

User's Guide
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DELTA Intkey Tutorial

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TABLE OF CONTENTS

General Information	3
The Intkey Screen	4
INTKEY Icons	5
The Information Box	6
Using INTKEY	7
Changing a character state selection	11
The Subset Button 	13
Character notes	14
Flipping between subsets	15
Mismatches	16
The Differences between taxa button 	18
Displaying information about a taxon	20
The Find Button 	22

GENERAL INFORMATION

INTRODUCTION

This tutorial was created as a basic guide to Intkey identification and introduction to some of the features available through the toolbars. The guide uses data from the **DELTA Sample Data** set provided by L. Watson and M. J. Dallwitz. This sample data set is available when downloading Intkey from the web (see below). The tutorial is constructed so the user can be shown as many features of Intkey as possible.

ABOUT INTERACTIVE KEYS

Interactive keys differ from printed, dichotomous keys in that there is no predetermined path that the user must follow to effect identification. Interactive keys allow the flexibility of viewing characters in different orders and of selecting them in a sequence that suits the information available to the user. The characters can be presented in the 'natural' order, i.e. grouped together by feature, e.g. all leaf characters together, or by 'best' order, in which characters with the best power to separate the taxa in the group are presented first. Both these arrangements are interchangeable within the identification process and changing from one mode to another does not affect the previous choices.

ABOUT THE SAMPLE DATA

The data on grass genera were collected in DELTA format by L. Watson of the Australian National University. They are an extract from the full data set, which contains descriptions of about 800 genera in terms of more than 500 characters (Watson and Dallwitz 1981; Watson, Dallwitz and Johnston 1986; Watson and Dallwitz 1992). The extract was chosen to illustrate the use of the DELTA programs, and is not intended to be a biologically meaningful subset. The DELTA system is provided free-of-charge.

DOWNLOADING DELTA INTKEY

As of 2013, the DELTA Intkey program (and others) have been rewritten in Java. For instructions on how to install DELTA Intkey, please visit <http://florabase.dec.wa.gov.au/help/keys/>.

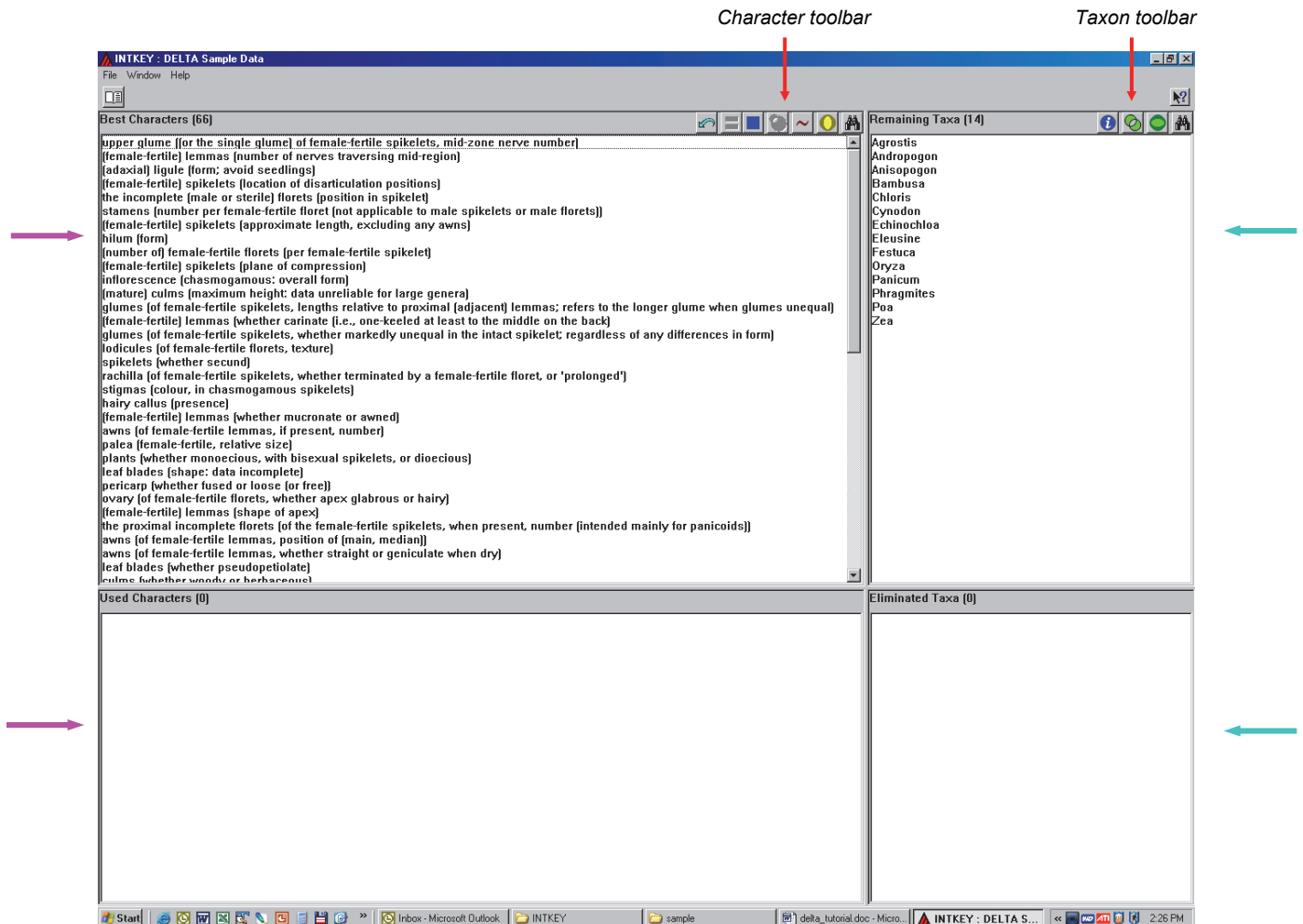
CITATION

L. Watson and M. J. Dallwitz (1998 onwards). DELTA Sample Data: Descriptions, Illustrations, Identification, and Information Retrieval. Version: 21st September 2000.

THE INTKEY SCREEN

This screen is the first screen you will see as you begin your identification. It is divided into 4 panes – two for characters (left side) and two for taxa (right side).

Each set of panes has its own set of toolbar icons placed on the top of the upper panes:



There are four panes – the two on the left displaying lists of characters and the two on the right containing lists of taxa

- best characters (top left): the best characters to use are listed at the top
- used characters (bottom left): the characters used so far in your identification
- remaining taxa (top right): the set of taxa which match the used character values
- eliminated taxa (bottom right): the set of taxa which no longer match the characters used

Initially only the top two panes contain information.



The character list can be displayed in two ways – 'best' order or 'natural' order. This view shows the character list in 'best' order (see next page for explanation).







Stay on this screen and use it to follow the Intkey icon explanations on the next page.





INTKEY ICONS

The Intkey icons are found under the menu bar and within the character and taxon toolbars, along the top of the uppermost panes. Holding the mouse over the icons reveals their function.

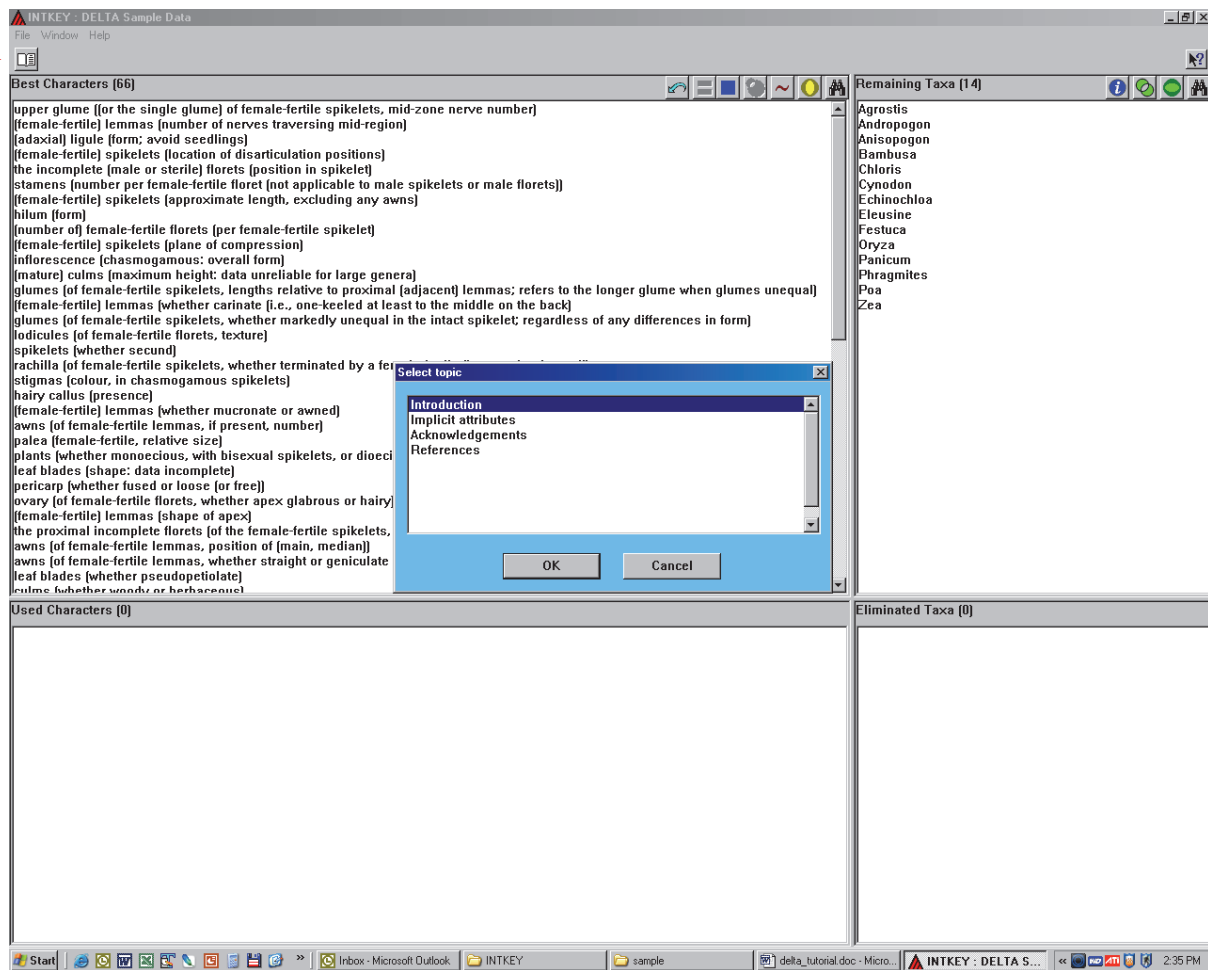


	Introduction and references – this enables you to read extra information on the data set and view the author's reference file.
	Help button – to find out more information about any button in the set, press 'help' then the button for which you need an explanation.

	Restart Identification – if you want to re-start your identification click this button.
	Best order – displays the characters in the top-left pane in order of their merit for separating the remaining taxa in the identification. This icon is greyed out on the screen because the characters ARE in 'best' order.
	Natural order – displays the characters in the top-left pane in the order in which the author placed them in the character list. Warning. Unless you are familiar enough with the data to know that certain character values exhibited by your specimen will eliminate a good proportion of the taxa at the current stage of the identification, you should consider using the 'Best' order.
	Set error tolerance – A taxon will remain under consideration until the number of differences between it and the specimen is greater than the error tolerance. You should increase the current value by 1 if you are aware that you have made a mistake in an identification (because the illustration or description of the remaining taxon does not correspond to your specimen) but you do not know what the mistake is.
	Use a subset of the characters. This button allows you to choose a set of characters to be used in subsequent operations. THIS IS A VERY USEFUL INTKEY TOOL
	Search – enables you to find text in characters or in taxon names.

	Information about taxa – allows you to display any information about the selected taxon eg descriptions, images
	Differences between taxa – displays the differences between selected taxa. Two or more taxa must be selected in either or both of the 'Taxa' panes before pressing the button.
	Use a subset of the taxa – allows you to choose a subset of the taxa, rather than the whole set. The subsets are defined by the author
	Search – enables you to find text in characters or in taxon names

THE INFORMATION BOX

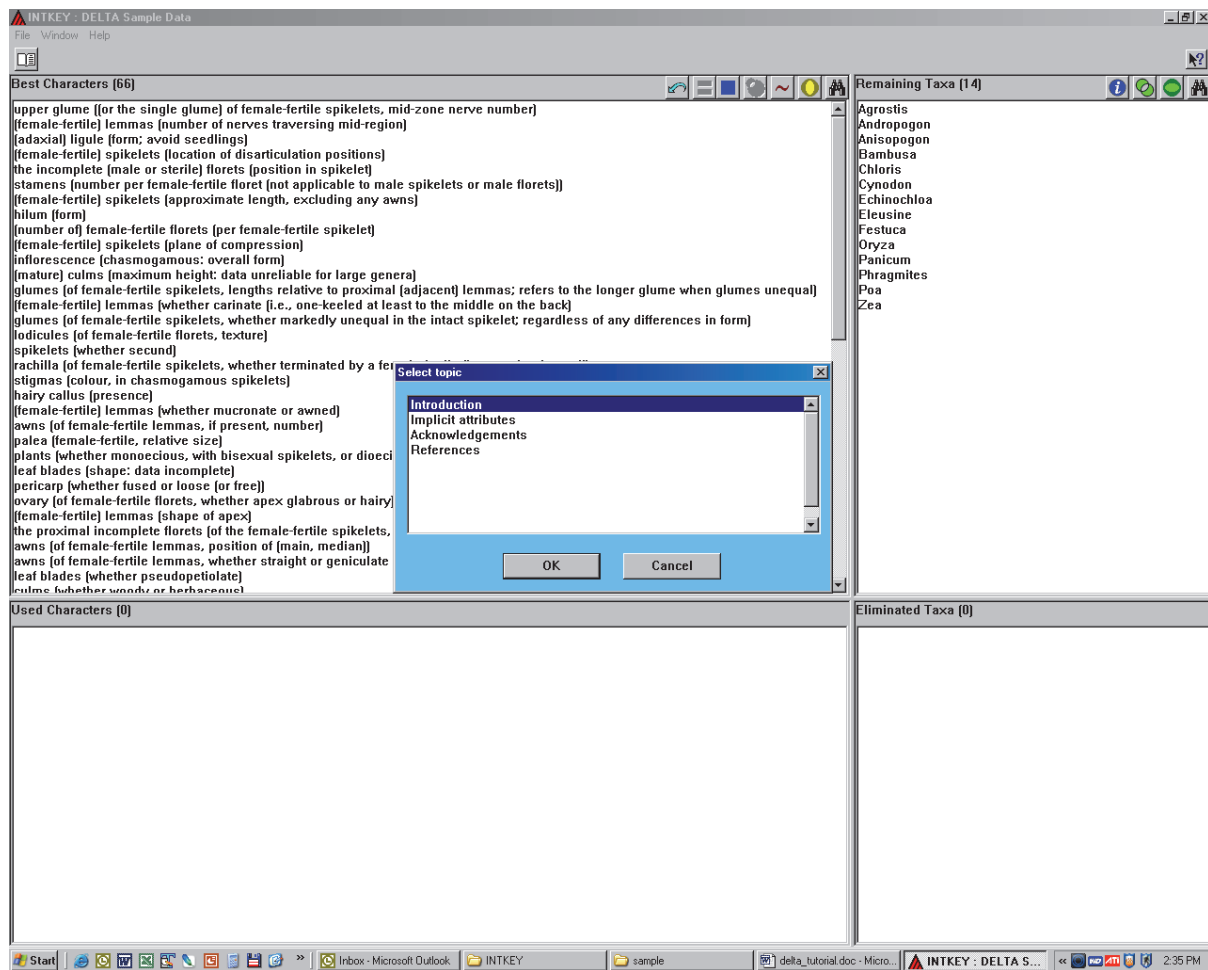


This screen shows the information dialogue box (in blue), which is accessed by clicking the book icon in the upper left corner (see arrow). Within this box are links to other information that the author has compiled for the data set.

HINT

Always check here first, as there may be special instructions from the author, which will help you to use a particular Intkey set

USING INTKEY

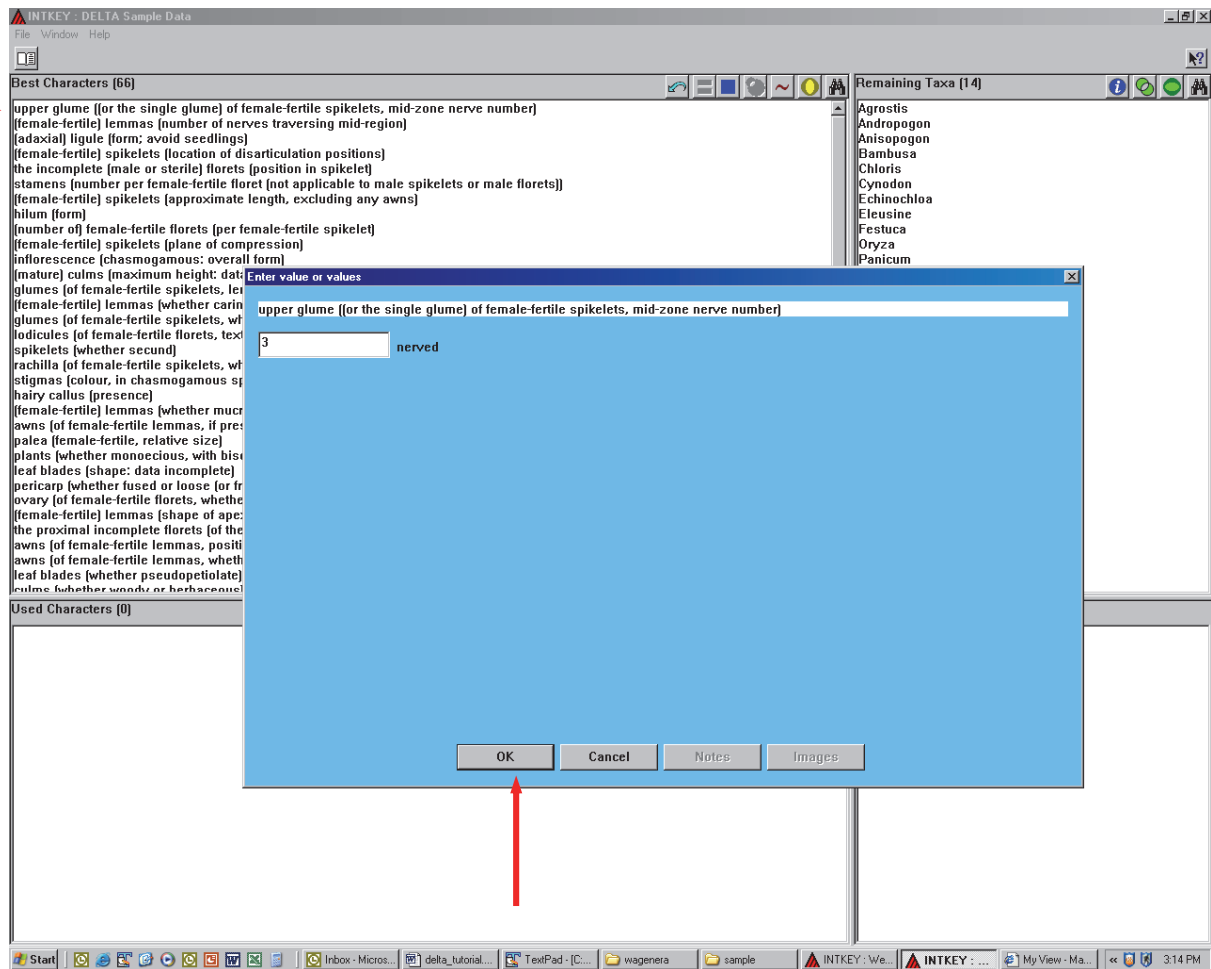


Examine the characters in the top left pane. In this screen the characters are sorted in the 'best' order i.e. the characters with the stronger discriminating power are listed first.

The first character is the best character to use (it is the most efficient character for eliminating the most taxa from your list), however, it is not necessary to start with this character; neither is it necessary to choose characters in the order in which they are presented.

Select the first character **by clicking on it...**

CHOOSING THE FIRST CHARACTER



On selecting this character, a character dialogue box appears. In Intkey there are two types of characters:

- numeric: requiring a real number or integer or a range of numbers
- multistate: requiring choice of one or more states

This character is a numeric character and requires an integer to be entered into the space – we entered 3

Enter 3, and then click the OK button on the box...

RESULTS...

Best Characters (60)

- the incomplete [male or sterile] florets [position in spikelet]
- [number of] female-fertile florets [per female-fertile spikelet]
- [female-fertile] spikelets [location of disarticulation positions]
- inflorescence [chasmogamous: overall form]
- [female-fertile] lemmas [whether carinate (i.e., one-keeled at least to the middle on the back)]
- stigmas [colour, in chasmogamous spikelets]
- [adaxial] ligule [form; avoid seedlings]
- palea [female-fertile, relative size]
- [female-fertile] spikelets [approximate length, excluding any awns]
- spikelets [whether secund]
- hairy callus [presence]
- [female-fertile] spikelets [plane of compression]
- glumes [of female-fertile spikelets, lengths relative to proximal [adjacent] lemmas; refers to the longer glume when glumes unequal]
- [female-fertile] lemmas [number of nerves traversing mid-region]
- [female-fertile] lemmas [whether mucronate or awned]
- hilum [form]
- rachilla [of female-fertile spikelets, whether terminated by a female-fertile floret, or 'prolonged']
- lodicules [of female-fertile florets, texture]
- leaf blades [shape: data incomplete]
- awns [of female-fertile lemmas, if present, number]
- spikelet-bearing axes [whether disarticulating; note that spikelet-bearing axes may be greatly reduced]
- fruit [or grain surface pattern]
- pericarp [whether fused or loose [or free]]
- [mature] culms [maximum height: data unreliable for large genera]
- spikelets [whether in regular 'long-and-short' combinations, as exemplified in typical andropogonoids]
- glumes [of female-fertile spikelets, whether markedly unequal in the intact spikelet; regardless of any differences in form]
- [female-fertile] lemmas [shape of apex]
- plants [whether monoecious, with bisexual spikelets, or dioecious]
- glumes [of female-fertile spikelets, whether carinate (i.e., one-keeled to middle or below)]
- awns [of female-fertile lemmas, whether straight or geniculate when dry]
- the proximal incomplete florets [of the female-fertile spikelets, when present, number [intended mainly for panicoids]]
- awns [of female-fertile lemmas, position of [main, median]]
- spikelets [termining: recorded mainly in spikes and racemes]

Remaining Taxa (8)

- Andropogon
- Chloris
- Cynodon
- Eleusine
- Festuca
- Panicum
- Phragmites
- Poa

Used Characters (2)

- glumes present
- upper glume 3 nerved

Eliminated Taxa (6)

- [1] Agrostis
- [1] Anisopogon
- [1] Bambusa
- [1] Echinochloa
- [1] Oryza
- [1] Zea

In each of the panes, the lists have now changed:

- Top left:** the computer has recalculated the best characters to use to discriminate between the remaining taxa.
- Bottom left:** this shows the characters and values that have been used so far in the identification
- Top right:** shows a list of taxa which match the character values entered so far and therefore remain in the list to be identified
- Bottom right:** shows the list of taxa that don't match the data you have entered and have therefore been eliminated from the identification process

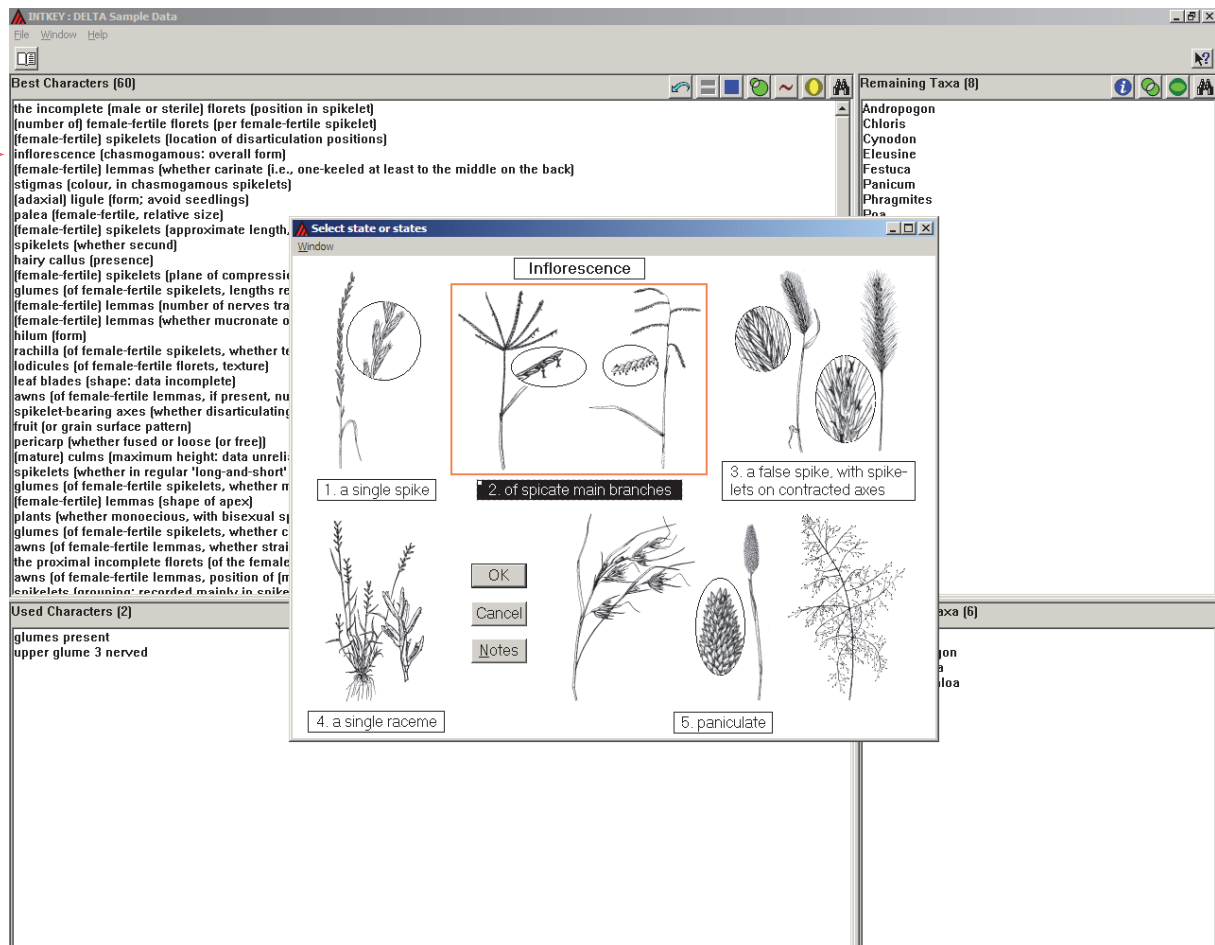
DEPENDENT CHARACTERS

The programme has scored a character you did not select – **'glumes present'** – see red arrow.

Throughout Intkey data sets there will be a number of characters that must be answered before the character you have chosen can be considered. Sometimes, as in the above case, the computer will automatically assign the correct state needed for the program to continue. Or you will have to provide the answer: in that case the character dialogue box for the controlling character will be presented. e.g. when choosing a leaf character you may be asked to answer a character about the presence of leaves. Answer this and the character you selected will be presented for scoring.

Do not be scared if this happens

NOW, SELECT ANOTHER CHARACTER



Select the character “inflorescence (chasmogamous – overall form)”

Note that this character is NOT the first character on the list.

This character has 5 states. These states are presented as diagrams within the character dialogue box. Highlight the state(s) you choose (in this case, state 2), then click the OK button on the box or double-click the state description.

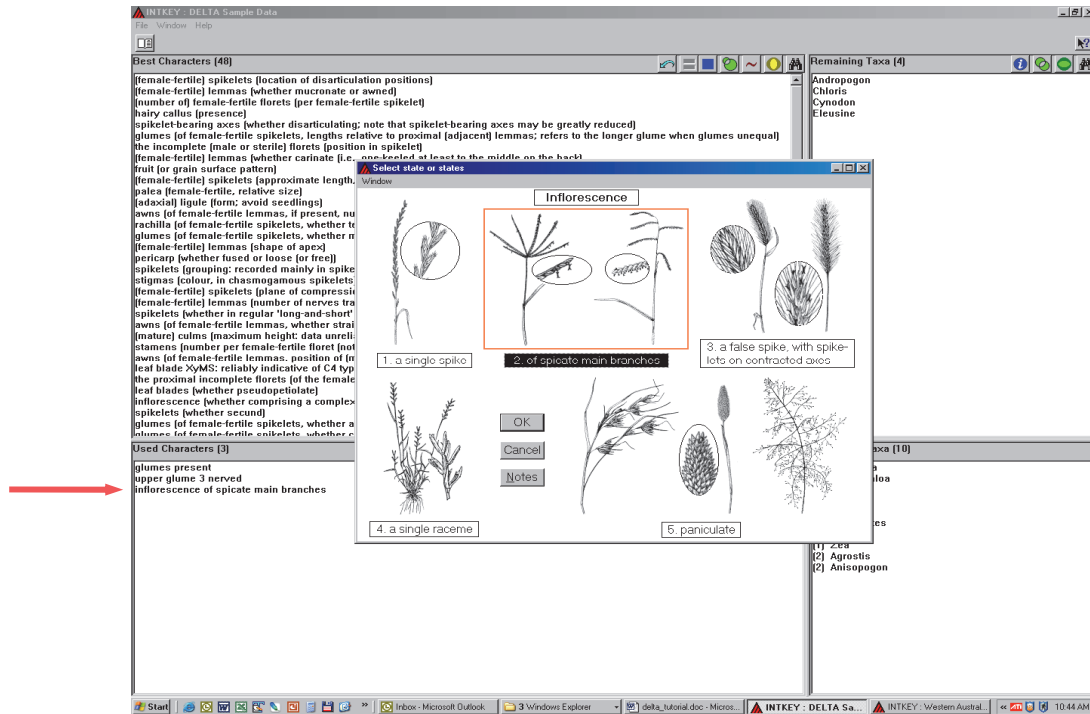
Note that on initial presentation of the character states, the first state looks as if it is already highlighted. It is not. To choose State 1, you must click on it.

CHOOSING MORE THAN ONE STATE

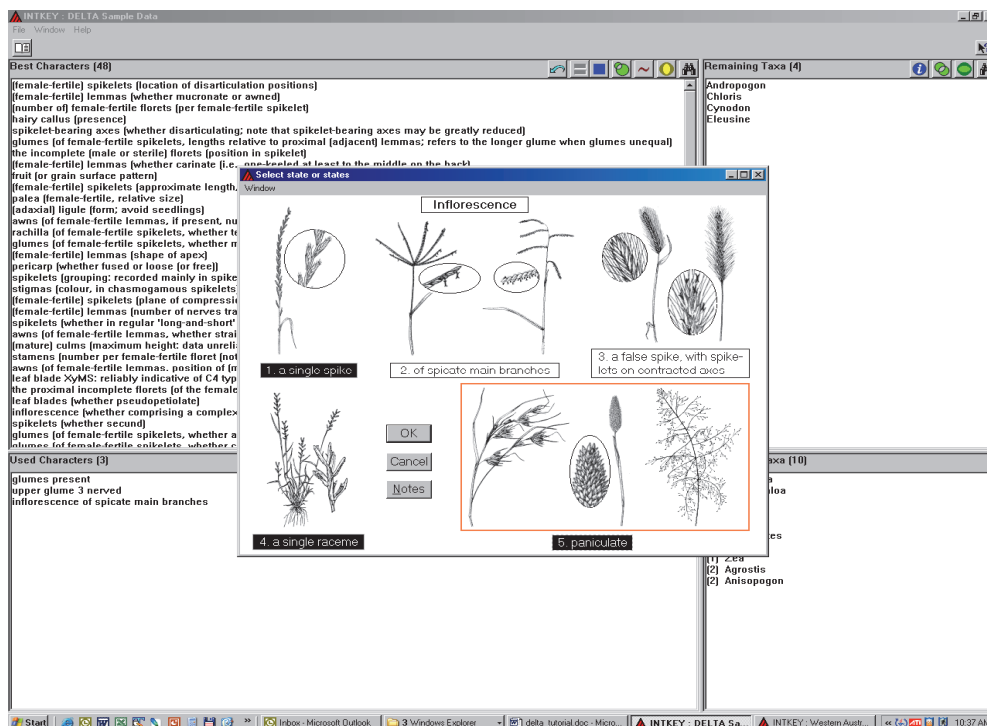
You can choose more than one state if you are unsure which is represented in your specimen. Just highlight as many as you need by clicking on the state name and then click the OK button. There is no need to hold down the shift or control keys for multiple selections. To un-select a state while in the dialogue box, just click it again.

CHANGING A CHARACTER STATE SELECTION

If, at any stage, you think you have made a mistake and want to correct it, click on the appropriate character in the 'Used Characters' (bottom-left) pane. The character dialogue box will be displayed with your original selection highlighted...

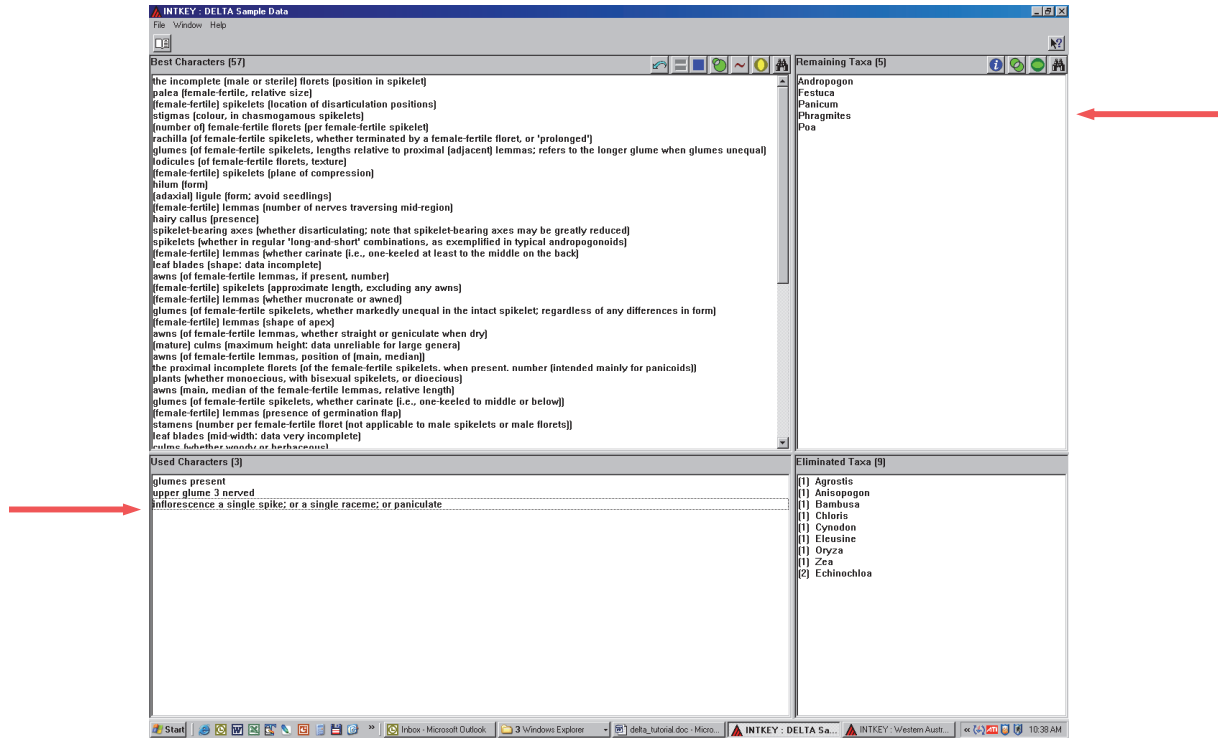


To change the previously entered information, click on the highlighted state. This un-selects it. Then click on the state(s) you do want and click OK. The example below shows a selection of states 1, 4 & 5. Select these states and click OK.



CHANGING A CHARACTER STATE SELECTION (CON'T)

Now the original selection has been replaced with the new selection and the data recalculated.



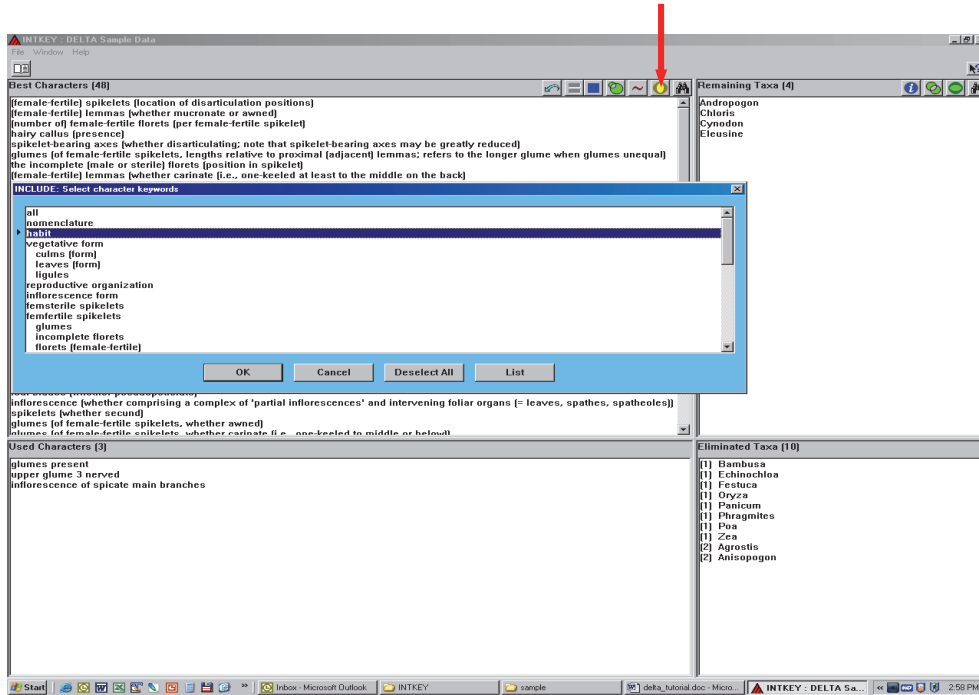
Return the data to the original selection of 'inflorescence of spicate main branches', i.e. State 2


TO REMOVE A CHARACTER SELECTION COMPLETELY

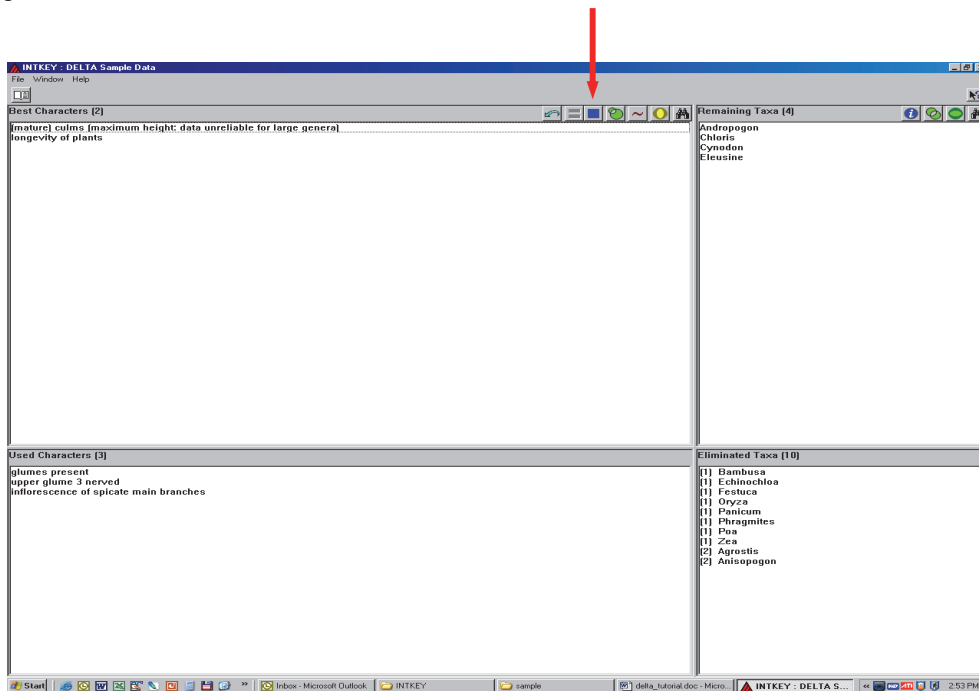
Click on the character in 'Used Characters'. This returns the character dialogue box with the chosen state(s) highlighted: Click on the highlighted state(s) to de-select. **Then click OK.** This causes the character to be returned to the 'available characters' pane and any taxa that were eliminated by the character you have just cancelled, to be replaced.

THE SUBSET BUTTON 

Most authors create a set of subsets of the character list. This allows you easy access to groups of characters without looking through the entire character list for them. This is very useful when working with large character sets such as the Western Australian Herbarium's WAGENERA Delta set. The picture below shows the list of subsets available for the Sample set. Choose the 'habit' set.



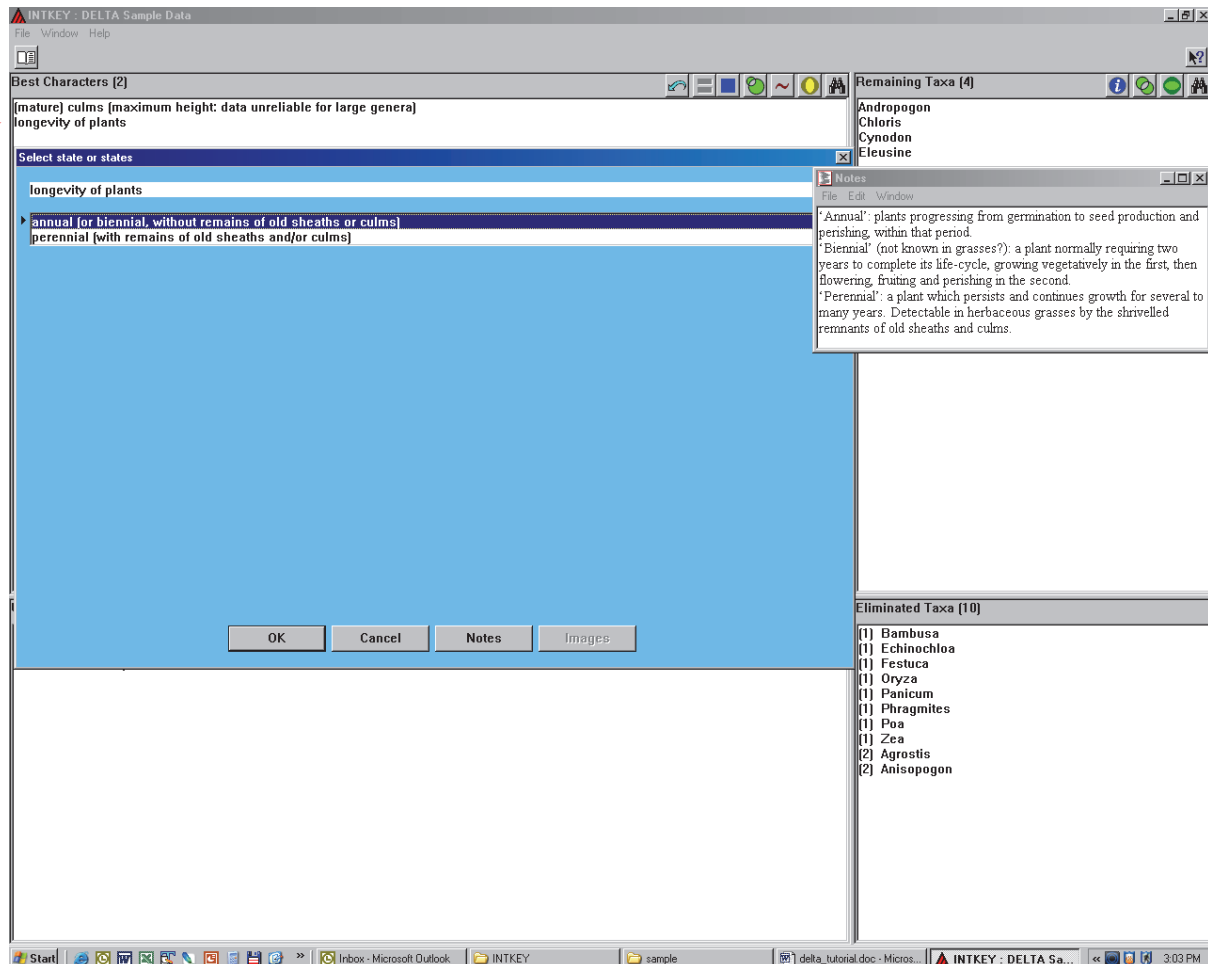
The screen below shows that there are 2 characters available for this set, in the 'best' view. Other characters may be available in the 'natural' view. To change to 'natural' order, click on the 'natural' button, shown by the red arrow below. Now 4 characters are available for use. Go back to 'best' view by clicking the 'best' icon 



CHARACTER NOTES

To help you interpret the character states, the author may have provided notes and images for various characters throughout the set, accessible when you select that character. If supplementary character information is available, the NOTES and IMAGES buttons in the character dialogue box will be active.

Select another character. In this case we have chosen 'longevity of plants'.



This character has two states and is presented in a normal blue character dialogue box.

NB: Sometimes if there are more states than will fit into the space provided, a scroll bar is provided. In this case all states are visible.

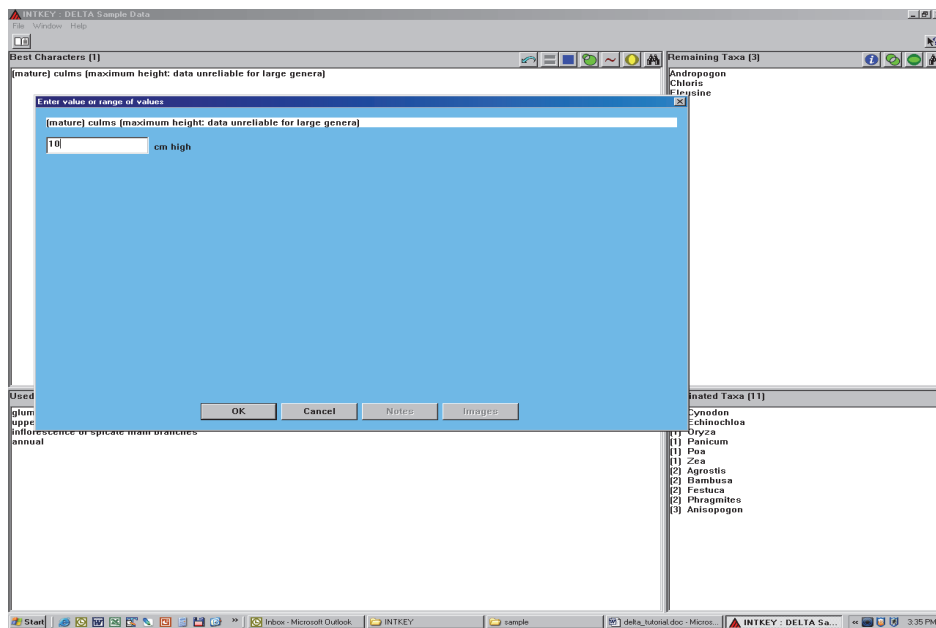
If you are uncertain about definition of the states or require more information, click the NOTES button within the dialogue box. This displays a Notes window near the upper right corner of the character dialogue box.

Note that in this case the image button is greyed out, as no character image is available.

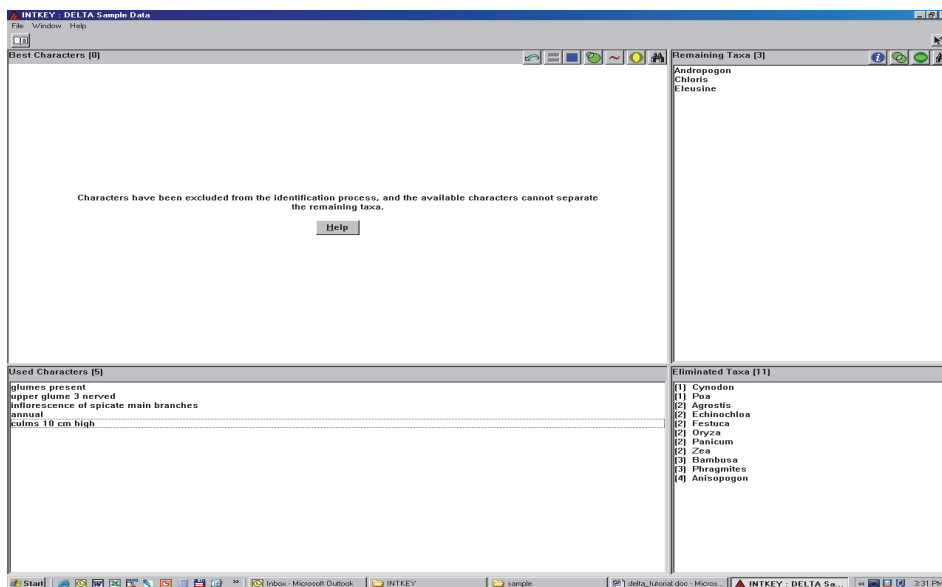
To continue, highlight 'annual', then click the OK button on the box.

FLIPPING BETWEEN SUBSETS

Remember you are still in the 'habit' subset. Choose the remaining character in this subset and type in '10' in the dialogue box:



This will result in message on the screen below. It is sent when you are using a subset of characters whose attributes cannot separate the remaining taxa. To return to the full list of remaining taxa, in order to continue the identification process, click on the subset button and choose 'all'. This will return all the remaining characters to the left hand pane. In this way you can flip between specialised sets of characters and the full list.

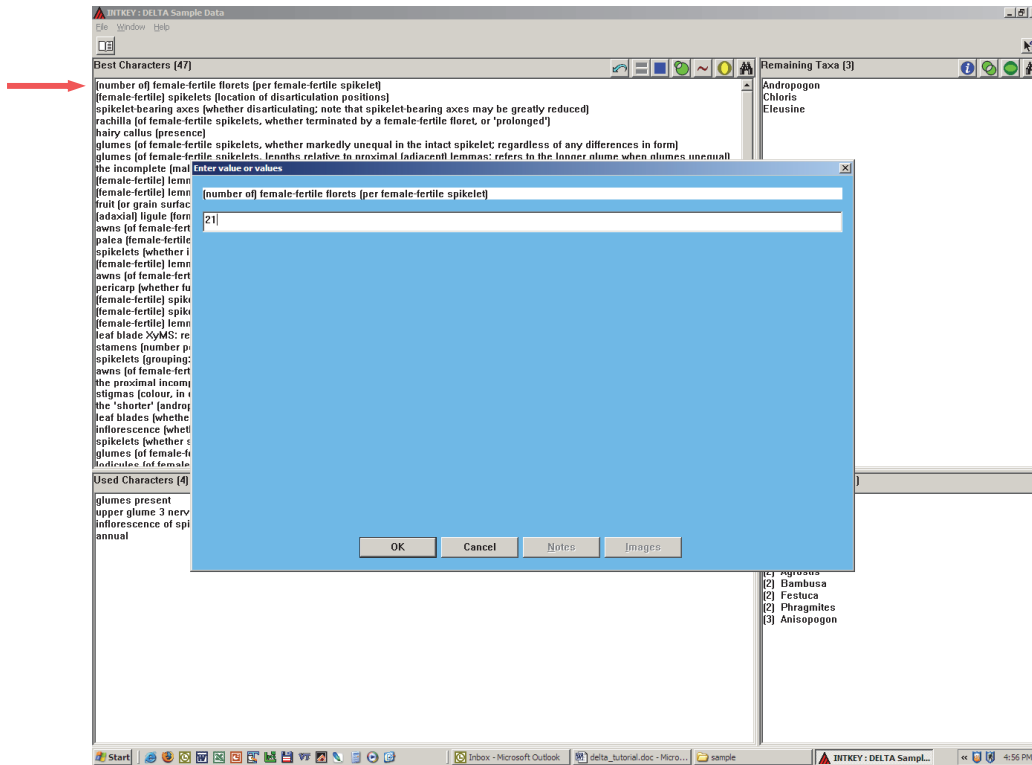


SWAPPING BETWEEN SUBSETS

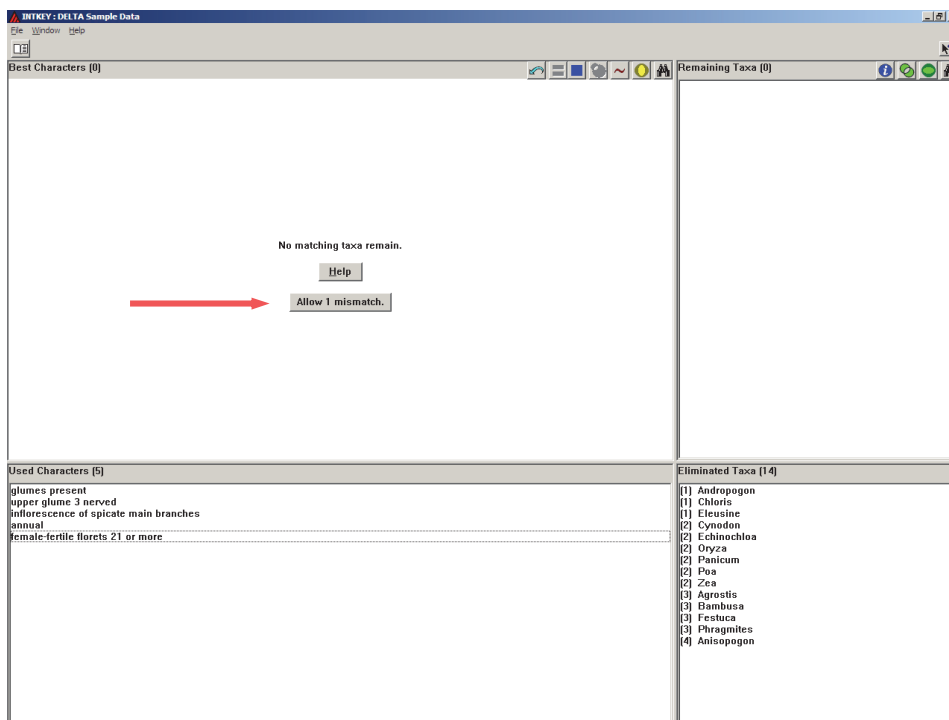
You can swap between subsets as often as you like. To return to the full character list choose 'all' from the subset list. Any characters which you have chosen whilst in 'subset' mode will remain as 'used characters' when you choose another subset.

MISMATCHES

Sometimes it is possible to exclude all the taxa depending on the character values you select. This is called 'mismatching'. The software will tell you this and displays a button allowing the programme to accept mismatches. To illustrate this, remove the 'culm' character by clicking on it, removing the '10' and clicking **OK**. Then choose the top character in the 'best characters' pane and type '21' in the dialogue box.



As you can see a 'mismatch' has occurred...



MISMATCHES (CONTINUED)

Clicking on the 'Allow 1 mismatch' button instructs the software to recalculate the list of remaining taxa and 'best' characters and allows you to continue identification, as seen below...

The screenshot shows the INTKEY: DELTA Sample Data software interface. The window is divided into several panes:

- Best Characters (46):** A list of 46 botanical characters, including:
 - [female-fertile] spikelets (location of disarticulation positions)
 - spikelet-bearing axes (whether disarticulating; note that spikelet-bearing axes may be greatly reduced)
 - rachilla (of female-fertile spikelets, whether terminated by a female-fertile floret, or 'prolonged')
 - hairy callus (presence)
 - glumes (of female-fertile spikelets, whether markedly unequal in the intact spikelet; regardless of any differences in form)
 - glumes (of female-fertile spikelets, lengths relative to proximal (adjacent) lemmas; refers to the longer glume when glumes unequal)
 - the incomplete (male or sterile) florets (position in spikelet)
 - (female-fertile) lemmas (whether mucronate or awned)
 - (female-fertile) lemmas (whether carinate (i.e., one-keeled at least to the middle on the back)
 - fruit (or grain surface pattern)
 - (adaxial) ligule (form; avoid seedlings)
 - awns (of female-fertile lemmas, if present, number)
 - palea (female-fertile, relative size)
 - spikelets (whether in regular 'long-and-short' combinations, as exemplified in typical andropogonoids)
 - (female-fertile) lemmas (shape of apex)
 - awns (of female-fertile lemmas, whether straight or geniculate when dry)
 - pericarp (whether fused or loose (or free))
 - (female-fertile) spikelets (approximate length, excluding any awns)
 - (female-fertile) spikelets (plane of compression)
 - (female-fertile) lemmas (number of nerves traversing mid-region)
 - leaf blade XyMS: reliably indicative of C4 type
 - stamens (number per female-fertile floret (not applicable to male spikelets or male florets))
 - spikelets (grouping; recorded mainly in spikes and racemes)
 - awns (of female-fertile lemmas, position of (main, median))
 - the proximal incomplete florets (of the female-fertile spikelets, when present, number (intended mainly for panicoids))
 - stigmas (colour, in chasmogamous spikelets)
 - the 'shorter' (andropogonoid) spikelets (sessile or shorter-pedicelled, sexuality)
 - leaf blades (whether pseudopetiolate)
 - inflorescence (whether comprising a complex of 'partial inflorescences' and intervening foliar organs (= leaves, spathes, spatheoles))
 - spikelets (whether secund)
 - glumes (of female-fertile spikelets, whether awned)
 - lodicules (of female-fertile florets, texture)
 - lodicules (of female-fertile florets, whether haired)
- Remaining Taxa (3):** A list of three taxa:
 - (1) Andropogon
 - (1) Chloris
 - (1) Eleusine
- Used Characters (5):** A list of five characters, with a red arrow pointing to the last one:
 - glumes present
 - upper glume 3 nerved
 - inflorescence of spicate main branches
 - annual
 - female-fertile florets 21 or more
- Eliminated Taxa (11):** A list of eleven taxa:
 - (2) Cynodon
 - (2) Echinochloa
 - (2) Oryza
 - (2) Panicum
 - (2) Poa
 - (2) Zea
 - (3) Agrostis
 - (3) Bambusa
 - (3) Festuca
 - (3) Phragmites
 - (4) Anisopogon

NOTE THAT THE CHARACTER YOU LAST SELECTED HAS REMAINED IN 'USED CHARACTERS'

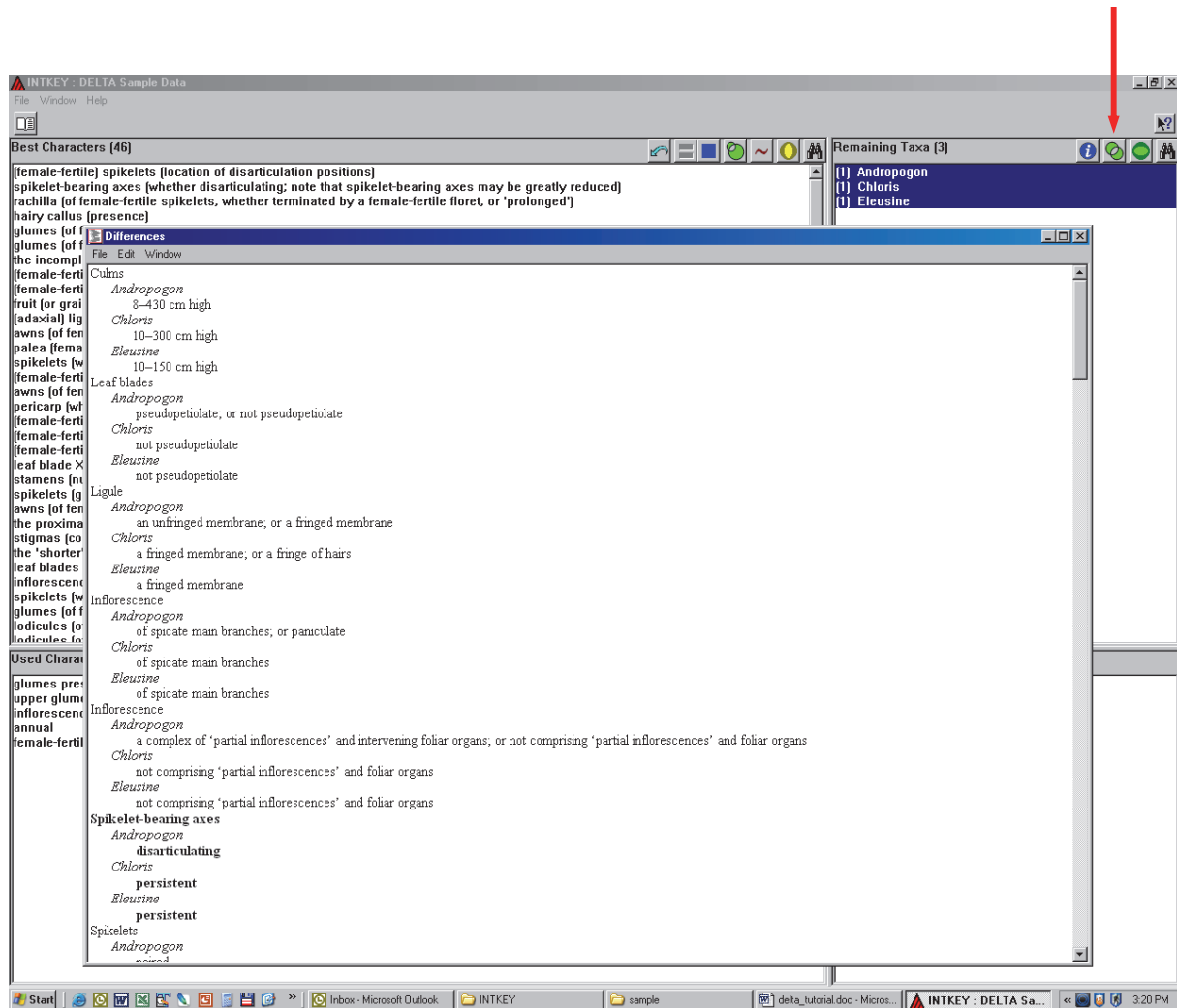
THE DIFFERENCES BETWEEN TAXA BUTTON



At any time during the identification you can display the differences between some or all of the remaining or eliminated taxa. This can be a useful tool in determining characters which may help you discriminate between a small number of remaining taxa.

To display the differences between taxa:

- Hold the **control key** down and highlight the taxa to be differentiated
- Click on the 'differences between taxa' button...



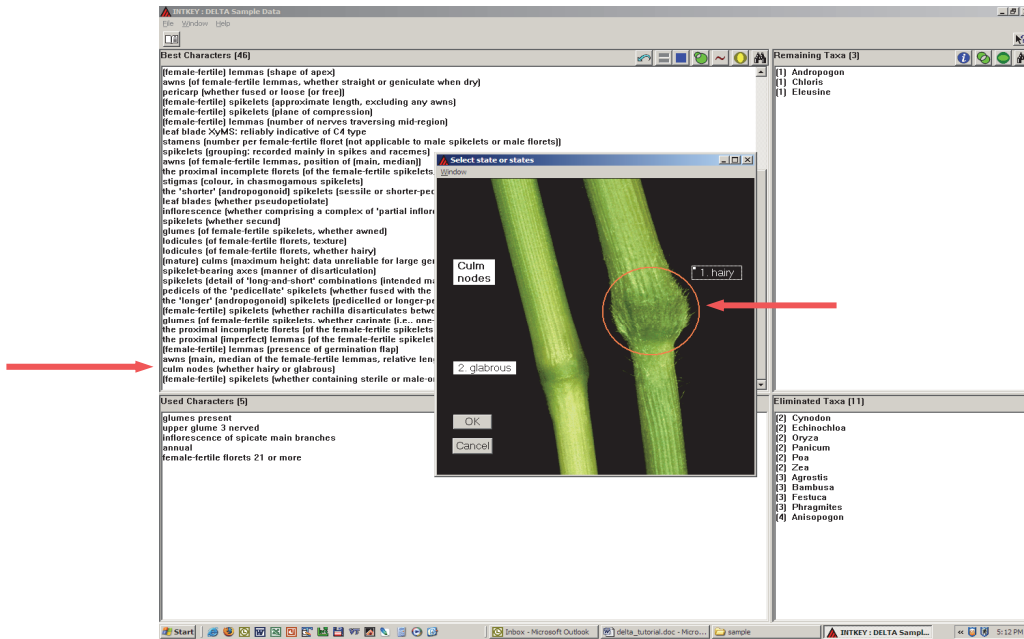
The resulting dialogue box lists the characters that differ between the chosen taxa.

Characters in bold signal a clear separation of values between all or some of the taxa.


To continue, close the 'Differences' box.

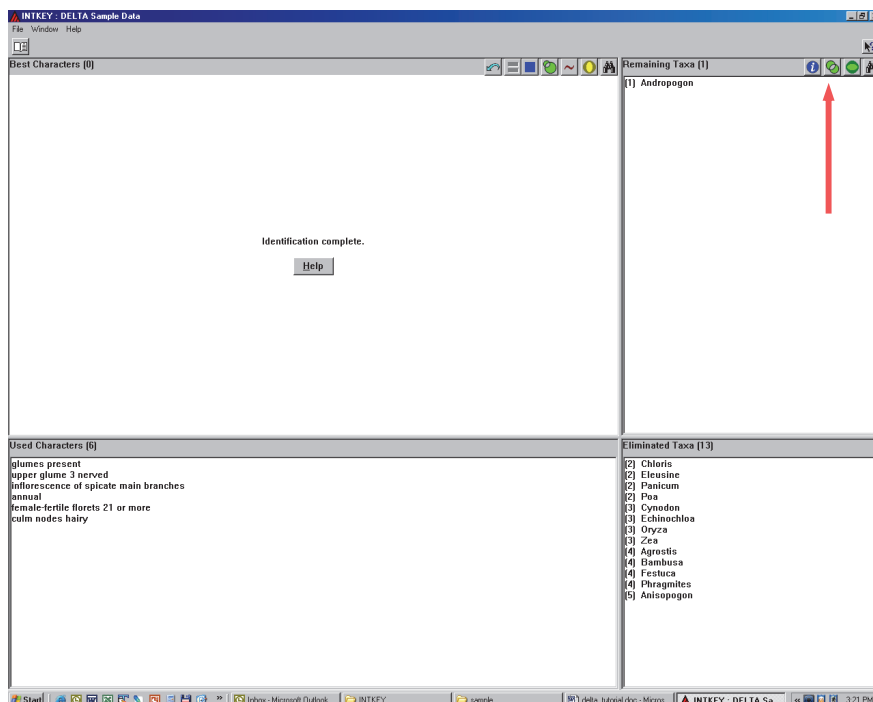
THE NEXT CHARACTER...

Scroll down the character list to the bottom and select 'culm nodes'. Note that you can choose characters to score from anywhere in the character list....

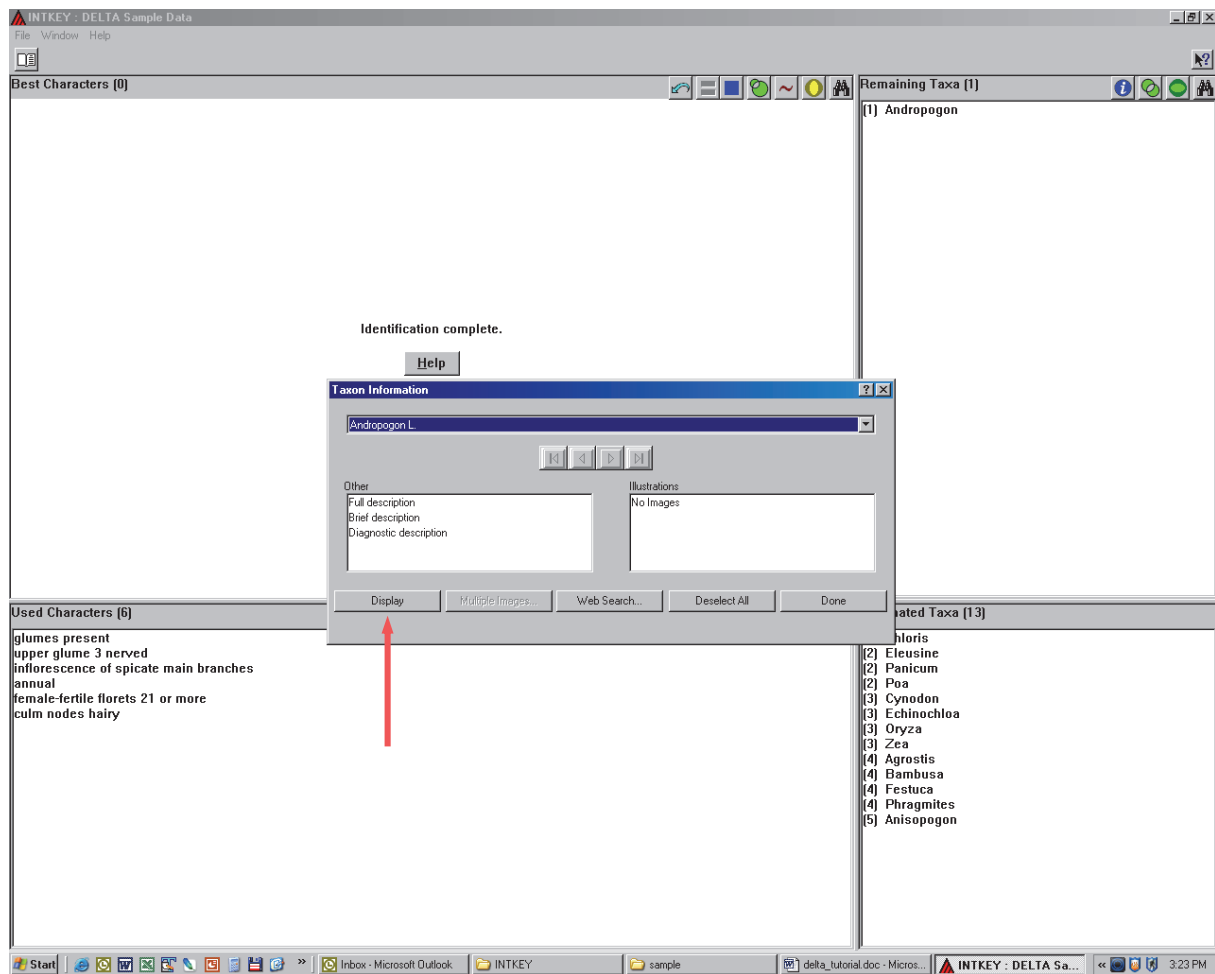


This character is presented as a photograph. In this example, the feature alluded to within the character state is shown by the red ring. Highlight this state (hairy), and click the OK button on the box or double-click in the red circle.

This character choice has resulted in a successful identification. There is only one remaining taxon – **Andropogon**. To see the extra information available for *Andropogon*, just click on the information button in the top right pane .



DISPLAYING INFORMATION ABOUT A TAXON

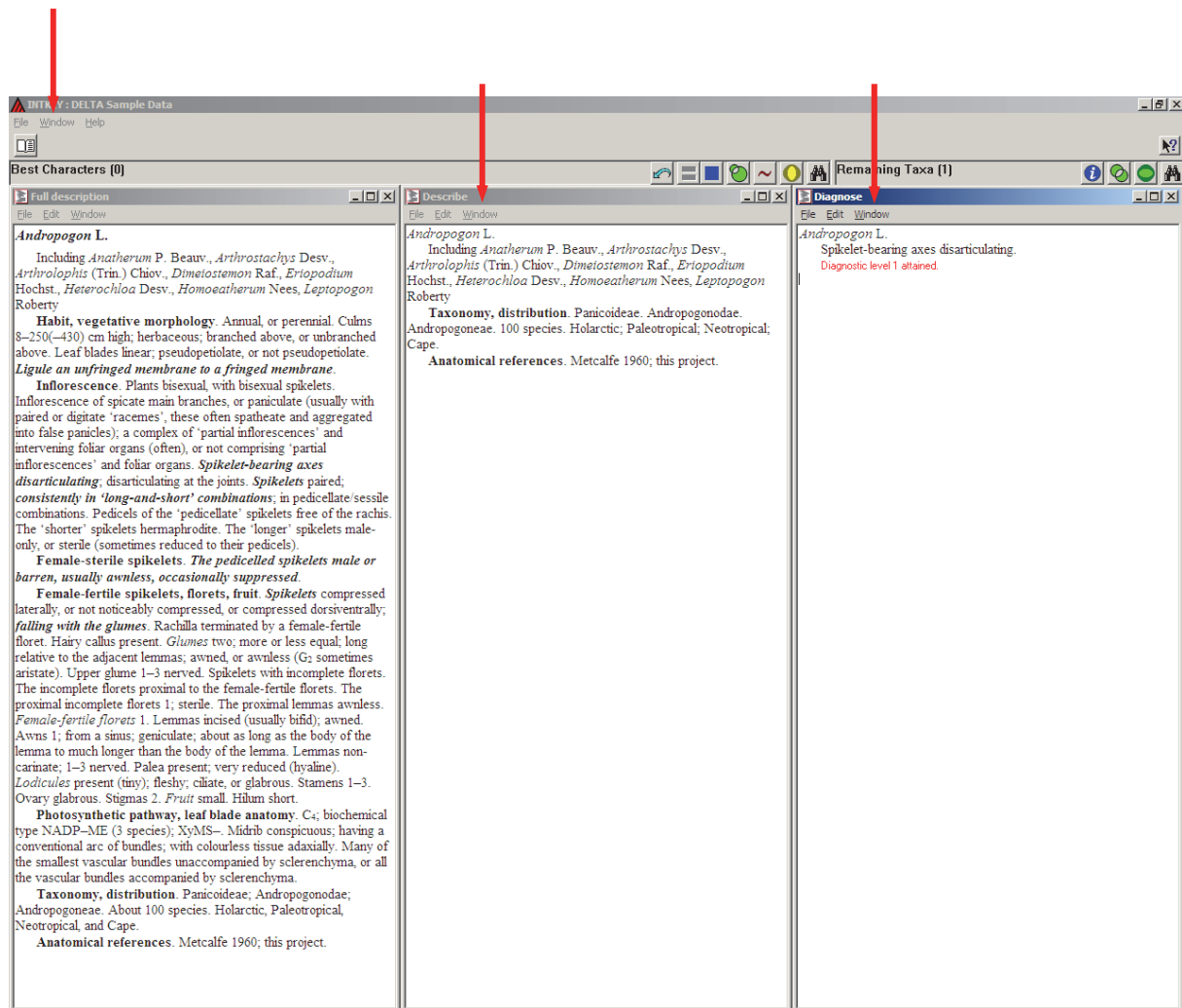


A Taxon Information dialogue box is displayed listing information for this taxon. For *Andropogon*, **full**, **brief** and **diagnostic** descriptions are available.

Often there are illustrations associated with the selected taxon, e.g. maps, taxon images or photographs of interesting or diagnostic features.

You can display any or all of the available information sets for this taxon. To continue highlight all descriptions and click the display button.

DESCRIPTIVE, DIAGNOSTIC AND IMAGE INFORMATION



All the information you have selected is tiled on the screen.

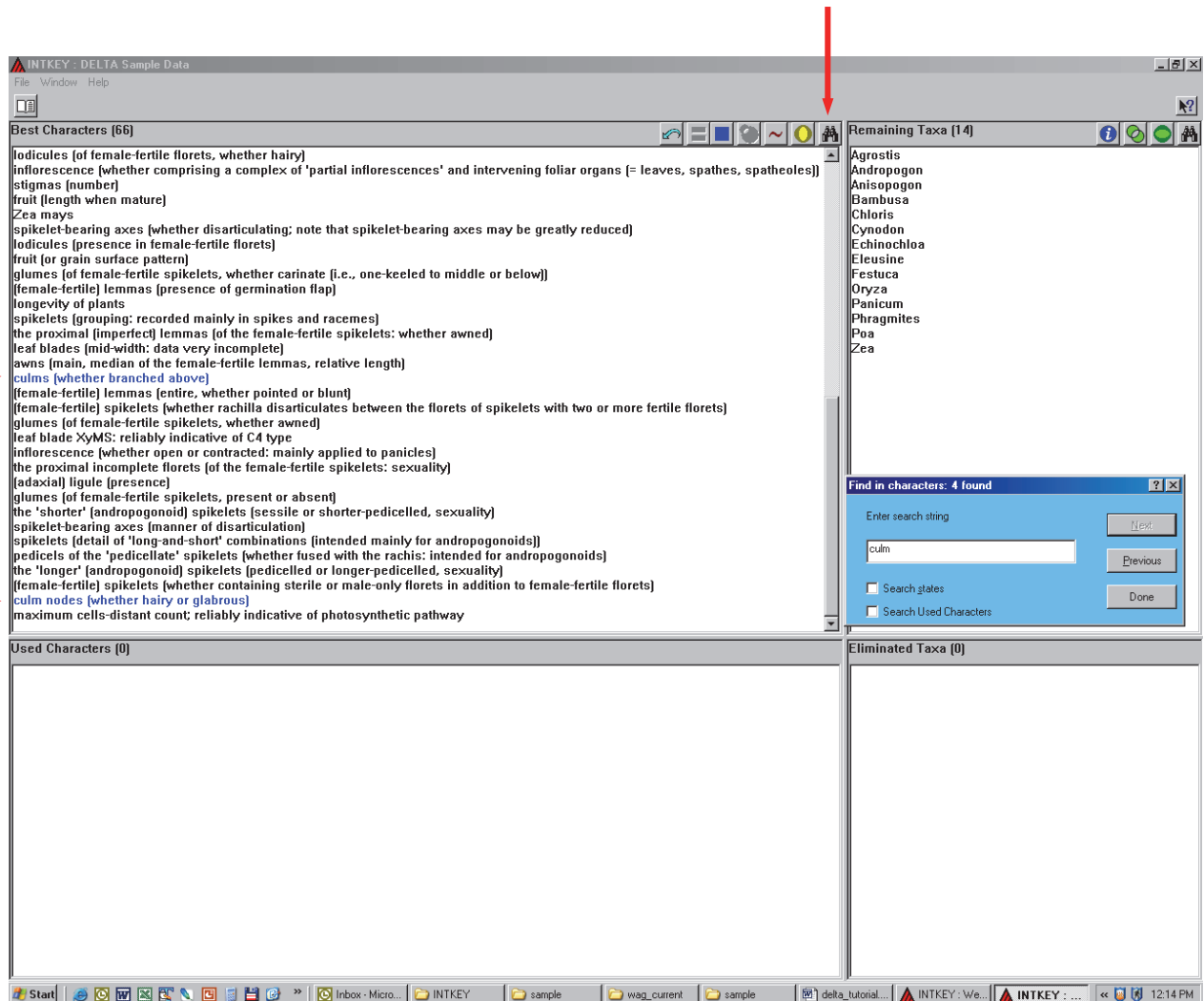
This can all be saved to another file on your computer or printed, in the usual Windows manner.

To continue, close the information windows by selecting 'Window – Close All' from the toolbars on any of the panes (see arrows). This returns you to the previous Taxon Information dialogue box. Click 'Done'.

THE FIND BUTTON 

FOR CHARACTERS

If you want to find a particular character or characters containing particular words, use the 'find' button on the left-hand toolbar. Click on the button, enter **culm** and click 'find'. All characters matching this search will be highlighted within the character list of the left.



The screenshot shows the INTKEY software interface. The 'Best Characters' list on the left contains 66 characters, with the following entries highlighted in blue:

- culms (whether branched above)
- (female-fertile) lemmas (entire, whether pointed or blunt)
- (female-fertile) spikelets (whether rachilla disarticulates between the florets of spikelets with two or more fertile florets)
- glumes (of female-fertile spikelets, whether awned)
- leaf blade XyMS: reliably indicative of C4 type
- culm nodes (whether hairy or glabrous)

The 'Remaining Taxa' list on the right contains 14 taxa:

- Agrostis
- Andropogon
- Anisopogon
- Bambusa
- Chloris
- Cynodon
- Echinochloa
- Eleusine
- Festuca
- Oryza
- Panicum
- Phragmites
- Poa
- Zea

A dialog box titled 'Find in characters: 4 found' is open, showing the search string 'culm' and buttons for 'Next', 'Previous', and 'Done'. The 'Search states' checkbox is checked.

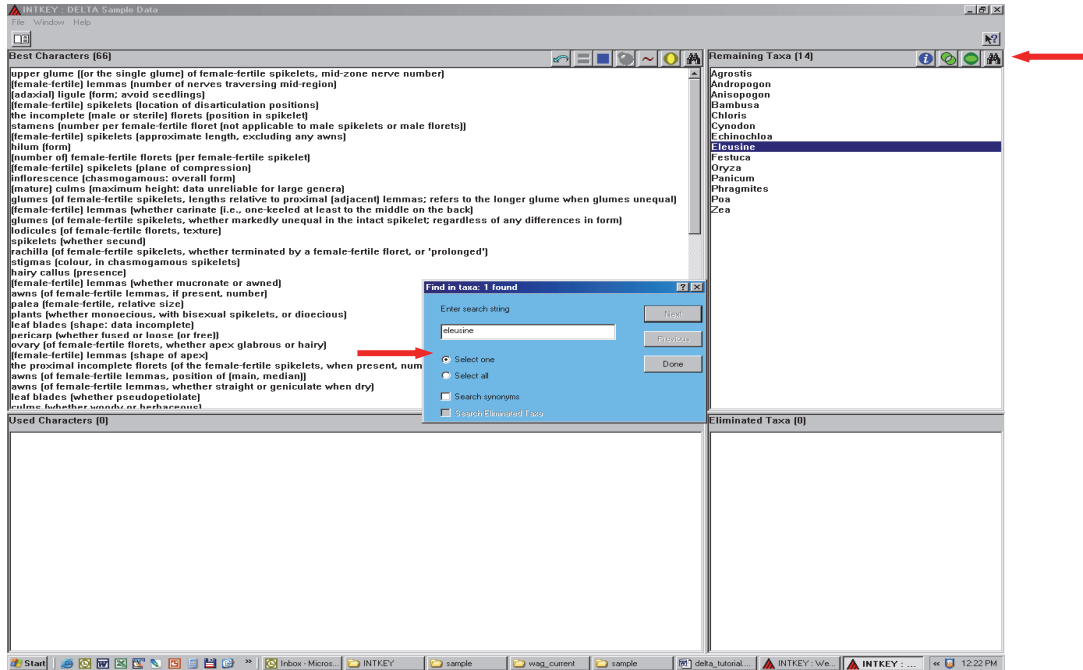
When searching through the character list there is a choice of searching the character names only or the characters and their states. Clicking on **'search states'** in the 'find' dialogue box will return more highlighted characters. 'Wildcard' symbols are not accepted but whole or partial words can be entered as the search program will match strings of letters. As an exercise, enter **lea** and also click 'Search states'

THE FIND BUTTON



FOR TAXA

If you are searching for a particular taxon, use the 'find' button on the right-hand toolbar and type in the name, and tick the 'select one' button. . Click 'find'...



You can also search on **parts of the word**, as shown below: no special 'wildcard' character, such as an asterisk * is needed. If you wish to search among remaining and eliminated taxa tick 'select all' and 'search eliminated taxa'. Click 'find'...

