonomic community that can only be met by overhauling traditional practices and applying appropriate up-to-date techniques. Single-access keys and the taxonomic terminology required to use them cannot adequately meet the growing requirement for accurate specimen identification. There is thus immense potential for the application of computerized identification. There have, however, been a number of practical difficulties that have prevented this potential from being fully realized. For example, the development of reliable software is very expensive and getting taxonomic data into a suitable format is tedious, time-consuming and error-prone. It is also difficult to design a user interface which is intuitively simple to use, especially for someone more

familiar with traditional printed keys, and yet which takes account of all the possibilities held out by the computerized polyclave. Nevertheless, it is reasonable to predict that these problems will be resolved before long.

Multi-access keys are a step forward, but further developments are required. These may include more use of expert systems, deploying not just raw taxonomic data but taxonomic knowledge and expertise (e.g. Diederich and Milton, 1988), and large-scale systems that directly link taxonomic expertise with the applied disciplines that make use of it, such as plant breeding and phytochemistry. There is a pressing need for methods that assist taxonomists in understanding their data, rather than merely processing it.

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