

MELISR MANUAL



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INTRODUCTION

Specify is a database software application designed to support the efficient computerisation and management of biological collections. Specify is distributed by the Specify Software Project, based at the Biodiversity Institute at the University of Kansas. The Specify Software Project and its predecessor, the MUSE Project, have been supported by the US National Science Foundation since 1987.

Specify was designed to the specifications of the collection community data model. Installations can be configured with multiple taxonomic collections as separate databases, or data can be managed together as a single, multi-disciplinary database. Specify's design and functions support botany, entomology, herpetology, ichthyology, invertebrate zoology, mammalogy, ornithology, palaeobotany, and vertebrate and invertebrate palaeontology.

The Specify Software Project website is located at <http://www.specifysoftware.org>.

Specify set-up

Installing Specify

To install Specify:

1. Navigate to the following folder: S:\PS&B\Specify
2. Double-click the Specify_windows.exe file (the version will be included in the file name)
3. Click **Run** in the **Open File – Security Warning** window:



- If you receive an error message about Java, run the Java runtime environment update file in Q:\SOE, and then try installing Specify again
4. When prompted, click **OK** to select English as the language:



5. Click **Next** for all options in the Specify **Installer** window to accept the default installation settings
6. Click **Done** to close the installer.

Opening and closing Specify

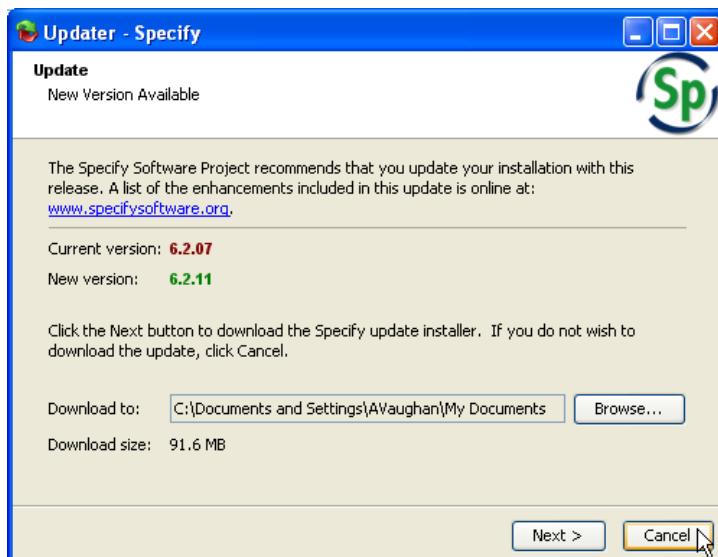
Logging in

1. Open Specify from the shortcut button or your programs list.

If you are presented with a window asking about internet connection settings, click **Cancel**. Once you have changed the edited your preferences (see below), you will no longer be presented with this window upon start-up.



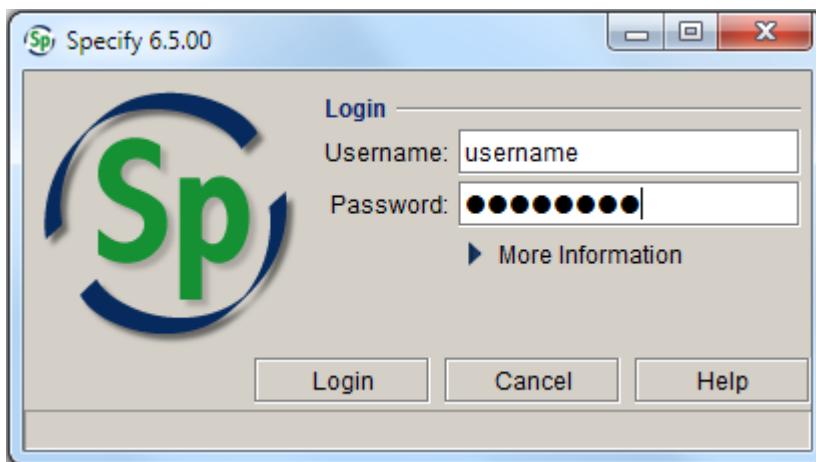
If you are presented with an **Updater** window, click **Cancel** to prevent Specify from updating your current installation. Updates to new versions must only be done by database administrators so we can ensure that the new version works properly with our customisation of Specify.



Click **Exit** when asked if you really want to exit (this will only exit you from the update installer, not from logging in to Specify):



2. Enter your user name and password in the login window
3. Click **Login**



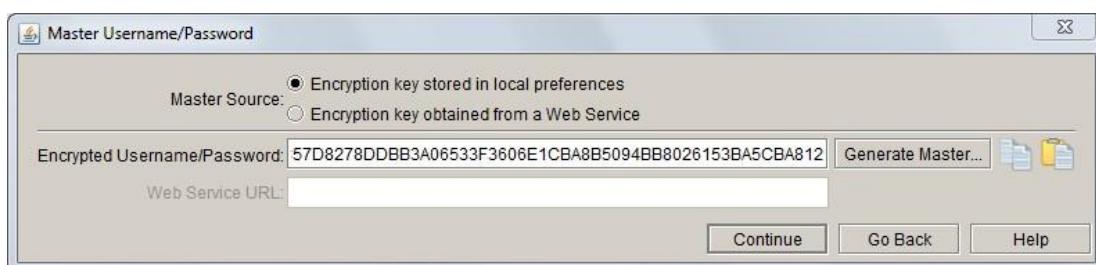
If your login fails, click on **More information** and check that the database settings match those below.



Configuring the master key

If you have just installed Specify on your computer, or if you are using Specify on a computer other than your own, you will need to enter your master key before you can log in. The master key for your username will have been e-mailed to you by the database administrator.

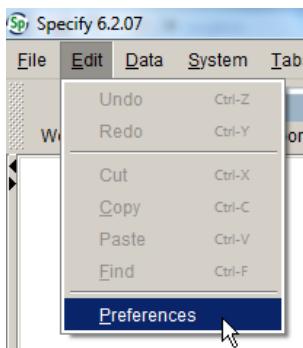
1. Click on the arrow next to **More Information** in the **Specify Login** window
2. Click on the **Configure Master Key** symbol
3. Enter your master key in the **Encrypted Username/Password** field
4. Click **Continue**
5. Click **Login** in the login window.



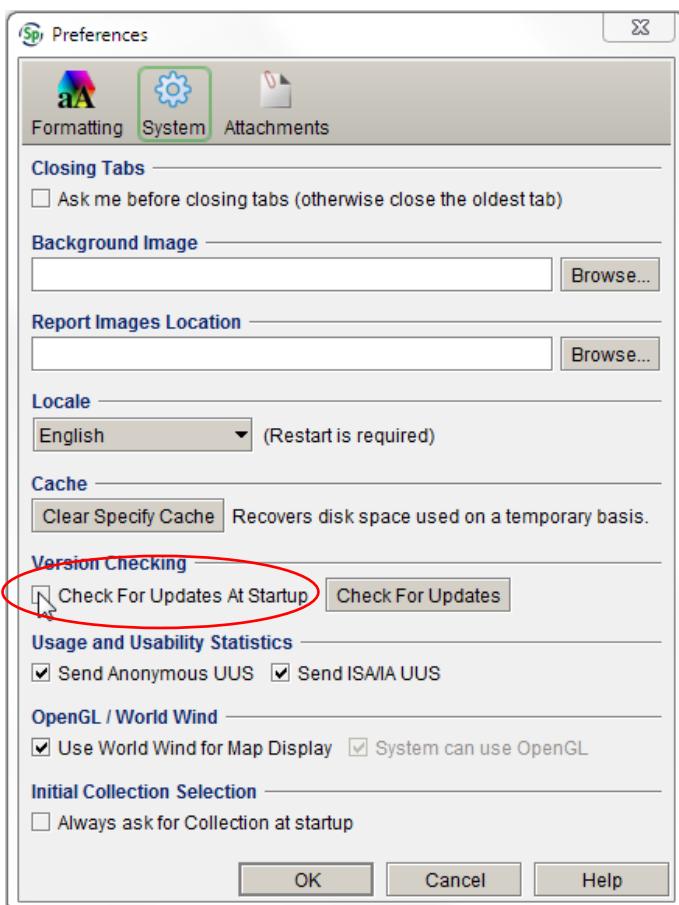
Editing preferences

When you first log in to Specify on your computer, you should edit the system preferences to stop Specify checking for updates each time you open the database:

1. Click on the **Edit** file menu, then select **Preferences**:



2. Under the **System** options, un-tick the **Check for updates at startup** box:



3. Click **OK** to save the changes.

Closing Specify

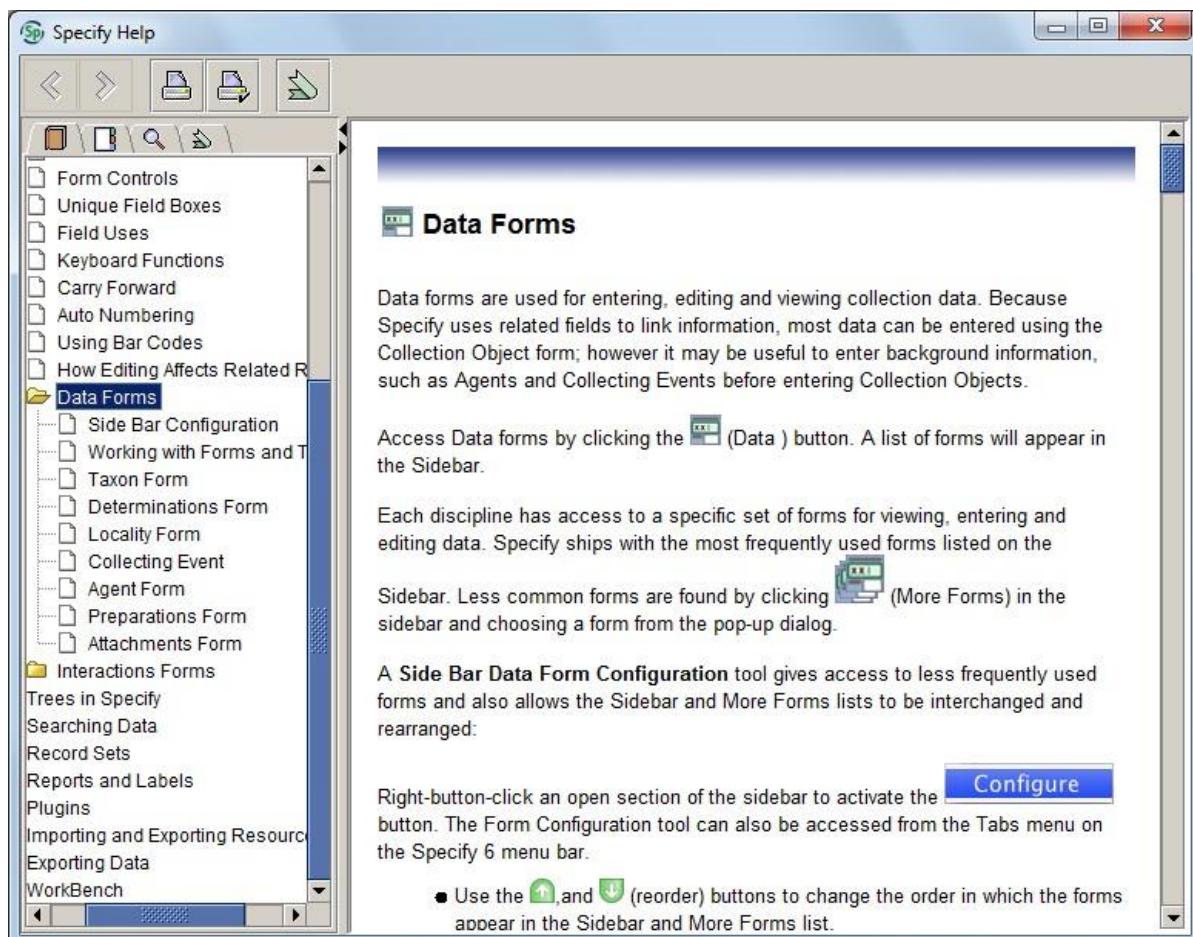
To close Specify, do one of the following:

- Click on the **Close** symbol in the top right corner of the window
- Select **Exit** from the **File** menu
- Press **Alt+F4**.

Using Specify

Specify Help

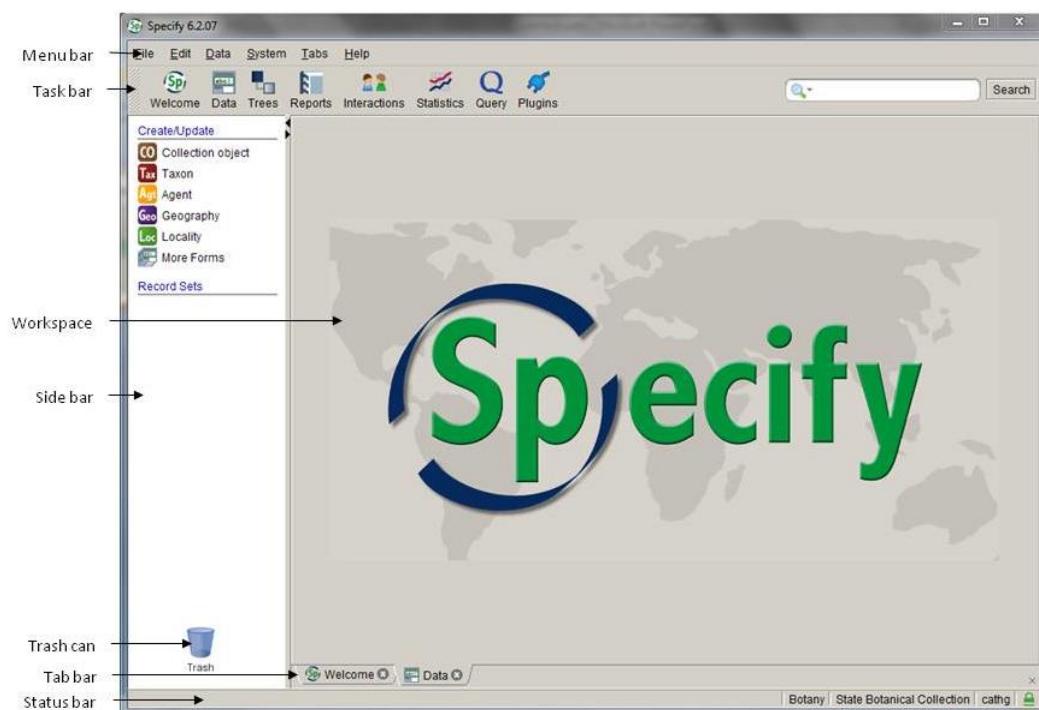
Specify contains an inbuilt help system that can be opened from anywhere in the application by pressing the **F1** key. The help system is designed to provide an overview of the modules within Specify, as well as context-sensitive help for a given task. When performing a task in Specify, press **F1** to open the **Specify Help** page that corresponds to the current task. **Specify Help** includes a table of contents, and full-text search capabilities.



The most relevant information in the Specify Help has been incorporated into this manual.

The Specify interface

The main sections of the Specify interface are described below.



Menu bar

The menu bar provides access to user preferences, system configuration settings and data entry settings.

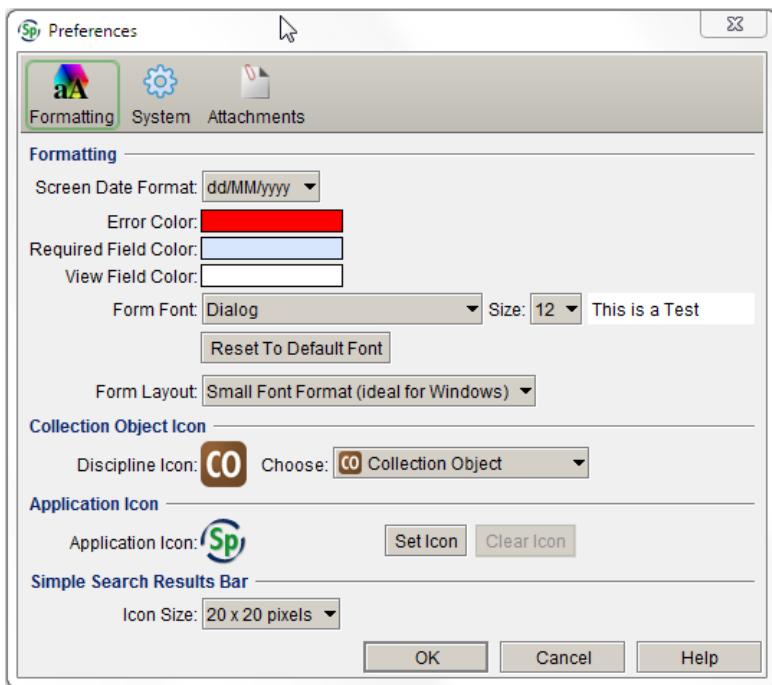
File

The file menu contains the **Exit** command. Specify can also be closed by pressing **Alt+F4** or clicking the **Close** symbol in the upper right corner of the window.



Edit

Formatting preferences (including font and font size) can be edited under **Preferences** in the **Edit** menu.



Tabs that are open in the workspace can be closed under the **Tabs** menu. You can either close the current tab, all tabs, or all tabs except the current tab. Tabs can also be closed by clicking on the **Close** symbol in the **Tab bar**.

The **Configure side bar** tool allows you to add or remove forms from the side bar. By default, the **Collection object**, **Taxon** and **Agent** forms are displayed in the **Data** module, and the **Collection object**, **Taxon**, **Agent** and **Loan** tables are displayed in the **Query** module. The side bar can also be configured by right-clicking the mouse in the side bar.

Help

The **Help** menu contains a link to the inbuilt **Specify Help**, plus a range of administrative functions, most of which can only be accessed by database administrators. The **Submit feedback** function allows users to send comments about particular aspects of the database to the Specify Software Project. To ensure that feedback is coordinated, and that bugs are properly documented, please provide feedback to the MELISR database administrators, rather than to Specify Software.

Task bar

The task bar contains buttons that are used to initiate database modules. Clicking on a button in the task bar will open a list of the components for that module in the side bar.

Welcome

The **Welcome** screen is viewed each time Specify is opened. It contains a summary of current loans and recent data entry activity.

Data

The **Data** module contains forms are used for entering, editing and viewing collection information. The main data forms used in MELISR are **Collection object**, **Taxon** and **Agent**.

Trees

The **Trees** module displays data in the **Geography**, **Taxon** and **Storage** tables as hierarchical trees. The data in these tables can also be viewed in forms.

Interactions

The **Interactions** module is used to create and manage loans, exchange and donations.

Statistics

The **Statistics** module provides a summary of the holdings, loans and data entry activity in Specify. Three graphical reports are also available in the side bar when the **Statistics** module is active.

Query

The **Query** module allows you to retrieve data stored in MELISR in an organised way. The main forms that are queried in MELISR are the **Collection object**, **Taxon** and **Agent** forms.

Plugins

The **Plugins** module contains web services that assist with georeferencing and visualising specimen records.

Side bar

The **Side bar** allows a list of components for each module to be activated in the workspace, such as data forms and record sets. The contents of the side bar will change to reflect the tools available within the active module.

The side bar can be resized by guiding the mouse over the line separating the side bar from the workspace until a crossbar appears, then clicking and dragging the side bar to the desired size.

Workspace

The **Workspace** is the area within which tasks are completed. Data entry forms, query forms, query results and reports all open in this space. Clicking a module component from the side bar list opens it in the workspace. Up to eleven workspace windows can be opened at one time, but you can only work in one window at a time.

Tab bar

The **Tab bar** indicates what tasks are open in the workspace. Tabs are labelled with an icon and module name. If the same module is opened in more than one window, the tab label will reflect the number of modules that are open. Click on the tabs to move between them. Click on the **Close** symbol to close a tab. If you close a tab before saving data or saving changes to a query, you will be prompted to save your changes.

Status bar

The right-hand side of the **Status bar** displays the current collection database and user name. MELISR currently includes three collections (*National Herbarium of Victoria*, *Victorian Reference Set* and *Non-MEL loans*). The discipline for the *National Herbarium of Victoria* and *Victorian Reference Set* collections is *Botany*. The discipline for the *Non-MEL loans* collection is also called *Non-MEL loans*.

The left-hand side of the status bar displays status reports for tasks that are being performed in the database, such as warnings for invalid data entry.

Trash can

A saved item listed in the side bar (such as a record set, query or report) can be deleted by dragging and dropping it onto the image of the trash can, or by right-clicking the item and selecting ‘Delete’.

Related information

The names of the forms in Specify represent the category of information that is stored in the corresponding table: the **Collection object** table stores information about herbarium specimens; the **Taxon** table stores information about taxon names; the **Geography** table stores information about geographic places; and the **Agent** table stores information about people and organisations. However, much of the information in one type of table is linked to information in a related table. For example, a **Collection object** record contains information about taxon names, geographic places and people that is stored in the **Taxon**, **Geography** and **Agent** tables respectively.

These links, or relationships, between different tables prevent users from having to re-type the same information in different records, which increases the efficiency of data entry and reduces the incidence of errors. Separating data into fields within related tables also allows the data to be searched in a more precise way.

Relationships between tables

There are three main types of relationships between tables in Specify: many-to-one, one-to-many and many-to-many.

One-to-one

A one-to-one relationship is a relationship between a primary and related table in which one record in the primary table can only be linked to a single record in the related table. For example, the collecting information for a single specimen is unique to that collection, thus a single record in the primary data table (in this case, **Collection object**) can only be linked to a single record in each related table that stores collecting information (such as the **Collecting event** table and the **Collection object attributes** table).

Many-to-one

A many-to-one relationship is a relationship involving a primary and related table in which many primary records are linked to a single related record in the related table. For example, many specimens are collected on a single collecting trip, thus there are many records in the primary data table (in this case, **Collection object** records) that are linked to a single record in the related table (in this case, the **Collecting trip** table).

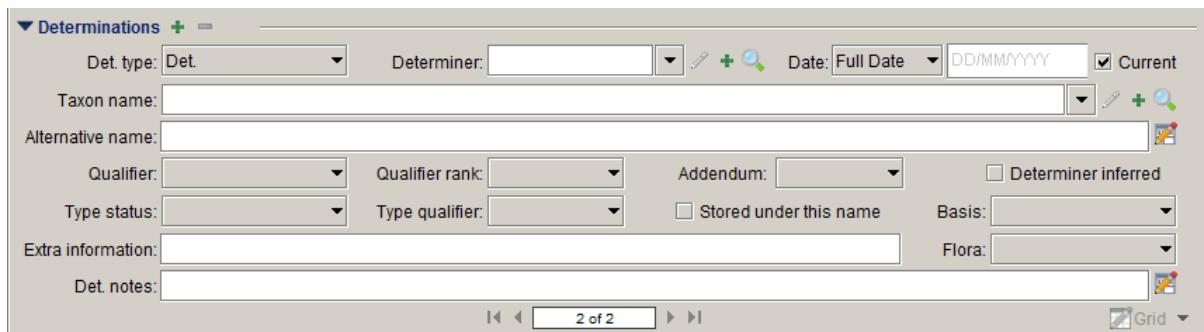
Related tables with a many-to-one relationship to the primary table are represented on the form as a query combo box with buttons to edit, add and search for a record within the table:



One-to-many

A one-to-many relationship is a relationship involving a primary and related table in which a single primary record links to many related records in the related table. For example, there might be more than one determination on a specimen, thus a single record in a primary table (in this case, a **Collection object** record) is linked to many records in a related table (in this case, the **Determinations** table).

Related tables with a one-to-many relationship are represented on the form as a subform (in either a grid or form view) with navigation controls that allow records in the related table to be added to or deleted from the primary table:



Many-to-many

A many-to-many relationship exists where multiple records in one table can be linked to multiple records in a related table. For example, more than one agent can be collectors for a single collection object, and more than one collection object can be collected by the same agent. Many-to-many relationships between tables require an associative table to link the two tables. In this example, the **Collectors** table is the link between the **Collecting event** table and the **Agent** table.

Form controls

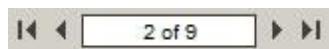
The following controls are used to enter and display data in the forms. Unless otherwise noted, all actions can be performed by clicking on the symbol using the mouse or pressing the spacebar when the symbol is in focus. The **Tab** key can be used to navigate between fields and form controls.

Symbol	Definition	Action
	Incomplete	Opens a dialogue box listing the required fields that are incomplete (this action cannot be performed using the keyboard) <i>Note:</i> The shield only appears once a change has been made inside the form and will disappear once all required fields contain data
	Warning	Opens a dialogue box listing fields that contain incorrect data (this action cannot be performed using the keyboard) <i>Note:</i> The shield will only display when the form contains errors

	Collapse	Hides the form or subform (this action cannot be performed using the keyboard)
	Expand	Opens the form or subform (this action cannot be performed using the keyboard)
	Add	Opens a new form or subform to add a new record
	Delete	Deletes the form or subform record. A Collection object cannot be deleted if it links to any other records.
	Edit	Opens the related record in a subform for editing
	Search	Opens a search dialogue box to search for a record in the form or subform. The fields in the related form will be available to search <i>Note:</i> This search treats all search criteria independently. For example, when searching for an agent 'John Smith', entering 'John' in the First name field and 'Smith' in the Last name field will return results for all agents with the last name 'Smith', as well as all agents with the first name 'John'.
	Information	Opens the associated form, in view mode
	View form	Displays the data in a table as a form in view mode
	View grid	Displays the data in a table as a grid in view mode
	Edit form	Displays the data in an editable table as a form in edit mode
	Edit grid	Displays the data in an editable table as a grid in edit mode
	Close	Closes the window or tab

Navigating between records

Navigation control buttons are found at the bottom of each primary form (e.g. the **Collection object** form), and the bottom of each subform (e.g. the **Determinations** form) when viewed as a form:



Browse through the records by clicking on the appropriate arrow (first, previous, next or last) or press the spacebar when the appropriate button is in focus.

You can also use keyboard controls to navigate between different records (see [Keyboard functions](#)).

Field types

Text box

Text boxes accept any input. The maximum length of text boxes varies between different fields.

Map reference:

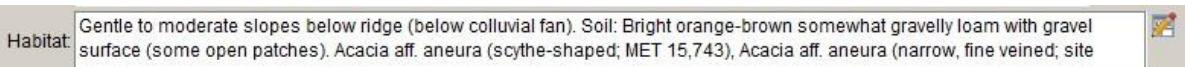
Number box

Number boxes look the same as text boxes, but will only accept numeric characters.

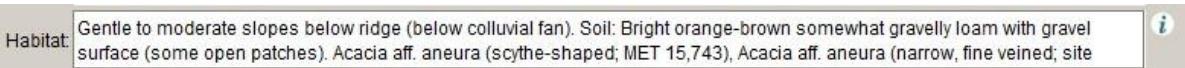
Quantity:

Expandable fields

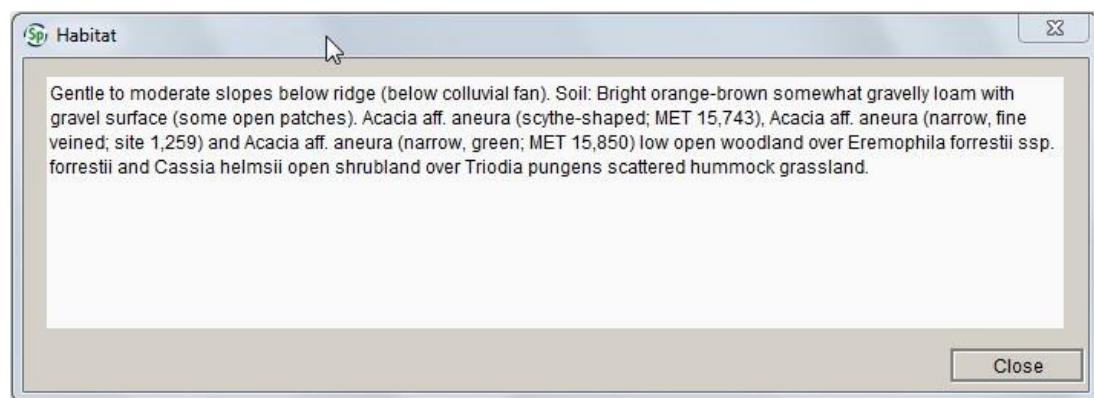
Expandable text fields allow longer strings of text to be entered. To save space, only the first one or two lines of an expandable text field are displayed on the form. In data entry or edit mode, expandable fields are indicated by an **Edit form** symbol to the right of the field:



In view mode, an **Information** symbol appears to the right of the field:



Clicking on the **Edit form** symbol or the **Information** symbol opens the field in a new window for editing or viewing, respectively:



Query combo box

A query combo box allows data to be searched and chosen from a related table; information cannot be typed directly into the box.



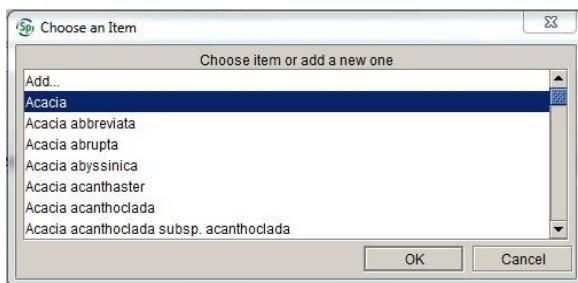
You can select the data in the related table from a drop-down list, or by searching the related table. If there is no corresponding record in the table, a new record needs to be added to the related table before it can be entered in the primary form. Records in related tables can also be edited.

To select data from a list:

1. Type the first few letters of the term you wish to use in the box, then either press the down-arrow key on the keyboard, or click on the arrow to the right of the combo box. A list of corresponding records in the related table will appear:



If the list of matching records is long, it will appear in a separate window:



You can also press the **Tab** key after entering text. If there is only one record in the table that corresponds to the text you entered, the matching record will be automatically selected when you press **Tab**.

2. Select a record from the results by clicking on it or scrolling through the list and pressing **Enter**

If a match cannot be found, 'Add...' will appear in the drop-down list. Either select 'Add...' or press **Enter** to add a new record to the related table. Pressing **Esc** will clear the list.

To search for data in the table:

1. Click on the **Search** symbol to the right of the combo box. A search window will appear:

(You may wish to place an '' before or after the word(s), for a wild card search.)*

Agent Info			
Last Name/Org:		First Name:	
Address:		State:	
City:		Country:	
Postal Code:		<input type="button" value="Search"/>	
<p><i>(You may wish to place an '*' before or after the word(s), for a wild card search.)</i></p> <p>Search Results</p> <div style="border: 1px solid black; height: 150px;"></div>			
<input type="button" value="OK"/> <input type="button" value="Cancel"/> <input type="button" value="Help"/>			

2. Type in either the entire name, or the first few letters followed by a wildcard (*):

Agent Info																																																																																																			
Last Name/Org:	macp*	First Name:																																																																																																	
Address:		State:																																																																																																	
City:		Country:																																																																																																	
Postal Code:		<input type="button" value="Search"/>																																																																																																	
<p><i>(You may wish to place an '*' before or after the word(s), for a wild card search.)</i></p> <p>Search Results</p> <table border="1" style="width: 100%; border-collapse: collapse;"> <thead> <tr> <th colspan="8">▼ Agent-12</th> </tr> <tr> <th>Initials</th> <th>Last name</th> <th>E-mail</th> <th>Address</th> <th>City</th> <th>State</th> <th>Post code</th> <th>Country</th> </tr> </thead> <tbody> <tr><td>M.</td><td>Macphail</td><td></td><td></td><td></td><td></td><td></td><td></td></tr> <tr><td>C.S.</td><td>MacPhee</td><td></td><td></td><td></td><td></td><td></td><td></td></tr> <tr><td></td><td>MacPherson</td><td></td><td></td><td></td><td></td><td></td><td></td></tr> <tr><td>C.</td><td>MacPherson</td><td></td><td></td><td></td><td></td><td></td><td></td></tr> <tr><td>J.</td><td>Macpherson</td><td></td><td></td><td></td><td></td><td></td><td></td></tr> <tr><td>J.H.</td><td>Macpherson</td><td></td><td></td><td></td><td></td><td></td><td></td></tr> <tr><td>J.K.</td><td>Macpherson</td><td></td><td></td><td></td><td></td><td></td><td></td></tr> <tr><td>K.</td><td>Macpherson</td><td></td><td></td><td></td><td></td><td></td><td></td></tr> <tr><td>W.</td><td>Macpherson</td><td></td><td></td><td></td><td></td><td></td><td></td></tr> <tr><td>W.A.</td><td>Macpherson</td><td></td><td></td><td></td><td></td><td></td><td></td></tr> </tbody> </table>				▼ Agent-12								Initials	Last name	E-mail	Address	City	State	Post code	Country	M.	Macphail							C.S.	MacPhee								MacPherson							C.	MacPherson							J.	Macpherson							J.H.	Macpherson							J.K.	Macpherson							K.	Macpherson							W.	Macpherson							W.A.	Macpherson						
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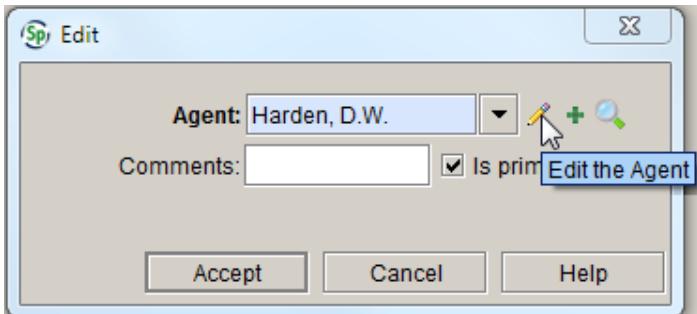
3. Select a record from the results by clicking on it or scrolling through the list and pressing **Enter**.

If a match cannot be found, close the search window and click on the **Add** symbol to add a new record.

To edit an existing record:

1. Select a record from the drop-down list or the search window

- Click on the **Edit** symbol to the right of the combo box. The record will open in a new window:



Caution!

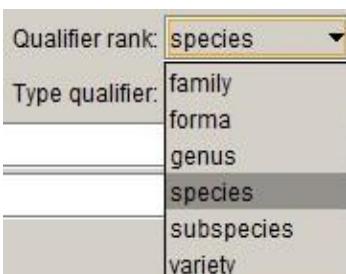
When editing records, remember that the data changes in each record that references that record. For example, if the spelling of a name in the **Last name** field is changed in an **Agent** record, the agent's name will be changed in the **Collectors** field in all **Collection object** records that link to that **Agent** record, and not just in the **Collection object** that is currently open. If the wrong collector was entered, the link to the wrong agent record needs to be deleted and a link to the correct agent needs to be added.

Pick lists

- A pick list presents a restricted set of values for a field. The values in a pick list can only be edited by a database administrator.



- Select an entry from the pick list by pressing the down-arrow, scrolling to the appropriate entry, then pressing **Enter**:



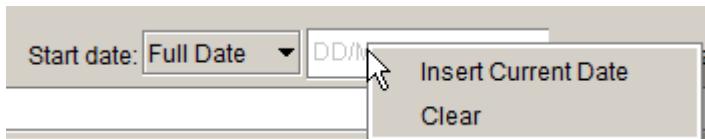
- Alternatively, enter the first letter of the appropriate pick list entry to select it. If there is more than one value in the pick list that begins with the same letter, press the first letter of the word until the right value is selected.
- Pick list fields can be cleared by pressing **Esc**.

Date fields

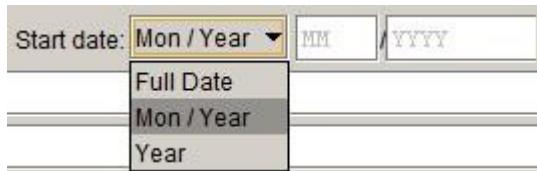
Date fields are formatted fields that only allow valid dates to be entered.



- Right-clicking inside a date field will allow you to either insert the current date, or clear the field:



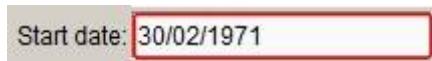
- Some date fields are preceded by a date type pick list, which allows you to choose from a full date, a month and year, or a year only. Press the down-arrow on the keyboard to open the pick list, scroll to the appropriate date type, then press **Enter** to select it:



- Other date fields only allow full dates to be entered:



- If an invalid date is entered, the date field will be highlighted in red, and you won't be allowed to save the record:



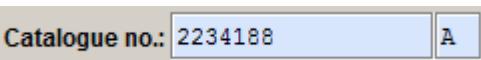
Check boxes

Check boxes are used to indicate the presence of an attribute. Click the check box to tick or un-tick the box.



Required fields

Fields that are required have a bold label and the text area is shaded blue:



Records cannot be saved until all required fields contain valid data. An **Incomplete** symbol will appear at the bottom of the form if required fields have not been completed.

Read-only fields

Read-only fields are used either to display a field in a different form than the one that it is edited in (e.g. the **Geography** field in the **Collecting event** form), or to display data that is automatically filled in (e.g. the **Created by** and **Last edited by** fields, or **IBRA region**, which is calculated from the **Latitude** and **Longitude** fields).

There is no border around read-only fields:

Created by: Macheda, D.R.	Created: 14/10/2010
Last edited by: Macheda, D.R.	Last edited: 14/10/2010

Form tools

Keyboard functions

Specify uses standard keyboard functions for filling out forms via keyboard entry. Keystrokes for the form controls are described in the [Form controls](#) section. The following keyboard functions apply to data entry and editing in forms:

- **Tab** moves the focus to the next field
- the spacebar activates a button
- the down-arrow key opens a query combo box or a pick list and moves focus to the next item in the list
- **Esc** closes a query combo box or pick list
- **Enter** selects a highlighted item within a list
- **Ctrl+S** will save a record or a query
- **Ctrl+C** will copy data within a field
- **Ctrl+P** will paste data into a field
- **Ctrl+X** will cut data from a field.

The following keyboard shortcuts can be used to navigate between different records in **Data view**:

- **Alt+Up** will take you to the first record in the set
- **Alt+Right** will take you to the previous record in the set
- **Alt+Left** will take you to the next record in the set
- **Alt+Down** will take you to the last record in the set.

You can also use keyboard shortcuts to close tabs in the workspace:

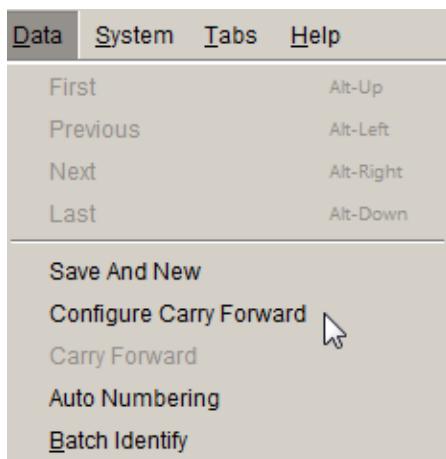
- **Ctrl+W** will close the current tab
- **Ctrl+Shift+W** will close all tabs.

Carry forward

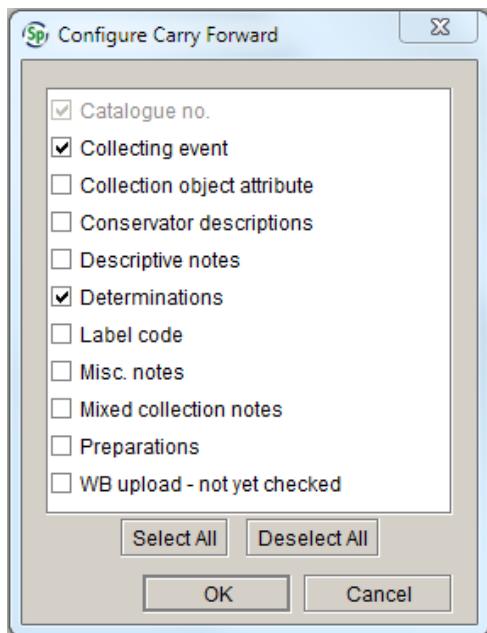
Specify allows you to carry forward data from certain fields into new **Collection object**, **Taxon** or **Agent** records during data entry. **Carry forward** needs to be configured before it can be selected from the **Data** menu.

To configure **Carry forward**:

1. Click on the **Data** menu in the menu bar (or right-click the mouse within the form)
2. Select **Configure carry forward**



3. Choose which fields you want to carry forward to the next record
4. Click **OK**.

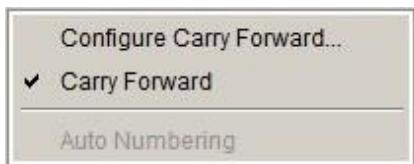


Carry forward automatically turns on after it has been configured. When configuring **Carry forward**, bear in mind that, if **Carry forward** is enabled for **Determinations**, *all* determinations from the previous record will be carried forward, not just the current determination.

The list of items in the **Configure carry forward** list cannot be changed. It includes fields that you would never want to share between different records, such as **Catalogue number** and **Mixed collection notes**.

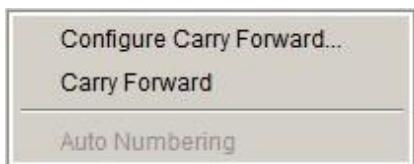
To turn **Carry forward** on:

1. Click on the **Data** menu in the menu bar (or right-click the mouse within the form)
2. Select **Carry forward**. A tick will appear next to **Carry forward** in the menu.



To turn **Carry forward** off:

1. Click on the **Data** menu in the menu bar (or right-click the mouse within the form)
2. Select **Carry forward**. The tick next to **Carry forward** will disappear.



Carry forward (or **Configure carry forward**) can only be selected from the **Data** menu when a form is being entered or edited in the **Data** module.

Caution!

When carrying forward locality data from one record to another, remember that if a **Locality** record is shared between two or more records, then subsequently edited, the locality will be changed in *all* **Collection object** records that share that locality, not just in the **Collection object** that is open when the **Locality** record is edited. You should only carry forward locality data if ALL of the details in the **Locality** form (and the associated **Locality details** and **Geocoordinate details**) are EXACTLY the same for the different collecting events, such as is the case for multisheet collections.

DATA ENTRY FORMS

General conventions

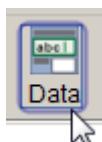
- Information added or interpreted by data entry staff should be entered in brackets [], unless it is entered in the **Curation notes** field or the **Georeferencing notes** field.
- Include a full stop after information in the following text fields: **Locality**, **Habitat**, **Associated taxa**, **Descriptive notes**, **Collecting notes**, **Miscellaneous notes**, **Ethnobotanical info.**, **Toxicity** and **Curation notes**.
- Include a space between measurements and the unit of measurement (e.g. '4 km', '1500 ft').
- Where it is necessary to abbreviate words, use only standard abbreviations (see [Appendix 1. Abbreviations](#)).

Creating and editing records

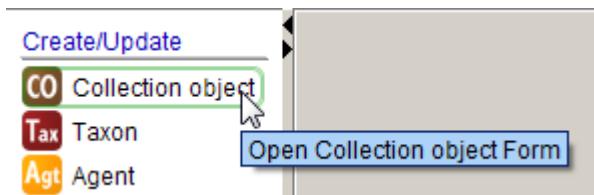
Opening a form

To open a blank data entry form:

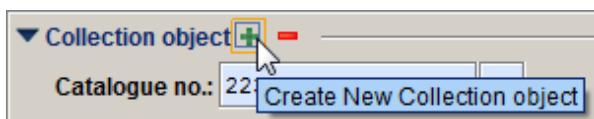
1. Click on the **Data** button in the task bar:



2. Select the form that you want to use from the side bar:

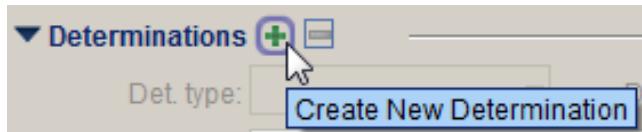


To open a new **Collection object** form after saving a record, click on the **Add** symbol at the top of the **Collection object** form:



Adding records to subforms

To add a record to subform of a primary form (e.g. to add a **Determination** record to a **Collection object** record), click on the **Add** symbol in the relevant subform:



If you accidentally add an extra record to a subform, you can delete it by clicking the **Delete** symbol in the relevant subform:



Note that, before you can delete a record in a subform, or add a new record to a subform, the form must contain data in at least one field, and any required fields must be completed.

Saving a record

To save a record, press **Ctrl+S**, or click the **Save** button at the lower right-hand corner of the form. The **Save** button will not be activated if there are errors in formatted fields or if any required fields have not been completed. Note that, although the record has been saved, it will remain in 'edit' mode unless you click the **View** button, which makes the record read-only (the **View** button appears next to the **Save** button once a record has been saved).

Editing a record

To edit a record, click the **Edit** button at the lower right-hand corner of the form to change it from view (read-only) mode to edit mode. See [Querying Specify](#) for instructions on how to query for records and open them in form view.

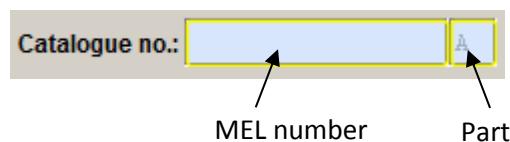
Collection object form

Collection object

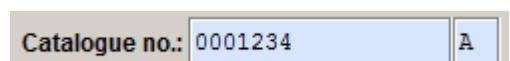
A collection object refers to an individual item collected during a collecting event. At MEL, a collection object either comprises an entire sheet, packet etc. for non-mixed collections, or the individual component of the sheet, packet etc. for mixed collections. The **Collection object** form contains (or links to) all the collecting and curatorial information known about the herbarium specimen.

Catalogue number

The **Catalogue number** is made up of the MEL number and part (see details below):



In order for the transactions to work in Specify, each record needs to have a **Catalogue number** in a standard format consisting of seven digits and one letter. Because not all MEL numbers contain seven digits, MEL numbers less than 1 000 000 need to be padded with leading zeroes. For example, the **Catalogue number** for MEL 1234 A would be 0001234A:



MEL number

All specimens at the National Herbarium of Victoria should be assigned a unique identification number of up to seven digits. Older specimens often have a MEL number stamped on the sheet. If there is no MEL number assigned to the specimen, assign the next number from your batch of MEL numbers (see the [Numbers](#) section for details of how to get a new batch of MEL numbers).

MEL numbers are assigned to spirit collections as well as to dry material in sheets or packets. If you come across a spirit collection that has the same MEL number as its corresponding sheet or packet, allocate a new MEL number to the spirit collection (note that only one MEL number should be assigned to the spirit collection, regardless of how many spirit jars there are). Carpological collections, fungal cultures and photographs of specimens held at other institutions all receive a separate MEL number to any corresponding sheet, packet or spirit material.

Microscope slides only receive a unique MEL number if there is no corresponding dry material or spirit collection. Silica gel samples and photographic slides do not receive a MEL number, but are listed as additional preparations of the corresponding sheet, packet or spirit (see [Preparations](#)).

Note

Do not reassign MEL numbers from deaccessioned specimens or from specimens that originally had more than one MEL number stamped on the sheet, just in case the specimen (or data associated with it) has been referenced in a publication or in someone's research notes. The only time we should re-use MEL numbers is if the specimen is still in the process of being accessioned into the collection when we decide to discard it, and the number hasn't been published online or elsewhere.

Part

MEL accession numbers are appended by a letter, which is used to differentiate between different parts of mixed collections. The default for **Part** is 'A'. The only instance where anything other than A is entered in this field is where there is more than one component on a herbarium sheet (or in a packet or spirit jar), such as more than one taxon on the sheet, or more than one set of collecting

information (note that the host of a parasitic plant should not be entered as a separate record unless there is value in doing so, e.g. if it's a rare taxon or a new record for an area). Thus, the MEL number always refers to the entire sheet, packet or spirit jar, and the part refers to the individual component.

Only one label is printed for a mixed collection. The MEL number, part and taxon name for parts B, C etc. will automatically be printed at the bottom of the label for part A. Where there is more than one set of collecting information on the sheet, the **Mixed collection notes** can be used to provide a brief indication of how parts B, C etc. differ from part A. If there is more than one taxon on the sheet, but the separate components share the one set of collecting information, there is no need to enter anything in the **Mixed collection notes** field.

When you have databased all components of a mixed collection, indicate in pencil on the specimen which component corresponds to part A, B, C etc. If it is unclear which parts of the specimen belong to which set of collecting information, only label the collecting information.

Type

This is a read-only field. If the collection object is a type, the **Type** box will automatically be ticked.

Imaged

This read-only field is used to indicate that a high-quality image of the specimen has been generated at MEL, in accordance with the standards of the GPI project. This field will be populated as soon as practicable after the specimen has been imaged.

GPI

This read-only field is used to indicate that a high-resolution image of the specimen has been delivered to JSTOR and is available to be viewed on the [Global Plants](#) website.

Multisheet

This is a read-only field. If the collection object is part of a multisheet relationship, the **Multisheet** box will automatically be ticked.

Parts

This is a read-only field. If the collection object is part of a mixed collection, the total number of parts in the mixed collection will be displayed in the **Parts** field.

Other identifier

The **Other identifier** table is used to record the institution from which incoming exchange specimens were received, and the accession or catalogue number applied to the specimen at the source institution, if known. This table may be used to record other types of identifiers in future.

Type

The type of other identifier that is being recorded. The options are:

- Ex herbarium – where the specimen is known to have been received as a duplicate or donation from another herbarium
- Duplicate – where the specimen is known (or has been inferred) to be a duplicate held at another herbarium based on collector, collecting number and collecting date.

Institution

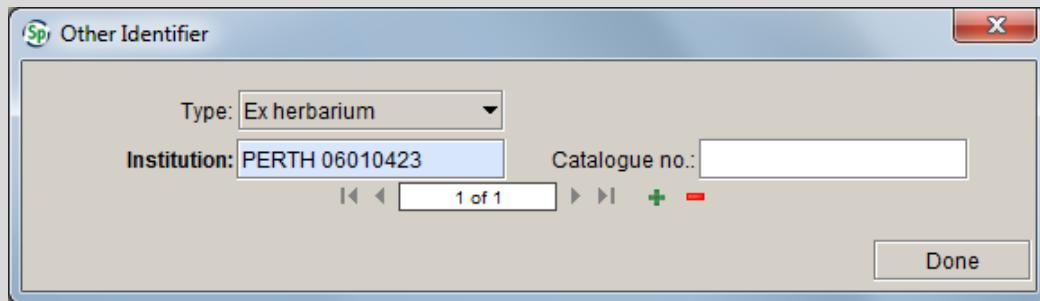
The Index Herbariorum code of the institution from which the specimen was received, or where the specimen was originally held. If the institution's accession number is provided, enter it in the **Catalogue no.** field in the **Other identifier** table. If the specimen has come from the private herbarium of an individual collector, enter that information in the **Original collection** field in the **Collection object attributes** table. Please use the code that the issuing herbarium is using on the specimen. For example, for a specimen from CANB that has the barcode 'CBG 025665', enter 'CBG' in the **Institution** field and '025665' in the **Catalogue no.** field (or scan the entire barcode in the **Institution** field – see below).

Catalogue no.

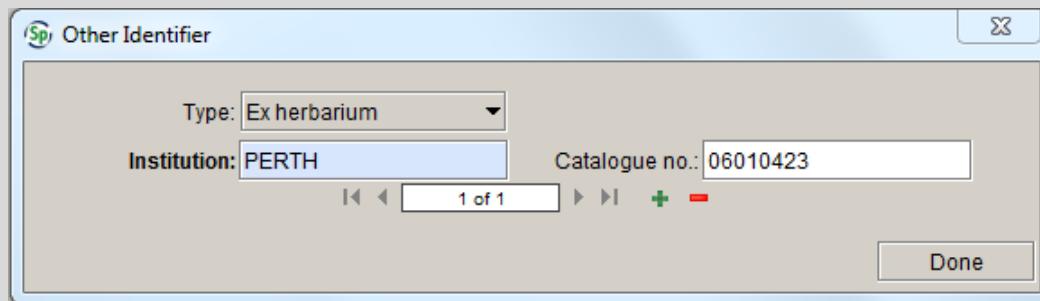
The catalogue or accession number that was assigned to a specimen (or its duplicate) at the herbarium from which it was received. For example, a duplicate of 'BRI AQ 814849' would have 'BRI' entered in the **Institution** field, and 'AQ 814849' entered in the **Catalogue no.** field.

Barcodes on exchange specimen labels

You can populate the **Institution** and **Catalogue no.** fields by scanning the barcode on most exchange specimen labels into the **Institution** field:



When you save the **Collection object** record, the herbarium code will be saved in the **Institution** field and the accession or catalogue number will be saved in the **Catalogue no.** field:



Note that DNA barcodes do not include the herbarium code, so you need to scan the barcode directly into the **Catalogue no.** field and type the herbarium code into the **Institution** field. Also, the MEL barcode scanners don't read the older NT barcodes, so these have to be entered by hand.

Determinations

Specify supports multiple determinations, which allows the determination history of a specimen to be accurately recorded. The same set of fields is used for all determination types, and the **Det. type** field is used to indicate what type of determination is being recorded.

Records that have a Conf. should always have a Det., even if the original determiner is unknown. For specimens that have a single determination covering both the type status and the current name, the information should be entered as a 'Det.' as well as a 'Type status' determination.

Older specimens often have handwritten labels bearing more than one name. These should all be treated as determinations, regardless of whether or not the determiner or date of determination is known. If there is more than one name on a single label, and the names are written in the same handwriting, they can be treated as a single determination. Unless there is reason to think otherwise, treat the first or most prominent name on the label as the name the specimen was determined to, and enter all the names that appear on the label in the **Det. notes** field.

Where a specimen of a parasitic plant or fungus bears a separate identification for the host taxon, you can just record the determination in the **Miscellaneous notes** field, instead of creating a separate collection object record.

See [Appendix 2. Examples of determination records](#) for specific examples.

Det. type

The type of determination. The following values can be selected from the pick list:

- Acc. name change – Accepted name change
- AVH annot. – AVH annotation
- Annot. – annotation
- Conf. – confirmavit
- Det. – determinavit
- Type status – type status determination.

If there is an annotation on the specimen that is only there for curation purposes, or is only there to correct the spelling of a taxon name on a previous det. slip, there is no need to enter the annotation in the database. See [Taxon name](#) for instructions on how to deal with misspelt taxon names in determinations.

Determiner

The name of the person who made the determination. Enter the determiner's name from the **Agent** drop-down list. If the determiner is not in the list, press the **Add** symbol to open the **Agent** form.

Where there is more than one determiner, the agent names will be separated by a semicolon, e.g. 'Stajsic, V.; Klazenga, N.'. If the combination of determiners is not listed in the drop-down list, it will need to be added to the **Agent** table as a 'Group agent'.

If the determiner is given as an institution code, e.g. BRI, select the relevant organisation agent from the list (e.g. 'BRI -- Queensland Herbarium').

If the determiner's name is difficult to read and has been interpreted, you can enter details about how it has been interpreted in square brackets in the **Det. notes** field. For example, if the determiner is given as 'Paul Wilson', but you have inferred that it is 'Paul G. Wilson', select 'Wilson, Paul G.' from the **Determiner** drop-down list, and record in Det. notes that '[The determiner is given as 'Paul Wilson'].':

The screenshot shows the 'Determinations' input form. At the top, there are dropdown menus for 'Det. type' (set to 'Det.'), 'Determiner' (set to 'Wilson, Paul G.'), and 'Date' (set to 'Full Date' with the value '23/05/2008'). A checked checkbox labeled 'Current' is present. Below these are fields for 'Taxon name' ('Correa baeuerlenii'), 'Alternative name' (empty), 'Qualifier' (empty), 'Qualifier rank' (empty), 'Addendum' (empty), and 'Basis' (empty). There are also checkboxes for 'Determiner inferred' (unchecked) and 'Stored under this name' (unchecked). To the right of these are dropdowns for 'Type status' (empty), 'Type qualifier' (empty), 'Flora' (empty), and 'Extra information' (empty). At the bottom of the form is a text area labeled 'Det. notes' containing the text '[The determiner is given as 'Paul Wilson'].']'. The entire form is contained within a grey border.

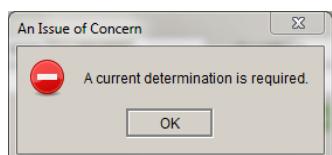
If you are certain of the identity of the determiner, there is no need to enter a message in the **Det. notes** field.

Date

The date of the determination. The determination date can be a full date, a month and year, or just a year. Select the appropriate date type from the date pick list, and then enter the date using the number keys. Note that if you enter a full date, then change the date type to 'Mon/Year' or 'Year', the month and/or date will revert to '01' if you then change the date type back to 'Full date'.

Current

This field is used to indicate which of the determinations is current, for records that have more than one determination. Tick the **Current** box in the current determination. If there is no current determination, a warning will appear when you try to save the record:



The current determination should never be a 'Type status' determination; where a single determination covers both the type status and the current name, the information should be entered as a 'Det.' as well as a 'Type status' determination. If a specimen has a 'Conf.' that is more recent than a 'Det.' of the same name, the 'Conf.' is the current determination.

The **Current** check box is automatically ticked when you add a new determination. For this reason, it makes most sense to enter determinations in chronological order. If the determination you are adding is not the current determination, uncheck the **Current** box and use the navigation bar to scroll through the other determinations to find the current one:

Determinations

Det. type: Det. Determiner: George, A.S. Date: Full Date 02/04/1967 Current

Taxon name: Pomaderris bilocularis

Alternative name:

Qualifier: Qualifier rank: Addendum: Determiner inferred

Type status: Type qualifier: Stored under this name Basis:

Extra information: Flora:

Det. notes:

1 of 3

Grid

Taxon name

The name of the taxon that the specimen has been determined to. This field links to the **Taxon** table. To look up a name, start typing the taxon name and then press the down-arrow or the **Tab** key to see a list of names that start with the letters you just typed in. It may take several seconds to populate the list if there are a lot of matching names. If the name is not in the list, it will need to be added to the **Taxon** table using the **Taxon** form.

If the name on the label is an orthographic variant of a name already in the **Taxon** table (or is just misspelt), select the correctly spelt name from the **Taxon name** drop-down list, and enter the name as it appears on the sheet in the **Det. notes** field.

If an incorrect author is given, but it's not clear whether the name is a homonym, an isonym or an error, select the valid name from the **Taxon name** list and enter the name and author combination given on the label in the **Det. notes** field.

Alternative name

The **Alternative name** field is used to record unpublished or unofficial names that have previously been applied to the specimen. This field should never be used for current determinations.

Before entering a name in this field, check to see if the name (or a variation of the name) is in the **Taxon** table. If the name is in the **Taxon** table, it should be entered in the **Taxon name** field (even if it is an unofficial or unpublished name). If the name is not in the **Taxon** table, check to see if it is listed in IPNI or Tropicos. If it is listed in either IPNI or Tropicos, add the name to the **Taxon** table. If you cannot find the name in IPNI or Tropicos, or if the name on the sheet has a different author, enter it in this field exactly as it appears on the label.

Qualifier

The determination qualifier, for uncertain determinations. The following values can be selected from the pick list:

- ?
- aff.
- cf.

In the past 'sp. aff.' has often been used in this field. 'sp. aff.' is not a determination qualifier, but indicates a different entity.

If a specimen has been determined to '*Somegenus* sp. aff. *someepithet*', then 'sp. aff. *someepithet*' needs to be added as a species to the **Taxon** table. If a 'sp. aff.' name is not already in the **Taxon** tree, and is not in APNI or Viclist, please see Neville or Val before adding it to the **Taxon** table.

Qualifier rank

The rank at which the determination qualifier applies. Select the appropriate rank from the pick list. By default, the **Qualifier rank** will be set to the lowest rank to which the specimen has been determined. This happens in the background after the record is saved, so you will not be able to see it immediately. You only need to fill in the **Qualifier rank** field if the qualifier is applied to a rank higher than the lowest rank to which the specimen has been determined. For example:

- '*?Eucalyptus camaldulensis*' – the **Qualifier rank** should be set to 'genus'
- '*Chamaecrista nomame* var. *?nomame*' – the **Qualifier rank** will automatically be set to the lowest rank, so you don't need to enter anything in this field.

Addendum

A suffix added after the name to indicate a concept for that name. The following values can be selected from the pick list:

- s.l. – *sensu lato*: in a broad sense
- s.str. – *sensu stricto*: in a narrow sense
- group
- intergrade
- intermediate
- complex
- vel aff.

Type status

The type status of the specimen, as recorded in the determination. The following type statuses are recognised at MEL:

- Holotype – the one specimen or illustration used by the author or designated by the author as the nomenclatural type
- Isotype – a duplicate specimen of the holotype
- Syntype – any specimen cited in the protologue when there is no holotype, or any of two or more specimens simultaneously designated as types
- Isosyntype – a duplicate of a syntype
- Lectotype – a specimen or illustration designated from the original material as the nomenclatural type if no holotype was indicated at the time of publication, or if it is missing
- Isolectotype – a duplicate specimen of the lectotype, if the lectotype has been chosen from among syntypes (if a lectotype has been chosen from among isotypes, the other isotypes remain just isotypes)

- Neotype – a specimen or illustration selected to serve as the nomenclatural type if no original material is extant or as long as it is missing
- Isoneotype – a duplicate specimen of the neotype (again only when the neotype was chosen from among syntypes; isotypes remain isotypes)
- Paratype – a specimen cited in the protologue that is neither the holotype nor an isotype, nor one of the syntypes if two or more specimens were simultaneously designated as types (*Note:* paratypes need to be cited as paratypes in the protologue; not every specimen cited in a protologue that is not an isotype or a syntype is a paratype)
- Residual syntype – used for the remaining syntypes when a lectotype has been selected from among syntypes (*Note:* in HISPID the term ‘Paralectotype’ is used for this and that is what goes into the database when ‘Residual syntype’ is selected from the pick list)
- Paraneotype – used for the remaining syntypes when a neotype has been selected from among syntypes
- Epitype – a specimen or illustration selected to serve as an interpretative type when the holotype, lectotype, or previously designated neotype, or all original material associated with a validly published name cannot be identified for the purpose of precise application of the name of a taxon
- Authentic specimen – the original specimen of an invalid name, i.e. any specimen cited in the protologue of an invalid name
- Type – used when we know it is a type, but are uncertain of the type status.

Type qualifier

The uncertainty of the type status determination, if recorded by the determiner. The options for type status qualifier are ‘probable’, ‘possible’ and ‘?’. If the determiner has included an explanation of why the type status is uncertain, include this in the **Det. notes** field.

Stored under this name

For type specimens, this field is used to indicate that the specimen is stored under the basionym. It does not need to be checked for non-type specimens. **Note that, contrary to prior herbarium procedure, if the specimen is a type of more than one name, it should be stored under the most recent basionym (the date of publication can be checked in the Taxon table).**

Stored under this name must only be ticked in one determination record; if there is more than one type status determination for the name that the specimen is stored under, only tick **Stored under this name** in the most recent (or the most authoritative) determination.

Basis

If the determination of a specimen is not based on examination of the actual specimen, but on a duplicate or an image, the basis of determination should be recorded here. The following values are currently in the pick list:

- Duplicate – we either have the catalogue number of the specimen at the original herbarium in MELISR, or the catalogue number is not available, but the collector, collecting number and collecting date match
- Image.

If additional values need to be added to the pick list, see the Collections Information Officer.

Extra information

The **Extra information** field should be used to record recognised form and variant names, or any other information that tells you something about the taxon or group concept, but is not part of the taxon name. For example:

- ‘alpine form’
- ‘broad phyllode variant’
- ‘var. indet.’.

Information entered in the **Extra information** field will be printed on the label directly below the taxon name.

Any nomenclatural notes relating to the taxon name (e.g. ‘nom. nud’, ‘nom. inval.’) should be entered in the **Nom. note** field in the taxon name record.

Flora

If the det. slip indicates that the specimen was viewed for a flora project, select the flora from the pick list. Do not enter any flora notes from the det. slip (e.g. ‘Seen for Flora of Australia’ or ‘Flora of Australia Project’) in the **Det. notes** field. The **Flora** pick list currently lists ‘Algae of Australia’, ‘Flora of Australia’ and ‘Flora Malesiana’. Additional flora projects can be added if needed. Make sure you only use this field in the determination record that corresponds to the relevant det. slip.

Det. notes

Det. notes should be used to record additional notes that relate to the determination or the particular specimen, and not to a taxon or group concept. For example:

- ‘glabrous variant with atypically short phyllodes’
- ‘form with more or less petalous flowers’
- ‘the awn is shorter than usual in this species’
- ‘female’
- ‘primocane’
- ‘fruit needed for identification to species level’
- ‘Determination taken from NSW 574242, Australia's Virtual Herbarium, 30/10/14’.

Lichen chemistry should be recorded in the **Det. notes** field if it is part of a determination. If it was provided by the collector, it should be recorded in **Collecting notes**. For example:

- ‘TLC in C: salazinic (major), consalazinic, norstictic (faint trace), protocetraric (trace) and usnic acids’
- ‘P-, K+, yellow, C-, KC-’.

What goes where?

Name usage

Where an observation about the use of a name has been made by data entry staff, it should be recorded as an annotation in the **Determinations** table (i.e. a separate **Determination** record with the **Det. type** set as ‘Annot.’). Examples of observations about the use of a name include:

- ‘Incorrectly reported from Australia, Checklist of Australian Lichens, Aug 2003’
- ‘Listed under doubtful and excluded names, Checklist of Australian Lichens, August 2003’
- ‘Listed under excluded names, Fl. Aust. 55: 162 (1994)’.

But, if an observation about the use of a name is written on a det. slip, then it should be recorded in the **Det. notes** field for that determination.

Source of name

An indication of where the name comes from should be entered in the **Det. notes** field. For example:

- ‘species name taken from I.G. Stone’s red collecting book’.

Variants and forms

Short, informal variant or form names should be entered in the **Extra information** field. For example:

- ‘Brisbane Range variant’
- ‘Daylesford form’
- ‘large flower form’
- ‘sessile-head variant’.

But, if the variant or form has been listed in Viclist or APNI, it should be entered in the **Taxon** tree. For example:

- ‘*Grevillea* aff. *oxyantha* (Mt Burrowa)’
- ‘*Betula* aff. *pubescens* (Mt Macedon)’.

If the variant or form information is a short description, rather than a short, informal name, it should be entered in the **Det. notes** field. For example:

- ‘variant with pubescent calyces’
- ‘variant with short, ovate-obovate leaves’
- ‘small, dark and short-headed form’.

If you are unsure whether something belongs in **Extra information** or **Det. notes**, enter the information in **Det. notes**.

Field names

Field names for fungi that have not been identified to species level should be entered in **Extra information**. For example:

- *Elaphomyces* ‘yellow crusty’ – only enter ‘yellow crusty’ in the **Extra information** field.

The formal part of the identification (in this example, ‘*Elaphomyces*’) should be entered in the **Taxon name** field as per usual.

Informal names

Informal names for current determinations should be entered in the **Taxon** table. There is a CHAH-endorsed format for informal names, but any informal name that is used in a determination may be added to the **Taxon** table, if you are sure that’s what it is. There are many informal names already in the **Taxon** tree, Viclist, FloraBase and APNI, so please consult these sources before adding a new informal name to the **Taxon** table. If in doubt, enter the informal part of the name in the **Extra information** field.

Redeterminations of duplicates

If the determination of a specimen is based on the redetermination of a duplicate specimen held at another herbarium, enter the name of the person who redetermined the duplicate in the **Determiner** field, and use the **Basis** field to record that the determination was based on a duplicate.

If the determination was taken from a duplicate, record an appropriate message in **Det. notes** to make it clear that the determiner hasn’t redetermined our specimen in person, e.g. ‘Determination taken from NSW 574242, Australia’s Virtual Herbarium, 30/10/14’. Enter the herbarium code and catalogue number of the inferred duplicate in the **Other identifier** table, recording ‘Duplicate’ in the **Type** field.

Nomenclatural notes

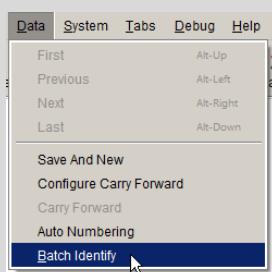
Any nomenclatural notes that need to be printed with the taxon name, such as ‘non. R.Br.’, ‘nom. nud.’, ‘nom. inval.’ etc. should be entered in the **Nom. note** field in the taxon name record, not in the determination record.

Batch identify

The **Batch identify** tool in Specify can be used to add new determination records to multiple collection objects at the same time. The newly added determination becomes the current determination, and the previous determinations are retained in the database.

To add a new determination to a batch of records:

1. Create a record set of the collection objects that you want to redetermine. Make sure that the record set only contains collection objects for which the new determination details are identical, as all the records in the set will get the same details added for the new det.
2. Select **Batch identity** from the **Data** menu:



3. Select **Record Sets** from the **Choose** window
4. Select the appropriate record set from the list and click **OK**

A window with all the determination fields and a summary of the collection objects in the record set. Before redetermining your record set, scroll through the list of records to check for any collection objects that shouldn't be there.

A screenshot of the 'Batch Identify' dialog box. The top section contains fields for 'Det type' (set to 'Det'), 'Determiner' (with a dropdown and search icon), 'Taxon name' (with a dropdown and search icon), 'Alternative name' (text input), 'Qualifier' (dropdown), 'Qualifier rank' (dropdown), 'Addendum' (dropdown), 'Determiner inferred' (checkbox), 'Type status' (dropdown), 'Type qualifier' (dropdown), 'Stored under this name' (checkbox), 'Basis' (dropdown), 'Extra information' (text input), 'Flora' (dropdown), and 'Det. notes' (text input). Below this is a table titled 'Collection Object' with columns: Catalogue no., Date, Type status, and Taxon. The table lists several entries, all of which have 'Pterostylis ingens' listed under 'Taxon'. At the bottom of the dialog are buttons for 'Identify', 'Select Specimens', and 'Close'.

5. Enter the details of the new determination and click **Identify**. All records will be redetermined, unless you select specific records from the list.

Preparations

The **Preparations** form is a subform of the **Collection object** form. It is used to store information about what type of specimen the collection object relates to (sheet, packet, spirit etc.), where it is stored, and information about where the specimen came from and where duplicates are held.

Preparation type

The type of preparations belonging to the collection object. The following preparation types are used at MEL:

- Sheet – a pressed and dried specimen mounted on archival paper and stored in a manila folder
- Packet – a dried specimen stored in a packet. The majority of fungi, lichen and bryophyte specimens are packet preparations.
- Spirit – material preserved in ethanol and stored in the Spirit Room
- Carpological – dried fruiting material that is too bulky to be pressed and mounted as a sheet
- Microscope slide – a glass slide prepared for microscopic examination of all or part of the specimen
- Photographic slide – a photographic slide that accompanies the specimen
- Cibachrome – an image of a specimen from a colour slide that has been reproduced on photographic paper
- Silica gel sample – plant material stored in silica gel to be used for molecular analysis
- Photograph of specimen – a photograph of a specimen held at another institution. If a printed photograph accompanies a pressed plant specimen (i.e. a habitat photo), this should be flagged in the **Photograph** field instead.
- Fungal culture – a dried fungal culture. All fungal cultures are stored in packets within the fungi collection.
- Display Set – a specimen that is stored in the Display Set on the first floor of the herbarium extension
- Seed collection – a seed sample, which is stored in the basement and may be used for germination trials or revegetation work
- Duplicate – duplicate material that is sent to another herbarium
- Seed duplicate – a duplicate seed collection that is sent to another herbarium
- Shipping material – a fragment of a specimen that is sent to another herbarium for analysis
- Vic. Ref. Set – a duplicate specimen that is held in the Victorian Reference Set, and has been curated as part of the separate *Victorian Reference Set* collection
- Vic. Ref. Set (old) – a duplicate specimen that is held in the Victorian Reference Set, but has not yet been curated in line with the new Vic. Ref. Set procedures.

A single collection object cannot have more than one of the following preparation types: ‘Sheet’, ‘Packet’, ‘Spirit’, ‘Carpological’, ‘Cibachrome’, ‘Photograph of specimen’, ‘Fungal culture’ or ‘Display Set’. The only preparation types that can occur with other preparation types in the one collection object record are ‘Microscope slide’, ‘Photographic slide’, ‘Silica gel sample’, ‘Vic. Ref. Set’, ‘Vic. Ref. Set (old)’, ‘Seed collection’, ‘Duplicate’, ‘Seed duplicate’ and ‘Shipping material’.

Quantity

The number of objects of a particular **Preparation type**. The default quantity is ‘1’. The value of this field should only ever be greater than one for those preparation types that do not receive individual numbers for each object (i.e. microscope slides and spirit jars).

For ‘Duplicate’ and ‘Seed duplicate’ preparations, the number in the **Quantity** field should match the number of institutions listed in the **MEL duplicates at** field in the **Preparation attribute** form.

For ‘Vic. Ref. Set’ specimens, the **Quantity** should always be ‘1’.

Number

The number assigned to the spirit jar, microscope slide, silica gel sample or Vic. Ref. Set specimen, or the library reference number for a photographic slide.

We have previously used the same numbering scheme for spirit and slide material. From now on, we will use a separate series of numbers for each type of preparation. The next available storage number for a preparation type is automatically generated when you save the record.

If there are multiple photographic slides with a specimen and they have each been assigned a Library reference number, they should be entered as separate preparations with the relevant Library reference number entered in the **Number** field for each preparation record.

Note that only one number is assigned for each spirit collection, regardless of whether or not there is more than one spirit jar in the collection. Likewise, only one number is assigned to microscope slides that belong to the same collection. Where there is more than one spirit jar or microscope slide for the one collection, use the **Quantity** field to indicate how many items there are.

For Vic. Ref. Set specimens, the number will become the **Catalogue number** in the corresponding **Collection object** record in the *Victorian Reference Set* collection.

Jar size

The size of the spirit jar (A, B, C or D). A is the smallest jar size, B is the medium jar size and C is the largest jar size. D is used to indicate that the specimen is an algal collection, irrespective of the jar size.

On loan

The **On loan** check box will automatically be ticked if a preparation is on loan.

Loans

The **Loans** button is a link to the entry in the **Loan** table that relates to the preparation. If a preparation is currently on loan, clicking on the **Loans** button will open the details of the **Loan** in a new tab.

Multisheets

Information about multisheet relationships between different specimens. The multisheet message must include the part (A, B, C etc.) after the MEL number, to indicate which parts of a mixed collection are involved in the multisheet relationship. The part should also be included for specimens that are not part of a mixed collection. The total number of sheets should reflect the number of database records, not the number of physical objects. All numbers should be spelt out in full, and there should not be a space between the number and the part. For example:

- ‘Sheet 1 of 3 (MEL 12345A, MEL 12345B, MEL 12346A)’.

For non-sheet collections or non-packet collections, include the preparation type before the MEL number, followed by a colon. For example:

- ‘Sheet 1 of 2 (MEL 2142735A, Carpological: MEL 269770A)’
- ‘Sheet 1 of 3 (MEL 691579A, MEL 691579B, Spirit: MEL 2040692A)’.

If the multisheet relationship is between a mature plant and its cultivated seedling, enter ‘Cultivated seedling(s):’ before the relevant MEL number(s). For example:

- ‘Sheet 1 of 3 (MEL 12345A, Cultivated seedlings: MEL 12346A, MEL 12347A)’.

MEL duplicates at

The Index Herbariorum codes of the herbaria that duplicates of a MEL specimen were sent to. Institution codes should be separated by a comma and a space, e.g. ‘AD, CANB, HO’; do not enter a full stop at the end of the string.

This field should only be completed for ‘Duplicate’ or ‘Seed duplicate’ preparations. Institutions that hold duplicates of specimens sent to MEL as exchange or donations should be listed in the **Other duplicates at** field in the record for the primary MEL preparation (i.e. ‘Sheet’, ‘Spirit’, ‘Carpological’, ‘Fungal culture’ or ‘Display Set’).

Other dupl. at

The Index Herbariorum codes of the herbaria (or the name of other institutions) that also hold duplicates of specimens sent to MEL as exchange or donations. The **Other duplicates at** field should never be filled in for ‘Duplicate’ or ‘Seed duplicate’ preparations. Herbaria that hold duplicates of specimens sent by MEL should be listed in the **MEL duplicates sent to** field for the ‘Duplicate’ preparation type.

Orig. herb.

The Index Herbariorum code of the institution where the actual specimen is held, where we have received a photograph or cibachrome of the specimen from a different herbarium. For example, if we receive an image of a type specimen from CANB, but the image is of a specimen held at K, 'CANB' would be entered in the **Ex herbarium** field, and 'K' would be entered here. The **Orig. herb.** field should never be filled in for 'Duplicate' or 'Seed duplicate' preparations.

Databasing MEL duplicates

Duplicate preparations

In Specify, 'gifts' (outgoing exchange and donations) are linked to preparations. When a new gift transaction is created, preparations are added to the **Gift** record, creating a register of what duplicates have been sent where. To distinguish between preparations that are held at MEL and those that have been sent to other institutions, any specimen that has duplicates must have a 'Duplicate' preparation entry in the **Preparations** table, in addition to the preparation type(s) held at MEL ('Sheet', 'Spirit' etc.).

A single **Collection object** record should only ever have one 'Duplicate' preparation record in the **Preparations** table, regardless of the number of duplicate specimens that have been sent out. The **Quantity** field should be used to indicate the number of herbaria to which a duplicate has been sent. (There is no need to record that more than one 'sheet' has been sent to a single herbarium, as we have no guarantee that they will retain all the material.)

The **MEL duplicates at** field is used to list the herbaria that duplicate material has been sent to, and should only be populated for 'Duplicate' or 'Seed duplicate' (see below) preparation types. Institution codes should be separated by a comma and a space, and full stops should not be used. Do not enter anything in the **MEL duplicates at** field for preparations that are retained at MEL.

Duplicates of multisheet collections

Where a duplicate of a multisheet collection has been sent to one or more herbaria, a 'Duplicate' preparation should only be added to the **Collection object** record for one component of the multisheet. This will generally be Sheet 1, but in rare cases, it may be Sheet 2 (e.g. if duplicate spirit material is sent of a multisheet collection comprising dry material and a spirit collection).

Victorian Conservation Seedbank duplicates

Victorian Conservation Seedbank specimens generally have duplicate herbarium material as well as a duplicate seed collection, which need to be entered as separate 'Duplicate' and 'Seed duplicate' preparations. Because the duplicate seed sample and duplicate herbarium material are not always sent to the same institutions, the information in the **MEL duplicates at** field for the 'Duplicate' and 'Seed duplicate' will usually be different.

Printing duplicate labels

The number of duplicate labels that need to be printed will be calculated from the **Quantity** fields for preparation types that require duplicate labels.

Victorian Reference Set specimens

Specimens in the Vic. Ref. Set are databased in their own collection and also recorded as a ‘Vic. Ref. Set’ preparation in the corresponding MEL specimen record. Each Vic. Ref. Set specimen will be assigned a six-digit VRS catalogue number, which will be stored in the **Number** field when the record is saved. The Vic. Ref. Set specimens all need to have unique VRS catalogue numbers so, if there is more than one Vic. Ref. Set duplicate of a MEL specimen, the MEL record will need to have a separate ‘Vic. Ref. Set’ preparation for each Vic. Ref. Set sheet; the value of the **Quantity** field in a ‘Vic. Ref. Set’ preparation must always be ‘1’.

Once the ‘Vic. Ref. Set’ preparation has been saved in the *National Herbarium of Victoria* collection, a collection object record will be automatically created in the *Victorian Reference Set* collection, with the VRS number as the **Catalogue number**. The *Victorian Reference Set* record will include the most recent determination and all other data (except the preparation records and links to transactions) from the corresponding *National Herbarium of Victoria* record. The *Victorian Reference Set* record should be edited to include any annotations on the Vic. Ref. Set sheet, or to delete any annotations from the *National Herbarium of Victoria* record that don’t relate to the Vic. Ref. Set specimen.

Given that all Vic. Ref. Set specimens are duplicates of specimens in the main collection, they should always be databased via the *National Herbarium of Victoria* collection; records can be edited in, but should not be directly added to, the *Victorian Reference Set* collection.

Vic. Ref. Set specimens will be labelled with distinct labels, and ‘Vic. Ref. Set’ will still appear in the ‘Dupl:’ string on the corresponding MEL label.

Storage

The storage system at MEL is quite outdated, and doesn’t reflect current taxonomic knowledge. In Specify, taxon names have been decoupled from the storage system, which allows us to query MELISR by up-to-date higher level taxonomy.

The **Storage** field provides a link to the **Storage** tree, so that changes in taxonomic classification in the **Taxon** tree do not necessarily have to lead to changes in storage. When you add a new taxon record for ranks above species, you also need to define its storage location; see [Adding new genus and higher taxon names](#) for instructions.

The **Storage** field will be populated when the record is saved. The storage location will be automatically printed on labels, regardless of whether or not the script that populates the **Storage** field has run.

Hort. Ref. Set

This field is used to indicate that the specimen is in the Horticultural Reference Set. It is legacy data from MELISR, and probably won’t be used in future. When the rest of the Hort. Ref. Set is databased, it will probably be entered as a separate collection in Specify.

Collecting event

The **Collecting event** table stores information about when and where the specimen was collected, and who it was collected by.

Collectors

All collectors associated with the collecting event should be entered here. Click on the **Add** symbol to open the **Collectors** subform. When adding multiple collectors, make sure that the primary collector is listed first (although the order of the collectors doesn't really matter from a database point of view, entering them in a consistent way will help us detect potential errors in the database). If you need to change the order of collectors, click on the collector's name that you want to move, then use the up and down arrows at the right-hand side of the **Collectors** grid:

Last name	Initials	Comments	Is primary
West	J.G.		No
Stajsic	V.		Yes
Albrecht	D.E.		No

If there is no collector's name on the specimen, do not enter anything in the **Collectors** field. Instead, enter '[Unknown]' in the **Verbatim collectors** field in the **Collecting event attributes** form. If the label actually states that the collector is unknown, enter 'Unknown' (i.e. without brackets) in the **Verbatim collectors** field. If the collector(s) name is illegible, enter '[Illegible]' in the Verbatim collectors field. If the collector's name is not on the label, but has been inferred from their handwriting or the collecting information, entered '[Inferred]' in the **Verbatim collectors** field.

Collecting no.

The collecting number of the primary collector(s). If there is no collecting number, type 's.n.' (*sine numero*) in the **Collecting no.** field. The **Collection object** form cannot be saved if this field is left blank.

If the collecting number is prefixed with the collector's initials, there is no need to enter their initials in the **Collecting no.** field.

If someone other than the listed collectors has assigned a collecting number to an unnumbered collection, enter the number in square brackets in the **Collecting no.** field, preceded by the initials of the person assigning the number. A note explaining who assigned the number should also be entered in **Miscellaneous notes**. For example:

- 'D. Rouse [JAJ 1301] & M. Duncan' – '[JAJ 1301]' would be entered in the **Collecting no.** field and '[Collecting number assigned by J.A. Jeanes]' should be entered in **Miscellaneous notes**.

If someone other than the listed collectors has assigned a collecting number to a specimen that already has a number, enter the primary collector's number in **Collecting no.**, and record the additional number in **Miscellaneous notes**. For example:

- 'F. Robbins 106 (ACB 17097)' – '106' would be entered in the **Collecting no.** field, and '[A.C. Beaglehole assigned collecting number 17097 to this specimen.]' would be entered in **Miscellaneous notes**.

Start date

The collecting date, or the earliest date if the collecting date is given as a range. The collecting date can be entered as a full date (day, month and year), a month and year, or a year only. Select the date type from the date drop-down list, then enter the date using the number keys.

In Texpress, if the collecting date was unknown but the collector was known, biographical notes would be entered in the Notes field to indicate the collector's lifespan or period of activity (where possible). In Specify, this information should be entered in the collector's record in the **Agent** table, so that it is linked to every record collected by that agent.

End date

The end date of collection, if the collecting date is given as a range. The collecting date can be entered as a full date (day, month and year), a month and year, or a year only. Select the date type from the date drop-down list, then enter the date using the number keys.

Flowering and fruiting dates

Specimens with a flowering date OR a fruiting date

If the collecting notes mention a flowering (or fruiting) date, and the specimen is in flower (or fruit), it is safe to assume that the date corresponds to the date of collection. If the specimen is not in flower (or fruit), enter the flowering (or fruiting) date in the **Collecting notes** field.

Specimens with a flowering date AND a fruiting date

If the specimen is in flower, but not in fruit, enter the flowering date as the date of collection, and the fruiting date in **Collecting notes** (or vice versa). You can also add a note in the **Data entry notes** field to explain that a fruiting date is given, but the specimen only bears flowers.

If the sheet contains separate plant specimens, one of which is bearing flowers and one of which is bearing fruit, assume that the flowering and fruiting dates represent the collecting dates of the separate plant specimens, and treat them as a mixed collection.

If the specimen has both flowers and fruits, but it doesn't appear to be a mixed collection, enter the flowering and fruiting dates in **Collecting notes**.

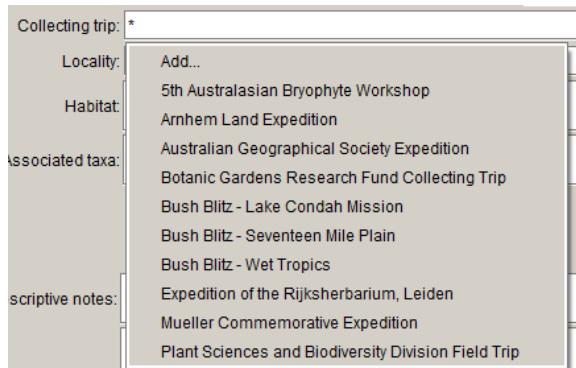
Flowering and fruiting dates without years

If the flowering and/or fruiting dates have been interpreted as collecting dates but do not include the year, enter them in the **Verbatim collecting date** field.

Collecting trip

The collecting trip or expedition on which the specimen was collected, e.g. 'Victorian Exploring Expedition', 'Mueller Commemorative Expedition'. Select the relevant collecting trip from the drop-

down list. To see a list of all the collecting trips in the **Collecting trip** table, enter a wildcard (*) in the query combo box and press the down-arrow:



If the collecting trip is not there, add it in the **Collecting trip** form.

Geography

This is a read-only field that displays the **Geography** full name string, if it has been entered in the **Locality** form. The geography details will not display in this field until the record has been saved.

Locality

The locality description, as provided by the collector. Click on the **Add** icon to open the **Locality** form.

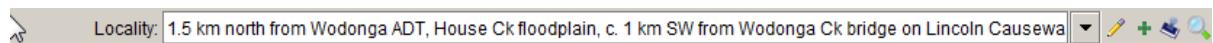


You will see that the locality field has a drop-down list that allows you to select a locality that has already been entered, but this must be used with great caution. Only use an existing locality record if ALL of the details in the **Locality** form (and the associated **Locality details** and **Geocoordinate details**) are EXACTLY the same. If a **Locality** record is shared between two or more **Collection object** records then subsequently edited, the locality will be edited in *all* the **Collection object** records that share that locality, not just in the **Collection object** record that is open when the **Locality** record is edited. If the locality is similar to a previous record, use the **Clone** feature outlined below.

If there are no locality details provided, DO NOT select 'No details given' from the drop-down list, as many of the records with 'No details given' in the **Locality** field have data in other fields in the **Locality** and **Geography** tables that will not correspond to the specimen you are databasing.

If you use 'carry forward' for the **Collecting event** information, the **Locality** query box in the new record will contain the locality of the previous record. Do not **Edit** this **Locality** record unless to correct an error, as it will change the locality for all records you entered before that use the same **Locality** record. If the specimen you are databasing was collected in the exact same spot (including at the same altitude) as the specimen you databased previously, you can use the same **Locality** record and don't have to do anything. If some, but not all, of the locality information is the same as in the previous record, you can use the **Clone** button – the stamp symbol just to the right of the **Add** icon. This will create a new **Locality** record with all the locality information from the previous record,

so you can just change in the **Locality** form what needs to be changed. It will almost always be safer to **Clone** an existing **Locality** record than to **Edit** it.

A screenshot of a software interface. On the left is a small icon of a hand cursor. Next to it is a text input field containing the text "Locality: 1.5 km north from Wodonga ADT, House Ck floodplain, c. 1 km SW from Wodonga Ck bridge on Lincoln Causewa". To the right of the input field is a dropdown arrow icon. Further to the right are several small, semi-transparent icons: a pencil, a plus sign, a magnifying glass, and a circular arrow.

Habitat

A general description of the habitat that the plant, alga or fungus was growing in. Lists of associated taxa should be entered in the **Associated taxa** field if they are given as a distinct list prefixed by 'associated species', 'in association with', or similar text.

Habitat or Associated taxa?

<i>Collecting information</i>	<i>Data entry</i>	<i>Comments</i>
Growing in a dry creek bed in dry sclerophyll forest on the property of Bush Hide-a-way Log Cabins, in association with <i>Poa sieberiana</i> var. <i>sieberiana</i> .	Habitat: Growing in a dry creek bed in dry sclerophyll forest on the property of Bush Hide-a-way Log Cabins. Associated taxa: <i>Poa sieberiana</i> var. <i>sieberiana</i> .	
Growing in creek bed with rather coarse sand and broken shells on surface. In association with * <i>Asphodelus fistulosus</i> , etc.	Habitat: Growing in creek bed with rather coarse sand and broken shells on surface. Associated taxa: * <i>Asphodelus fistulosus</i> .	
Growing on sand in association with <i>Ecdeiocolea monostachya</i> , amongst mallee eucalypts of a yellow sand-plain.	Habitat: Growing on sand in association with <i>Ecdeiocolea monostachya</i> , amongst mallee eucalypts of a yellow sand-plain. Associated taxa: <i>Ecdeiocolea monostachya</i>	<i>Ecdeiocolea monostachya</i> can be entered in Associated taxa , but should also be left in the habitat description so the original description is not corrupted.
Interdunal low-reddish, loamy, non-calcareous sands with <i>Eucalyptus oleosa</i> , mallee, <i>Casuarina</i> , <i>Heterodendrum</i> open woodland and sparse shrubs and Spinifex.	Habitat: Interdunal low-reddish, loamy, non-calcareous sands with <i>Eucalyptus oleosa</i> , mallee, <i>Casuarina</i> , <i>Heterodendrum</i> open woodland and sparse shrubs and Spinifex. Associated taxa:	In this description ' <i>Eucalyptus oleosa</i> , mallee, <i>Casuarina</i> , <i>Heterodendrum</i> ' is describing the woodland, rather than associated taxa.
Button grass plain, head of Melaleuca Inlet. Grows on recently burnt areas of plain. In Jungle thicket in Horizontal Scrub areas. Usually in association with <i>Bauera</i> .	Habitat: Button grass plain, head of Melaleuca Inlet. Collecting notes: Grows on recently burnt areas of plain. In Jungle thicket in Horizontal Scrub areas. Usually in association with <i>Bauera</i> .	It's not clear whether the three sentences that follow the habitat description apply only to the specimen in question or if they are a general description of where the taxon grows, so it's better to enter that information in the Collecting notes field, rather than in Habitat and Associated taxa .

Collecting information	Data entry	Comments
In deep sand in association with <i>Casuarina paludosa</i> .	Habitat: In deep sand. Associated taxa: <i>Casuarina paludosa</i> .	
Growing in association with [MGC] 5547.	Habitat: Associated taxa: [MGC] 5547	If you can determine the identity of MGC 5547 from MELISR, enter the taxon name in parentheses after the collecting number, e.g. '[MGC] 5547 (<i>Eremophila longifolia</i>)', but don't leave out the collecting no..
Located in dry sclerophyll forest, by the roadside. In association with <i>Eucalyptus sieberi</i> and other eucalypts which are dominant.	Habitat: Dry sclerophyll forest, by the roadside. In association with <i>Eucalyptus sieberi</i> and other eucalypts which are dominant. Associated taxa: <i>Eucalyptus sieberi</i> , <i>Eucalyptus</i> spp.	Only taxon names should be entered in the Associated taxa field.
Below the south facing cliffs of the wall of a large gully on the west side of a large hill. Soil: red-brown pebbly-rocky loam amongst boulders. <i>Eucalyptus leucophloia</i> , <i>Acacia rhodophloia</i> , <i>A. aneura</i> low woodland over <i>Eremophila</i> sp. high open shrubland over <i>Ptilotus obovatus</i> low shrubland over <i>Polectachne</i> sp. Mt Ella, <i>Triodia pungens</i> open hummock grassland. Associated species: <i>Rhodanthe margaretha</i> e, <i>Taplinia saxatilis</i> , <i>Sida</i> aff. <i>filiformis</i> , <i>Chenopodium saxatile</i> , <i>Oxalis</i> aff. <i>corniculata</i> , <i>Canthium latifolium</i> , <i>Astrotricha hamptonii</i> (on the cliffs), <i>Lobelia</i> sp., <i>Eriachne mucronata</i> , <i>Cheilanthes humilis</i> ?	Habitat: Below the south facing cliffs of the wall of a large gully on the west side of a large hill. Soil: red-brown pebbly-rocky loam amongst boulders. <i>Eucalyptus leucophloia</i> , <i>Acacia rhodophloia</i> , <i>A. aneura</i> low woodland over <i>Eremophila</i> sp. high open shrubland over <i>Ptilotus obovatus</i> low shrubland over <i>Polectachne</i> sp. Mt Ella, <i>Triodia pungens</i> open hummock grassland. Associated taxa: <i>Rhodanthe margaretha</i> e, <i>Taplinia saxatilis</i> , <i>Sida</i> aff. <i>filiformis</i> , <i>Chenopodium saxatile</i> , <i>Oxalis</i> aff. <i>corniculata</i> , <i>Canthium latifolium</i> , <i>Astrotricha hamptonii</i> (on the cliffs), <i>Lobelia</i> sp., <i>Eriachne mucronata</i> , <i>Cheilanthes humilis</i> ?	Taxa that are describing the habitat should not be entered in the Associated taxa field.

Collecting notes

Any notes provided by the collector that do not belong in other fields (e.g. information about distribution or abundance). Annotations made by someone other than the collector and notes made by data entry staff should be entered in either the **Miscellaneous notes** or **Curation notes** fields.

Annotations made by people other than the collector, such as Nancy Burbidge or Jim Willis, should be entered in the **Curation notes**, **Miscellaneous notes** or the **Georeferencing notes** field. For example:

- ‘Field label removed to handwriting file J.H. Willis 15/5/1961.’ should be entered in **Curation notes**
- ‘No. 88 from J.H. Willis to G.O.K. Sainsbury.’ should be entered in **Miscellaneous notes**
- A comment about the collecting locality by J.H. Willis, e.g. ‘Not Kallista, but could be Monbulk’, should be entered in **Georeferencing notes**
- ‘Common in lawns of Melbourne Botanic Gardens. J.H. Willis.’ should be entered in **Miscellaneous notes**.

Notes on the sheet by curators of personal herbaria (such as Steetz or Sonder) should be entered in the **Miscellaneous notes** field.

Collecting event attributes

The **Collecting event attributes** subform is used to enter additional information about the collecting event, including plant origin, host and substrate.



Collecting event attachments

Any attachments that relate to the collecting event, such as habitat photos or a photo of the plant at the collecting site.



Collectors

Agent

To look up a name, start typing the collector’s last name and then press the down-arrow or the **Tab** key to see a list of matching names. What you type in the field is only matched against the **Last name** field, so don’t type a comma or any initials when you are looking up a collector’s name. Scroll the list of matching names, then press **Enter** or click **OK** when you have found the right agent.

When adding multiple collectors, make sure that the primary collector is listed first (although the order of the collectors doesn't really matter from a database point of view, entering them in a consistent way will help us detect potential errors in the database). If you need to change the order of collectors, click on the collector's name that you want to move, then use the up and down arrows at the right-hand side of the **Collectors** grid:

Last name	Initials	Comments	Is primary
West	J.G.		No
Stajsic	V.		Yes
Albrecht	D.E.		No

If you have selected the wrong name, press **Esc** to clear the field, then search again.

If the collector's name does not appear in the list, select 'Add' from the drop-down list, or click the **Add** symbol next to the field to add a new agent record.

Comments

The **Comments** field can either be used to record collecting numbers assigned by one of the additional collectors, or uncertainty about the interpretation of the collector's name.

The collecting number for the primary collector(s) (see **Is primary**) should be entered in the **Collecting no.** field. For example:

- 'A.C. Beaglehole 58278 & E.G. Errey 1978' – '1978' should be entered in **Comments** for E.G. Errey. **Comments** should be left blank for A.C. Beaglehole, and '58278' should be entered in the **Collecting no.** field.

If you are unsure that the collector is the person you have selected from the drop-down list, enter a question mark in this field.

Is primary

Where there is more than one collector, the **Is primary** check box is used to indicate which of the collectors are the primary collectors. The **Is primary** check box is ticked by default, so it only needs to be un-ticked for collectors who are not considered to be primary collectors.

The primary collector is the collector whose name appears before the collecting number or 's.n.' (if 's.n.' is recorded in the collecting information). If more than one collector's name appears before the collecting number (or 's.n.'), they can all be considered as primary collectors. If there is more than one collector, but no collecting number or 's.n.', all collectors should all be considered as primary collectors. For example:

- 'N.G. Walsh 4901 & F. Anderson' – N.G. Walsh is the primary collector
- 'L.A. Craven & C.R. Dunlop 6663' – both collectors are primary collectors
- 'J.G. & M.H. Simmons s.n. & K.C. Rogers' – J.G. Simmons and M.H. Simmons are the primary collectors
- 'D. Rouse [JAJ 1301] & M. Duncan' – D. Rouse is the primary collector.

Note that these examples are only a guide; feel free to apply your own knowledge of the collectors when assessing which are the primary collectors and which are the additional collectors. For

example, Nigel Sinnott labels are sometimes formatted with two collectors listed before the collecting number (e.g. 'A.E.M. & N.H. Sinnott 2989'), even though the collecting number is from his sequence and he should be considered the only primary collector.

Collecting trip

Trip name

The name of the collecting trip, or expedition.

Start date

The start date of the collecting trip or expedition, or the earliest date if a range is given. The collecting trip start date can be entered as a full date (day, month and year), a month and year, or a year only. Select the date type from the drop-down list, then enter the date using the number keys.

End date

The end date of the collecting trip or expedition if the date is given as a range. The collecting trip end date can be entered as a full date (day, month and year), a month and year, or a year only. Select the date type from the date drop-down list, then enter the date using the number keys.

Verbatim start date

If the collecting trip start date is given in a format that cannot be entered in the **Start date** field, it should be entered here (e.g. 'late March', 'Spring', 'Christmas 1912'). If the collecting trip start date is given in a non-standard form but includes a year, or a year and a month, the year and/or month should also be entered in the collecting trip **Start date** field.

Verbatim end date

If the collecting trip end date is given in a format that cannot be entered in the **End date** field, it should be entered here (e.g. 'late March', 'Spring', 'Christmas 1912'). If the collecting trip end date is given in a non-standard form but includes a year, or a year and a month, the year and/or month should also be entered in the collecting trip **End date** field.

Sponsor

The sponsor of the collecting trip or expedition, e.g. 'Australian Geographic', 'Churchill Fellowship Trust'.

Comments

Any additional information about the collecting trip that does not fit in the above fields.

Collecting event attributes

Label data

Verbatim collectors

The collector(s) name(s) exactly as they appear on the label, without interpretation. If the label contains a collector's name, you only need to complete this field if the names entered in the **Collectors** field have been interpreted, or if the name on the label is spelt differently or provides additional information, including honorifics (Miss, Mrs, Prof., Dr, Mr etc.). By recording the collector(s) name(s) verbatim, it is much easier to correct this information where the original interpretation of a name was incorrect, and it's also enormously useful for historical research. Do not include collecting numbers in the **Verbatim collector** field.

If there is no collector's name on the specimen, enter '[Unknown]' in the **Verbatim collectors** field. If the label actually states that the collector is unknown, enter 'Unknown' (i.e. without brackets). If the collector(s) name is illegible, enter '[Illegible]' in the **Verbatim collectors** field. If the collector's name is not on the label, but has been inferred from their handwriting or the collecting information, entered '[Inferred]' in the **Verbatim collectors** field.

If there is more than one collector, but only one of the collectors' names has been interpreted, you should still enter them both in the **Verbatim collector** field. For example, if the collectors were given as 'Mr & Mrs T.P. Richards', you would enter the collectors as 'T.P. Richards' and 'A.F. Richards', and the verbatim collectors would be recorded as 'Mr & Mrs T.P. Richards', not just 'Mrs T.P. Richards'.

A guide to when the name on the label should be recorded in the **Verbatim collectors** field is provided below:

Name on label	Collectors	Record verbatim collector(s)?
Chas. Walter	Walter, C.	No – there is no interpretation, and the additional information on the label is not particularly important
Mrs T.P. Richards	Richards, A.F.	Yes – the name in the Collector field has been interpreted
O. Tepper	Tepper, J.G.O.	Yes – the name in the Collector field has been interpreted
Sir W. McGregor	MacGregor, W.	Yes – the name on the label is spelt differently to the interpreted name in the Collector field, and includes an honorific
Rev. J. Chalmers	Chalmers, J.	No – there is not really any interpretation of the name here. 'Rev.' will be recorded as the Title in the Agent record for James Chalmers.

Th. Kotschy	Kotschy, C.G. T.	Yes – the name in the Collector field has been interpreted
Dr Hooker	Hooker, J.D.	Yes – the name in the Collector field has been interpreted
Bowm.	Bowman, E.	Yes – the name in the Collector field has been interpreted
Fr. Nicolas	Nicolas, G.	Yes – ‘Fr.’ has been interpreted as a title, rather than an abbreviated first name
Thwaites	Thwaites, G.H.K.	Yes – the initials have been interpreted

Collector inferred

If the collector has been inferred, tick the **Collector inferred** check box. Information about how the collector has been inferred can be entered in the **Miscellaneous notes** field, along with any relevant sources.

Collector unknown

If there is no collector’s name on the sheet, and the collector cannot be inferred, tick the **Collector unknown** check box. ‘However, if the collecting label says ‘Unknown’, enter ‘Unknown’ in the **Verbatim collectors** field.

Collector illegible

If the collector’s name is on the sheet, but is illegible, tick the **Illegible** check box.

Verbatim collecting date

If the collecting date is given in a format that cannot be entered in the date field, it should be entered here (e.g. ‘late March’, ‘Spring’, ‘Christmas 1912’). If the collecting date is given in a non-standard form but includes a year, or a year and a month, the year and/or month should also be entered in the collecting date fields (**Start date** and **End date**).

Date inferred

If the collecting date has been inferred, tick the **Date inferred** check box. Do not infer collecting dates from other database records; collecting dates should only be inferred from published sources, such as expedition journals, exsiccatum lists, or other publications.

Information about the source of an inferred date can be entered in the **Miscellaneous notes** field; however, if the date has been inferred from the collector's lifespan or known period of activity, enter that information in the **Agent** table instead.

Plant origin

Introduced status

The introduced status of the specimen at the collecting locality. This information will either be provided by the collector, in the exchange data, or assessed by a botanist at a later date. Data entry staff do not need to assess introduced status. Where this information is provided by the collector or in the exchange data, enter the exact wording in the **Collecting notes** field, and select the corresponding category from the pick list. The following values can be selected from the pick list:

- Native – the taxon is native to the collecting locality
- Not native – the taxon is not native at the collecting locality
- Unknown – the introduced status of the taxon at the collecting locality is unknown.

If the **Introduced status** field is filled in, the introduced **Source** field must also be completed.

Introduced source

The source of the introduced status. The following values can be selected from the pick list:

- Collector – the introduced status was provided by the collector
- Exchange data – the introduced status was provided in the exchange data
- NGW – the introduced status was assessed by Neville Walsh
- VS – the introduced status was assessed by Val Stajsic.

If other values need to be added to the pick list, please see the Collections Information Officer.

Introduced status date

The date that the introduced status was assessed, if known.

Cultivated status

The cultivated status of the specimen at the collecting locality. This information will either be provided by the collector, in the exchange data, or assessed by a botanist at a later date. Data entry staff may also make an assessment of whether the specimen was 'Presumably cultivated' or 'Possibly cultivated' if the collecting information is ambiguous, but do not need to assess the cultivated status otherwise. Where this information is provided by the collector or in the exchange data, enter the exact wording in the **Collecting notes** field, and select the corresponding category from the pick list. The following values can be selected from the pick list:

- Cultivated – the specimen is known to have been grown in cultivation at the collecting locality

- Presumably cultivated – the specimen is presumed to have been cultivated, based species distribution, collecting information (e.g. ‘Ex. horto bot. Berolinensi’) or other information
- Possibly cultivated – the specimen is thought to have possibly been cultivated, based on species distribution or collecting information
- Not cultivated – the specimen is known to have not been cultivated
- Unknown – the cultivated status of the specimen is unknown.

If the **Cultivated status** field is filled in, the cultivated **Source** field must also be completed.

Note that if a plant was collected from the wild and grown on for a brief period of time until it developed features needed for identification, then it should not be considered cultivated. For example, if a liverwort is collected and then left on a windowsill for a week until it has formed antheridia, or if a flowering plant is left in water for a week until its flowers open, then they should not be considered cultivated. Details about how the specimen was treated after being collected from the wild should be entered in the **Collecting notes** field, if provided by the collector, or in the **Miscellaneous notes** field if inferred by the data entry person.

Cultivated source

The source of the cultivated status. The following values can be selected from the pick list:

- Collector – the cultivated status was provided by the collector
- Data entry person – the cultivated status was assessed by the data entry person
- Exchange data – the introduced status was provided in the exchange data
- Other – the introduced status was assessed by someone else.

If other values need to be added to the pick list, please see the Collections Information Officer.

Cultivated status date

The date that the cultivated status was assessed, if known.

Provenance

The provenance details for cultivated specimens, if provided by the collector.

Habitat

Associated taxa

A list of other plants, algae or fungi growing in association with the specimen. If the collector has provided a distinct list of associated taxa, enter it in the Associated taxa field, rather than in the Habitat field; if the associated taxa are listed as part of the general habitat description, they can be entered in Associated taxa, but should also be included in the full habitat description to avoid losing meaning or context. Where genus names have been abbreviated, and it is clear which genus is being abbreviated, spell them out in full in order to facilitate querying. Any associated species that are included as part of the general habitat description should not be listed in this field. If in doubt, only enter associated taxa if the collector has prefaced the list with ‘associated species’, ‘growing in association with’ or similar wording. Examples of what should be entered in the Habitat and Associated taxa fields are provided on page 47.

Host taxon

The taxon name of the host of the specimen, if known. The **Host taxon** field will eventually be linked to the **Taxon** table, but, for now, simply enter the taxon name as a string of text. If the collector has only provided a common name, only add the taxon name if it is unambiguous and easy to determine.

Note: If the specimen bears a separate identification for the host taxon of a parasitic plant or fungus, you can just record the determination in the **Miscellaneous notes** field, instead of creating a separate collection object record.

Common name

The common name of the host, if provided by the collector. Sometimes a brief description of the host will be provided (e.g. ‘some sort of caterpillar’); this information can also be entered in the host **Common name** field.

Substrate

Information about what the specimen is growing on, if provided by the collector. This field should only be used to record the microhabitat that a cryptogam is growing in; descriptions of the soil or underlying geology of the collecting locality should be included in the habitat description. Examples of what should be entered in the **Habitat**, **Host** and **Substrate** fields are provided below.

Habitat, Host or Substrate?

<i>Collecting information</i>	<i>Data entry</i>	<i>Comments</i>
On moss on granite outcrop in scrub.	Habitat: On moss on granite outcrop in scrub. Substrate: moss	Moss needs to be put in the Habitat field as well as in the Substrate field to make it clear that the specimen is not growing directly on the granite outcrop.
On old bark at base of tree in eucalypt woodland.	Habitat: At base of tree in eucalypt woodland. Substrate: old bark	It is not clear if the tree is a eucalypt, so don't record eucalypt as the Host common name .
Beneath leaf litter under <i>Quercus</i> .	Habitat: Beneath leaf litter under <i>Quercus</i> .	An example would be <i>Amanita phalloides</i> growing under an oak. The fungus is mycorrhizal with oak, but mycorrhizal associations should not be recorded in the Host field.
On the ground amongst litter.	Habitat: On the ground amongst litter.	Ground, or soil, is not a substrate.
In <i>Eucalyptus</i> woodland, fruiting body growing out of roots of <i>Eucalyptus baxteri</i> .	Habitat: In <i>Eucalyptus</i> woodland. Substrate: roots Host taxon: <i>Eucalyptus baxteri</i>	
Growing out of Witchety Grub in <i>Acacia</i> root.	Habitat: In <i>Acacia</i> root. Host taxon: <i>Xyleutes</i> Host common name: Witchety Grub	The substrate is what it is growing on, so in this case it could be dead caterpillar, or part of the caterpillar, such as arising from head of caterpillar. Only enter the Host taxon name if there is no ambiguity about what taxon the common name is referring to.
Growing on <i>Eucalyptus polyanthemos</i> in open eucalypt woodland with grassy understory.	Habitat: Growing on <i>Eucalyptus polyanthemos</i> in open eucalypt woodland with grassy understory. Host taxon: <i>Eucalyptus polyanthemos</i>	If a plant is parasitic, its host should be recorded in the Host taxon field, not in Substrate .
Growing on sandy soil derived from granite..	Habitat: Sandy soil derived from granite.	Soil information should not be included in substrate.

Collection object (continued)

Descriptive notes

A description of the specimen provided by the collector. **Descriptive notes** includes information about the habit of the specimen, as well as information such as flower colour, the shape and size of leaves, etc.

Descriptive notes that were written by someone other than the collector should generally be entered in the **Det. notes** field in the **Determination** form. As an exception, if the descriptive notes have been written by an Identifications Botanist, who has seen the fresh material and clearly indicates that this should be databased as a descriptive note, not a det. note, it can be added in this field, but the author and date of the descriptive notes should be provided in brackets. For example:

- ‘Skin very thin, egg very soft, gleba jelly-like, phallus firmer textured. Eggs to 35 x 20 mm, mature phalli to 70 x 24 mm, generally cylindrical, straight or often curved to some degree. White rhizomorphs. Smell is similar to rotting bananas. [Description by V. Stajsic, 15/6/2012.]’.

Miscellaneous notes

Any notes relating to the specimen or collecting event that are not provided by the collector. Notes provided by the collector should not be entered here, but should go in **Collecting notes**. This field can be used for any annotations or curatorial comments about the specimen that may be of interest to anyone using the specimen data. This includes comments about how specimen information has been interpreted, and notes authored by curators of personal herbaria (such as Steetz or Sonder). If the annotation appears on the specimen, it doesn't need to be enclosed in brackets, but if it's entered at the time of data entry, it should be enclosed in brackets (this will help us distinguish one annotation from the next). For example:

- ‘[There are two labels on the sheet but only one specimen.]’
- ‘[Extract from letter from H.I. Ashton to R.O. Belcher, 6 July 1981 which explains collecting information is attached to sheet.]’
- ‘Donated by Miss Lecky, May 1931. ’
- ‘misit amicus Dr. Short, 1843’.
- ‘[Collecting no. above represents Whinray's despatch no. to MEL. Duplicates of this collection sent to other herbaria may have different despatch nos.]’
- ‘[The original label says 'Portland V. May 1931 (Miss Lecky) ... Miss M. Wise Sept. 1895'. Miss May Wise collected in 1895, but not at Portland. Miss Lecky did collect at Portland. It's probable that either Miss Wise did not collect the specimen, or the specimen is not from Portland. It's also possible that there are two separate collections represented on the sheet. -- A.C. Vaughan, Oct. 2013]’.

Where annotations involve matters of interpretation, they should always include the author of the annotation and the date, and any relevant sources. Preface the name of the person who authored the annotation with a double hyphen and space (as in the last example above).

Information about projects that the specimen has been used or collected for should also be entered in **Miscellaneous notes**. For example:

- ‘Sampled for the Victorian Conservation Seedbank’
- ‘Seen by Bentham’.

Note that information on exchange labels that relates to the curation or use of a specimen held at another herbarium (e.g. ‘Spirit material at BRI’; ‘Voucher for DNA sample’, ‘Voucher for essential oils analysis...’) should not be entered in the MEL collections database.

In future, details of projects for which the MEL specimen is a voucher will be recorded in a separate table. In the meantime, information about projects should be entered in the **Miscellaneous notes** field (and never in **Collecting notes**). Note that information about destructive sampling should be entered in the **Conservator description** table.

Collection object attributes

The **Collection object attributes** table records additional information that is specific to the **Collection object**, including phenology, label data, curation notes and other information.



Conservator description

The **Conservator description** table is used to record information about damage to specimens.



Collection object attachments

Any attachments that relate to the collection object, such as images of letters or illustrations associated with the specimen, or a digital image of the specimen.



Label printing information

Label code

This field can be used to flag records that you want to print labels for, in order to make it easier to query for them when making record sets for label printing (but the field does not need to be populated in order to print labels for that record). It is purely an administrative field, and there are no restrictions on what can be entered.

Mixed collection notes

Only one label is printed for a mixed collection. The **MEL number**, **Part** and **Taxon name** for parts B, C etc. will automatically be printed at the bottom of the label for part A. If there is more than one taxon on the sheet, but the separate components share the one set of collecting information, there is no need to enter anything in the **Mixed collection notes** field. Where there is more than one set of collecting information on the sheet, the **Mixed collection notes** can be used to provide a brief indication of how parts B, C etc. differ from part A, as follows:

- If there is more than one collector on the sheet, enter the collector's name (initials and last name), preceded by 'Leg.', e.g. 'Leg. C. Stuart'
- If there is more than one collecting locality, enter a very brief description of the locality, e.g. 'Mt Buffalo', 'near Halls Gap'
- If there is more than one collecting date on the sheet, enter the date
- If there is more than one collecting number on the sheet, enter the collecting number preceded by the collector's initials. Never enter a collecting number in this field without including the collector's initials.

Only enter locality or date information if there is more than one specimen from the same collector on the sheet.

Collection object attributes

The **Collection object attributes** table records additional information that is specific to the **Collection object**, including phenology, label data, curation notes and other information.

Phenology

If the specimen has flowers, fruits, buds, or is leafless, fertile or sterile, enter a '1' in the appropriate boxes. Note that the '1' is only used to indicate the presence of features; it is not used to indicate how many flowers, fruit etc. there are on the sheet. Only enter a '1' if you are absolutely sure of the presence or absence of these features. Additional fields for phenology (and reproductive and vegetative status) will be added in the future.

Label data

Ethnobotanical info.

Notes about the ethnobotanical usage of the plant, alga or fungus, if provided by the collector. For example:

- 'Bark and roots used as fish poison'
- 'Incolis medicamentum [?=used as medicine]'
- 'Before the introduction of cats natives used a piece of the root – squeezing sap into food & placing it near their feet to be eaten by rats & mice & in the morning these would be found

dead. The mice have a particular liking for the soles of the feet – hence their placing the poison near their feet’.

Data entered in this field will be printed on MEL labels, so do not repeat any ethnobotanical information in other fields.

Toxicity

Information about the toxicity of the specimen, if provided by the collector. For example:

- ‘When fed to horses, produces fatal results’
- ‘Poisonous to cattle’.

Longer descriptions about a poisoning case should also be entered here, rather than in **Collecting notes**. For example:

- ‘Dog from this locality very sick and thought to have ingested this fungus. Dog from same locality died same time last year. Severe gastro-intestinal irritation, damage to wall of bowel. Specimen of fungus brought in by vet.’

Data entered in this field will be printed on MEL labels, so do not repeat any toxicity information in other fields.

Common name

Any vernacular name for the plant, alga or fungus, if provided by the collector. For example:

- ‘Common Broom’
- ‘Kodhiro’
- ‘Sikat’.

This field has a limit of 50 characters (including spaces).

Usage

Any remarks about the usage of the common name, such as the language in which the common name is given, or the ethnic group who uses the name. This field can also be used to record information about the appearance of the common name on the collecting label. For example:

- ‘Enga language’
- ‘This is called the Cardwell plum here’
- ‘Name followed by a word in non-Latin script’
- ‘Local name’.

In the second example, ‘Cardwell plum’ would also be entered in the **Common name** field. This field has a limit of 64 characters (including spaces).

Label language

This field is used to record the language(s) that the original specimen data is written in. Recording this information allows records to be queried by label language for the purpose of translating collecting information. Separate multiple languages with a space and a comma, e.g. ‘Spanish, German, English’.

Translation confidence

This field is used to indicate the level of confidence applied to the translation of collecting information into English. The following values can be selected from the pick list:

- Native or bilingual proficiency – translated by someone who speaks, reads and writes the language with a proficiency equivalent to that of an educated native speaker
- Full proficiency – translated by someone who is able to use the language fluently for most purposes
- Limited proficiency – translated by someone who has enough knowledge of the language to translate collecting information without the aid of a dictionary or translation service
- Bilingual dictionary – translated with the aid of a bilingual dictionary (printed or electronic)
- Online translation service – translated using an online translation service (such as Google Translate).

Translated by

The person who provided the translation and the date provided, if known. Enter names and dates in the following format:

[initials] [preposition] [last name] [suffix], [dd] [mmm] [yyyy]

For example:

- ‘D. Sinkora, 12 Dec 1977’
- ‘B. Meurer-Grimes, Feb 2001’.

Data entry notes

Curation notes

Notes about the specimen that are only of relevance for internal curation purposes, e.g. missing specimens, notes about MEL numbers being reassigned. Data in this field will not be delivered to AVH.

- ‘Specimen could not be located, April 2014.’
- ‘Extracted from Victorian Reference Set and returned to the main collection, 12/11/2013.’

Annotations made by people other than the collector or data entry staff, such as Nancy Burbidge or Jim Willis, should also be entered in the **Miscellaneous notes** (unless they relate to the collecting locality, in which case they should be entered in **Georeferencing notes**). For example:

- ‘Field label removed to handwriting file J.H. Willis 15/5/1961.’ should be entered in **Curation notes**
- ‘No. 88 from J.H. Willis to G.O.K. Sainsbury.’ should be entered in **Miscellaneous notes**
- A comment about the collecting locality by J.H. Willis, e.g. ‘Not Kallista, but could be Monbulk’, should be entered in **Georeferencing notes**
- ‘Common in lawns of Melbourne Botanic Gardens. J.H. Willis.’ should be entered in **Miscellaneous notes**.

Curation sponsor

The organisation or individual who sponsored the curation of the specimen, e.g. CASS Foundation. Only the sponsor’s name should be entered in this field; a script will prefix the sponsor’s name with ‘The curation of this specimen was generously sponsored by’ when printed on the specimen label.

Other

Original collection

Information about the personal herbarium, exsiccata series or other collection from which the specimen originates. For example:

- ‘Herbarium O.W. Sonder (1812–1881)’
- ‘Lichenes Rariores et Critici Exsiccati’
- ‘Plantes des Tunisie’
- ‘Plantae Mexicanae’
- ‘Plantes d’Espagne’.

This is a temporary field. Information about the original collection will eventually be moved to the **Exsiccata** table, which has not yet been fully implemented. The **Exsiccata** table allows more than one set of **Original collection** information to be entered per specimen. If the specimen has come from more than one collection (e.g. via both Steetz’s and Sonder’s personal herbaria), enter all the information in this field. If it does not all fit, it can be abbreviated to ‘Ex Herbarium Steetz, Ex Herbarium Sonder’, etc. Once the **Exsiccata** table is functioning, we will standardise the **Original collection** messages and they won’t need to be entered manually.

Fascicle

The fascicle number in an exsiccata series.

This is a temporary field. Information about the original collection will eventually be moved to the **Exsiccata** table, which has not yet been fully implemented.

Original collection:	Musc Frondosi Exsiccati Fascicle	
Fascicle:	3	Number:

Number

The specimen number in an exsiccata series or a number within a personal herbarium. For example:

Original collection:	Lichenes Rariores et Critici Exsiccati	
Fascicle:		Number: 54

Original collection:	Ex Herbarium Raleigh A. Black	
Fascicle:		Number: 349.020 (3)

This is a temporary field. Information about the original collection will eventually be moved to the **Exsiccata** table, which has not yet been fully implemented.

Illustration

This field is used to indicate that there is an illustration associated with the specimen.

Photograph

This field is used to indicate that there is a printed photograph with the specimen, such as a habitat photo. If the specimen is a photograph of a specimen held at another institution, ‘Photograph of specimen’ should be entered as the **Preparation type**, and this field should be left blank.

The existence of high-resolution digital images created for the GPI project will be flagged in the **GPI** field. Other digital images relating to the specimen should be attached the relevant table (see [Attachments](#)).

Spore print

This field is used to indicate that there is a spore print with a fungi specimen.

Conservator description

The **Conservator description** table is used to record information about destructive sampling and damage occurring to specimens.

Preparation

Select the preparation type that has been damaged or destructively sampled. If more than one preparation type of a specimen has been damaged or sampled from, a separate Conservator description will need to be entered for each preparation.

Event type

Select the event type: 'Destructive sampling' or 'Damage to specimen'. If a specimen has been subjected to more than one event type (i.e. has been destructively sampled from **and** damage has occurred), a separate Conservator description will need to be entered for each event.

Events

The **Events** section of the **Conservator description** form is used to record the details of a single instance of damage or destructive sampling of a preparation. If the preparation has been damaged or sampled from more than once (and if it is possible to distinguish between the different damage events), each instance of damage or destructive sampling should be treated as separate events. The form is split into three sections: fields relevant to Destructive sampling events, fields relevant to Damage to specimen events, and fields relevant to both event types.

Researcher

The name of the person who has carried out the destructive sampling or on whose behalf destructive sampling was undertaken by a staff member.

Sampling date

The date the destructive sampling occurred. If a partial date (e.g. year, or month and year) has been given, enter the date here. Enter unknown days and months as '01' - e.g. a date given as '1984' should be entered as '01/01/1984'. Use the **Date precision** field to record whether the sampling date is precise to the nearest day, month or year.

Date precision

The precision of the date entered in the **Sampling date** field (day, month or year). For example, a sampling date given as 'Oct 1985' and entered in the **Sampling date** field as '01/10/1985' should have 'month' entered as the date precision.

Purpose

The intended purpose of the destructive sampling (e.g. DNA sequencing, pollen sample, leaf cuticle analysis).

Results

A statement of the results of destructive sampling (e.g. whether DNA was successfully extracted). Information about DNA sequences (e.g. GenBank accession numbers) will be recorded in the **DNA sequence** table once this has been implemented.

Cause of damage

The organism or event that damaged the specimen. The following values are currently available in the pick list (if another value needs to be added, see the Collections Information Officer):

- beetle
- cigarette beetle
- fire
- human
- inadequate packaging
- insect
- mould
- psocid
- silverfish
- unknown
- water.

Where more than one option applies, always choose the most descriptive term.

Severity

The severity of the damage to the specimen. The following values are available in the pick list:

- minor
- moderate
- severe.

If different parts of the specimen have received different levels of damage (e.g. minor damage to stem and moderate damage to leaves), only enter the most severe category of damage present. If additional information about the severity of damage needs to be recorded, enter it in the **Comments** field.

Verbatim date noticed

If the date damage was noticed is given in a format that cannot be entered in the date field, it should be entered here (e.g. 'late October', 'summer of 1964'). If the date noticed is given in a non-standard

format but includes a year or a year and a month, the date should also be entered in the **Date noticed** field.

Date noticed

The date damage to the specimen was noticed. If a partial date (e.g. year, or month and year) has been given, enter the date here. Enter unknown days and months as '01' - e.g. a date given as '1984' should be entered as '01/01/1984'). Use the **Date precision** field to record whether the date noticed is precise to the day, month or year.

Date precision

The precision of the date entered in the **Date noticed** field (day, month or year). For example, if the date damage was noticed is recorded as '1995', this should be entered in the **Date noticed** field as '01/01/1995' and 'year' should be entered as the date precision.

Assessed by

The staff member who assessed the damage to a specimen.

Date assessed

The date when damage to a specimen was assessed by a staff member.

Treatment report

Information about the treatment provided to the specimen, such as the names of the agents or organisations providing the treatment, when the treatment occurred, a description of the treatment, and any notes about how the damage to the specimen has been documented.

Part of specimen

The part/s of the specimen that have been destructively sampled from or damaged. The value of the field can be one or more of the following:

- alga
- fungus
- lichen
- liverwort
- moss
- buds
- inflorescence
- fruit
- cone
- leaves

- rhizome
- roots
- stem
- bark
- label
- seeds
- sori.

Comments

Any additional information about destructive sampling or damage to the specimen.

Conservator event attachments

Any attachments documenting the damage to the preparation.



Locality form

Locality

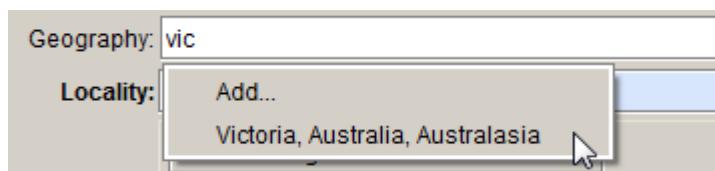
The **Locality** form contains all the details of the collecting locality. It contains two subforms: **Locality details** and **Geocoordinate details**.

Geography

The higher level geography for the collecting locality. If the geography is unknown, enter 'Earth' in this field (this will allow us to tell the difference between records where the geography is unknown, and where it has been accidentally omitted). There are four levels of geography in the **Geography** table: **Continent**, **Country**, **State** and **County**.

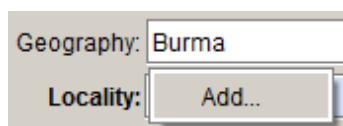
Start typing the country, state or county name, then press the down-arrow to see a list of corresponding entries. Note that there are no county names for Australia in the **Geography** tree.

If any of the four levels is selected from the list, the parent geography will be automatically filled in, so enter the most specific information possible. For example, if you look up the state 'Victoria' in the query combo box, the full name will include the country ('Australia') and continent ('Australasia'):

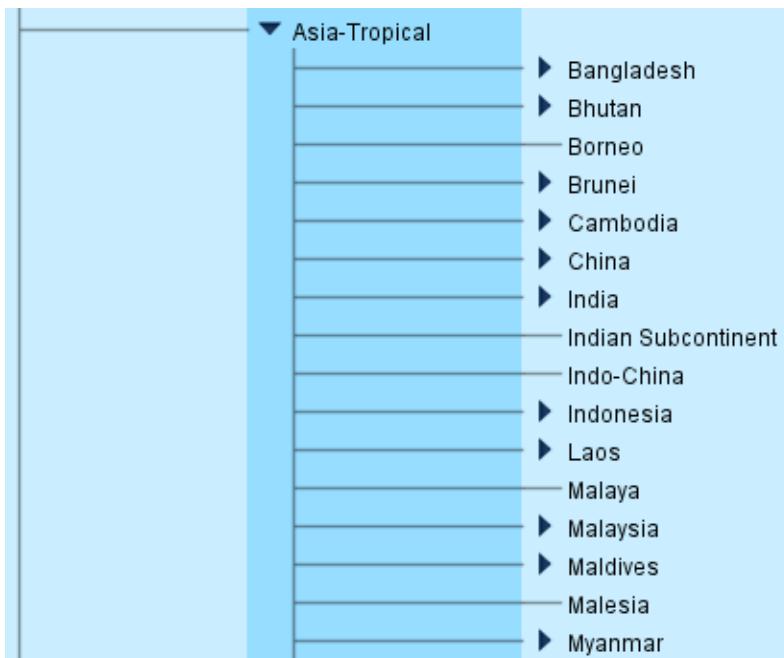


The continent number and name come from the World Geographic System for Recording Plant Distributions (WGS). The continent names and numbers are used in the storage system for specimens collected outside Australia

The country, state and county names in the **Geography** tree come from the International Organization for Standardization (ISO 3166 standard), and many may have unfamiliar spellings. If you can't find the place name you are looking for in the drop-down menu, browse the **Geography** tree to see if you can find it. For example, Burma is listed by its official name, Myanmar, so a search for 'Burma' in the **Geography** drop-down list won't return any results:



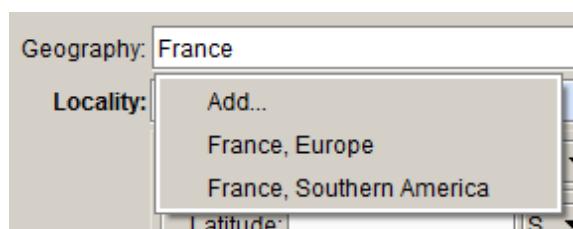
If you browse the **Geography** tree, you will see that it is listed as Myanmar:



Specify allows for entries in the **Geography** tree to be synonymised, which means that a query on either name in a **Collection object** query will return the same results. See [Search synonyms](#) for more information. If you would like a synonym of a place name to be added to the **Geography** tree, please see the Collections Information Officer.

Note that, in WGS, Russia occurs in Europe as well as in Asia – Temperate. If the collecting locality only gives ‘Russia’ as the collecting locality, select ‘Russia, Europe’ from the **Geography** drop-down list.

Be aware that countries that have dependencies in other continents will also be listed under more than one continent. For example, France is in Europe, but it also has a dependency in Southern America (Clipperton Island):



The option ‘France, Southern America’ should never need to be selected, because if the label has enough information for you to know that the specimen was collected in a French dependency in Southern America, then it probably also gives you enough information to select the relevant entry from the **State** level in the **Geography** tree.

Note that it is not possible to enter a combination of geographic place names. If the collecting locality traverses two or more regions, enter the next region in the hierarchy. For example, if the collecting locality is given as ‘Murray River’ (which borders New South Wales and Victoria, and flows through South Australia), ‘Australia, Australasia’ should be selected from the **Geography** drop-down list.

Cultivated plant records

Cultivated plant specimens were previously databased with 'Cultivated' in the geography fields instead of the geographic place names. This practice is no longer used at MEL. Cultivated plant records should be databased with the geographic hierarchy entered in the **Geography** field, and other relevant details entered in the **Locality** form. The **Collecting event attributes** subform contains fields to record the **Cultivated status** and the **Source** of the cultivated status.

Locality

The description of where the specimen was collected, as provided by the collector. No punctuation is added to labels, so include a full stop after the locality, even if it is not a proper sentence.

If there are absolutely no locality details provided (and thus 'Earth' has been entered in the **Geography** field), enter '[No details given]' in the **Locality** field. If there is no description of the locality other than what has already been entered in the **Geography** field, repeat the lowest ranked place name in the **Geography** name in the **Locality** field. For example, if the collecting locality is only given as 'Victoria', 'Victoria' should be entered in the **Locality** field as well as in the **Geography** field:

Geography: Victoria, Australia, Australasia
Locality: Victoria

If the only description of the collecting locality is UTM coordinates, a map reference, a botanical region or a Victorian grid reference, enter it in the **Locality** field, as well as in the field where it belongs:

Locality

Geography: Victoria, Australia, 5. Australasia

Locality: Melway 29 J8

Degrees Minutes Decimal Seconds

Latitude: N (Source)

Longitude: E (Source)

Datum: Source: Precision: Original precision:

Min. altitude: Max. altitude: Unit: Altitude precision:

▼ Locality details + -

Grid: Zone: Easting: Northing:
UTM: Map reference: Melway 29 J8

Botanical region: Victorian grid ref.:

Min. depth (m): Max. depth (m):

Generalised locality: Relation: Gazetteer:

GEOLocate Display in WorldWind Display in GoogleEarth GCD 0

Created by: Vaughan, Alison Created: 18/03/2011
Last edited by: Last edited: 18/03/2011

Save Cancel Help

The screenshot shows the Locality software interface. The 'Geography' field is set to 'Victoria, Australia, 5. Australasia'. The 'Locality' field contains 'Vic. Volcanic Plain', which is circled in red. Below this, there are fields for Latitude and Longitude in various formats (Degrees Minutes Decimal Seconds), Datum, Min. altitude, Max. altitude, Precision, Unit, Original precision, Altitude precision, and a 'Locality details' section. In the 'Locality details' section, the 'UTM' dropdown is also circled in red. Other fields in this section include Grid, Zone, Easting, Northing, Map reference, Victorian grid ref., Relation, and Gazetteer. At the bottom, there are buttons for 'GEOlocate', 'Display in WorldWind', 'Display in GoogleEarth', and a 'Gd' button with a value of 0. Log-in information and creation details are at the bottom left, and save/cancel/help buttons are at the bottom right.

If only altitude or latitude and longitude have been provided, enter them in the relevant fields, and enter '[No details given.]' in the **Locality** field:

The screenshot shows the Locality software interface. The 'Geography' field is set to 'Earth'. The 'Locality' field contains '[No details given.]', which is circled in red. Below this, there are fields for Latitude and Longitude in various formats, Datum, Min. altitude, Max. altitude, Protocol, Uncertainty, Unit, Alt. method, Coll. uncertainty, and Alt. uncertainty. At the bottom, there are buttons for 'GEOlocate', 'Display in WorldWind', 'Display in GoogleEarth', and a 'Gd' button with a value of 0. Log-in information and creation details are at the bottom left, and save/cancel/help buttons are at the bottom right.

Minor corrections to, or interpretations of, the locality description should be entered in brackets in this field. For example:

- 'Balarrat [=Ballarat].'
- '6 m[iles] west of Horsham'.

Any comments about the locality description or an explanation of why the locality could not be georeferenced should be entered in the **Not geocoded because** and **Georeferencing notes** fields.

Locality information should be entered exactly as it appears on labels (unless the description exceeds the field size – see below). Do not convert miles to kilometres. If the unit of distance has been given as 'm' and you suspect that it refers to miles rather than metres, append the m with '[iles]' to make it clear that only 'm' has been given on the label; do not write 'miles'.

The **Locality** field has a limit of 255 characters (including spaces). If the locality description exceeds the field length, first check if there is information in the locality description that belongs in other fields, such as map references or original uncertainty values. If necessary, the locality description can be shortened by using standard abbreviations in place of whole words. Refer to the list of abbreviations in [Appendix 1. Abbreviations](#) for the correct formatting.

If the locality description still exceeds 255 characters, if possible, ask the collector to shorten the description, or shorten it at your own discretion. Locality descriptions that are particularly long may need to be split between the **Locality** field and the **Collecting notes**. In this case, ensure that the most important locality information is in the **Locality** field.

Latitude and longitude

Geocodes can be entered in one of the following formats:

- Decimal degrees – e.g. 37.8272°
- Degrees and decimal minutes – e.g. 37° 49.629'
- Degrees, minutes and decimal seconds – e.g. 37° 49' 37.74"

Select the lat/long type from the drop-down list, and enter the latitude and longitude in the fields provided.

The lat/long type is set to default to ‘Degrees, minutes and decimal seconds’, and the hemisphere fields are set to default to ‘S’ and ‘E’. The default preferences can be changed by clicking on the **Information** symbol at the right of the lat/long form. Note that the changes will only come into effect after the current **Collection object** record has been saved. Changing the default preferences will only affect your own user account.

Once the geocode has been entered, you can convert it to the different lat/long types using the drop-down list. The original geocode format is recorded in the database (and is visible on the form), and is used as the source for conversions between geocode formats. Note that editing the geocode will overwrite the source geocode.

Geocode information can be entered as a point, line or polygon. For botanical specimens, latitude and longitude are generally provided for a single point, but if the collector has provided line data (i.e. two sets of latitude and longitude that define a line between two places), or polygon data (i.e. three or more points that define a polygon around a certain area), these can be entered by selecting the line or polygon button.

If the collector has only provided UTM coordinates, you can choose to leave the **Latitude and longitude** fields blank (but note that the record cannot be mapped unless the latitude and longitude are provided). UTM coordinates are not currently being automatically converted to latitude and longitude, but they will be in future.

Datum

The geodetic datum of the geocode.

The datum refers to how the earth is modelled and affects where exactly lines of latitude and longitude occur on the ground. There are a number of different datums in use and each results in a slightly different latitude and longitude grid. **Datum** should be recorded where the geocode was determined by the data entry person, if the geocode was determined by GPS, or if the collector has indicated which datum was used. Note that MGA94 is UTM projection of GDA94 coordinates; if the collecting label states ‘MGA94’, select ‘GDA94’ from the pick list.

Where the **Protocol** is ‘GEOLocate’, ‘GeoNames’ or ‘Google Earth’, the **Datum** will be automatically set to ‘WGS84’ when the record is saved. Where the **Protocol** is ‘GA gazetteer’, the **Datum** will be set to ‘GDA94’.

A guide to determining which datum was used is provided below.

GPS readings

Most GPS units are set to use the WGS84 datum by default. If the datum has not been recorded, check with the collector, if possible.

Google Earth and Google Maps

Google map products use the WGS84 datum.

Australian map references

Maps could be based on any datum. Newer maps will probably be based on GDA94 and older maps will be AGD66 or AGD84. Check near the title of the map for the datum and/or coordinate system used. If the coordinate system is AMG66, then the datum is AGD66. If it is a newer map the coordinate system might be MGA94, in which case it the datum is GDA94. Most of the maps in the Royal Botanic Gardens Library use AGD66.

Reader’s Digest Atlas of Australia

The Reader’s Digest *Atlas of Australia* (1994) is assumed to be in AGD66.

Melway

Melway directories up to edition 30 use AGD66. From edition 31 (2004) onwards, the datum is GDA94.

VicRoads State Directory

VicRoads used AGD66 up to edition 4. From edition 5 onwards, the datum is GDA94.

Source

The source of the geocode. The following values are available in the pick list:

- Collector
- Data entry person
- Exchange data.

Where the data entry person is the same as the collector, **Source** will default to ‘Collector’ when the record is saved. If the data entry person is not the same as the collector, and if the **Protocol** is ‘GA gazetteer’, ‘GEOLocate’, ‘GeoNames’ or ‘Google Earth’, **Source** will default to ‘Data entry person’ when the record is saved; if **Protocol** is ‘GPS’, **Source** will default to ‘Collector’.

Protocol

The method by which the geocode was determined. The following values are available in the pick list:

- AMG conversion – the geocode was converted from an AMG reference that was provided by the collector
- GA gazetteer – the geocode was found on the Geoscience Australia place names of Australia gazetteer
- GEOLocate – the geocode was determined using GEOLocate
- GeoNames – the geocode was found on the GeoNames website
- Google Earth – the geocode was determined using Google Earth
- GPS – the geocode was determined by GPS
- Map or atlas.

If the **Source** is ‘Exchange data’, you don’t need to fill in **Protocol** unless it’s provided in the exchange data. Where GeoLocate is used to georeference the locality, **Protocol** and **Source** will be automatically filled in.

In Texpress, we included a category for conversions from *Melway* references, however, due to the differences in *Melway* references between editions, *Melway* references should not be converted to latitude and longitude.

Uncertainty

The level of uncertainty in the geocode. The following categories of geocode uncertainty apply:

- 1. 0 – 50 m
- 2. 50 m – 1 km
- 3. 1 – 10 km
- 4. 10 – 25 km
- 5. > 25 km.

Collector’s uncertainty

If the collector has provided an uncertainty value with the geocode, this should be entered here, along with the units in which the uncertainty is given.

Min. altitude

The altitude, if provided by the collector. If altitude is given as a range, enter the lower value here. If the altitude is provided in feet, enter it in feet, rather than converting it to metres.

Max. altitude

If the altitude is given as a range, enter the higher value here. If the altitude is provided as less than a certain value, e.g. ‘<1200 feet’, enter the measurement here, leave **Min. altitude** blank, and enter the verbatim text in **Verbatim altitude**.

Unit

The units in which the altitude is provided (metres or feet).

Altitude method

The method by which the altitude was determined. The pick list contains the following values:

- Altimeter
- Altimeter (corrected)
- DEM [digital elevation model]
- Field estimate
- Google Earth
- GPS
- Map
- Unknown.

Verbatim altitude

If the altitude is provided in a format that can’t be unambiguously recorded in the other altitude fields, enter it here as it appears on the label (but record relevant parts of the altitude in other fields as well). For example:

- ‘<500 ft’ (also enter ‘500’ in **Max. altitude** and ‘feet’ in **Unit**)
- ‘c. 5 m’ (also enter ‘5’ in **Min. altitude** and ‘metres’ in **Unit**)
- ‘about sea level’ (also enter ‘0’ in **Min. altitude**).

GEOLocate

Clicking the **GEOLocate** button launches the GEOLocate georeferencing service. GEOLocate uses the **Locality** description and geographic location to find latitude and longitude coordinate data for specimen records. See the Plugins section for more information.

Display in World Wind

Clicking the **Display in World Wind** button will open the World Wind application. The link to World Wind is available in the **Locality** form at any time. See the Plugins section for more information.

Display in Google Earth

Clicking the **Display in Google Earth** button will map the current record in Google Earth. The record must have a latitude and longitude for the **Display in Google Earth** button to become active.

Locality attachments

Any attachments that relate specifically to the collecting locality (and not to the specimen itself), such as a map of the locality.



Locality details

UTM Grid

The grid system used for the UTM coordinates, if known. The pick list currently includes the following values:

- AMG – Australian Map Grid
- MGA – Map Grid of Australia
- UTM – Universal Transverse Mercator.

If other entries need to be added to the pick list, please see the Collections Information Officer.

UTM Zone

The zone for UTM coordinates. In the UTM system, the world is divided into 60 zones (numbered 1–60), each of which is six degrees of longitude wide. UTM zones are sometimes followed by a letter that indicates the Military Grid Reference System (MGRS) Zone, e.g. ‘55H’. MGRS Zones should also be entered here.

UTM Easting

The easting is a measure of how far east the location is within the zone. Easting values should be six digits long.

UTM Northing

The northing is a measure of how far north the location is within the zone. Northing values should be seven digits long.

Map reference

If a map reference has been provided, such as the mapsheet on which the easting and northing are based, or a reference from a street directory, enter it here. For example:

- ‘Melway ref. 211 K8’
- ‘Eltham mapsheet’
- ‘AMG – (Lerderderg 7722-1-2 map, 1:25000) 726-248’
- ‘Wimmera Study Area Sector: f, Sub-block: 37f’.

Exchange labels from BRI often include a numerical map reference after the AMG coordinates (e.g. ‘7867-764725’), which can also be entered in this field.

If the edition of a street directory or the date of publication of a map is provided, make sure it is recorded in the database.

IBRA region

This is a read-only field that is used to record the Interim Biogeographic Regionalisation of Australia (IBRA) region, which is determined from the latitude and longitude. If a botanical region that is different to the IBRA region has been recorded by the collector, or provided on an exchange label, it should be recorded in the **Botanical region** field.

IBRA subregion

A read-only field that records the IBRA subregion, as calculated from the latitude and longitude entered in the **Locality** form.

Victorian grid ref.

This is a read-only field that is used to record the Victorian 10-minute grid reference for records that were entered in Texpress.

Botanical region

The botanical region in which the specimen was collected, if provided by the collector or recorded on an exchange label. If the collector has recorded an IBRA region, there is no need to record it in this field.

Min. depth

The depth that the specimen was collected at, in metres. If depth is given as a range, enter the shallower value here.

Max. depth

If depth is given as a range, enter the deeper value here, in metres. If depth is given as another unit (e.g. fathoms), convert it to metres.

Depth unit

The units of measurement in which the depth is given. The values in the pick list are:

- fathoms
- feet
- metres.

Generalised locality

An accurate, but less precise, version of the collecting locality that can be used when we wish to obscure the exact locality (e.g. for rare and threatened plants). This field is populated automatically, and cannot be edited by data entry staff.

Relation

The relation of the collecting locality to the generalised locality (e.g. ‘10 km SW’). This field is populated automatically, and cannot be edited by data entry staff.

Gazetteer

The place name in the gazetteer that is the source of the geocode. This information is useful when the locality provided on a label is quite detailed but, because the exact locality cannot be found on a map, the geocode assigned may be less precise than the locality description would lead you to think. Recording which gazetteer entry the geocode is based on will give an indication of the uncertainty of the geocode. For example:

- ‘Sugarloaf Mountains, track from Tale River Valley, S of Wapenamanda’ – **Gazetteer:** Wapenamanda
- ‘Cometville’ – **Gazetteer:** Comet
- ‘King Leopold Range, Diamond Gorge Road, 15 km E of Fitzroy River, c. 170 km WNW of Halls Creek, c. 70 km NE of Fitzroy Crossing’ – **Gazetteer:** Diamond Gorge.

In Texpress, this information was often entered as a note in the **Locality** field, for example, ‘Yandarloo via Wilcannia, Darling River. [Lat/long is for Wilcannia.]’.

Geocoordinate details

The **Geocoordinate details** form provides additional information about the locality, and how (or why) the geocode was (or was not) determined.

Georeference date

The date the specimen was georeferenced. This field will be automatically filled in when the record is saved. Where the geocode **Source** is ‘Collector’, the **Georeference date** will be the same as the date of collection. Where the geocode **Source** is ‘Data entry person’, the **Georeference date** will be the date of record creation. Where the geocode **Source** is ‘Exchange data’, the **Georeference date** will be left blank.

Geocode source

The source of the geocode, if it has been taken from an obscure source. For example:

1. ‘Western Australian Phytogeographic Regions map, 1980’
2. ‘Ampol Road Map, Queensland’
3. ‘Uncommon locality index’.

This field has a limit of 64 characters (including spaces).

Georeferencing notes

Any notes about how the locality information has been interpreted, why a particular geocode was assigned, or any extra information about why a geocode was not assigned. For example:

- ‘Lat/long taken for Cobar, as collector was in this area on this date.’
- ‘Collector was known to be in Western Australia at this time.’
- ‘There are several Bluff Mountains. Coordinates are for the Bluff Mountain closest to Tenterfield, as Stuart was known to be in that area on this date.’
- ‘There are three Herbert Creeks in Queensland. It is unclear which Bowman collected at.’
- ‘Locality not found on any maps or gazetteers.’
- ‘There are several Mount Mitchells in New South Wales.’

Annotations about the collecting locality made by people other than the collector or data entry staff should also be entered in the **Georeferencing notes** field. For example:

- A comment about the collecting locality by J.H. Willis, e.g. ‘Not Kallista, but could be Monbulk, J.H. Willis.’.

Notes that only indicate which locality has been selected, and not why it has been selected, (e.g. ‘Lat/long is for Rockingham’) should not be entered here. Instead, ‘Rockingham’ should be entered in the **Gazetteer** field.

Verified status

Verified status is used to indicate whether the geocode of a record has been verified, or if it is awaiting verification. The values in the pick list are:

- Requires verification
- Verified by collector
- Verified by curator.

This field has been populated with ‘Requires verification’ for specimen records that have been identified as outliers in Australia’s Virtual Herbarium. If anyone from MEL verifies or corrects a georeference, the value should be changed to ‘Verified by collector’ or ‘Verified by curator’, depending on who verified the georeference.

Not geocoded because

If you have attempted to assign a geocode to the locality, but were not able to, select one of the following values from the pick list:

- Locality ambiguous – e.g. there multiple localities with the same name and it is unclear which one the collector was at
- Locality not found – the locality name could not be located on maps or in gazetteers.

Any additional explanation of why the collecting locality could not be geocoded should be entered in the **Georeferencing notes** field.

If the locality is obviously vague (e.g. ‘South-eastern Australia’, ‘China’), it is not necessary to explain why a geocode was not assigned to the record.

Administrative fields

The following fields are automatically completed and cannot be edited.

Created by

The person who created the database record.

Created

The date the record was created.

Last edited by

The person who last edited the record.

Last edited

The date the record was last edited.

Geography form

The **Geography** form is used to enter geographical information at the continent, country, state and county levels. The data in the **Geography** table should be complete, so please see the Collections Information Officer before adding or editing any records in the **Geography** form.

Parent

To enter a new geographical area name, you need to indicate what place name the new name sits under in the **Geography** tree. For example, the parent of ‘Victoria’ is ‘Australia’, and the parent of ‘Australia’ is ‘Australasia’.

Geographic rank

The rank of the geographic place name. The rank must be one of the following:

- Continent – the continent number and name from the World Geographic System for Recording Plant Distributions (WGS). The continent names and numbers are used in the storage system for specimens collected outside Australia.

- Country – the ISO standard country name. There are also some WGS place names at this level, where the WGS name could not be mapped to an ISO country name (e.g. ‘Indian Subcontinent’, ‘Southwestern Pacific’).
- State – the ISO standard state or province name
- County – subdivisions of the state or province.

Name

The name of the continent, country, state or county.

Name on label

The geographic name, including diacritical marks. The name field (which does not include diacritical marks) will be used for querying and data entry, and this field will be used to record the geographic place name with diacritical marks, as it should appear on the label.

Comments

Any comments about the usage of the place name, or the history of the place. For example:

- ‘Previously part of the Netherlands Antilles, which were dissolved in 2010.’
- ‘Istria was part of Italy between 1919 and 1947.’

Subdivisions

The **Subdivisions** section lists the geographic place names that occur below the geographic place in the **Geography** tree.

Name

The name of the geographic subdivision.

Taxon form

The **Taxon** form is used to enter new taxon names. In Specify, taxa or taxon names are stored in a taxon tree (or classification) with the genus, species, subspecies, variety and forma parts of the taxon name stored as individual records, which are linked through parent–child relationships.

Parent

The name of the parent taxon. For species names, this is a genus name; for genus names, a family name, etc. If a parent name is not in the drop-down list, it needs to be added using the **Taxon** form. If a parent of a family or higher rank is not in the drop-down list, it is probably easier to look up the lowest ranked ancestor in the **Taxon** tree and then open the **Taxon** form to enter the new names.

Rank

The rank of the taxon: genus, species, etc. Select the appropriate name from the drop-down list. Only ranks below the rank of the parent taxon to the next mandatory rank are available in the list.

Name

For names of taxa above the species level this is the taxon name; for species names it is the species epithet; and for names of infraspecific taxa, it is the infraspecific epithet. See [Formatting of taxon names](#) for information on what to enter in this field for hybrid names etc.

Author

The author of the name, formatted according to the standard abbreviations listed in Brummit & Powell or [IPNI](#). The **Author** field should be completed for genus and higher taxon names, as well as for species and infraspecific taxa.

Where the author of the taxon is different to the author of the publication in which the name is published, the author of the publication may be included in the **Protologue** field.

Protologue

The original article the name was published in. This is compulsory for basionyms of which MEL holds a type, and is optional for other names.

The protologue string should include the following elements:

- the standard abbreviation of the article or book in which the name was published
- the volume of the book or journal, if relevant
- the issue of the journal, in parentheses (note that the issue is only required if the page numbers are not contiguous between different issues in the same volume)
- the page number separated by a colon and the year the name was published.

For publications whose author is different to that of the name, the author of the publication may be prepended, preceded by 'in'. As this is the author of a publication rather than a name, author names should not be abbreviated here. The 'in' is important to make sure the protologue string prints correctly on labels.

Parent:	Cyrtostylis
Name:	huegelii
Protologue:	in Lehmann, J.G.C., Plantae Preissianae 2(1): 6 (1846)

Year

The year of publication of the protologue. This must be entered for taxon names for which MEL holds a type specimen, but can also be entered for other taxon names.

ms

If the taxon name has not yet been published, enter 'ms' in this field. Names flagged with 'ms' will be reported on periodically to check if the name has been published.

Full name

The full taxon name. This is a read-only field.

Nom. note

This field should be used to record nomenclatural notes that need to be printed with the taxon name, such as 'non. R.Br.', 'nom. nud.', 'nom. inval.' etc.

If the name is illegitimate, the preference is to indicate the correct authorship instead of using 'nom. illeg.', e.g. *Acacia tenuifolia* F.Muell. non (L.) Willd. (1806) would be entered as follows:

Author:	F.Muell.		
Year:	1855	ms:	<input type="text"/>
Nom. note: non (L.) Willd. (1806)			

If the nomenclatural status has been filled in, it will be appended to the full name that appears in the **Taxon** name drop-down list, so that homonymous names can be distinguished.

Taxon name:	Acacia tenui
Alternative name:	Add...
Qualifier:	Acacia tenuifolia
Type status:	Acacia tenuifolia [non (L.) Willd. (1806)]
Family information:	Acacia tenuinervis
Det. notes:	Acacia tenuispica
	Acacia tenuissima

Cultivar

This field is used to indicate the rank of the cultivar taxon. The items in the pick list are:

- cultivar
- cultivar group.

The value of the **Cultivar** field will replace the taxon **Rank** when in data that is delivered to AVH. In Specify, you need to fill in both the **Rank** field and the **Cultivar** field for taxon names.

Is hybrid

This box needs to be ticked to indicate a hybrid or intergrade. Ticking this box will enable the **Hybrid parent** fields.

Hybrid category

This field is a pick list that lists the hybrid categories. The items in this list are:

- Hybrid name
- Hybrid formula
- Intergrade or intermediate.

If 'Hybrid name' is selected, a multiplication sign ('×') will print in front of the name or epithet.

Hybrid rank

The rank at which the hybrid flag applies for hybrid names (e.g. *×Glossadenia tutelata* vs. *Potamogeton ×sparganiifolius*). The items in this pick list are:

- genus
- species
- infraspecific taxon.

Hybrid parent 1

The first parent of a hybrid or intergrade. To avoid having more than one entry in the **Taxon** table for hybrids, intermediates or intergrades between the same taxa, hybrid parents should always be entered in alphabetical order, regardless of how they are listed on the det. slip. If the order of the names on the det. slip is deemed important, it can be recorded in the **Det. notes** field.

Hybrid parent 2

The second parent of a hybrid or intergrade.

Preferred name

The accepted name for a synonym. This is a read-only field. Synonymies can only be made in the **Taxon** tree.

Is preferred

This is a read-only field that indicates that the taxon name is the preferred name.

Source of synonymy

This field is used to record where (or who) the synonymy comes from.

Comments

Any additional comments about the taxon name.

Synonyms

The **Synonyms** subform lists the synonyms of the current name that have been synonymised in the **Taxon** tree. This part of the form is read-only.

Full name

The full name of the synonym.

Child taxa

This subform lists the child taxa of the current taxon. If the current taxon is a genus, for example, the child taxa are species.

Full name

The full name of the child taxon.

Attachments

Taxon attachments

Any attachments that relate to a taxon name, such as PDFs of publications.

Adding new genus and higher taxon names

Because the higher classification is decoupled from the MEL storage location in MELISR, when you add a new taxon record for ranks above species, you also need to define its storage location. The storage location is updated in the **Genus and higher taxon storage** page of the MELISR website: 10.15.15.99/melisr/index.php/genusstorage. If you add a new genus or higher taxon name that will be used in a **Collection object** record, it's best to define its storage location straight away, so that the storage location can be printed on the MEL label.

To enter the storage location of a new genus or higher taxon:

1. Click **Add** next to the taxon name you just entered:

Genus and higher taxon storage		
TaxonID	Name	Add
75817	Aleurocystis	Add...
75110	Brevicellirium	Add...

The higher classification for the taxon name will be displayed:

Edit genus and higher taxon storage

Aleurocystis

Life: Life
Kingdom: Fungi
Division: Basidiomycota
Class: Basidiomycetes
Subclass: Agaricomycetidae
Order: Russulales
Family: Stereaceae

2. In the **Stored under** drop-down list, select the MEL storage location (family or other grouping) for that taxon:

Stored under

(Select storage)
316. Valerianaceae
317. Dipsacaceae
318. Calyceraceae
319. Asteraceae
320. Butomaceae
Indet.
F. Fungi
Ascomycetes
Basidiomycetes
Chytridiomycetes

3. Click the **Insert** button:

Stored under



Taxon names

Formatting of taxon names

In Specify, taxon names are stored entirely differently than in Texpress. While in Texpress parts of the taxon name were stored in a genus, species epithet and infraspecific epithet field in the same record, in Specify taxa or taxon names are stored in a taxon tree (or classification) with the genus, species, subspecies, variety and forma parts of the taxon name stored as individual records, which are linked through parent–child relationships. Taxa at supra- and infrageneric ranks are stored the same way.

One advantage of this is that taxa may be determined to any level in the **Taxon** tree, so if a specimen has only been identified to, say, order, you can just enter the name of the order in the **Determination** form. Another advantage is that we have many more options for, and much more control over, the formatting of names.

Names of infraspecific taxa

In Texpress you could (or really should) only have one infraspecific epithet. In Specify, you can enter subspecies, variety and forma (all as separate records) for a single taxon. However, while you can enter more than one infraspecific rank for a taxon in the taxon tree, botanical names still may have only one infraspecific epithet. So, for example, for the taxon that has been stored in the taxon tree as genus: *Bedfordia*, species: *linearis*, subspecies: *oblongifolia*, variety: *curvifolia*, the name that will be printed on labels and all other reports is *Bedfordia linearis* var. *curvifolia* Orchard. In the names in the drop-down list in the **Determination** form, all epithets will be printed so that people can see the difference between *Bedfordia linearis* var. *curvifolia* and *Bedfordia linearis* subsp. *oblongifolia* var. *curvifolia*.

Note: ‘Names’ like *Bedfordia linearis* subsp. *oblongifolia* var. *oblongifolia* that have been entered in Texpress as autonyms are, in fact, not autonyms. Such names need to have an author and, if you encounter one on a herbarium sheet or det. slip, you should check if the name has been validly published.

Note: In Texpress we religiously entered the authorship of both the name of the infraspecific taxon and the name of the species that the taxon belonged to. While the ICBN states that it is often advisable to cite the author of a name, it doesn’t say anywhere that you can insert the name of a different taxon, so we do not do that anymore. That is, the author of the species name will still be entered with the species name, but will not be printed on labels and in reports for infraspecific taxa.

Hybrid names

Hybrid names are written with a multiplication sign (‘×’) in front of the name or epithet. In order for the name to show in the right position in the drop-down list in the **Determination** form, and to avoid duplication of the same name with and without the multiplication symbol, the multiplication symbol is not entered in the **Taxon** table, but will appear automatically on the label if ‘Hybrid name’ has been selected from the **Hybrid category** pick list. This allows us also to deal correctly with infraspecific hybrid names. Such names do not have multiplication symbols, but have ‘notho’ prefixed to the infraspecific rank prefix.

Hybrid formulae

Hybrid formulae have the format *Parent 1 × Parent 2*, e.g. *Eucalyptus baxteri × Eucalyptus obliqua*. In order to print the formula correctly on the label, ‘Hybrid formula’ has to be selected from the **Hybrid category** pick list and the **Hybrid parent 1** and **Hybrid parent 2** entered. Both parents need to be in the **Taxon** tree. In accordance with the recommendation in ICBN, we enter the parents in alphabetical order. In order for the hybrid formula to show in the drop-down list in the **Determination** form, the formula also needs to be entered correctly in the **Name** field. For ease of data entry and reliability of queries we use a lower case ‘x’ in the **Name** field.

Hybrid formulae are entered at the rank to which the first parent is identified, so the above example is entered as a species with parent *Eucalyptus* and ‘*baxteri* x *Eucalyptus obliqua*’ in the **Name** field. *Eucalyptus camaldulensis* var. *camaldulensis* × *Eucalyptus obliqua* will be entered as a variety with the **Name** ‘*camaldulensis* x *Eucalyptus obliqua*’ and **Parent** ‘*Eucalyptus camaldulensis*’. For clarity and unambiguity we do not abbreviate or leave out any parts of the parents’ names:

The screenshot shows the 'Taxon' entry screen. The 'Name' field contains 'baxteri x Eucalyptus obliqua'. The 'Is hybrid' checkbox is checked, and the 'Hybrid category' dropdown is set to 'Hybrid formula'. The 'Hybrid parent 1' field contains 'Eucalyptus baxteri' and the 'Hybrid parent 2' field contains 'Eucalyptus obliqua'.

We cannot deal with uncertainty in hybrid parents, so, if one of the parents is uncertain or unknown, only add **Hybrid parent 1** and write ‘<Parent1> hybrid’ in the **Name** field:

The screenshot shows the 'Taxon' entry screen. The 'Name' field contains 'oxycedrus hybrid'. The 'Is hybrid' checkbox is checked, and the 'Hybrid category' dropdown is set to 'Hybrid formula'. The 'Hybrid parent 1' field contains 'Acacia oxycedrus' and the 'Hybrid parent 2' field is empty.

Intergrades and intermediates

Intergrades and intermediates are dealt with in a similar way to hybrid formulae and have the format *Taxon 1 – Taxon 2*. ‘Intergrade/intermediate’ should be selected in the **Hybrid category** pick list and Taxon 1 and Taxon 2 are entered in the **Hybrid parent** fields. Like in hybrid formulae, the taxa between which the plant is intermediate are entered in alphabetical order (if considered important, the names of the taxa can be written in the order they are on the herbarium sheet or det. slip in the **Det. notes** field in the **Determination** form):

The screenshot shows the 'Taxon' entry screen. The 'Name' field contains 'brachybotrya - Acacia dictyocarpa'. The 'Is hybrid' checkbox is checked, and the 'Hybrid category' dropdown is set to 'Intergrade/intermediate'. The 'Hybrid parent 1' field contains 'Acacia brachybotrya' and the 'Hybrid parent 2' field contains 'Acacia dictyocarpa'.

'Intergrade' or 'intermediate' should be selected from the **Addendum** field in the **Determination** form to indicate which term was used by the determiner.

The screenshot shows the 'Determinations' section of a software interface. It includes fields for 'Det. type' (dropdown), 'Determiner' (Maslin, B.R.), 'Date' (Full Date, 25/07/2011, checked for 'Current'), 'Taxon name' (Acacia brachybotrya - Acacia dictyocarpa), 'Alternate Name' (empty), 'Qualifier' (dropdown), 'Qualifier rank' (dropdown), 'Addendum' (dropdown set to 'intermediate'), 'Type status' (dropdown), 'Type qualifier' (dropdown), 'Extra information' (empty), 'Det. notes' (Branchlet indumentum suggests that this might be an intermediate between A. dictyocarpa and A. brachybotrya), and several checkboxes: 'Determiner inferred' (unchecked), 'Stored under this name' (unchecked), 'Basis' (dropdown), 'Flora' (dropdown), and icons for edit, add, search, and delete.

Intergrades between infraspecific taxa of the same species are far from uncommon (that's why they're infraspecific taxa, not species) and adding them to the taxon tree should be avoided. For such determinations the species name should be entered in the **Taxon name** field in the **Determination** form, while the information about the intergradedness between the infraspecies can be entered in the **Extra info.** field

Administrative fields

The following fields are automatically completed and cannot be edited.

Created by

The person who created the database record.

Created

The date the record was created.

Last edited by

The person who last edited the record.

Last edited

The date the record was last edited.

Agent form

The **Agent** form is used to record information about people and organisations who are involved in the collection, determination or curation of specimens. Note that when the **Agent** form is opened from within the **Collection object** form (i.e. when adding a new collector), you may not be able to see the **Agent attachment** icon at the bottom of the form, depending on the size of your screen. If you wish to add (or view) an **Agent** attachment, click the **Collapse** symbol next to the **Agent geographies** heading to collapse that subform.

Agent type

The type of agent. **Agents** can be one of the following:

- Person: an individual botanist, collector, student or data entry person
- Organisation: an institution or organisation that acts as a collector (e.g. 'Ballarat Field Naturalists Club') or that is involved in transactions (e.g. 'National Herbarium of New South Wales')
- Group: more than one individual who act together as, for example, determiners
- Other: any other type of agent (it is unlikely that we will need to use this category).

Institution/Last name

The last name (for a 'person' agent), or the organisation/institution name (for an 'organisation' agent).

If the agent's last name consists of a preposition and a substantive, as in many European names (e.g. C.G.G.J. van Steenis), then the preposition is in lower case and should be entered in the **Initials** field:

Agent type: Person Institution/Last name: Steenis
Title: First name: Initials: C.G.G.J. van

If the name has been anglicised the preposition is treated as part of the substantive, and should be entered in the **Last name** field:

Agent type: Person Institution/Last name: De Nardi
Title: First name: Initials: J.C

If the agent is an organisation that is involved in loan or exchange transactions with MEL, prefix the organisation name with the Index Herbariorum acronym, and use two hyphens with a space either side to separate it from the institution name:

Institution/Last name: TRT -- Royal Ontario Museum Botany Department

Prefixing the institution name with the herbarium code makes it much easier to look up an institution in the gift and loan forms. It is important that two hyphens are used as the separator, as that is what the transaction paperwork program uses to identify which part of the name to print on reports and labels.

Title

The agent's salutation or honorary title (for a 'person' agent). If a title is not in the pick list, see the Collections Information Officer.

First name

The agent's first name (for a 'person' agent). Entering data in the **First name** field is not as important as entering data into the **Initials** field.

Initials

The agent's first and middle initials. If the first name needs to be spelt out to avoid ambiguity, it should be repeated here (as well as being entered in the **First name** field). For example:

- Paul G. [Wilson]
- Peter G. [Wilson]
- Stephen [Johnson]
- Sidney [Johnson].

Agent type: Person	Institution/Last name: Wilson	
Title:	First name: Paul	Initials: Paul G.

If a person agent's name includes a preposition that has not been anglicised, e.g. 'de', 'van', 'zu', it should be entered after the initials:

Agent type: Person	Institution/Last name: Wied	
Title:	First name:	Initials: M.A.P. zu

If the preposition has been anglicised (and thus capitalised), it should be included as part of the **Last name**.

Abbreviation

The Index Herbariorum code for the organisation agent, or for the institution that an agent works for.

E-mail

The agent's e-mail address.

Job title

The agent's job title (for a 'person' agent).

CITES no.

The CITES permit number of an organisation agent involved in transactions.

Date type

Different types of date ranges can be entered in the **Agent** record, depending on the type of agent, or the information available. The following date types can be selected from the drop-down list:

- **Birth/Death** – the birth and/or death dates of a person agent
- **Collected** – the period of activity for a collector (either a person or an organisation)
- **Received specimens** – the period during which an organisation agent received specimens on loan or exchange.

Start date

The earliest date corresponding to the date type, i.e. the agent's date of birth (for a 'person' agent), the earliest date of a period of collecting activity, or the earliest date that an organisation received specimens. The **Start date** can be entered as a full date, a month and year, or a year only.

End date

The latest date corresponding to the date type, i.e. the agent's date of death (for a 'person' agent), the latest date of a period of collecting activity, or the latest date that an organisation received specimens. The **End date** can be entered as a full date, a month and year, or a year only.

Comments

Any comments about the agent, such as period of collecting activity (for people agents, if the date entered in the **Start date** and **End date** fields is 'Birth/Death') or history of the institution (for organisation agents).

Web link

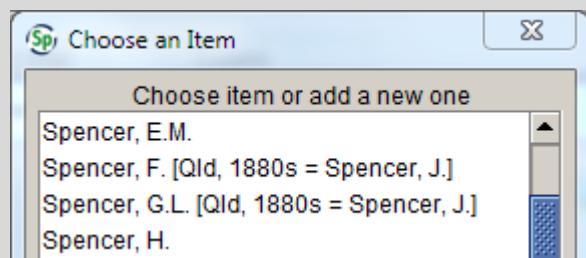
A link to a website about the agent (whether a 'person' agent or an 'organisation' agent). The web link must include the protocol (i.e. 'http://').

Recording incorrect or misinterpreted versions of agent names

Sometimes collectors' names have been recorded incorrectly on herbarium labels, or are frequently misinterpreted, for example, Jessie Spencer, who Mueller mostly referred to as Mrs F. Spencer (he mistook her initial for an F, and it can also be hard to tell the difference between Mueller's capital I, T, J and F). Jessie was also incorrectly referred to as 'Mrs G.L. Spencer' in a 19th-century newspaper, and Jim Willis has pencilled those initials on some specimens. In cases such as this, it is useful to add the incorrect version of the name to the **Agent** table, with an indication of which name should be used instead. For example:

Institution/Last name:	Spencer
First name:	
Initials:	F. [Qld, 1880s = J. Spencer]

The correct version of the name should be recorded in the Initials field so it shows up in the agent list:



Make sure you include enough information to distinguish the name from other collectors with the same name: in the above example, the 'Qld, 1880s' is important in case we ever come across a collector whose initials and last name actually are 'F. Spencer'.

Please always include an explanation of why the name has been assumed to be incorrect or misinterpreted, and references to the evidence that backs up your interpretation.

Comments:	Mueller appears to have interpreted Jessie Spencer's initial as an F instead of a J. See: Maroske, S. & Vaughan, A. (2014). Ferdinand Mueller's female plant collectors: a biographical register. <i>Muelleria</i> vol. 32.
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Note: You should never select one of these entries from the agent list; always use the entry it refers you to, and record the name as it appears on the label in the Verbatim collector field:

Last name	Initials
Spencer	J.

Label data

Verbatim collectors: Mrs F. Spencer

Addresses

Multiple addresses can be entered for a single agent. If more than one address is entered, use the **Is current** check box to indicate the primary (or current) address, which will be used on mailing labels.

Attn:

The person or position to whom correspondence should be forwarded (for organisation agents).

Address

The organisation and/or street address of the agent.

City

The city that the agent resides or works in.

State

The state or province that the agent resides or works in.

Post code

The postal code of the city that the agent resides or works in.

Country

The country that the agent resides in.

Phone

The agent's primary telephone number.

Fax

The agent's fax number, if known.

Is current

The **Is current** field is used to record which of the agent's addresses is current. An agent can only have one current address.

Start date

If an agent has more than one address, the date at which MEL started using a new address should be entered in the **Start date** field. The **Start date** will default to the date that a new address record was added.

Exchange

This is a read-only field that is used to indicate whether or not MEL has an exchange agreement with an institution agent. Changes to this field can only be made by a database administrator.

Loan p'work

The e-mail address of the person to whom loans paperwork should be sent.

Exchange p'work

The e-mail address of the person to whom exchange paperwork should be sent.

Data format

The institution's preferred format for exchange data.

Agent geographies

Region

The geographical region of interest to the agent. This field links to the **Geography** tree, so only places listed in the **Geography** tree can be entered.

Comments

Enter any comments about the agent's interest in the geographic region (e.g. whether they collected in the region, or if it was a topic of research).

Attachments

Agent attachments

Any attachments that relate to the agent, such as images of handwriting samples, letters, or PDFs of articles about the agent.



Administrative fields

The following fields are automatically completed and cannot be edited.

Created by

The person who created the database record.

Created

The date the record was created.

Last edited by

The person who last edited the record.

Last edited

The date the record was last edited.

Attachment forms

Specify allows many types of files to be attached to various tables. It's important that attachments are properly curated so they can be effectively queried and can be made available to external researchers and projects such as Australia's Virtual Herbarium (AVH), and not just used internally by herbarium staff. The requirements for curating non-image attachments (such as Word documents, PDF files and spreadsheets) are fairly straightforward, but the metadata requirements for curating images are more complex.

Images should be only attached to specimen records if they augment the specimen data and are of sufficient quality and relevance to be of interest to other data users. Once the mechanisms are in place for delivering images to AVH, certain categories of images attached to specimen records will be delivered to AVH by default.

Please ensure images have the correct orientation before importing them into MELISR; you cannot alter the orientation once they've been imported, and we don't want to deliver sideways images to AVH or other services.

Attachment file formats

The following file formats can be attached to records in Specify:

- JPEG
- GIF
- PNG
- TIFF
- PDF
- CSV

Do not attach Word or Excel files to records. Note that Specify will not generate a thumbnail image for TIFF files. Avoid creating new TIFF images to attach to MELISR records, but if you are provided with TIFF images by a collector, don't change them to another format.

Types of attachments

Attachments can be added to the following forms:

- **Collection object** – attachments that relate to the collection object, e.g.
 - images of the specimen in the field (but not general habitat photos)
 - images of the specimen in the lab (e.g. prior to being curated)
 - images of the pressed or dried specimen (whether or not it has been mounted or curated)
 - letters associated with herbarium specimens
 - illustrations associated with herbarium specimens
- **Collecting event** – attachments that relate to the collecting event more broadly, rather than to the individual specimen (or specimen-to-be), e.g.

- general habitat images (as opposed to a photo focussing on the specimen-to-be in the field; if in doubt, add the image as a **Collection object attachment**)
 - a photo of the collector/s in the field
- **Locality** – attachments that relate specifically to the collecting locality (and not to the specimen itself), e.g.
 - a map of the collecting locality
- **Agent** – attachments that relate to an agent, e.g.
 - images of handwriting samples
 - portraits
 - letters (if a letter is from a herbarium specimen, add it as a **Collection object attachment**)
 - PDFs of papers about the agent
- **Conservator event** – attachments that relate to a conservator event, e.g.
 - images of damage to a preparation
 - treatment reports
- **Taxon** – attachments that relate to a taxon name, e.g.
 - PDFs of publications
- **Loan** – attachments that relate to a loan, e.g.
 - preparation lists for loans of unaccessioned material
 - import permits
- **Exchange** – attachments that relate to an exchange transaction, e.g.
 - species lists for consignments of shipping material without preparations.

Collection object attachment or Collecting event attachment?

An image of the habitat in which the specimen was growing, or of collectors at the collecting site, should be added as a **Collecting event attachment**. An image of the specimen, either before or after it was collected, should be added as a **Collection object attachment**. Sometimes an image of the plant, alga or fungus in the field will show habitat detail as well as the specimen itself. Use your own judgment to decide whether the main subject of the image is the specimen (or specimen-to-be), or the habitat. If in doubt, make the image a **Collection object attachment**.

Attachment metadata

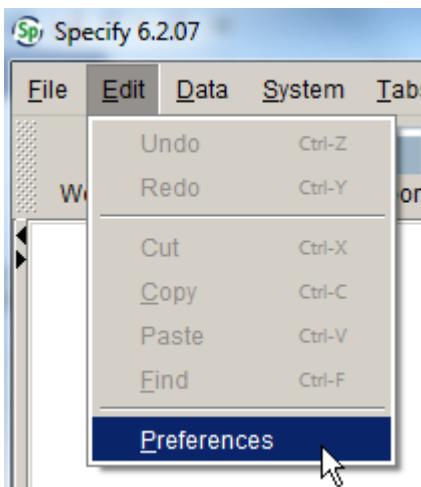
Two tables are used to record information about attachments. The first is the **Attachment** table, which is used to record some of the technical, content and curatorial metadata. A second table, **Additional metadata**, is used to record additional metadata.

Attachment metadata can either be added and edited within Specify, or, for attachments that have already been uploaded into Specify, you can add or edit metadata using the **Attachment metadata workbench**.

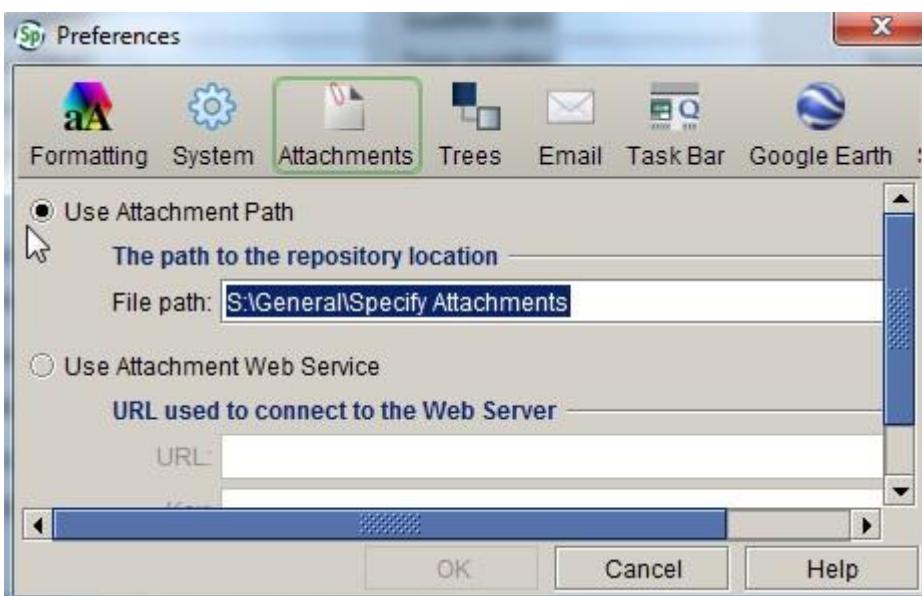
Attachment storage location

Before adding any attachments in Specify, the attachment storage location needs to be set. To set the storage location:

1. Go to **Preferences** under the **Edit** file menu:



2. Under the **Attachments** tab, set the attachment storage location as S:\General\Specify Attachments :



Note that the file path is not case-sensitive on Windows computers.

Attachment

Original file name

The original file name of the attachment. The **Original file name** will be automatically taken from the file being uploaded.

Title

The title of the attachment (the **Original file name** without the file path). The title will be automatically filled in from the **Original file name**; the **Title** does not have to be meaningful.

Subject

The subject of the attachment. There is no need to repeat information that is elsewhere in the record, such as **Catalogue number**, **Taxon name** or **Collector**.

Examples of **Subject** for specimen-related images include:

- ‘Part of inflorescence’
- ‘Testa surface’
- ‘Ascus with imm. spores’
- ‘Whole plant’
- ‘Internal view of spadix’
- ‘Young fruit capsules’
- ‘Flower’
- ‘Fruiting body’.

If the attachment is a PDF of a published article, enter its title here. If a non-specimen-image attachment does not have a formal title, enter a brief description of it here. For example:

- ‘Letter from McHard to Mueller, dated 1885’
- ‘2014-0008 preparations list’.

Image creation date

The date an image attachment was created (creation date is not required for non-image attachments such as PDF or Excel files). The **Image creation date** will be automatically filled in from the EXIF data embedded in the image when needed.

Copyright holder

The person or organisation who owns copyright in an image. The **Copyright holder** will default to the photographer (in the **Image attributes** table), if left blank. Where the photographer was a member of staff at the time the photograph was taken, the **Copyright holder** should be entered as ‘RBG Melbourne’.

Copyright date

The date that copyright in the image was asserted. **Copyright date** will default to the year in the **Image creation date** if left blank.

Restrictions on use

Any restrictions on use of the image instructed by the copyright holder or photographer (such as an embargo period). If a **Licence** has been provided and there are no restrictions on use entered, we will assume that we can use the image for any purpose that fits within the **Licence**.

Attribution

How the image should be attributed. If **Attribution** is left blank, it will default to **Photographer**.

Additional metadata

The **Additional metadata** table contains additional metadata that is mostly only used for images, however, the **Category** field should be used for non-image attachments if there is a relevant category in the pick list (e.g. 'Notes' for a PDF of notes provided by the collector).

Photographer

The name of the person who took the photograph. There is currently no link within Specify between the attachment metadata tables and the **Agent** table, so the photographer's name will need to be entered by hand. We will make our own link between the **Photographer** field and the **Agent** table so we can properly attribute images when used outside of MELISR. For this to work, photographers' names need to be entered in a standard format, as follows:

[last name], [initials (separated by full stops)] [preposition (where applicable)]

e.g. 'Ratkowsky, D.A.', 'Heul, T. van der'

Make sure that there's an entry for the photographer in the **Agent** table, and check that their **First name** has been entered, if known.

Image type

The method by which the image was produced. The values in the pick list are:

- SEM
- Light microscope image.

More terms can be added to the pick list as needed.

Category

The **Category** field is used to indicate the broader subject of the image (more detail must be provided in the **Subject** field). These categories will allow us to determine which attachments are appropriate for different uses (e.g. which are suitable for sending to AVH, which could be used for VicFlora, which could be used in an online database of collectors). There is some overlap in the categories (e.g. ‘Label’ is part of a ‘Herbarium specimen’); where more than one **Category** option applies, always use the more specific term.

The values currently in the pick list are:

- Habitat – an image of the general habitat in which the plant, alga or fungus was growing (as opposed to an image of the specimen while still in the field) (used for **Collecting event attachments**)
- Handwriting – a handwriting sample attached to an agent record (used for **Agent attachments**)
- Herbarium specimen – all or part of a dried or pickled specimen that is (or will become) a herbarium specimen, regardless of whether or not it has been mounted or curated yet (used for **Collection object attachments**)
- Illustration – an illustration associated with a herbarium specimen (used for **Collection object attachments**)
- Label – detail of one or more labels on a herbarium specimen (used for **Collection object attachments**)
- Letter – a letter attached to a herbarium specimen (if a **Collection object** attachment), or a non-specimen-related letter (if attached to an **Agent** record) (used for **Collection object attachments or Agent attachments**)
- Notes – an image of any notes accompanying the specimen, such as lengthy notes with fungi, descriptions by Mueller, or Sonder’s diagnoses (used for **Collection object attachments**)
- Person/s – a photo of a person or persons involved in a collecting event (used for **Collecting event attachments**, if relevant, or **Agent attachments**)
- Specimen in field – all or part of the specimen in the field (i.e. an image of the individual specimen taken in the field, as opposed to a general habitat photo) (used for **Collection object attachments**)
- Specimen – an image of all or part of the specimen taken somewhere other than in the field or once it has been curated, e.g. in the lab prior to being pressed and/or dried; use this category if you are unsure where the image was taken or whether or not it has been preserved yet (used for **Collection object attachments**).

Magnification

The magnification of images taken under a microscope. Magnification should only be included for images that have a scale bar. You do not need to include the magnification symbol (x). Be careful not to confuse the size of the scale bar with the magnification.

Licence

The licence under which an image can be used. The pick list has the following values:

- CC BY
- CC BY-SA
- CC BY-ND
- CC BY-NC
- CC BY-NC-SA
- CC BY-NC-ND
- Unknown.

If the licence is unknown, please select ‘Unknown’ in the pick list.

Comments

Any additional remarks about the attachment.

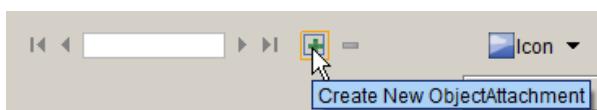
Adding attachments

To add an attachment to a record:

1. Click on the attachment symbol in the relevant form:



2. Click on the **Add** symbol at the bottom of the **Attachment** form:



3. Navigate to the file that you want to attach to the record (if the file browser window doesn't open automatically, click the **Browse** button)
4. Enter as much metadata as you can about the image (see field descriptions above)
5. Click **Done** to save the **Attachment** record.

TRANSACTIONS

Information about herbarium transactions is recorded in the **Interactions** module in Specify. Two separate collections are used to record details of MEL transactions: outgoing loans, donations and exchange are recorded in the *National Herbarium of Victoria* collection, and incoming loans are recorded in the *Non-MEL loans* collection.

Loans

In MELISR, loans of MEL specimens to other institutions are recorded in the **Loan** table. The Loan table has two views: **Loan** and **Loan w/o preps**. The **Loan w/o preps** table allows you to enter data about the loan before specifying which specimens will be part of the loan. See the **Databasing loans** section for more information on how to use the two Loan views.

Loan form

Loan

Loan number

The MEL loan number comprises two parts, separated by a forward slash:

- Year – the year the loan was prepared
- Number – a sequential, four-digit number. The sequence restarts at 0001 each year.

Old loan numbers have been converted to this format based on the year they were sent out (e.g. MEL loan 210 = 1974/0210).

This field fills automatically when the loan record is saved; however, the loan number needs to be entered manually for the first loan in each calendar year and for transferred loans.

Note that the abbreviation for the recipient institution (e.g. CANB) appears after the loan number but is not part of the loan number. The abbreviation is drawn from the institution in the **Sent to** field.

Loan status

The current status of the loan. The following values can be selected from the pick list:

- Awaiting acknowledgement – loan sent but yellow acknowledgement form not received at MEL
- Complete – all loan preparations have been returned to MEL (or transferred to another institution)
- Current – all or some preparations still on loan

- New – loan is being prepared
- Not serviced – loan request received but not serviced
- Written off – loan closed because specimens have been lost or destroyed.

Quantity on loan

The number of preparations that are on loan. This field fills automatically when loan preparations are added or returned.

Date requested

The date the recipient institution requested the loan (i.e. date of formal loan request).

Current due date

The date by which the loan is due to be returned to MEL. For loans where an extension has been granted, the **Current due date** should be updated.

Extension granted

A check box indicating if an extension has been granted. The new due date should be recorded in **Current due date**. Details of who granted the extension and the date are recorded in the **Description** field, and should be prefixed by a double pipe (||).

Original due date

The date by which the loan was originally due to be returned to MEL. For loans where no extension has been granted, the **Original due date** will be the same as the **Current due date**.

Description

A short summary of the contents of loan. For example:

- ‘*Utricularia* specimens set aside during visit to MEL on 13 Sep 2010’
- ‘Selected Victorian specimens of *Epacris impressa*’

This description appears on the loan paperwork. Subsequent comments should be prefixed by ‘||’, for example:

- ‘Selected Victorian specimens of *Epacris impressa*. || Extension granted by J.Smith, 4/4/2011.’

Project

This field is used to indicate if a loan was requested for a particular project. ‘Flora of Australia’ is currently the only project in the pick list.

Destructive sampling permitted

A check box to indicate if destructive sampling has been approved (either at the time the loan was prepared, or subsequently). Details of destructive sampling permission should be included in **Conditions**.

Conditions

Any conditions other than the standard MEL loan conditions, such as details of permission for destructive sampling to be undertaken.

Acknowledged

The date of receipt of the loan at the receiving institution (as recorded on yellow acknowledgement slip).

Received comments

Comments noted by the receiving institution on the yellow acknowledgement slip (e.g. damage to specimen(s), discrepancies between specimens sent and loan list).

Loan notice

Details of the most recent notice sent to the receiving institution regarding the loan. Details of previous notices are recorded in the **Description** field (prefixed by | |). The following values can be selected from the pick list:

- Acknowledgement request
- Extension
- Overdue
- Recall
- Reminder.

Notice sent

The date on which the most recent notice was sent to the receiving institution.

Loan closed

The date on which all loaned specimens are processed as returned. For full loan transfers, this is the date on which the loan is acknowledged as received by the institution to which it was transferred.

Loan transfer no.

For transferred loans (full or partial), the loan number to which the loan has been transferred. For loan transfers, the year and number components stay the same, but the institution code changes to

that of the institution to which the loan has been transferred. For example, if loan 1974/0210 CANB is transferred to AD, the transferred loan number is 1974/0210 AD.

Loan agents

Name

The botanist(s) and/or student(s) on behalf of whom the loan was requested. A loan may have multiple loan agents (e.g. student and supervisor(s)).

Role

The role of the agent in the loan. The following values can be selected from the pick list:

- Botanist
- Other
- Student
- Supervisor.

Shipments

Sent to

The institution to which the loan was sent. This corresponds to **Last name** in the **Agent** table and is formatted as the herbarium code followed by ‘--’ then the title of the institution (e.g. CANB -- Australian National Herbarium).

Shipment number

An auto-generated identifier for the shipment.

Date sent

The date the loan was prepared for dispatch. This date prints on the loan paperwork.

Prepared by

The Curation Officer(s) who prepared the loan. This prints on the loan paperwork.

Method

The method by which the loan was shipped. The pick list values relevant to loans are:

- Air Mail – Customs Insured (loans to overseas institutions)
- Collected from MEL

- Courier
- Express Post
- Hand delivered
- Registered Post (loans to Australian institutions)
- Sea Mail – Customs Insured (very large or heavy loans to overseas institutions)
- Transfer.

Reference no(s)

Tracking numbers for each parcel in the shipment (from the Registered Post or Customs Insured label).

Number of parcels

The number of parcels in the shipment.

Weight

The total weight of the parcels in the shipment, in kilograms (e.g. 450 g = 0.45).

Postage

The total postage cost for all parcels in the shipment.

Comments

Any comments relevant to the shipment, for example:

- ‘sent with exchange MEL ref. 1987’.

Loan preparations

The **Loan** preparations subform is used to record the details of the preparations in the loan. Only loans sent after 1 January 1996 are linked to loan preparations. Specimens sent on loan prior to 1996 were not databased.

Catalogue no.

The catalogue number of the specimen.

Preparation type

The preparation type of the specimen that is being sent on loan. Preparations that can be sent on loan are:

- Sheet
- Packet
- Spirit collection
- Microscope slide
- Fungal culture
- Carpological
- Display set
- Cibachrome
- Photograph of specimen.

Is resolved

This field indicates whether the loan of an individual preparation has been resolved. ‘Yes’ indicates that the preparation has been returned to MEL (or otherwise accounted for). ‘No’ indicates that the preparation is on loan.

Quantity

The number of preparations relating to a single collection object that have been sent on loan. For example, if there are three microscope slides for a given specimen, and all are sent on loan, the quantity will be ‘3’.

Outgoing comments

Comments specific to the preparation at the time the loan is sent (e.g. permission for destructive sampling; specimen not scanned when loan sent).

Borrower's comments

Specific comments noted by the receiving institution (e.g. that the specimen was damaged on receipt of the loan).

Incoming comments

Comments specific to the preparation when it is returned to MEL (e.g. damage to specimen; notes about updates required when specimen returned).

Status

The status of a preparation that is resolved, but not returned. The following values are available in the pick list:

- Destroyed
- Lost
- Transferred

- Written off.

Loan return preparations

The preparation type and quantity returned.

Loan return preparations

The **Loan return preparations** table is used to record details relating to the return of individual specimens from loan.

Processed by (agent)

The Curation Officer who processed the loan return.

Date returned

The date on which the preparation is processed as returned.

Quantity returned

The number of preparations returned from loan. When all components of a given preparation are returned, the quantity returned will equal the quantity sent. In cases where preparations are lost, destroyed or written off, the quantity returned will not be equal to the quantity sent.

Quantity resolved

The number of preparations resolved. When all components of a given preparation are returned, the quantity resolved will equal both the quantity returned and quantity sent. In cases where preparations are lost, destroyed or written off, the quantity resolved will not be equal to the quantity returned.

Note: all preparations for a given loan must be resolved before a loan can be closed.

Loan return

Returned comments

A summary of the material returned, including the number of specimens, date returned and comments. For example:

- ‘5 returned, 3/3/2010. Quarantined material VM10002535.’

This information must be entered for all pre-1996 loans. It is not required for post-1996 loans; details of previous partial returns can be deleted if all information correlates with the loan information summary in the loan returner.

Quarantine

A check box to indicate if the loan was quarantined when it was returned to MEL. The Quarantine Entry Number is entered in **Returned comments**.

Administrative fields

The following fields are automatically completed and cannot be edited.

Created by

The person who created the database record.

Created

The date the record was created.

Last edited by

The person who last edited the record.

Last edited

The date the record was last edited.

Databasing loans

Entering a new MEL loan

New loans are entered by the Curation Co-ordinator once approved by the Collections Manager and Chief Botanist.

To enter a new **Loan** record:

1. Open the **Interactions** module
2. Click **Loan w/o preps** in the side bar
3. Enter details in the following fields:
 - **Loan status** – i.e. ‘New’
 - **Date requested**
 - **Description**
 - **Destructive sampling permitted**
 - **Conditions** – e.g. details of destructive sampling permitted; quarantine message for all loans to overseas institutions
 - **Loan agent(s) Name and Role** – check that a first name is recorded for each agent involved in a loan

- **Sent to** – check and/or add or all agent details, including Index Herbariorum code, title, address and CITES or Department of the Environment registration code
 - **Prepared by**
4. Save the loan record. The **Loan number** will be automatically completed when the record is saved.

Adding preparations to a loan

Preparations are added to a loan by a Curation Officer. Note that it's not possible to add a preparation to a loan while databasing a specimen.

To add preparations to an existing **Loan** record:

1. Create a record set using one of the following methods:
 - Open the **Record set creator** and scan barcodes into the **MEL barcodes** text box. Select **Create record set** and name the record set with the loan number (e.g. 2011/0011 NSW). Note that you'll need to exit and log back into MELISR to access the record set.
 - Open the **Record set creator** and scan barcodes into the **MEL barcodes** text box. Select **Create barcode string**. Copy and paste the barcode string into the **Barcode** field in the **Collection object** table in the **Query builder**. Select 'In' as the **Operator** and run the query. Save the results as a record set by clicking on the **Record set** symbol in the results bar. Name the record set with the loan number – note that '/' should be replaced with '-' (e.g. 2011-0011 NSW).
 - Scan barcodes directly into the **Barcode** field in the **Collection object** table in the **Query builder**. Use a comma after each barcode. Select 'In' as the **Operator** and run the query. Save the results as a record set by clicking on the **Record set** symbol in the results bar. Name the record set with the loan number – note that '/' should be replaced with '-' (e.g. 2011-0011 NSW).
 - For spirit or microscope slide preparations, create a record set by querying on the spirit/slide number in the **Preparation** table.

Note: more than one record set can be added to a loan record.

2. In MELISR, find the loan by searching for the loan number in either the **Simple search** (e.g. '2011/0001*') or the **Loan number** field in the **Query builder** (in the **Loan** table)
3. Open the **Loan** form and click **Edit**
4. Click the **Add** symbol in the **Loan preparations** form
5. Select **Record sets and information requests** when prompted to choose the source of the preparations
6. Select the relevant record set from the list and click **OK**
7. In the **Create loan from preparations** window, click **Select all**, scan through the list and deselect any preparations that are not part of the loan (e.g. microscope slides). Note that duplicate preparations don't need to be deselected at this point.
8. Click **OK**
9. Save the **Loan** record
10. Open the [**Herbarium transaction paperwork**](#) and, in the **Loans** section, select the loan from the drop-down list and click **Delete 'duplicate' loan preparations**.

Deleting preparations from a loan

The Curation Co-ordinator and Curation Officers can delete preparations from a loan. A loan preparation should only be deleted if it was erroneously added (e.g. if the wrong MEL number was entered), and only before the loan is dispatched. See the Curation Co-ordinator if a preparation needs to be deleted after the loan has been sent.

Adding shipment details to a loan

Shipment details are added to a loan by a Curation Officer once the specimens have been checked, scanned and packed.

1. Add details to the following fields:
 - **Date sent**
 - **Method** – the postal category used to send the shipment
 - **Reference no(s)** – the tracking reference number(s) for parcels (e.g. registered post, customs insured). Scan labels directly into this field, using a comma to separate entries. Ensure that the shipment method matches the label type.
 - **Number of parcels**
 - **Weight** – total weight of all parcels in the consignment
 - **Postage** – total cost of postage (calculate the postage using the online [Australia Post calculator](#))
 - **Comments** – e.g. notable damage to a specimen
2. Change the **Loan status** from ‘New’ to ‘Awaiting acknowledgement’
3. Save the **Loan** record.

Printing loan paperwork

1. Go to the [Herbarium transaction paperwork](#) page
2. Select the relevant loan from the list (sorted in descending order by loan number; greyed-out numbers are loans without preparations)
3. Print paperwork as follows:

White copy: send with loan	Yellow copy: send with loan	Pink copy: retain at MEL
<ul style="list-style-type: none">• Loan paperwork• List of preparations• Loan conditions (on reverse of loan paperwork)	<ul style="list-style-type: none">• Loan paperwork	<ul style="list-style-type: none">• Loan paperwork• List of preparations

4. Print the required number of **Parcel labels** and an **Envelope**.

Returning a databased MEL loan

1. Open the [Loan returner](#)
2. Select the relevant loan from the drop-down list

3. Scan the returned specimens into the loan returner one by one (or scan into a Word or Excel document and copy and paste list of MEL numbers with each on a separate line)
4. Select **Update batch**
5. If necessary, adjust the **Quantity returned** (e.g. if multiple spirit or microscope slide preparations were sent, but not all have been returned)
6. Select the **Curation officer**
7. Enter the **Date returned**
8. If necessary, enter the quarantine reference number in **Quarantine message**
9. Click **Return batch**
10. Open the relevant loan in MELISR and check that the **Loan preparation** table, **Quantity on loan**, **Loan status** and **Loan closed** are correct
11. Update **Returned comments** if details of previous returns have been entered
12. **Save** the loan form.

Returning an undatabased MEL loan (pre-1996 loans)

1. Open the **Loan form** for the relevant loan and select **Edit**
2. Enter the number of specimens returned and the date in **Returned comments**, along with any relevant comments (quarantine reference number, discrepancies in number of specimens, etc. For example:
 - ‘5 returned, 3/3/2010.’
 Use a full stop between each entry.
3. Update the **Quantity on loan** (in the top right-hand corner of the form). The quantity needs to be calculated manually.
4. For complete returns:
 - change the **Loan status** to ‘Complete’
 - enter the date in **Loan closed**
 - flag the **Closed** check-box (bottom right-hand corner of form)
5. **Save** the loan form.

Transferring a databased MEL loan

Loan transfers are entered by the Curation Co-ordinator. Loan transfers must be formally requested by the institution to which they are to be transferred.

1. Create a record set and barcode string for the loan preparations to be transferred
2. Open the **Loan returner** (<http://10.15.15.99/melisr/index.php/loanreturn>)
3. Select the relevant loan from the list and enter the barcode string
4. Select the **Curation officer**
5. Enter the **Date returned**
6. Select the **Transferred** checkbox
7. Click **Return batch**
8. In MELISR, open the **Loan form** for the relevant loan and select **Edit**

9. Enter the **Transfer loan no** (the existing MEL loan number, but with the institution code for the institution to which the loan is being transferred)
10. Check that the relevant loan preparations are flagged as returned, resolved and transferred in the Loan preparations table
11. Check that the **Loan status** and **Quantity on loan** are correct
12. **Save** the loan record
13. Create a new **Loan record**, add the relevant record set and add loan details:
 - **Loan status** – i.e. ‘Awaiting acknowledgement’
 - **Date requested**
 - **Description**
 - **Destructive sampling permitted**
 - **Conditions** – e.g. if destructive sampling permitted
 - **Loan agent(s) and Role(s)**
 - **Institution** – enter or check all details, including title, Index Herbariorum code, address and CITES or Department of the Environment registration code
 - **Date sent** – i.e. date of transfer
 - **Prepared by**
 - **Method** – i.e. ‘Transfer’
 - **Comments** – i.e. [Quantity] transferred from [original institution]
14. **Save** the loan record.

Transferring an undatabased MEL loan (pre-1996 loans)

Loan transfers are entered by the Curation Co-ordinator. Loan transfers must be formally requested by the institution to which they are to be transferred.

1. Open the loan form for the loan to be transferred and select **Edit**
2. Update the **Loan status** (if necessary) and **Quantity on loan**
3. Enter the **Transfer loan no** (the existing MEL loan number, but with the institution code for the institution to which the loan is being transferred)
4. Update Returned comments: ‘[Quantity] transferred, [date].’
5. Enter **Loan closed** (= date on which the loan is acknowledged as received by the institution to which it was transferred)
15. **Save** the loan record
16. Create a new **Loan record** and add loan details:
 - **Loan status** – i.e. ‘Awaiting acknowledgement’
 - **Date requested**
 - **Description**
 - **Destructive sampling permitted**
 - **Conditions** – e.g. if destructive sampling permitted
 - **Loan agent(s) and Role(s)**
 - **Institution** – enter or check all details, including title, Index Herbariorum code, address and CITES or Department of the Environment registration code
 - **Date sent** – i.e. date of transfer
 - **Prepared by**

- **Method** – i.e. ‘Transfer’
- **Comments** – i.e. [Quantity] transferred from [original institution]

17. Save the loan record.

Outgoing exchange and donations

Outgoing consignments of exchange, donations and shipping material are recorded in the **Gift** table.

Gift form

Gift

Gift number

The MEL reference number for a consignment of outgoing exchange, donation or shipping material. The gift number is generated automatically when a record is saved. The same sequence is used for both incoming and outgoing consignments (i.e. gift numbers and exchange numbers are allocated sequentially).

Category

The category of material being sent. The following options are in the pick list:

- Donation – duplicate specimens sent to an institution with which MEL does not have a formal exchange agreement
- Exchange – duplicate specimens sent to an institution with which MEL has a formal exchange agreement
- Shipping material – material other than duplicate specimens (e.g. samples for destructive analysis).

Quantity

The number of specimens (or samples) in the consignment. This field fills automatically once preparations are added.

File name

The file name for electronic data for the consignment.

Description

A summary of the contents of the consignment. For example:

- ‘Miscellaneous vascular plants and cryptogams (incl. two types)’.

This description appears on the MEL paperwork. Subsequent comments should be prefixed by ‘||’.

For example:

- ‘Miscellaneous vascular plants and cryptogams (incl. two types). || Request for acknowledgement of receipt sent 18 May 2011.’

Acknowledged

The date on which the recipient institution processed the consignment (as recorded on the yellow acknowledgement form).

Received comments

Any comments noted by the recipient institution on the yellow acknowledgement form (e.g. damage to specimen(s); discrepancies between specimens sent and specimen list).

Gift agents

Name

Usually the person to whom the electronic data was sent (for exchange or donations), or the botanist(s) and/or student(s) who requested the material (e.g. for shipping material). A consignment can have more than one agent.

Role

The role of the agent in the exchange, donation or shipping material transaction. The following values can be selected from the pick list:

- Botanist
- Other
- Recipient of exchange file
- Student
- Supervisor.

Shipments

Sent to

The institution to which the consignment was sent. This corresponds to **Last name** in the **Agent** table and is formatted as the herbarium code followed by ‘ -- ’ then the title of the institution (e.g. CANB -- Australian National Herbarium).

Shipment number

The auto-generated identifier for the shipment.

Date sent

The date on which the consignment was dispatched. This date appears on the MEL paperwork.

Prepared by

The Curation Officer(s) who prepared the consignment. If the consignment was prepared by more than one Curation Officer, they should be entered as a 'Group agent'.

Method

The method by which the shipment was sent. The following options are available in the pick list:

- Air Mail – Customs insured (no longer used)
- Air Mail – Customs non-insured
- Collected from MEL
- Courier
- Express Post
- Express Post International
- Hand delivered
- Pack & Track International
- Registered Post (within Australia only)
- Sea Mail – Customs insured (no longer used)
- Sea Mail – Customs non-insured (very large or heavy consignments).

Reference no(s)

The tracking number for each parcel in the shipment. Tracking numbers should be scanned from the consignment note or label (e.g. Registered Post label, Pack & Track International consignment note), rather than entered manually. Multiple numbers should be separated by commas.

Number of parcels

The number of parcels in the shipment.

Weight

The total weight of the parcels in the shipment, in kilograms (e.g. 450 g = 0.45).

Postage

The total postage cost for the consignment, as calculated using the [Australia Post postage calculator](#).

Comments

Any comments relevant to the shipment, for example:

- ‘Sent with MEL loan 2011/0006’.

Gift preparations

Catalogue no.

The catalogue number of the gift preparation.

Quantity

The number of duplicate preparations for a given catalogue number that are included in the consignment. For exchange, donations and shipping material, the quantity will usually be ‘1’.

Preparation type

The following preparation types can be sent as exchange/donation/shipping material:

- Duplicate
- Seed duplicate
- Silica gel sample
- Shipping material.

Quantity

The total number of duplicate preparations for a given catalogue number (e.g. if a specimen has duplicates assigned to BRI, CANB and NSW, the quantity is ‘3’).

Description

A description specific to the individual duplicate or shipping material preparation (e.g. for shipping material, the description might denote the type of material (leaf material, anthers, etc.)).

Migration comments

This field is used to record any problems noted when data was imported into Specify from the Loans and Exchange database in April 2011. These comments generally relate to a discrepancy between the number of specimens noted in the Loans and Exchange database, and the number of records in the electronic file for the consignment.

Administrative fields

The following fields are automatically completed and cannot be edited.

Created by

The person who created the database record.

Created

The date the record was created.

Last edited by

The person who last edited the record.

Last edited

The date the record was last edited.

Databasing outgoing donations and exchange

How to process outgoing exchange, donation or shipping material

1. Create a record set for the preparations in the consignment using one of the following methods:

For large consignments (more than ten specimens):

- Open the **Record set creator** and scan barcodes into the **MEL barcodes** text box and select **Create record set**. You'll need to exit and log back into MELISR to access the record set.

OR

- Open the **Record set creator** and scan barcodes into the **MEL barcodes** text box. Select **Create barcode string**. Copy and paste the barcode string into the **Barcode** field (**Collection object** table) in the **Query builder**. Select 'In' as the **Operator** and run the query. Save the results as a record set by clicking on the **Record set** symbol in the results bar.

OR

For small consignments (fewer than ten specimens):

- Open the **query builder** and select the **Barcode field** from the **Collection object** table. Select 'In' as the **Operator** and scan the barcodes into the search box (use a comma between each barcode). Run the query and save the results as a record set by clicking on the **Record set** symbol in the results bar.

Note: multiple record sets can be added to a gift record.

2. In MELISR, click **Interactions** in the task bar
3. Click **Gift** in the side bar
4. Select **Record sets** when prompted to choose source of preparations
5. Select the relevant record set
6. Select the **preparation type** and **quantity** for each preparation by either:
 - Manually flagging each preparation
 - OR
 - **Select all**, then **Save** the Gift record. Open the herbarium transactions page (<http://10.15.15.99/melisr/index.php/transactions>), select the relevant exchange consignment from the list and click on **Clever button thing**. This will remove any silica gel sample preparations as well as non-giftable preparations (e.g. sheet, packet, spirit, etc.). You will still have to check the **Gift** record and manually remove any other preparations that are not included in the consignment (e.g. Seed duplicates).
Note: only ‘Duplicate’, ‘Seed duplicate’, ‘Silica gel sample’ and ‘Shipping material’ preparations should be added to Gift records.
7. Enter details in the following fields:
 - **Category**
 - **Description**
 - **Gift agent(s) Name(s) and Role(s)**
 - **Sent to**
 - **Date sent**
 - **Prepared by**
 - **Method**
 - **Reference no(s)**
 - **Number of parcels**
 - **Weight**
 - **Postage**
 - **Comments** – e.g. notable damage to a specimen
8. **Save** the form. Select **Exit** when prompted to print a Gift invoice
9. Open the **Exchange metadata** page (<http://10.15.15.99/melisr/index.php/exchangedata>) and select the relevant exchange consignment from the **Exchange** drop-down list
10. If the consignment contains records that have been created or edited on the day they’re being sent, click on the **Update BioCASE** button
11. Select the **Output format** (refer to the agent record to check which file type to send) and press **Submit**
12. Name the file using the gift number (e.g. MEL exchange 1602 PAL) and save it to the relevant folder in S:\COLLECT\Loans & exchange\Exchange\Outgoing exchange
13. Add the **File name** to the **Gift** record in MELISR
14. Open the herbarium transactions page (<http://10.15.15.99/melisr/index.php/transactions>) and select the relevant exchange consignment from the drop-down list
15. Select ‘Exchange paperwork’ and print three copies – one each on white, yellow and pink paper. The white and yellow copies are sent with the consignment (box 1) and the pink copy is attached to the paperwork kept at MEL.
16. Save a copy of the exchange paperwork as a PDF file to email to the recipient institution

- 17.** Select ‘List of preparations’ and print two copies (one to send with the consignment and one to retain at MEL). Printed double-sided if necessary.
- 18.** Select ‘Parcel labels’ and print the required number
- 19.** Using the HerbMEL account, email the exchange paperwork and data to the recipient institution (refer to the agent record for contact details). Record the file name in the subject line (e.g. MEL exchange 1602).

How to enter outgoing shipping material using a dummy record

MEL occasionally ships specimens, samples or other materials that are not linked to MEL specimens (e.g. recently collected non-MEL specimens, unvouchered pollen samples). In such cases, a dummy record needs to be used in order to create a **Gift** record:

- 1.** Open the dummy record MEL 999999A in MELISR and edit the preparation type and quantity in accordance with the type and quantity of material to be sent
- 2.** Open the **Interactions** module and click **Gift** in the side bar
- 3.** Select **Enter Catalogue Numbers** when prompted to choose source of preparations
- 4.** Enter 999999A
- 5.** Select the **Preparation type** and **Quantity** and follow steps 7 and 14–19 as above
- 6.** Return to the **Gift** record, delete the dummy preparation and save the record.

Deleting preparations from a gift record

The Curation Co-ordinator and Curation Officers can delete preparations from a gift. A preparation should only be deleted from a gift before the consignment is dispatched (except in the case of shipping material consignments created using a dummy record). See the Curation Co-ordinator if a preparation needs to be deleted after a consignment has been sent.

Sending silica gel samples as shipping material

Where material from a silica gel sample is sent to a researcher to be used for destructive sampling, the silica gel sample preparation should be added to the relevant **Gift** record (i.e. there is no need to create a separate shipping material preparation). When adding silica gel sample preparations to a **Gift** record, each preparation needs to be flagged manually. Do not ‘Select all’ and use the ‘Clever button thing’, as this will delete the silica gel sample preparations from the record.

If the entire silica gel sample is used, the quantity in the silica gel sample preparation record should be changed to ‘0’ after the material is sent. If only part of the silica gel sample is used, the quantity will need to be adjusted retrospectively to reflect the number of consignments of shipping material that the silica gel sample preparation is linked to (e.g. if material from a single silica gel sample preparation is sent to two separate researchers, and there is still material at MEL, the quantity in the silica gel sample preparation record should be ‘3’).

Remember to follow the destructive sampling procedure when processing material, including filling in the **Destructive sampling** fields in the **Conservator event** table.

Incoming exchange

Incoming consignments of exchange, donations and shipping material are recorded in the **Exchange In** table.

Exchange In form

Exchange in

Exchange number

The MEL reference number for a given consignment of incoming exchange, donation or shipping material. The exchange number is generated automatically when a record is saved. The same sequence is used for both incoming and outgoing consignments (i.e. gift numbers and exchange numbers are allocated sequentially).

Date received

The date on which the consignment was checked and processed at MEL.

Category

The category of material received. The following options are in the pick list:

- Donation – specimens received from an institution (or individual) with which MEL does not have a formal exchange agreement
- Exchange – duplicate specimens received from an institution with which MEL has a formal exchange agreement
- Shipping material – material that will not be accessioned at MEL (e.g. material for destructive sampling).

Processed by

The Curation Officer(s) who processed the consignment. If the consignment was prepared by more than one Curation Officer, they should be entered as a ‘Group agent’. *Note:* consignments received prior to May 2011 are all flagged as being processed by Alison Vaughan as this field was not recorded in the previous Loans and Exchange database.

Received from

The institution from which the consignment was received. This corresponds to **Last name** in the **Agent** table and is formatted as the herbarium code followed by ' -- ' then the title of the institution (e.g. CANB -- Australian National Herbarium).

Date sent

The date on which the consignment was sent to MEL (as noted on the paperwork received with the material).

Quantity

The number of specimens (or samples) in the consignment.

Description

A short summary of the contents of the consignment. For example:

- 'Miscellaneous vascular plants and cryptogams'.

File name

The file name for electronic data for the specimens in the consignment.

Administrative fields

The following fields are automatically completed and cannot be edited.

Created by

The person who created the database record.

Created

The date the record was created.

Last edited by

The person who last edited the record.

Last edited

The date the record was last edited.

Databasing incoming exchange, donation or shipping material

1. Open MELISR and click **Interactions** in the task bar
2. Click on **Exchange In** in the side bar
3. Enter details in the following fields:
 - **Exchange number**
 - **Date received**
 - **Category**
 - **Processed by**
 - **Received from**
 - **File name**
 - **Date sent**
 - **Quantity**
 - **Description**
4. Save the form
5. Record the exchange number (MEL ref. no.) in red pen on the top right-hand corner of the paperwork.

Non-MEL loans

The non-MEL loan database is in a separate collection from the main MELISR database. To access the non-MEL loans module, log into MELISR and select ‘non-MEL loans’ in the **Choose a Collection** window.

Non-MEL loan form

Loan

MEL reference number

A four-digit reference number allocated when a loan is received at MEL. This field fills automatically when a new loan record is created.

Loan status

The current status of the loan. The following values are available in the pick list:

- Requested – formal loan request sent but specimens not yet received at MEL
- Current – all specimens still at MEL (or some returned and confirmed as received)
- Returning – all or some specimens returned but not confirmed as received
- Complete – all specimens returned and confirmed as received
- Written off – all specimens lost or destroyed.

Quantity outstanding

The number of specimens currently on loan (i.e. the quantity borrowed minus the quantity returned). For loans with loan preparations, **Quantity outstanding** is calculated automatically when a new **Shipment** record is added (i.e. when a return or transfer is processed).

Loan number

The loan number allocated by the lending institution. The loan number is automatically prefixed with the abbreviation of the lending institution when the record is saved (e.g. BM 2626M).

Quantity borrowed

The number of specimens received in the loan.

Received

The date on which the loan was checked and acknowledged at MEL.

Current due date

The date by which the loan is to be returned. The loan period is generally 12 months from the date of receipt, unless specified otherwise. The **Current due date** will be the same as the **Original due date** unless the loan has been extended.

Original due date

The date by which the loan is to be returned. The loan period is generally 12 months from the date of receipt, unless specified otherwise.

Loan closed

A check box used to indicate that all specimens have been returned (or transferred) and acknowledged.

Taxa

The families and genera or taxa in the loan. Taxa should be entered in the following formats:

For loans containing multiple taxa:

- MOSS: Aloina, Crossidium, Desmatodon, Tortula
- ASTERACEAE: Abrotanella, Arrhenechthites, Bedfordia, Brachylottis, Crassocephalum, Delairea, Emilia, Erechtites, Euryops, Gynura, Othonna, Roldana, Vernonia

For loans containing a single taxon:

- MYRTACEAE: Eucalyptus globulus

- MYRTACEAE: Isotype of Eucalyptus globulus.

Conditions

Any special conditions specified by the lending institution. For example:

- ‘Six month loan period’
- ‘Destructive sampling permitted subject to K destructive sampling policy’.

Comments

Any comments pertinent to the loan. For example:

- ‘Released from quarantine NM12000784’
- ‘44 received 02/07/2001. 3 received 12/02/2003.’
- ‘1 packet and 32 spirit’
- ‘41 packets and 108 sheets (306 specimens)’.

Loan transfer

Details of loan transfers, both to and from MEL. For example:

- ‘Transferred from CANB’
- ‘Transferred to AD’.

Extension

A summary of loan extensions requested and granted. For example:

- ‘12 month extension granted 13/10/2005. 12 month extension requested 02/11/2007.’

Extension requested

The date of the most recent request to extend the loan.

Loan extended

A check box used to indicate that the most recent request for extension has been granted.

Old MEL ref.

The MEL ref. no. for loans that pre-date the current MEL ref. sequence. For example:

- ‘Page 15’.

Loan agents

Agent

The institution from which the loan originated (lending institution) and the MEL botanist(s) and student(s) on behalf of whom the loan was requested.

Role

The role of the agent in the loan. The following values can be selected from the pick list:

- Botanist
- Lending institution
- Student.

Note: The loan agents should ideally appear in the following order: Lending institution, Botanist, Student. The loan agents currently appear in random order, and the order changes every time the record is saved.

Shipments

The **Shipment** table provides a record of all returns and/or transfers for a given loan.

Note: Loans that have been returned or transferred in parts have multiple shipment records. It's easiest to view these in grid form. Multiple shipment records should ideally appear in reverse chronological order, but they currently appear in random order.

Shipped to

The institution to which the loan was returned or transferred.

Shipment no.

An auto-generated identifier for the shipment.

Date sent

The date on which the consignment was processed at MEL.

Prepared by

The Curation Officer(s) who processed the return of the loan.

Method

The method by which the loan was shipped. The pick list values relevant to loans are:

- Air Mail – Customs Insured (loans to overseas institutions)
- Collected from MEL
- Courier
- Express Post
- Hand delivered
- Registered Post (loans to Australian institutions)
- Sea Mail – Customs Insured (very large or heavy loans to overseas institutions)
- Transfer.

Reference no(s)

The tracking number for each parcel in the shipment. Tracking numbers should be scanned from the consignment note or label (e.g. Registered Post label, Pack & Track International consignment note), rather than entered manually. Multiple numbers should be separated by commas.

Quantity sent

The number of specimens in the consignment.

No. parcels

The number of parcels in the consignment. This number should correspond to the number of reference nos.

Weight

The total weight of all the parcels in the consignment.

Postage

The total shipping cost for the consignment.

Comments

Any comments pertaining to the return of the loan. For example:

- ‘Spirit material’
- ‘Sent with MEL exchange 1234’
- ‘Sent with H loan 12/07 (MEL ref. 1234)’.

Acknowledged

The date on which the consignment is confirmed as received. *Note:* this is a text field but dates should be entered in dd/mm/yyyy format.

Administrative fields

The following fields are automatically completed and cannot be edited.

Created by

The person who created the database record.

Created

The date the record was created.

Last edited by

The person who last edited the record.

Last edited

The date the record was last edited.

Creating and editing non-MEL loans

Entering a new non-MEL loan

New non-MEL loan records are created by the Curation Co-ordinator when the Collections Manager requests a loan:

1. Log in to MELISR and open the *non-MEL loans* collection
2. Open the **Interactions** module
3. Click **Loan w/o Preps** in the side bar
4. Enter the following details:
 - **Loan status** – ‘Requested’
 - **Taxa**
 - **Conditions**
 - **Comments**
5. Add **Loan agents (Lending institution, Botanist(s) and Student)**
6. Delete the blank **Shipment** record
7. Save the **Loan** record.

Processing an incoming non-MEL loan

1. Open the online **Loans** processing tool
(<http://10.15.15.99/melisr/index.php/loanreturn/loans>)
2. Find the relevant loan using the **Find loan** function

- Select ‘non-MEL loans’ the relevant Institution and ‘Requested loans’ and press **Submit**
 - Select the relevant loan based on the Botanist (and/or Student) and click on ‘Borrower’ to check that the taxa accord with the loan paperwork and specimens.
3. Log in to MELISR and open the *non-MEL loans* collection
 4. Find and open the loan record by entering the MEL ref. no. in the **Simple Search** box. (*Note:* **Simple search** needs to be configured for non-MEL loans).
 5. Select **Edit** and enter the following details:
 - **Loan number**
 - **Current due date**
 - **Loan status** – ‘Current’
 - **Date received**
 - **Original due date**
 - **Quantity outstanding**
 - **Quantity borrowed**
 - **Taxa** – if different to what was recorded when loan was requested
 - **Conditions** e.g. permission for destructive sampling
 - **Comments** – if required
 6. Save the record
 7. If the loan contains specimens with barcodes, scan them in via the **Borrower** (<http://10.15.15.99/melisr/index.php/borrower/>):
 - Select the relevant **MEL reference number** from the drop-down list
 - Scan the specimens into the **Enter barcodes** box (one barcode per line)
 - In the **Add preparations** box, select the relevant **Preparation type** and **Curation Officer** (if the loan contains more than one type of preparation, you will need to scan them in multiple batches)
 - Click **Add to loan**
 - In lieu of marking off specimens on the loan list, annotate paperwork with ‘[no. specimens] received via Borrower, [date and initials]’.

Returning a non-MEL loan without associated loan preparations

1. Log in to MELISR and open the *non-MEL loans* collection
2. Find and open the loan record by entering the MEL ref. no. in the **Simple Search** box. (*Note:* **Simple Search** needs to be configured for non-MEL loans).
3. Select **Edit** and create a new **Shipment** record
4. Enter the following details:
 - **Shipped to** – this should always be the lending institution unless the loan is being transferred
 - **Date sent**
 - **Prepared by**
 - **Method**
 - **Reference no(s)**
 - **Quantity sent**
 - **No. parcels**

- **Weight**
 - **Postage**
 - **Comments**
5. Edit **Loan status** to 'Returning'
 6. Save the record
 7. Check that **Quantity outstanding** has updated automatically and that it accords with the loan paperwork
 8. Create paperwork for the consignment using the **Herbarium transactions paperwork** page: <http://10.15.15.99/melisr/index.php/transactions>
 9. Create a PDF of the paperwork and email it to the relevant Curator via the HerbMEL account
 10. Print three copies of the paperwork (pink copy to be retained at MEL, white and yellow copies to be sent with specimens).

Returning a non-MEL loan with associated loan preparations

1. Open the **Borrower**: <http://10.15.15.99/melisr/index.php/borrower/>
2. Select the relevant **MEL reference number** from the drop-down list
3. Scan the specimens into the **Enter barcodes** box (one barcode per line)
4. In the **Return preparations** box, select the relevant **Curation Officer** and edit the **Return date** if necessary (default is the current date)
5. Select **Prepare for return** and check that the relevant preparation and quantities are flagged in the loan preparation list
6. Select **Return**. The Borrower automatically adds a new shipment record to the relevant non-MEL loan record. Several fields need to be updated in MELISR.
7. Log in to MELISR and open the *non-MEL loans* collection
8. Find and open the loan record by entering the MEL ref. no. in the **Simple Search** box. (*Note: Simple Search needs to be configured for non-MEL loans; refer to MELISR Manual*).
9. Select **Edit** and enter the following details in the relevant **Shipment** record:
 - **Method**
 - **Reference no(s)**
 - **No. parcels**
 - **Weight**
 - **Postage**
 - **Comments**
10. Save the record
11. Check that **Quantity outstanding** has updated automatically and that it accords with the loan paperwork
12. In lieu of marking off specimens on the loan list, annotate paperwork with '[no. specimens] returned via Borrower, [date and initials]'
13. Create paperwork for the consignment using the **Herbarium transactions paperwork** page: <http://10.15.15.99/melisr/index.php/transactions>
14. Create a PDF of the paperwork and email it to the relevant Curator via the HerbMEL account
15. Print three copies of the paperwork (pink copy to be retained at MEL, white and yellow copies to be sent with specimens).

ATTACHMENTS

Attachment metadata workbench

The **Attachment metadata workbench** allows you to easily add and edit metadata for attachments, without opening each attachment in Specify. You can download a metadata spreadsheet for a batch of attachments, add missing metadata and/or edit existing metadata, then upload the metadata into MELISR. Note that you cannot use the **Attachment metadata workbench** to add new attachments to MELISR; they must have already been uploaded.

The screenshot shows the Attachment metadata workbench interface. At the top, there is a navigation bar with links: Labels | Numbers | Record set creator | Storage families | Fancy quality control machine | Attachment metadata. Below the navigation bar, the title "Attachment metadata workbench" is displayed. The interface includes several search and filter options:

- User name: (select a user) ▾
- Attachments added on or after (yyyy-mm-dd): 2014-05-21
- Attachments added before (yyyy-mm-dd): (empty field)
- Check for all attachment records with insufficient metadata
- Filter by attachment records with missing values in:
 - Copyright holder
 - Copyright date
 - Restrictions
 - Credit
 - Photographer
 - Context
 - Licence
- Extra fields: (select) ▾
 - taxon name
 - collector
 - collecting number
- Output format: HTML table ▾ Get attachment metadata

At the bottom left, there is a link: Upload file with attachment metadata.

The URL for the **Attachment metadata workbench** is
<http://10.15.15.99/melisr/index.php/imagemetadata>.

Downloading attachment metadata

To download metadata for a batch of attachments:

1. Select your Specify user name from the drop-down list
2. In the **Attachments added on or after** and **Attachments added before** fields, enter the date span in which the attachments requiring metadata were added to MELISR
 - You can limit your attachment records to those with insufficient metadata to be used for anything other than viewing in MELISR by ticking the **Check for all attachment records with insufficient metadata** box
 - Alternatively, you can limit your records to those missing certain pieces of metadata using the **Filter by attachment records with missing values in** option (selecting multiple fields will include records with no data in one or more of the fields selected)
 - You can include other fields from the specimen record in your metadata file for reference by selecting them in the **Extra fields** box. Hold the **Ctrl** key down to select more than one field. Note that these will all be ignored when the file is uploaded, so you can't use the **Attachment metadata workbench** to edit data in these fields.
3. Select the **Output format**. HTML table will provide a preview of the results in your browser.
4. Click **Get attachment metadata** to download the metadata file.

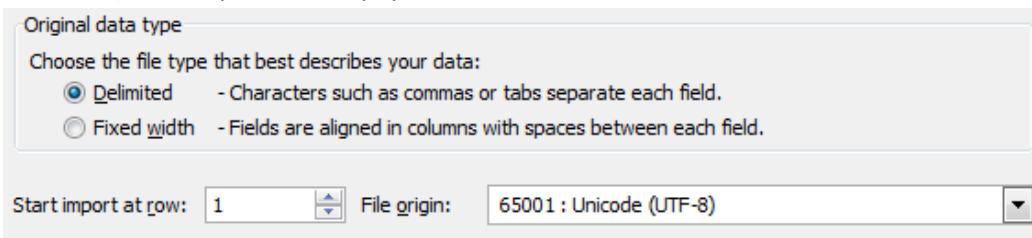
Editing attachment metadata

To edit the metadata file:

1. Open the attachment metadata file from within Excel or another text editor; don't open the file from the file manager. **If you open the file from the file manager, any special characters (umlauts, accents etc.) will be corrupted in Excel.**
 - If the file doesn't appear in the file browser, check that it is looking for all files, not just Excel files:



- In the **Text Import Wizard**, ensure that 'Delimited' is selected, and change the **File origin** to UTF-8 (this will preserve any special characters in the metadata):



2. Add or edit the metadata fields. Refer to the instructions for entering metadata in the **Note** that the file path is not case-sensitive on Windows computers.

3. Attachment and Error! Reference source not found. tables, and note the following:
 - You can change an attachment from a **Collection object attachment** to a **Collecting event attachment** (and vice versa) by changing the table name in the **Table** column. Make sure you spell the table name correctly, and use maximal capitals, i.e. ‘Collection Object’, ‘Collecting Event’.
 - Do not edit the **GUID** column as it is used to match the rows in the spreadsheet to records in the database
 - Data in the **CatalogNumber**, **MimeType**, **AttachmentLocation**, **Title**, **Created** and **CreatedBy** columns will be ignored when the file is uploaded, so those columns should not be edited
 - The **Modified** and **ModifiedBy** values will be automatically updated when the metadata is uploaded, so there’s no need to edit those columns
 - If you delete data from a field for an individual record, the value of that field will be cleared when the metadata file is uploaded.
4. Save the file once you’ve finished editing the metadata.

Uploading attachment metadata

To upload the edited metadata into MELISR:

1. On the **Attachment metadata workbench** page, click on **Upload file with attachment metadata**. This will open the **Upload attachment metadata** page.
2. Select your Specify user name from the drop-down list
3. Click on **Choose file** and navigate to the metadata file you wish to upload
4. Click **Submit** to load the file.
 - A record set will be created for the records in the upload file (if you’re already logged in to Specify when you upload the file, you’ll need to log out and back in before you can see the record set).

Attachment tools

The **Attachment tools** in Specify allow you to view all attachments in the workspace, open associated specimen records in form view, and import either single attachments or multiple attachments in a single action.

Open the **Attachment tools** by clicking the **Attachment** button on the task bar.

Four functions appear on the side bar:

- Show all attachments
- Show all images
- Import images
- Import image index

Show all attachments/Show all images

Click **Show all attachments** (or **Show all images**) in the side bar to browse thumbnail representations of all attachments (or just the image attachments) relevant to the current collection.

Note: Thumbnails are created for JPEG and PNG files and most PDFs. Other file types are represented by a default thumbnail based on their file type.

Image viewing controls

The following controls are available in the **Attachments** results view:

Symbol	Location	Action
	next to thumbnail	Displays information about the associated record, and allows the record to be opened in form view
	next to thumbnail	Opens the associated record in form view. Also indicates the table to which the attachment is linked.
	bottom of workspace	Displays some of the associated record information and displays the latitude and longitude from the associated Locality record on a map
	bottom of workspace	Displays attachment metadata from the original file when available. <i>Note:</i> Metadata captured at the time a digital photo is taken may include the date, and latitude/longitude. The metadata information may be stripped from the file when the image is loaded into an outside program such as a web-based image storage facility. Some file types such as PNG, BMP and GIF contain little or no metadata.
	bottom of workspace	Opens the Specify Help page for the Attachment tools

Viewing attachments

To display a larger version of the image within Specify:

- Double-click an individual image thumbnail to display it in a new tab in the workspace

To open an image in an image viewer :

1. Double-click an individual image thumbnail to display it in a new tab in the workspace
2. Right-click on the image and click **Open in external viewer**. The image will either open in your default image-viewing program, or you will have the option of selecting an external viewer from the file manager.

To open a non-image file in its native program:

- Double-click a non-image file to open it in its native program.

Exporting attachments

To export an attachment:

1. Right-click on the thumbnail and click **Export attachment**
2. Navigate to the folder you want to export the attachment to, and click **Save**.

Import attachments

The **Import attachments** tool allows multiple attachments to be associated to records by matching attachment names within a directory to a unique field within an existing record. For example, attachments can be linked to records within the **Collection object** table by giving the attachment files names that correspond to the **Catalogue number** or the **MEL number**. The **Import attachment** tool also gives you the option of linking files to records by ‘Field number’ (**Collecting number**), but these are not unique within MELISR, so cannot be used for this purpose. You can also link attachments to **Taxon** records by using the taxon **Full name**.

Table	Unique field value	File name example
Collection object	Catalogue number	2374514A.jpg
Collection object	MEL number	5142.jpg
Taxon	Full name	Crowea exalata subsp. magnifolia.png

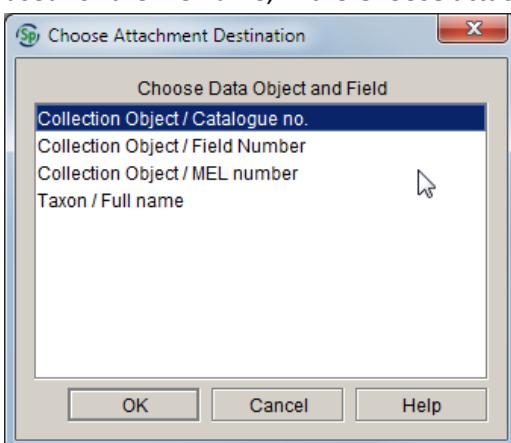
Multiple attachments can be associated to the same record by adding a number to the end of the **Catalogue number** in the file name. Note that you can't add multiple attachments to the same record if you are using **MEL number** as the unique field value.

Unique field value	Example of file names for multiple attachments
Catalogue number	2374514A1.jpg, 2374514A2.jpg, 2374514A3.jpg

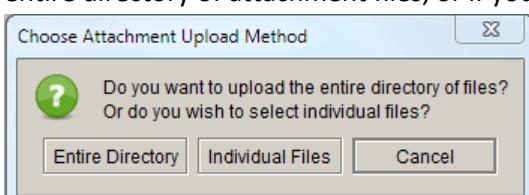
Importing attachments

To import attachments:

1. Click **Import attachments** in the side bar
2. Select the table that you want to link attachments to, and the unique field value that you've used for the file name, in the **Choose attachment destination** window:



3. Click **OK**
4. In the **Choose attachment upload method** window, choose whether you want to upload an entire directory of attachment files, or if you want to select individual files:



Note that you can select more than one file if you choose 'Individual files'.

5. Navigate to the files or folder that you want to upload and click **Open**. Specify will display a message once the upload is complete, and details of any file upload issues will be reported in a browser window.

Import attachment mapping file

The **Import image mapping file** tool allows multiple files to be attached to **Collection object** records in Specify by associating the files with the **Catalogue number** or **MEL number**, or to **Taxon** records by associating the files with the taxon **Full name**. This method of importing of multiple attachments is the preferred option when the attachment files have not been pre-named with the **Catalogue number** or **MEL number**. The **Import attachment mapping file** tool also gives you the option of linking files to records by ‘Field number’ (**Collecting number**), but these are not unique within MELISR, so cannot be used for this purpose.

An image mapping file is used to create the association between the attachment file and the unique field value. Note that you can only map to one field in each mapping file (i.e. either **Catalogue number**, **MEL number** or taxon **Full name**), and not to a combination of fields. The file must first be created in a spreadsheet program, then saved as either a tab-delimited or CSV file.

The mapping file must contain two columns: the first column records the unique field value within a record (i.e. **Catalogue number** or **MEL number**), and the second column includes the name of the attachment file:

	A	B
1	Catalogue number	File name
2	2062140A	IMG_1155.jpg
3	2062140A	IMG_1156.jpg
4	0015428A	notes.doc
5	0655148B	1161 colour sketch.jpg

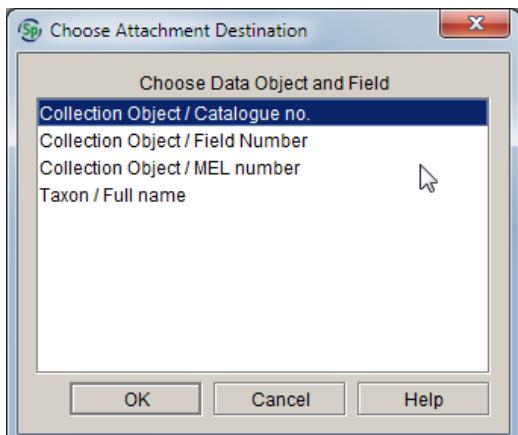
	A	B
1	MEL number	File name
2	2154874	habitat.png
3	12145	0049_001.pdf
4	336548	Fungi pictures.doc
5	7748	95.773.jpg

The unique field value and file names must match the respective field values and file names exactly, and the mapping file must be located in the same directory as the attachment files. More than one attachment can be associated with the same unique identifier, and the same attachment can be added to more than one record.

Importing attachments

To import an attachment mapping file:

1. Click **Import attachment mapping file** in the side bar
2. Select the table that you want to link attachments to, and the unique field value that you’ve used for the file name, in the **Choose attachment destination** window:



3. Click **OK**
4. Navigate to the attachment mapping file in the file manager and click **Open** (remember that the attachment files must be in the same directory as the mapping file).
Specify will display a message once the upload is complete, and details of any file upload issues will be reported in a browser window.

DNA SEQUENCES

Uploading DNA sequences

DNA sequences for both MEL specimens and specimens from other herbaria can be uploaded into MELISR using a comma-delimited text (CSV) file by going to <http://10.15.15.99/melisr/index.php/dnasequence> in your favourite browser.

The DNA sequence data is added to two tables: **Preparation** and **DNA sequence**.

The CSV file

CSV files are most easily created and edited in a spreadsheet program like Microsoft Excel or LibreOffice/OpenOffice Calc. A CSV file for uploading sequences into MELISR at a minimum consists of a column with catalogue numbers, *CatalogNumber*, and one or more columns (one column for each marker) with *GenBank accession numbers*.

Standard columns

If you want to include data in the following columns, the column headers have to exactly match those listed below. Any other column headers will be interpreted as markers (see below). Note that the *CatalogNumber* column is mandatory, but the other columns are optional. If you need additional columns for your own use, please let Niels know; additional columns can be added easily enough, but we need to make the upload script ignore them so they don't add to the processing time.

CatalogNumber

The *Catalogue number* or barcode. For MEL specimens, use the MEL number – i.e. without the suffix for the part. Make sure you have a space between the ‘MEL’ prefix and the number, as it is needed to recognise it as a MEL collection (and not a MELU one, for example). For collections of other Australian herbaria, it is best to use the *Catalogue numbers* used in AVH.

SampleNumber

The number of your DNA sample. If this has been filled in, a **Preparation** record with preparation type *Molecular isolate* will be created. You can already upload the Preparation record when you don't have sequences yet by leaving the marker fields blank.

PreparedBy

The name of the person who prepared the DNA sample. This is not a required field, but since the DNA samples are curated by yourself and the numbers are your own, it is strongly recommended for

the benefit of other Specify users and the Collections Branch. You can enter a default value in the next step, so you don't need to have it in your CSV file.

PreparedDate

The date the DNA isolation was done.

Sequencer

The name of the agent responsible for the sequence. This is more important for records of GenBank accession numbers we receive with returned loans. For these records it is probably best to enter the name of the institution the loan is returned from, rather than the person who did the sequencing. Also for this field a default value can be entered in the next step and, as with all **Agent** fields, a group of names can be entered.

Project

The name of the project as a part of which the sequence was made. Sequences don't have to belong to a project, but adding it to a project will be nice for future reference (and for other users) and will make it easier to retrieve your sequences from MELISR in a search. Projects need to be created in MELISR first before you can add sequences to them. You can read further down how to create a new **Project** record in MELISR.

BOLDSampleID

The identifier for the sample as used in the Barcode of Life Database (BOLD). This is your sample number with a suffix added by BOLD. This field will be useful mainly while we don't have a BOLD barcode yet.

BOLDBarcodeID

The BOLD ID for the DNA barcode.

TaxonName

The taxon name. This is for your own use only.

Marker columns

Any column header that is different to those listed above will be considered a marker and the column will be expected to contain GenBank accession numbers.

You can have multiple columns with *GenBank accession numbers*, one column for each marker. You can also have an 'unknown' marker, if the marker has not been supplied – which will mostly be the case for GenBank accession numbers that come with returned loans. If there is more than one

sequence for the same marker and the same specimen, just create a new row for each sequence. Multiple columns with the same header will create an uncaught error. You can also use multiple rows for the same *Catalogue number* if the data in any of the other columns is different.

When uploading the data from the CSV file, the content of the marker columns (or columns assumed to be markers) are tested against GenBank, and the data won't be uploaded if they are not valid GenBank accession numbers.

Adding new data to the CSV file

Preparation and **DNA Sequence** records will only be created once, so you can keep re-uploading the same CSV file over and over when new information is added. This means you can add data as it becomes available, rather than waiting until it is all ready (e.g. you can add a Sample number before you have sequences, or a GenBank accession number before you have a BOLD barcode). Also, if you have made an error in one of the non-identifier columns (i.e. any column other than *CatalogNumber*, *SampleNumber*, *BOLDSampleID* or *BOLDBarcodeID*), you can just change it in the CSV file and upload the file again.

Uploading DNA sequence data

The upload process consists of two steps.

Step 1

DNA sequences

You can add sequences to MELISR here by uploading a CSV file with catalogue numbers and Genbank accession numbers. A link to an example CSV file is provided below. Only the *CatalogNumber* column is required. *SampleNumber*, *PreparedBy*, *PreparedDate*, *Sequencer*, *Project*, *BOLDSampleID*, *BOLDBarcodeID* and *TaxonName* are optional. Column headers have to match exactly the headers given above; columns with any other headers will be considered markers. The taxon name is for your own use only and is not uploaded. If a Sample number is given, a Preparation record with prep type 'Molecular isolate' will be created, which you can query on in MELISR. Molecular isolate preparations may be uploaded without sequences and sequences may be uploaded without preparations. DNA Sequence and Preparation records will only be created once, so you can keep using the same spreadsheet.

You can upload sequences for both MEL and non-MEL collections here. Sequences for collections that are not from MEL will be loaded into the non-MEL collection, which is the collection we use to record incoming loans. If you don't have access to this collection you can ask one of the MELISR administrators for access.

The upload process comprises two steps. On this page you can select your *Specify* username from the drop-down list and select the file you want to upload. On the next page you can review the columns you are uploading and set default values for some of the columns.

[Example CSV file](#)

Specify user*

File* No file chosen

In the first upload step, apart from the CSV file, you also need to select a *Specify user*. Just select your username from the dropdown list. You do need a *Specify* user account to be able to upload sequences into MELISR, but you do not need editing privileges.

Specify user*

File* sequences_test.csv

When both fields have been filled in, you can hit ‘Continue’.

Step 2

When a sequence file is uploaded, the first thing the script does is parse and analyse the first row of the spreadsheet to establish what information it should get from which columns. The results of this are given back to the user to verify in Step 2.

Specify user*

	Column	Default value
Catalogue number	0	
Sample number	1	
Prepared by	2	
Prepared date	3	
Sequencer	4	
Project		
BOLD barcode ID		
BOLD sample ID		
Markers	rbcL	6
	matK	7
	rpL32-trnL	8
	ITS	9
	ETS	10
	bvgnhj	11

The table in the form at Step 2 indicates what information is found in which column (columns are numbered from 0).

As indicated above, any column header that is not recognised by the script is considered to be a marker. MELISR has a pick list with DNA markers. If a marker is not in the pick list, it will be indicated in the table. You can safely upload sequences with markers that are not in the pick list, as long as you have established that it is indeed a new marker, but a marker won’t display in the Specify form and you won’t be able to query for it unless it is in the pick list. You can add a new marker to the pick list on the [Markers](#) page. See ‘Add a new marker’ for more details.

You can enter default values for the *PreparedBy*, *PreparedDate*, *Sequencer* and *Project* columns. Default values will be used when a column is not in the spreadsheet or when a cell in a column is empty. Agent names – *PreparedBy* and *Sequencer* – need to be spelt exactly as in the **Agent** table.

No special code has been written yet to convert dates, so the only dates that can be uploaded for *PreparedDate* are complete dates in ISO date format ('yyyy-mm-dd').

Sequences – or the **Collection Objects** sequences are derived from rather – can be added to a sequencing **Project**. **Collection Object** records can only be linked to a **Project** if the project is already in the database. You can check what projects are in the database and add new projects on the [Projects](#) page. See ‘Add a new project’ for more details.

When you are satisfied that you are loading the correct data, hit *Continue*.

Specify user*		nielsk ▾
	Column	Default value
Catalogue number	0	
Sample number	1	
Prepared by	2	Birch, J.L.
Prepared date	3	
Sequencer	4	Birch, J.L.
Project	5	GrassBoL
BOLD barcode ID	7	
BOLD sample ID	6	
	rbcL	9
	matK	10
Markers	rpL32-trnL	11
	ITS	12
	ETS	13

Continue **Cancel**

Now the real work starts for the upload script. The script will do the following for each row in the spreadsheet:

1. First, the script will look up the *Catalogue number* in MELISR. If a MEL number can't be found an error will be recorded and the script will move on to the next row. If a *Catalogue number* of a non-MEL collection can't be found a new **Collection Object** record will be created in the *Non-MEL loans* collection and a warning will be recorded.
2. If a *SampleNumber* has been provided, the script will look for a **Preparation** with the same *Sample number* for the same **Collection Object** (*Sample numbers* do not have to be unique across the database). If such a **Preparation** cannot be found, a new **Preparation** record of type *Molecular isolate* will be created. If a **Preparation** already exists, the script will update the *Prepared by* and *Prepared date* fields if required.
3. For each *GenBank accession number* the script will look if a **DNA Sequence** record already exists. If it does, the script will check if any of the *Sequencer*, *BOLD sample ID* or *Bold barcode ID* fields need to be updated.
If a **DNA Sequence** record does not already exist, the script will try to retrieve the sequence from GenBank, using one of the GenBank web services. Only if a sequence can be retrieved from GenBank, a new **DNA Sequence** record will be created. If the sequence cannot be retrieved, a warning will be recorded.

4. If a **Project** has been provided, the script will try to link the **Collection Object** record to a **Project**. The **Project** has to exist in MELISR. If the **Project** does not exist a warning will be recorded.

When the script has finished – for initial uploads of largish data sets this may take a while because of the GenBank requests – a report of all the errors and warnings recorded during the running of the script and all the actions undertaken will be sent back to the screen.

Errors

Catalogue number		Error
MEL 2377035	error	Catalogue number not in MELISR.
MEL 570131	error	Catalogue number not in MELISR.
MEL 570134	error	Catalogue number not in MELISR.

Info.

Catalogue number		Error
AD 108301	info	Molecular isolate Preparation record iAF71 already exists.
AD 108301	info	Molecular isolate Preparation record iAF71 has been updated.
AD 108301	info	AD 108301 has been added to project 'GrassBoL'.
AD 226779	info	Molecular isolate Preparation record iAF67 already exists.
AD 226779	info	Molecular isolate Preparation record iAF67 has been updated.
AD 226779	info	AD 226779 has been added to project 'GrassBoL'.

Adding a new marker

New markers can be added to the pick list on the [Markers](#) page,
<http://10.15.15.99/melisr/index.php/dnasequence/markers>.

Markers

Marker	In pick list	Number of sequences
ETS	✓	111
ITS	✓	114
matK	✓	115
rbcL	✓	112
rpL32-trnL	✓	113

Add new marker

Specify user*	<input type="text"/>
Marker*	<input type="text"/> <input type="button" value="Add"/>

First on the page is a table showing how many sequences are in the database for each marker and whether the marker is in the pick list.

To add a new marker, just select a *Specify user* from the drop-down list and enter the name of a marker in the *Marker* field in the form under ‘Add a new marker’. Click ‘Add’ when you are done. The new marker will show in the table immediately.

Adding a new project

New projects can be added to MELISR on the [Projects](#) page,
<http://10.15.15.99/melisr/index.php/dnasequence/projects>.

DNA sequencing projects

Project name	Number of sequences
GrassBoL	565

Add new project

Specify user*

Project name*

As on the **Markers** page, there is first a table with projects and the number of sequences belonging to each project. These numbers won’t be entirely accurate if the same specimen has been sequenced for multiple projects.

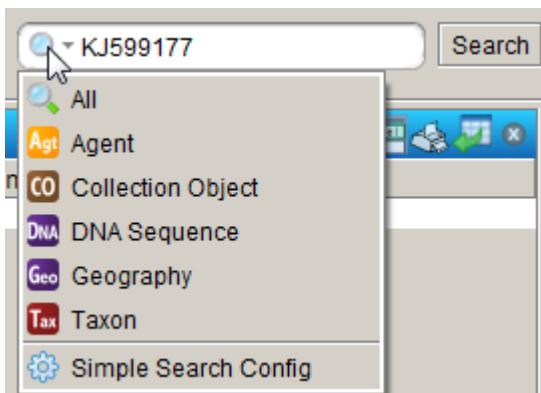
You can add a new project by filling in the fields in the form below and clicking ‘Add’. The new project will show in the table immediately.

Working with sequences in Specify

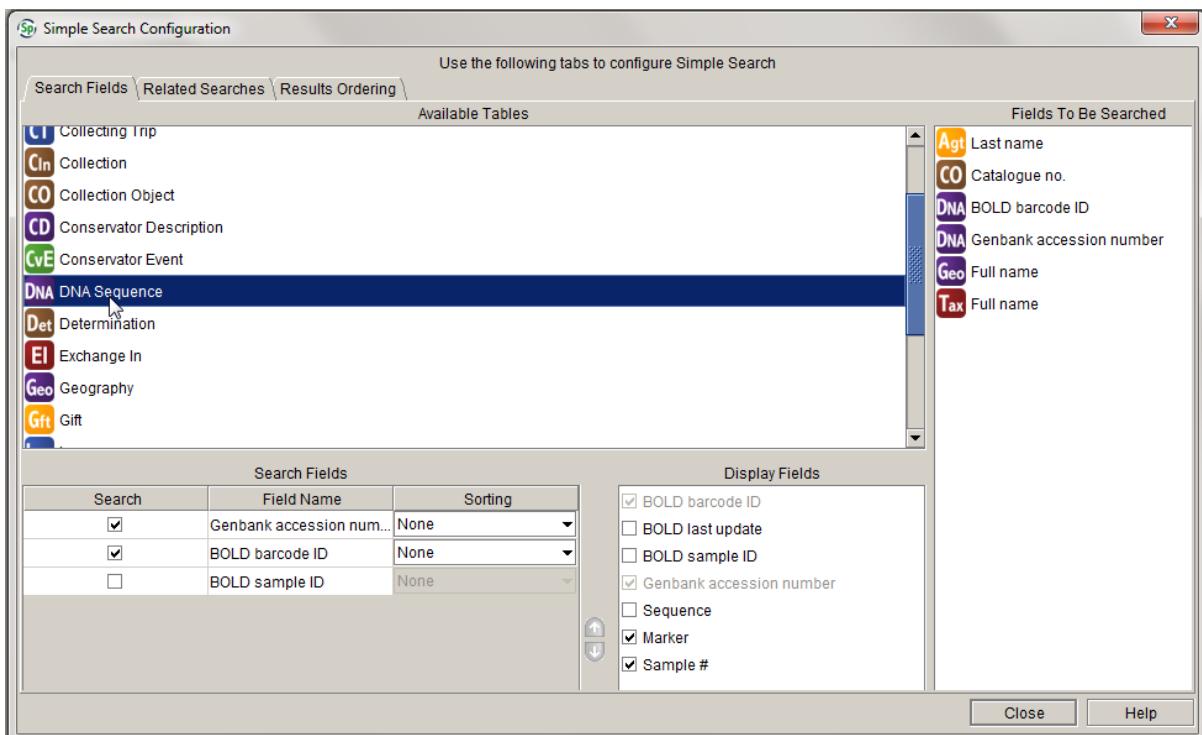
Finding sequences

Simple search

You can configure Simple search to find DNA sequences by *GenBank accession number* or *BOLD barcode ID*. To do so, open the Simple search configuration window, by clicking on the down arrow in the Simple search box in the top right-hand corner of your screen and select ‘Simple Search Config’ from the dropdown that will appear, as shown below.



In the window that appears (see below), select ‘DNA Sequence’ in the *Available Tables* pane, tick the fields you want the **Simple search** to be able to search on under *Search Fields* and additional fields you want to be displayed in the result under *Display Fields*. There are no *Related Searches* for **DNA Sequences**, so if you want to find sequences by a particular person, or of a particular taxon or from a geographic region, you have to use the Specify Query.



Query

The **Query module** section of the MELISR Manual (p. 104 onwards) details how to use the query in Specify. The best way to query for sequences in MELISR is as a **Collection Object** query:

		Not Operator	Criteria	Sort	Show Prompt	Always		
	Catalogue no.	<input type="checkbox"/> Contains ▾	<input type="text"/>	<input checked="" type="radio"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	
	Project name	<input type="checkbox"/> Contains ▾	<input type="text"/> GrassBoL	<input checked="" type="radio"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	
	Preparation type	<input type="checkbox"/> Contains ▾	<input type="text"/> Molecular isolate	<input checked="" type="radio"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	
	Number	<input type="checkbox"/> Contains ▾	<input type="text"/>	<input checked="" type="radio"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	
	Prepared by [Formatted]			<input checked="" type="radio"/>				
	Prepared date	<input type="checkbox"/> = ▾	<input type="text"/>	<input checked="" type="radio"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	
	Current	<input type="checkbox"/> Yes ▾		<input checked="" type="radio"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	
	Full name	<input type="checkbox"/> Contains ▾	<input type="text"/>	<input checked="" type="radio"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	
	Country	<input type="checkbox"/> Contains ▾	<input type="text"/>	<input checked="" type="radio"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	
	DNA sequences [Aggregated]							

Things to look out for are:

1. Only include the *Project name* field if you want to query on a project. If you include the field and leave it blank you'll still only get **Collection Objects** that have been assigned to a **Project** in your result.
2. This query will return one row for each **Collection Object**, because an aggregator on the **DNA Sequence** table has been used. A potential drawback of this is that you cannot query for only **Collection Objects** that have sequences. You can get around this to some extent by, in the search result, ordering the rows on the aggregated *DNA sequences* field and select only those rows that have a value in this field before you open the **Collection Object** form. If you really want only records with sequences in your result set, you have to include one or more fields from the **DNA Sequence** table in your query, but as soon as you do that you'll get a separate row for each sequence.

The results of the example query above are displayed below. You can open view details of records in the result by clicking on the **Collection Object form** button (where the mouse pointer is).

▼ Search Results - 454								
Catalogue no.	Project name	Number	Prepared by [Formatted]	Prepare...	Full name	Country	DNA sequences [Aggregated]	Collection Ob
0039900A	GrassBoL	iAC08	Birch, J.L.		Poa cookii	Australia		
0112799A	GrassBoL	iAE28	Birch, J.L.		Poa mollis	Australia	ETS: KJ599061 ITS: KJ599...	
0113076A	GrassBoL	iAE53	Birch, J.L.		Poa hothamensis var. parviflora	Australia		
0222049A	GrassBoL	iAE46	Birch, J.L.		Poa phillipsiana	Australia		
0223963A	GrassBoL	iAD43	Birch, J.L.		Psilurus incurvus	Australia		
0223992A	GrassBoL	iAH44	Birch, J.L.		Sclerochloa dura	Australia		
0225155A	GrassBoL	iAD36	Birch, J.L.		Cynosurus cristatus	Australia		
0225727A	GrassBoL	iAB85	Birch, J.L.		Briza minor	Australia		
0225734A	GrassBoL	iAB86	Birch, J.L.		Briza minor	Australia	ETS: KJ599006 ITS: KJ598...	
0225832A	GrassBoL	iAH41	Birch, J.L.		Puccinellia fasciculata	Australia		
0225866A	GrassBoL	iAH50	Birch, J.L.		Vulpia myuros f. megalura	Australia		
0225887A	GrassBoL	iAH49	Birch, J.L.		Vulpia myuros f. myuros	Australia		
0225891A	GrassBoL	iAD25	Birch, J.L.		Vulpia myuros f. myuros	Australia		
0225901A	GrassBoL	iAD14	Birch, J.L.		Vulpia ciliata	Australia	ETS: KJ599045 ITS: KJ598...	
0242835A	GrassBoL	iAH4	Birch, J.L.		Cynosurus cristatus	Australia		
0247784A	GrassBoL	iAC11	Birch, J.L.		Poa costiniana	Australia	ETS: KJ599011 ITS: KJ598...	
0250000A	GrassBoL	iAC00	Birch, J.L.			Australia	ETS: KJ599000 ITS: KJ598...	

You can't query for MEL and non-MEL sequences at the same time, as they are stored in different collections in Specify, the MEL collections in the *National Herbarium of Victoria* collection and the non-MEL ones in *Non-MEL loans*. However, if you save a query in one collection, you can use the same query in the other. If you don't have access to the *Non-MEL loans* collection, ask one of the MELSR administrators to let you in.

The DNA sequence form

The **DNA Sequence form** can be opened from the **Collection Object form** by clicking on the *DNA* button in the group of buttons near the bottom of the form:



In the **DNA Sequence form** you can link out to the information on the sequence in GenBank by clicking on the *Weblink* button:

Typically, you won't need to do any editing in the **DNA Sequence form**, as everything can be done in the CSV file you upload, but, if you have updated a sequence in GenBank, and you want the updated sequence in MELISR, you can ask a MELISR administrator for access. Deletion of sequence records from MELISR is something that has to be done by a MELISR administrator.

QUERYING

Querying Specify

One of the benefits of databasing specimens is the ability to query for and retrieve specimen information efficiently and effectively. Specify has two search functions: a **Simple search**, which enables quick searches on pre-indexed fields, and a **Query builder**, which allows for more structured and comprehensive querying of specimen data. Query results can be viewed in the workspace, saved as a record set, printed or exported as a spreadsheet. The main tables that are used for querying are the **Collection object**, **Taxon** and **Agent** tables.

When querying Specify, it is important to bear in mind that several records in some tables in the database (such as **Agent** and **Determinations**) may be linked to the one **Collection object** record, so the one specimen record may appear more than once in your results. If fields from the **Determinations** table are included in the query output, records that match the query terms – and which have more than one determination – will appear more than once in the results grid. For example, MEL 50834 has a det. for *Eucalyptus glaucescens* Maiden & Blakely by J.H. Willis, as well as a conf. by M.I.H. Brooker. A query for **Catalogue number** = ‘0050834A’ that includes the (Taxon) **Full name** in the query output will return two results for the same record in the results grid, because the collection object that matches the search criteria is linked to two records in the **Determinations** table:

The screenshot shows the Specify Query builder interface. The search criteria are:

Table	Field	Operator	Value	Sort	Show	Prompt	Always
CO	Catalogue no.	Contains	0050834a	<input checked="" type="radio"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Tax	Taxon name [Formatted]			<input type="radio"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Tax	Family	=		<input type="radio"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Tax	Full name	Contains		<input type="radio"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Det	Current			<input type="radio"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>

The results grid shows:

Catalogue number	Taxon name [Formatted]	Determinations [Aggregated]	Det. type
0050834A	<i>Eucalyptus glaucescens</i> Maiden & Blakely	<i>Eucalyptus glaucescens</i>	Det.
0050834A	<i>Eucalyptus glaucescens</i> Maiden & Blakely	<i>Eucalyptus glaucescens</i>	Conf.

If, however, the **Current** (determination) criteria is set to ‘Yes’, the record will only appear once in the results grid, as the query is only searching for the records where the current determination matches the search criteria:

The screenshot shows the Specify Query builder interface. The search criteria are the same as the previous one, but the 'Current' determination criteria is set to 'Yes'.

The results grid shows:

Catalogue number	Taxon name [Formatted]
0050834A	<i>Eucalyptus glaucescens</i> Maiden & Blakely

Similarly, if a **Collection object** query includes the collectors’ names in the query output, records for specimens with more than one collector will be duplicated in the results. For example, MEL 241014

was collected by A.C. Beaglehole with E.G. Errey as an additional collector. A query for **Catalogue number** = '0241014A' that includes (Collector) **Last name** in the query output will return two results for the same record in the results grid, because the collection object that matches the search criteria is linked to two records in the **Agent** table:

The screenshot shows the Query interface with two search criteria defined:

- Catalogue no.**: Contains 0241014a
- Last name**: Contains (highlighted)

The results grid displays two rows:

Catalogue no.	Last name
0241014A	Beaglehole
0241014A	Errey

If the **Is primary** field is included in the query with the **Operator** set to 'Yes', the matching collection object record will only appear once in the results, because there is only one primary collector linked to the record:

The screenshot shows the Query interface with three search criteria defined:

- Catalogue no.**: Contains 0241014a
- Last name**: Contains
- Is primary**: Yes (highlighted)

The results grid displays one row:

Catalogue no.	Last name	Is primary
0241014A	Beaglehole	Yes

However, a record with more than one primary collector will always appear more than once in the query results if the (Collector) **Last name** field is in the query output. MEL 696791 was collected by L.A. Craven and C.R. Dunlop, who are both recorded as primary collectors. If (Collector) **Last name** is included in the query output, and **Is primary** is set to 'Yes', the record will be duplicated in the query results:

The screenshot shows the Query interface with three search criteria defined:

- Catalogue no.**: Contains 0696791a
- Last name**: Contains
- Is primary**: Yes

The results grid displays two rows:

Catalogue no.	Last name	Is primary	Collectors [Aggregated]
0696791A	Craven	Yes	Craven , L.A; Dunlop, C.R.
0696791A	Dunlop	Yes	Craven , L.A; Dunlop, C.R.

If, however, the collectors are aggregated in the query output (by double-clicking on 'Collectors' instead of selecting fields from the **Agent** table), the record will only appear once in the query results:

The screenshot shows the Query interface with two search criteria defined:

- Catalogue no.**: Contains 0696791a
- Collectors [Aggregated]**

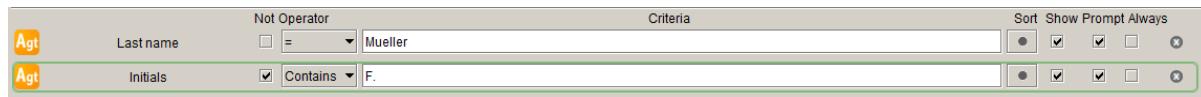
The results grid displays one row:

Catalogue no.	Collectors [Aggregated]
0696791A	Craven , L.A; Dunlop, C.R.

Query terms

Not

Checking the **Not** box will negate the **Operator**. For example, if the **Operator** is set to '=' and the **Not** box is checked, the query will return records that do not equal the value in the **Criteria** field:



This query will not return records where the collector's last name is Mueller, but the collector's initials do not contain 'F.':

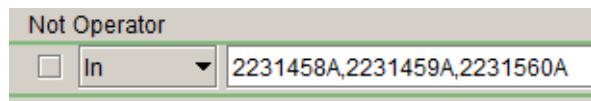
▼ Search Results - 18	
Last name	Initials
Mueller	U.I.
Mueller	T.
Mueller	R.
Mueller	M.M.

Operator

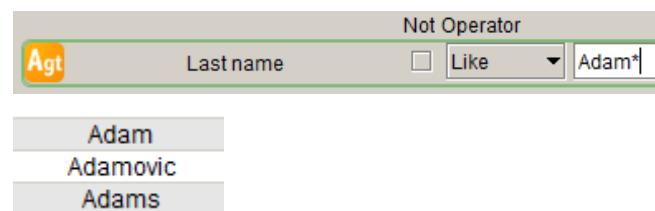
The **Operator** defines how the value(s) in the **Criteria** field should be interpreted. The following operators can be selected (note that not all operators are available for all field types):

Expression	Result	Available for
=	Finds all records for which the value of the selected field is equal to the specified criterion	Number, date and text fields
>	Finds all records for which the value of the selected field is greater than the specified criterion	Number and date fields
<	Finds all records for which the value of the selected field is less than the specified criterion	Number and date fields
>=	Finds all records for which the value of the selected field is greater than or equal to the specified criterion	Number and date fields
<=	Finds all records for which the value of the selected field is less than or equal to the specified criterion	Number and date fields
Between	Finds all records for which the value of the selected field is between the specified criteria	Number and date fields
In	Finds all records for which the value of the selected field is included in the list of criteria. Criteria in a list should be	Number and text fields

separated by commas:



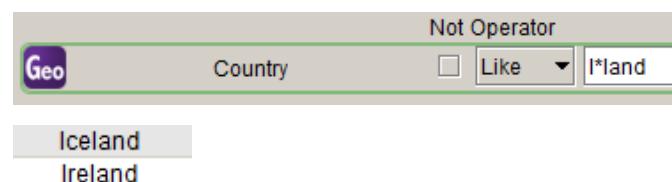
- Like** Finds all records for which the value of the selected field contains the pattern specified in the query term. A wildcard character (*) must be included in the query term to create the desired pattern. For example, the following query will return records for specimens where the collector's last name begins with 'adam':



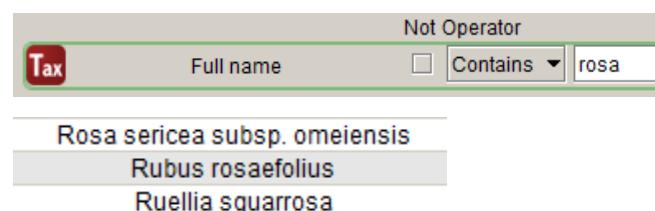
The following query will return records for taxa where the taxon name ends in 'folia':

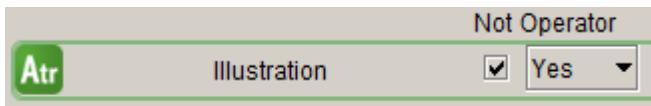


The following query will return records for all geographic place names that start with 'I' and end with 'land':



- Contains** Finds all records for which the value of the selected field contains a specified string of characters. The position of the query term in the field is not important. For example, the following query will find records where the **Taxon name** field contains 'rosa' at the start, the middle or the end of the locality description:



Empty	Finds all records for which the value of the selected field is empty. It is important to note that 'Empty' is a condition and not the same as leaving the Criteria field blank (if the Criteria field is left blank, the field will be included in the results, but not in the query).	Number fields, text fields and check boxes
Yes	Finds all records for which the check box for the selected field has been ticked	Check boxes
No	'No' is an option for check box fields, but it is not a very useful query term. If you wish to search for records for which a check box has not been ticked, use the 'Not' query term in combination with the 'Yes' operator. For example, the following query will return records for specimens that don't have an illustration:	Check boxes
		
Yes or Empty	Finds all records for which the check box for the selected field has either been ticked, or is empty	Check boxes
No or Empty	Finds all records for which the check box has not been ticked, or is empty (i.e. it includes records that might previously have been ticked, but have since been un-ticked)	Check boxes

Criteria

The **Criteria** box is used to enter the search terms for the field that is being queried.

Note that fields that are check boxes do not include **Criteria**, as all the possible values of the check box field are covered in the **Operator**.

Sort

The results of each field can be sorted in ascending or descending order, or left unsorted:

Symbol	Definition	Action
	Unsorted	Query results are unsorted
	Sort ascending	Query results are sorted in ascending order (A→Z; 0→99)
	Sort descending	Query results are sorted in descending order (Z→A; 99→0)

The default for **Sort** is unsorted. Click the **Sort** button to change it to ascending or descending.

Show

You can choose whether or not to display a field in the query form in the results. By default, all fields in a new query form are displayed in the results. Un-tick the **Show** box next to a field to exclude it from the results.

Note that the **Show** button has been un-ticked for most fields in the **Basic record info.** and **Template** queries. Remember to tick the **Show** box next to those fields that you want to see in the results grid.

Prompt

The **Prompt** command allows query terms to be customised when creating reports. It is not used for querying data.

Always

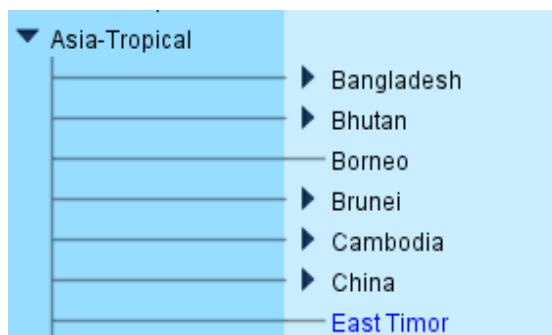
The **Always** command relates to report creation, and is not used for querying.

Search controls

Search synonyms

If **Search synonyms** is ticked, synonyms of the taxon name or geographic area name will be included in the query and the query results. The **Search synonyms** box is ticked by default.

For example: ‘East Timor’ has been added to the **Geography** table and synonymised with Timor-Leste (the blue text indicates that East Timor is a synonym):



A query for either ‘East Timor’ or ‘Timor-Leste’ will return records for both:

Collection object	Collecting event	Locality	Geography
Catalogue number	End date	Datum	Comments
Collecting event	End date (Day)	Geography	Continent
Collecting notes	End date (Month)	Latitude	Country
Collection object attribute	End date (Year)	Locality	County
Conservator descriptions	Habitat	Locality details	Full name
Created	Locality	Longitude	Name
Created by	Start date	Max. altitude (m)	Name on label
Descriptive notes	Start date (Day)	Min. altitude (m)	Preferred Geo

Not Operator: Criteria: Sort: Show Prompt Always
Geo Full name Contains Timor-Leste

Full name ▲
East Timor, Asia-Tropical
Timor-Leste, Asia-Tropical
Timor-Leste, Asia-Tropical
Timor-Leste, Asia-Tropical
Timor-Leste, Asia-Tropical
Timor-Leste, Asia-Tropical
Timor-Leste, Asia-Tropical
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Timor-Leste, Asia-Tropical
Timor-Leste, Asia-Tropical
Timor-Leste, Asia-Tropical

Distinct

If **Distinct** is ticked, only unique records are returned in the results. For example, the following query will produce a list of distinct years from the collecting date of specimens in MELISR collected by Ferdinand Mueller:

The screenshot shows the MELISR search interface. The search criteria are set as follows:

- Start date (Year)**: Set to "CE" with the operator "=".
- Agent [Formatted]**: Set to "Mueller".
- Last name**: Set to "Mueller".
- Initials**: Set to "F.". (Note: This field is labeled 'Initials' but contains a last name.)

At the bottom of the search interface, there are several checkboxes: Search Synonyms, Distinct, Count, and a **Search** button.

Because only distinct combinations of the values in the **Collector** and **Start date (Year)** fields are being returned, each year only appears once in the results:

Start date (Year)	Agent [Formatted]
1832	Mueller, F.
1842	Mueller, F.
1843	Mueller, F.
1844	Mueller, F.
1845	Mueller, F.
1846	Mueller, F.
1847	Mueller, F.
1848	Mueller, F.
1849	Mueller, F.
1850	Mueller, F.
1851	Mueller, F.
1852	Mueller, F.
1853	Mueller, F.
1854	Mueller, F.
1855	Mueller, F.
1856	Mueller, F.
1857	Mueller, F.
1858	Mueller, F.
1859	Mueller, F.
1860	Mueller, F.

If the **Distinct** box is not ticked, the same query returns a list of years from the collecting date of *all* specimens in MELISR collected by Mueller:

Search Results - 5000	
Start date (Year)	Agent [Formatted]
1832	Mueller, F.
1842	Mueller, F.
1843	Mueller, F.
1844	Mueller, F.
1845	Mueller, F.

When the **Distinct** option is selected, the query results can only be viewed in the workspace; they cannot be used to create a record set, nor can the results be viewed in data entry forms.

Count

If **Count** is checked, a count of the matching records will appear in a separate window in the workspace. The results grid will not be displayed when the **Count** function is active.

The screenshot shows a search interface with the following criteria:

- Start date (Year)**: Not Operator =
- Agent [Formatted]**: (empty)
- Last name**: = Mueller
- Initials**: = F.

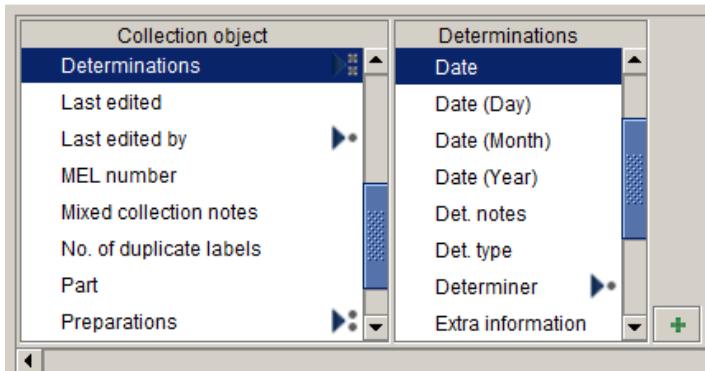
A modal dialog box titled "Search Complete" is displayed, stating "24121 matching records were located." with an "OK" button.

Search

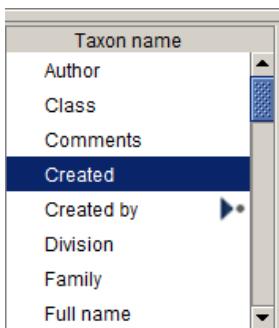
The **Search** button activates the query. Pressing **Enter** will also activate the query.

Querying dates

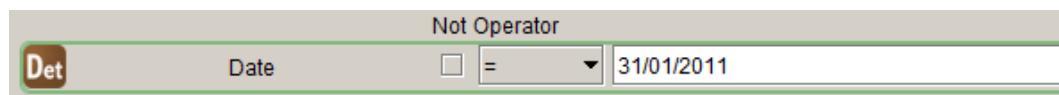
Dates that have a date type pick list next to the **Date** field (such as the determination date and the collecting date) can be queried as a full date, or by any combination of day, month and year:



Dates that only allow a full date to be entered (such as the date the record was created) can only be searched as a full date:



If querying by full date, the date entered must be formatted as dd/mm/yyyy (the query will not run if an incomplete date is entered):



Note that partial dates (i.e. a year only, or a month and a year) need to be stored as complete dates in the back end of the database (i.e. as a day, month and year), even though only part of the date is displayed in the front end. '01' is stored in the month and/or day field to complete partial dates. For example, a partial date that displays as '07/2007' is stored in the database as '01/07/2007' and a partial date of '2007' is stored in the database as '01/01/2007'. Therefore, if an exact date of '01/01/2007' is queried the partial date (2007) will be included in the results.

Querying by barcode

Barcode scanners can be used to input MEL numbers into the query form. Multiple MEL numbers can be queried by selecting the 'In' operator, and listing the MEL numbers in the **Criteria** field, separated by commas. MEL's barcode scanners are programmed to append a carriage return after the scanned data (which is equivalent to typing in a barcode and pressing **Enter**, which will activate the query). If you wish to enter more than one barcode in a search string, the barcode will need to be re-programmed to remove the carriage return.

Note that your query won't work if you scan barcodes into the **Catalogue number** field in the query form; they must be entered in the **Barcode** field.

To stop appending a carriage return to scanned data, scan the following code:



SET DEFAULTS

To append a carriage return to scanned data, scan the following codes in the order shown:



SCAN OPTIONS



<DATA><SUFFIX>



ENTER

Standard query forms

Four standard **Collection object** query forms have been created. Note that, while the standard query forms are useful for users unfamiliar with the database structure, they can be slow to run because they contain a lot of fields. It will generally be more efficient to build your own query that contains the fields you want to search by.

Catalogue number

The **Catalogue number** query allows you to search for records based on **Catalogue number**. If the **Operator** is set to 'Contains', you can enter the MEL number in the field (i.e. the **Catalogue number** without any leading zeroes), but be aware that you may get extra records in your results. For an exact match, set the **Operator** to '=' and enter the full **Catalogue number** (seven digits plus one letter).

CO	Not Operator	Criteria	Sort	Show	Prompt	Always
Catalogue number	<input type="checkbox"/> Contains	<input type="text"/>	<input type="radio"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

Basic record info.

The **Basic record info.** query allows you to search and retrieve basic record information for collection objects.

	Not Operator	Criteria	Sort	Show	Prompt	Always	X
CO Catalogue number	<input type="checkbox"/> Contains <input type="button" value="▼"/>	<input type="text"/>	<input type="radio"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Tax Taxon name [Formatted]	<input type="checkbox"/>	<input type="text"/>	<input type="radio"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Tax Family	<input type="checkbox"/> = <input type="button" value="▼"/>	<input type="text"/>	<input type="radio"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Tax Full name	<input type="checkbox"/> Contains <input type="button" value="▼"/>	<input type="text"/>	<input type="radio"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Det Current	<input type="checkbox"/> Yes <input type="button" value="▼"/>	<input type="text"/>	<input type="radio"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Agt Collectors/Last name	<input type="checkbox"/> Contains <input type="button" value="▼"/>	<input type="text"/>	<input type="radio"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Col Is primary	<input type="checkbox"/> Yes <input type="button" value="▼"/>	<input type="text"/>	<input type="radio"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
CE Collecting no.	<input type="checkbox"/> Contains <input type="button" value="▼"/>	<input type="text"/>	<input type="radio"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
CE Start date (Day)	<input type="checkbox"/> = <input type="button" value="▼"/>	<input type="text"/>	<input type="radio"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
CE Start date (Month)	<input type="checkbox"/> = <input type="button" value="▼"/>	<input type="text"/>	<input type="radio"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
CE Start date (Year)	<input type="checkbox"/> = <input type="button" value="▼"/>	<input type="text"/>	<input type="radio"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Geo Name	<input type="checkbox"/> Contains <input type="button" value="▼"/>	<input type="text"/>	<input type="radio"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Loc Locality	<input type="checkbox"/> Contains <input type="button" value="▼"/>	<input type="text"/>	<input type="radio"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Loc Latitude	<input type="checkbox"/> = <input type="button" value="▼"/>	<input type="text"/>	<input type="radio"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Loc Longitude	<input type="checkbox"/> = <input type="button" value="▼"/>	<input type="text"/>	<input type="radio"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Agt Created by/Last name	<input type="checkbox"/> Contains <input type="button" value="▼"/>	<input type="text"/>	<input type="radio"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
CO Created	<input type="checkbox"/> = <input type="button" value="▼"/>	<input type="text"/>	<input type="radio"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Agt Last edited by/Last name	<input type="checkbox"/> Contains <input type="button" value="▼"/>	<input type="text"/>	<input type="radio"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>

Note that, to reduce the chance of getting more than one result for a single collection object record, the **Current** (determination) and the **Is primary** (collector) fields are set to 'Yes'.

Created and Last edited

The **Created and Last edited** query is designed help you query for all the records you databased or edited on a single day, for quality control or label-printing purposes. **Created** and **Last edited** dates must be entered as full dates. You can use the '<', '>' or 'Between' operators to query for records databased or edited on more than one day. For example, to query for records that have been edited since the 1st of January 2010, set the **Operator** to '>' and enter '01/01/2010' in the **Criteria** box for the **Last edited** field:

CO	Last edited	<input type="checkbox"/> > <input type="button" value="▼"/>	<input type="text"/> 01/01/2010
----	-------------	---	---------------------------------

To query for all records edited in January 2010, set the **Operator** to 'Between' and '01/01/2010' and '31/01/2010' in the **Criteria** boxes for the **Last edited** field:

CO	Last edited	<input type="checkbox"/> Between <input type="button" value="▼"/>	<input type="text"/> 01/01/2010	and	<input type="text"/> 31/01/2010
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Data request

The **Data request** query is useful for extracting data to send to visitors or external researchers. Note that the **Current** determination field is set to 'Yes', so you will need to change that if you want to include type status determinations in the results.

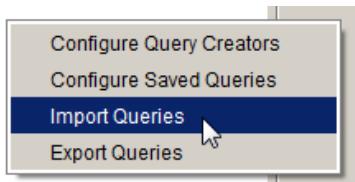
Importing standard queries

The standard queries are saved in the S:\PS&B\Specify\Queries folder. To import the queries into Specify:

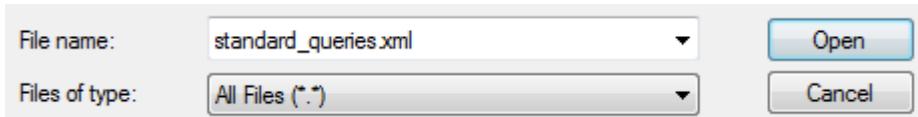
1. Open the **Query** module by clicking on the button in the task bar:



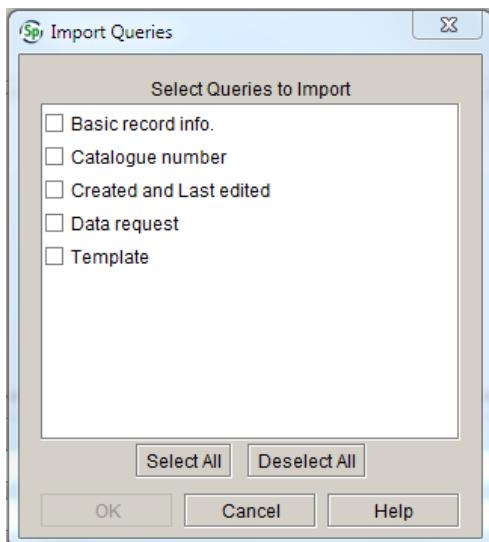
2. Right-click in the side bar under 'Saved Queries', then select 'Import Queries':



3. Navigate to S:\PS&B\Specify\Queries\standard_queries.xml and click **Open**:



4. Click **Select All** in the **Import Queries** window, then click **OK**:



After being imported, the queries will appear in the side bar.

Creating queries

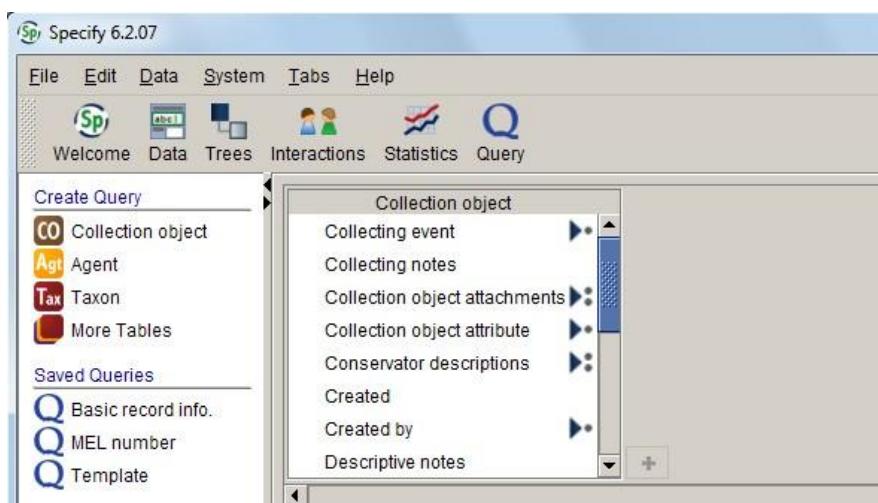
Queries can be made using the Specify **Query builder**, or modified from the query template.

Query builder

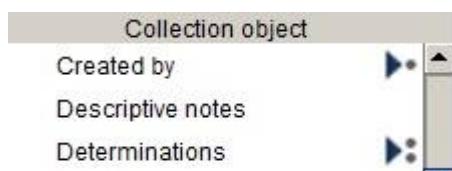
The **Query builder** allows you to select query fields from a primary table and its related tables.

To build a new query:

1. Select the table that you want to query in the side bar. The **Collection object** table is the main table used for querying specimen information. A list of fields and related tables will appear at the top of the workspace:

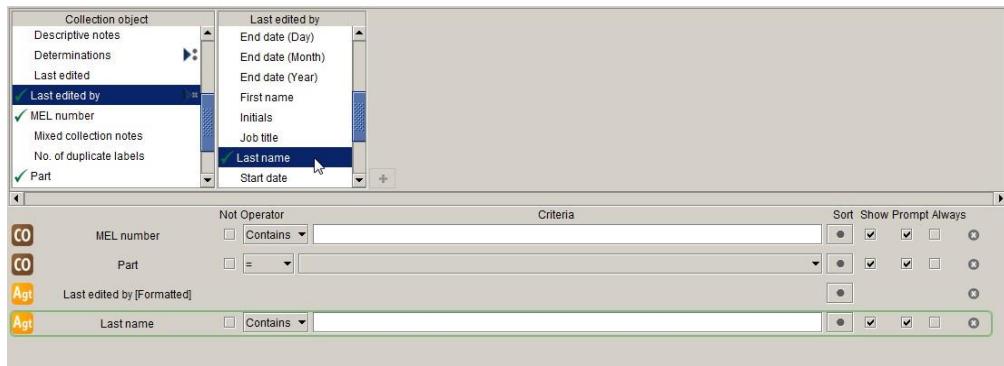


Related tables are indicated by an arrow to the right of the table name. One dot after the arrow indicates a one-to-many relationship between the related table and the primary table; two dots indicates a many-to-one relationship between the related table and the primary table:

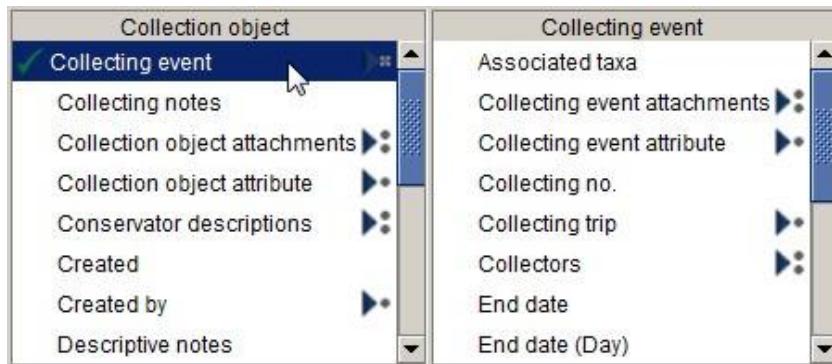


(Many collection objects can be created by the one person, and one collection object can have many determinations.)

2. Double-click on the fields that you want to include in your query. The field name will appear below the table list(s) in the workspace:



To display fields in other tables, single-click a table name in the field list:

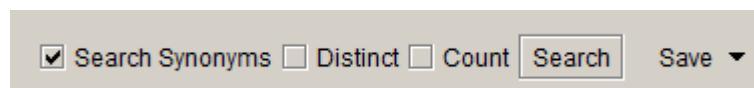


If you double-click on a table name, it will add an field containing aggregated data for that table to the query form. Search criteria cannot be entered for aggregated data fields, but the aggregated data will display in the results.

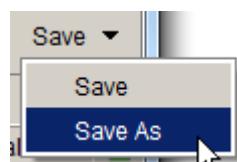
3. Bear in mind that for a field to be displayed in the query results, it must be listed in the query
4. There is no limit on the number of fields that can be added to a query, but larger, more complex queries will take much longer to run
5. Modify the query as required
6. Click the **Search** button to activate the query.

Saving queries

You can save a query by clicking the **Save** button at the bottom right-hand corner of the query screen.



If you have modified a query you can choose to save it as a new query, rather than overwriting the existing query, by selecting **Save As**:

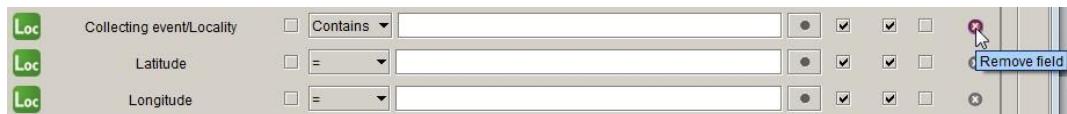


Query template

To use the **Query builder** most effectively, you need to have a good knowledge of the Specify data model. Users who are less familiar with the data model may wish to modify the query template. The query template lists most of the fields available in the **Collection object** table and related tables.

To modify the query template:

1. Click on **Template** in the side bar to open the query form
2. Click on the delete symbol at the right of the field name to delete unwanted fields:

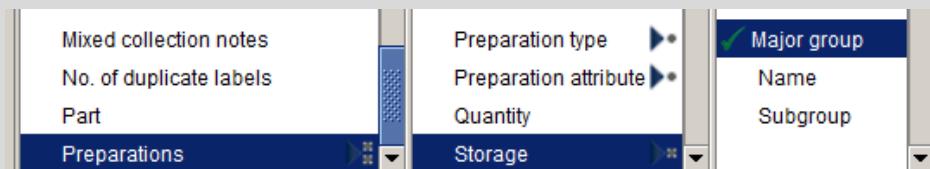


3. Modify the query syntax as required.

Tips for querying

Querying for major storage groups

Because not all the major storage groups (Fungi, Lichens, Dicots, Hepatics etc.) in the MEL collection are taxonomic groups, you can't easily search for a major group using the **Taxon** table. Instead, use the **Major group** field in the **Storage** table to search for storage groups:



The major group names are:

- A. Algae
- B. Bryophytes
- C. Hepaticas
- D. Dicots
- FER. Ferns
- F. Fungi
- G. Gymnosperms
- L. Lichens
- LYC. Lycophytes
- M. Monocots

Querying for type specimens

The easiest way to query for types is to use the **Det. type** field. Query for the name in the (Taxon) **Full name** field, and set **Det. type** to 'Type status':



If the **Current** determination field is in your query form, make sure it isn't set to 'Yes', as Type status dets are never set as the current determination.

Query results

Query results are limited to 20,000 records. A count of records matching the query term can exceed 20,000, but Specify can only display 20,000 result records at once. Use the **Count** function if you only want to know the number of records that match your query, otherwise break the query into smaller sections by adding more search terms. If you need to view more than 20,000 results, see the Collections Information Officer.

Viewing query results

Once a query is activated, the results are displayed in a grid in a separate query results tab. Only fields that were included in the query form are displayed in the results grid. The results can be sorted by clicking on the title bar of the field you wish to order by:

Collectors [Aggregated]	Collecting no.	Start date ▲	Locality
O'Shanesy, P.A.	27	01/01/1866	Rockhampton.
O'Shanesy, P.A.	16	01/01/1867	Rockhampton.
O'Shanesy, P.A.	1048	01/01/1869	Rockhampton.
O'Shanesy, P.A.	1708	01/01/1876	Gracemere.
O'Shanesy, P.A.	2045	01/01/1877	Blackwater Creek. Rockhampt
O'Shanesy, P.A.	3035	01/01/1877	Comet River.
O'Shanesy, P.A.	2051	01/01/1877	Blackwater Creek. Rockhampt
O'Shanesy, P.A.	3039	01/01/1878	Blackwater Creek. [There are .
O'Shanesy, P.A.	3033	01/01/1878	Blackwater Creek. [There are .
O'Shanesy, P.A.	4017	01/01/1879	Between Comet and Nogoa R
O'Shanesy, P.A.	4054	01/01/1879	Near Cometville [Comet]. Roc.
O'Shanesy, P.A.	4039	01/01/1879	Cometville. [Coordinates are f.
O'Shanesy, P.A.	39	01/02/1867	Near Table Mountain. Rockha.
O'Shanesy, P.A.	48	01/02/1867	Rockhampton.

Clicking the column header once will sort the results in ascending order (A→Z; 0→99); clicking the title again will sort the results in descending order (Z→A; 99→0).

Selecting records

Records in the results grid can be selected by pressing and holding the **Ctrl** key while clicking on records in the list:

Catalogue number
0041871A
0041892A
0041894A
0041895A
0230431A
0231115A
0231800A
0231898A
0231933A
0231998A
0232002A
0584472A
0584473A
0584474A
0584476A

You can select or deselect records by clicking the **Select all** or **Deselect all** buttons at the bottom of the query results:



Once records have been selected, you can use the results controls to perform further actions.

Results controls

Query results can be viewed and utilised in a number of ways using the controls on the results bar:

Symbol	Definition	Action
	Record set	Creates a record set from the selected records
	Attachments	Displays any attachments for records in the query results that are linked to the table that the query is based on
	Form	Opens the selected records in the relevant data form
	Print	Prints the selected records
	Export	Exports the results as a spreadsheet

Record set

Query results can be saved as a record set in the side bar. To create a record set:

1. Select the results that you want to save from the results grid. If you do not select any records, all records will be included in the record set.
2. Click the **Record set** symbol in the results bar:

Search Results - 553													
MEL number	Part	Taxon name ...	Collectors [A...]	Collectors/[L...]	Start date (D...)	Collecting no.	Start date (M...)	Start date (Y...)	Locality	Created by [F...]	Last modified [F...]	Actions	
41873	A	O'Shanesy, ...	O'Shanesy		6	67	6	1867	Rockhampto...	Thomas, J.E.	Naganowsk...		
41874	A	O'Shanesy, ...	O'Shanesy		6	207	6	1867	Rockhampto...	Thomas, J.E.	Naganowsk...		
41877	A	O'Shanesy, ...	O'Shanesy		6	208	6	1867	Rockhampto...	Thomas, J.E.	Naganowsk...		
230511	A	O'Shanesy, ...	O'Shanesy			61	3	1867	Rockhampto...	Pelina,	Pearce, E.		
230515	A	O'Shanesy, ...	O'Shanesy		1	74	12	1867	Gracemere...	Pelina,	Polikarpows...		
230516	A	O'Shanesy, ...	O'Shanesy		10	10	7	1867	Gracemere...	Pelina,	Polikarpows...		
231084	A	O'Shanesy, ...	O'Shanesy			60	3	1867	Rockhampto...	Pelina,	Alfaro, D.		
231124	A	O'Shanesy, ...	O'Shanesy			21	2	1867	Rockhampto...	Pelina,	Alfaro, D.		
705196	A	O'Shanesy, ...	O'Shanesy		1	73	12	1867	Rockhampto...	Pelina,	Alfaro, D.		
1609975	A	O'Shanesy, ...	O'Shanesy			6	1	1867	Near Rock...	Pelina,	Naganowsk...		
1613594	A	O'Shanesy, ...	O'Shanesy			68	3	1867	Rockhampto...	Pelina,	Naganowsk...		
1614168	A	O'Shanesy, ...	O'Shanesy		10	92	12	1867	Rockhampto...	Thomas, J.E.	Taylor, F.		
231866	A	O'Shanesy, ...	O'Shanesy		20	30	10	1867	Rockhampto...	Thomas, J.E.	Russell, J.		
1614143	A	O'Shanesy, ...	O'Shanesy			31	2	1867	Gracemere...	Thomas, J.E.	Taylor, F.		
231986	A	O'Shanesy, ...	O'Shanesy		6	204	6	1867	Rockhampto...	Thomas, J.E.	Currow, N.		
707237	A	O'Shanesy, ...	O'Shanesy		6	205	6	1867	Rockhampto...	Thomas, J.E.	Alfaro, D.		
231850	A	O'Shanesy, ...	O'Shanesy			7 (series 4)	1	1867	Rockhampto...	Thomas, J.E.	Alfaro, D.		
1614171	A	O'Shanesy, ...	O'Shanesy		12	8	7	1867	Rockhampto...	Thomas, J.E.	Naganowsk...		
1517651	A	O'Shanesy, ...	O'Shanesy		6	IV 31	6	1867	Gracemere...	Thomas, J.E.	Crabbe, J.		
1517652	A	O'Shanesy, ...	O'Shanesy		6	IV 31	6	1867	Gracemere...	Thomas, J.E.	Crabbe, J.		
607897	A	O'Shanesy, ...	O'Shanesy		15	57	11	1867	Rockhampto...	Jones, G.	Paull, M.F.		
88529	A	O'Shanesy, ...	O'Shanesy		10	91	4	1867	Rockhampto...	Volunteers,	Naganowsk...		
19946	A	O'Shanesy, ...	O'Shanesy		1	156	6	1867	Rockhampto...	Volunteers,	Gallagher, C.		
88509	A	O'Shanesy, ...	O'Shanesy		8	210	8	1867	Rockhampto...	Jones, G.	Polikarpows...		
726467	A	O'Shanesy, P.	O'Shanesy		22	39	4	1867	Rockhampto...	Jolley, H.M.	Macheda, D.		
726468	A	O'Shanesy, P.	O'Shanesy		22	122	5	1867	Rockhampto...	Jolley, H.M.	Macheda, D.		
726630	A	O'Shanesy,	O'Shanesy		22	57	4	1867	Curtis Island...	Jones, G.	Macheda, D.		
1059204	A	O'Shanesy, P.	O'Shanesy		24	13	12	1867	Gracemere...	Dawson, H.	Polikarpows...		
1059205	A	O'Shanesy, ...	O'Shanesy			55	3	1867	Near Mount...	Dawson, H.	Polikarpows...		
1004794	A	O'Shanesy, ...	O'Shanesy		25	26	4	1867	Rockhampto...	Thomas, J.E.	Russell, J.		
990064	A	O'Shanesy,	O'Shanesy		46	142	4	1867	Rockhampto...	Thomas, J.E.	Taylor, F.		

- Enter a name for the record set and click **OK** or press **Enter**:



To add new records to an existing record set:

- Select the results that you want to add to an existing record from the results grid
- Click the **Record set** symbol at the bottom of the form:

Last name	Initials
Fitzgerald	K.
FitzGerald	K.J.
Fitzgerald	N.
Fitzgerald	R.
Fitzgerald	R.D.
Fitzgerald	S.
Fitzgerald	S.M.C.C.
Fitzgerald	W.
Fitzgerald	W.F.
Fitzgerald	W.M.
Fitzgerald	W.V.

Buttons at the bottom: Select All, Deselect All, Click to select Record Set or Drag to Record Set in sidebar.

- Click on the name of the record set that you want to add the records to and click **OK** or press **Enter**:

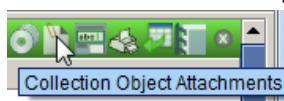


See [Using Record sets](#) for more information about working with record sets.

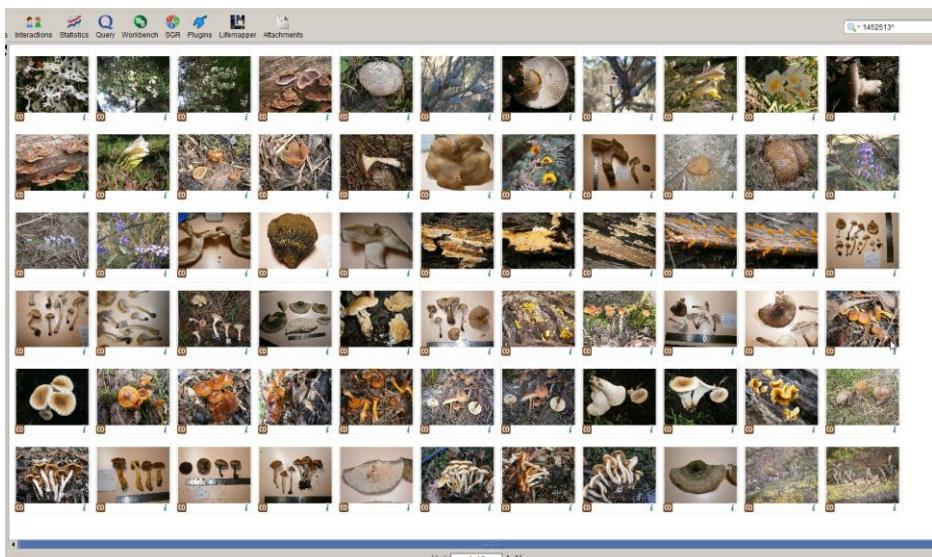
Attachments

You can view any attachments associated with the query results by clicking on the **Attachment** symbol:

- Select the results that you want to see attachments for from the results grid. If you do not select any records, all records will be included in the record set.
- Click the **Attachment** symbol in the results bar:

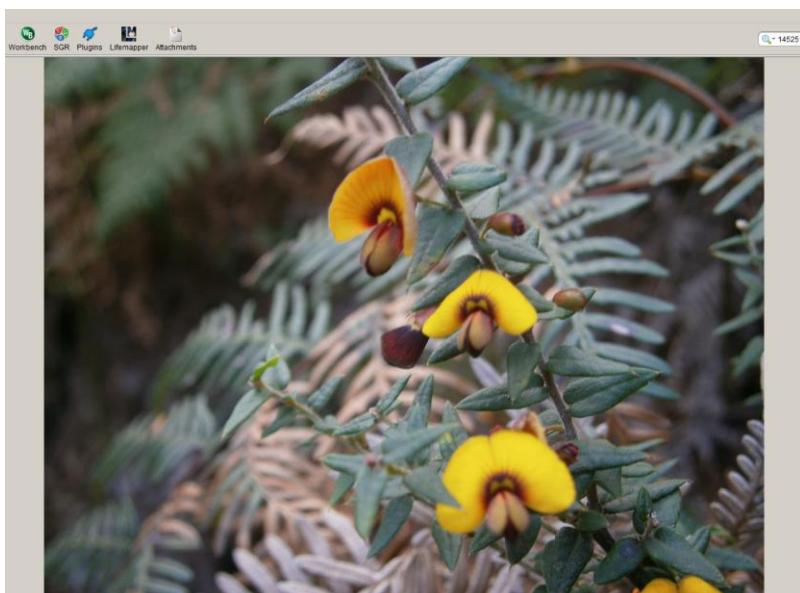


- An overview of the images associated with the results will open in a new tab:



4. From here you can examine the attachment information in three ways.

Double-clicking an image will open it in a new tab:



Clicking on the form icon underneath the image will open the associated record (in this case, the **Collection object** form):



Clicking on the **Information** symbol underneath the image will display a summary of the collecting information associated with the image:

Catalogue no.: 2371922A
 Field Number:
 Start date: 01/09/2013
 Locality: Rosebud, Mornington Peninsula, Arthurs Seat State Park, Northern side of circuit walk around McLaren's Dam.
 Latitude: -38.37508333
 Longitude: 144.93238889
 Geography: Victoria, Australia, 5. Australasia
 Taxon: Bossiaea cinerea
 Original file name: Fresh specimen - flowers.JPG

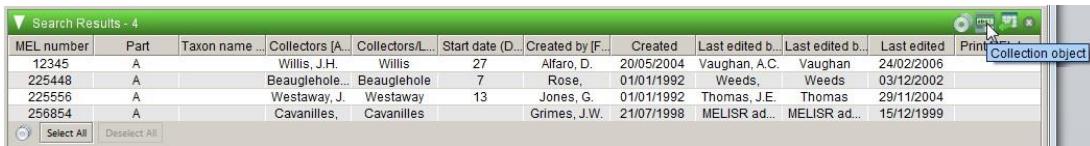
[Show Collection Object](#)

From here you can click on 'Show Collection Object' to open the full record in the **Collection object** form.

Form

Query results can be viewed in form mode by clicking on the **Form** symbol. The query results will open in the form that corresponds to the table that was queried (i.e. the results of a **Collection object** query will open in the **Collection object** form, and the results of an **Agent** query will open in the **Agent** form). To view results in a form:

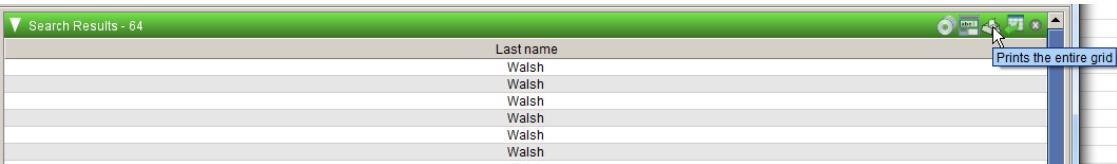
1. Select the results that you want to view from the results grid. If you do not select any records, all records will be included in the record set.
2. Click the **Form** symbol in the results bar:



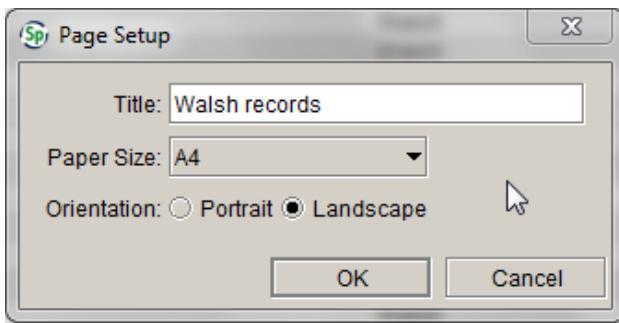
Print

Query results can be printed by clicking on the **Print** symbol. Note that all records in the results grid will be printed, regardless of whether or not certain records are selected. The results will be printed in the order they were retrieved; any subsequent sorting of the results in the grid will be ignored. To print results:

1. Select the results that you want to print from the results grid. If you do not select any records, all records will be included in the record set.
2. Click the **Print** symbol in the results bar:



3. In the **Page setup** window, enter a title, select the paper size and orientation, and click **OK**



4. A preview of the print file will open in the workspace. Only those fields included in the results grid will be printed.

5. Click the print icon to print the results to your local printer:

Export

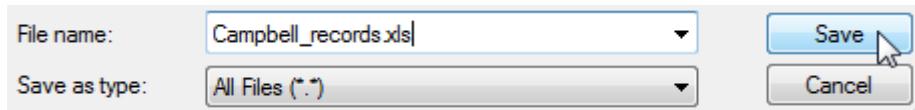
Query results can be exported by clicking on the **Export** symbol. Note that all records in the results grid will be exported, regardless of whether or not certain records are selected. To export results:

1. Click the **Export** symbol in the results bar:

Collecting ...	Start date ...	Start date ...	Geography...	Locality	Created by ...	Created by ...	Created	Last edited ...	Last edited ...	Last edited	Print MEL ...
s.n.	1890	1890	New South ...	Tooma Ra...	Jones, G.	Jones	01/01/1992	Hurley, M.	Hurley	30/08/2004	
s.n.	11	1890	Victoria, Au...	Werribee R...	Jones, G.J.	Jones	01/01/1992	Alfaro, D.	Alfaro	24/05/2002	
27			Victoria, Au...	Upper Mitta...	Petina,	Petina	01/01/1992	Gebert, W.A.	Gebert	08/12/2006	
s.n.			Victoria, Au...	Gippsland,	Petina,	Petina	01/01/1992	Alfaro, D.	Alfaro	26/04/2002	
731	2	1980	Victoria, Au...	Mt Buffalo, ...	Jones, G.	Jones	01/01/1992	Hennessy, ...	Hennessy	11/04/2006	

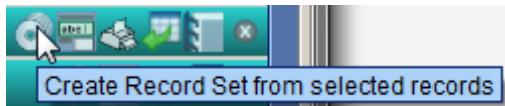
2. Enter a title for the file in the **Title** field, then click the **Browse** button to navigate to the directory in which you want to save the file:

3. Name the file and click the **Save** button. Note that the file name must include the file extension (e.g. xls, csv):



Using Record sets

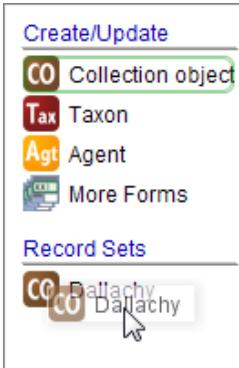
Record sets can be saved from the results of both a **Simple search** and a **Query** by clicking the **Record set** symbol in the results grid:



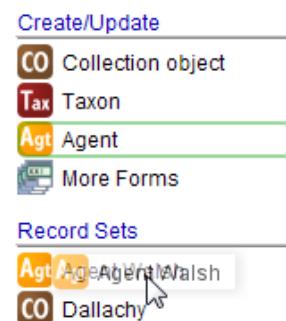
See [Record set](#) for instructions on how to save results as a record set.

Once a record set has been saved, it can be dragged and dropped on to items in the side bar for different modules. If you slightly drag a record set in the side bar, the items in the side bar that can interact with the record set will be highlighted with a coloured outline. For example:

- If you slightly drag a **Collection object** record set in the **Data** module, the **Collection object** form will be highlighted:



If you slightly drag an **Agent** record set in the **Data** module, the **Agent** form will be displayed:



Dragging and dropping a record set on an item in the side bar will open the records in the record set in the relevant form, interaction or plugin. For example, dragging an **Agent** record set on to the **Agent** form in the **Data** module will open the agent records for all the agents in the record set:

The screenshot shows a software interface for managing record sets. At the top, there's a section for 'Agent' with fields for Agent type (Person), Institution/Last name (Walsh), Title, First name, Initials, Abbreviation, E-mail, Job title, CITES no., Date type, Start, End, Comments, and a 'Web link' button. Below this is a section for 'Addresses' with fields for Attn, Address, Address 2, Address 3, Address 4, City, State, Post code, Country, Phone, Fax, and Exchange. There are also buttons for 'Is current', 'Start date', and a 'Grid' view. At the bottom of the form, there's a navigation bar with arrows and a '1 of 64' indicator. On the left side, there's a sidebar with a 'Attachments' section showing a file icon and '0' files.

The number of records in the record set will match the number of records displayed in the navigation bar at the bottom of the form. You can scroll through the records using the navigation controls.

Record set menu

The record set menu is accessed by right-clicking on the record set in the side bar:



Three options are available:

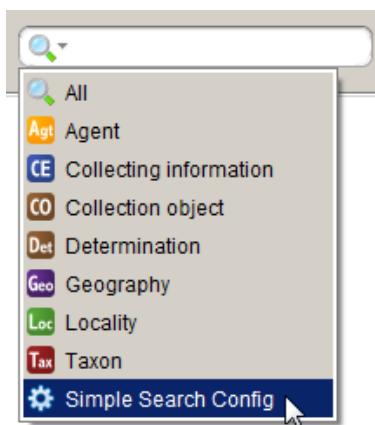
- Rename – activates a text field in which you can rename the record set. Type the new name into the text field and press **Enter** to save the record set under the new name.
- Delete – deletes the record set. Record sets can also be deleted by dragging and dropping them on to the trash can.
- View – opens the record set in a new results grid. Further actions can be taken by using the controls in the results grid.

Simple search

The **Simple search** is designed to eliminate the need to build complex queries to perform commonly executed searches. All the actions that can be applied to query results are available in the **Simple search**.

Configuring simple search

Simple search can be configured to query on different fields. The fewer fields that are queried, the faster the search will run. To configure **Simple search**, click on the arrow next to the **Simple search** icon, then select ‘Simple Search Config’ from the menu:



There are three configuration tabs: ‘Search fields’, ‘Related searches’ and ‘Results ordering’.

You can configure **Simple search** any way you like, but the following configuration is recommended to begin with.

1. In the ‘Search fields’ tab, click on **Collecting information** in the ‘Available tables’ panel, and uncheck the **Start date** and **Collecting no.** in the ‘Search fields’ panel:

The screenshot shows the 'Simple Search Config' window. At the top, there are three tabs: 'Search Fields', 'Related Searches', and 'Results Ordering'. Below them is a 'Available Tables' panel containing a list of tables with their abbreviations: Bor, BM, BrM, CE, CT, Cln, CO, CN, CD, and CvE. The 'CE Collecting information' table is highlighted with a dark blue background. Below this is a 'Search Fields' panel with a table:

Search	Field Name	Sorting
<input type="checkbox"/>	Start date	None
<input type="checkbox"/>	Collecting no.	None
<input type="checkbox"/>	End date	None

2. Click on **Determination** in the ‘Available tables’ panel and uncheck the **Date** field in the ‘Search fields’ panel:

The screenshot shows a software interface for managing search fields. At the top, there are tabs for 'Search Fields', 'Related Searches', and 'Results Ordering'. Below these are two main panels: 'Available Tables' and 'Search Fields'.

Available Tables:

- CO Collection object
- CN Common Name
- CD Conservator description
- CvE Conservator event
- Con Container
- DNA DNA sequence
- Dea Deaccession
- Det Determination** (highlighted in blue)
- Div Division
- EI Exchange In

Search Fields:

Search	Field Name	Sorting
<input type="checkbox"/>	Date	None
<input type="checkbox"/>	Type status	None

- Click on **Locality** in the 'Available tables' panel and un-tick **Locality** in the 'Search fields' panel.

The screenshot shows the same software interface as the previous one, but with a different set of available tables.

Available Tables:

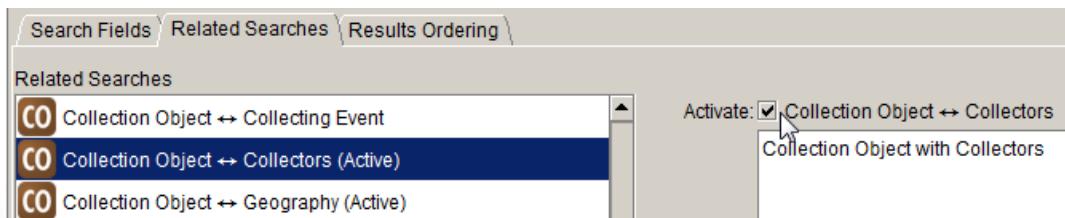
- FNP Field Notebook Page
- FNS Field Notebook Page Set
- Geo Geography
- Gft Gift
- Ins Institution
- Jou Journal
- Loa Loan
- LrP Loan Return Preparation
- Loc Locality** (highlighted in blue)
- LnA Locality Name Alias

Search Fields:

Search	Field Name	Sorting
<input type="checkbox"/>	Locality	None

- Under the 'Related searches' tab, check that the following relationships are marked 'Active':
 - Collection object ↔ Collectors
 - Collection object ↔ Geography
 - Collector ↔ Collecting event
 - Collection object ↔ Taxon (there are two of these relationships – check that they are both active)
 - Collection object ↔ Taxon (determined)
 - Taxon ↔ Collection object
 - Taxon ↔ Geography

To activate (or deactivate) a relationship, click on the relationship description in the 'Related searches' panel, then tick (or un-tick) the **Activate** box to the right of the panel:



- No changes need to be made in the 'Results ordering' tab.

Simple search is now configured to query on the following fields:

Fields To Be Searched	
Agt	Last name
CO	Catalogue no.
Geo	Full name
Tax	Full name

A query on one of these fields will return records from the primary table that the search term occurs in (e.g. the **Agent** table for a query on **Last name**) as well as from other tables that contain links to the field being queried (e.g. records from the **Collection object** table for specimens that were collected by the agent, or records from the **Taxon** table that link to determinations by the agent).

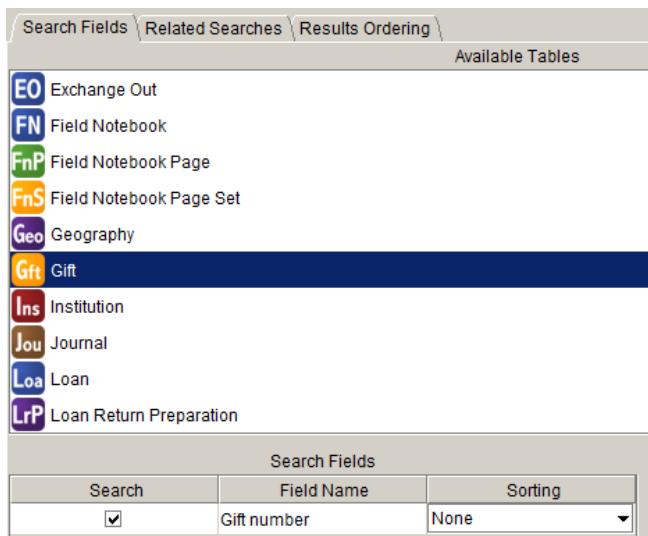
Curation staff might also wish to use **Simple search** to query for loan or gift transactions. To configure **Simple search** to query for loan and gift records:

- Click on **Loan** in the 'Available tables' panel and tick the **Loan number** field in the 'Search fields' panel:

Available Tables	
Geo	Geography
Gft	Gift
Ins	Institution
Jou	Journal
Loa	Loan
LrP	Loan Return Preparation
Loc	Locality
LnA	Locality Name Alias
Per	Permit
Prj	Project

Search Fields		
Search	Field Name	Sorting
<input checked="" type="checkbox"/>	Loan number	None

- Click on **Gift** in the 'Available tables' panel and tick the **Gift number** field in the 'Search fields' panel:



Wildcards and delimiters

More than one term can be used in a search specification, but the results will vary depending on the use of wildcards and delimiters. For example, if the search string is 'Lake Bolac', the **Simple search** results will include records that have either 'Lake' OR 'Bolac' in any search field. Records that contain the phrase 'Lake Bolac' in one field will also be found.

Wildcards and delimiters can be used in the **Simple search** criteria to define queries more narrowly. A wildcard (*) allows the criteria to be found as part of a string. Single or double quote delimiters (' or ") allow two or more words to be searched as a string rather than as separate criteria. The wildcard and delimiter can also be used together to further limit the search:

Query term	Result
*Clinton	Returns any string with Clinton at the end
Clinton*	Returns any string that begins with Clinton
Clinton	Returns any string that includes Clinton anywhere in the string
Clinton Lake	Returns any string that begins with Lake or ends with Clinton
"Clinton Lake" or 'Clinton Lake'	Returns any string where Clinton Lake is the entire string
"Clinton Lake" or *'Clinton Lake'*	Returns any string that includes Clinton Lake anywhere in the string

The search term is queried in all fields that have been selected in the **Simple search** configuration options, so a query for 'Laur*' will return a list of agents whose last name starts with 'Laur' (Laurer, Laurie, Laury etc.), as well as a list of all taxon names that begin with 'Laur' (Lauraceae, Laurencia, Laurus etc.).

The screenshot shows a software interface with two tables. The top table, titled 'Agent - 5', has columns for 'Initials' and 'Lastname'. It contains five rows with data: D.W., Laurer; D., Laurie; and D., Laury. Below this is a toolbar with 'Select All' and 'Deselect All' buttons. The bottom table, titled 'Taxon - 33', has a column for 'Full name'. It lists 33 entries starting with Laurensia, such as Laurensia arborea, Laurensia cymosa, Laurensia divaricata, Laurensia elongata, Laurensia filiformis, Laurensia forsteri, Laurensia furcata, Laurensia gracilis, Laurensia panicosa, Laurensia rigida, Laurensia shepherdi, Laurensia speciosa, Laurensia translucida, Laurensia pilosiflora, Laurella, Laurella philippiana, and Laurella sempervirens.

Initials	Lastname
D.W.	Laurer
D.	Laurie
D.	Laury

Full name
Laurensia arborea
Laurensia cymosa
Laurensia divaricata
Laurensia elongata
Laurensia filiformis
Laurensia forsteri
Laurensia furcata
Laurensia gracilis
Laurensia panicosa
Laurensia rigida
Laurensia shepherdi
Laurensia speciosa
Laurensia translucida
Laurensia pilosiflora
Laurella
Laurella philippiana
Laurella sempervirens

Simple search examples

'Wakefield'

A search for 'Wakefield' will first return results for agents with the last name 'Wakefield', and will then return the results for records in the **Taxon** table and **Collection object** table that contain links to the 'Wakefield' entries in the **Agent** table:

The screenshot shows a software interface with a search bar containing 'wakefield'. Below the search bar is a table titled 'Agent - 8' with a column for 'Initials'. It lists eight entries: A.T., Captain, E.M., F.W., N., N.A., R., and R.J. Below this table are two status bars: 'Taxon ↔ CollectionObject - 167' and 'Collection Object ↔ Collectors - 4083'.

Initials
A.T.
Captain
E.M.
F.W.
N.
N.A.
R.
R.J.

Select All	Deselect All
------------	--------------

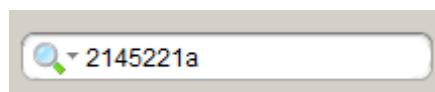
► Taxon ↔ CollectionObject - 167
► Collection Object ↔ Collectors - 4083

In this example there are:

- eight records in the **Agent** table for agents with the last name Wakefield
- 167 records in the **Taxon** table that link to records in the **Collection object** table that have determinations by someone with the last name Wakefield
- 4083 records in the **Collection object** table where one of the collectors has the last name Wakefield.

'2145221a'

A search for a **Catalogue number** will return the results from the **Collection object** table where the **Catalogue number** matches the query term:



Because the **Simple search** is configured to display results from linked tables, a search for **Catalogue number** presents the same result in different ways:

▼ Collection object - 1	
	Catalogue number 2145221A
<input type="checkbox"/> Select All	Deselect All
►	Collection Object ↔ Taxon - 1
►	Collection Object ↔ Collectors - 1
►	Collection Object ↔ Taxon (determined) - 1
►	Collection Object ↔ Geography - 1

In this example, the same result is described by five different relationships, but because catalogue numbers are unique, they don't provide any additional information:

- one record in the **Collection object** table contains the **Catalogue number** 2145221A
- one record in the **Collection object** table with the **Catalogue number** 2145221A has a determination (either current or non-current) that links to a record in the **Taxon** table
- one record in the **Collection object** table with the **Catalogue number** 2145221A has a current determination that links to a record in the **Taxon** table
- one record in the **Collection object** table with the **Catalogue number** 2145221A has a locality that links to a record in the **Geography** table.

'China'*

A search for 'China*' will first return results for names in the **Geography** table that start with 'China', and will then return results for records in the **Taxon** table and **Collection object** table that contain links to the 'China*' records in the **Geography** table:

 China*	
▼ Geography - 4	
	Full name
	China, Asia-Temperate
	China North-Central, China, Asia-Temperate
	China Southeast, China, Asia-Temperate
	China, Asia-Tropical
<input type="checkbox"/> Select All	Deselect All
►	Taxon ↔ Geography - 34
►	Collection Object ↔ Geography - 40

In this example there are:

- four records in the **Geography** table that start with 'China'
- 34 records in the **Taxon** table for taxa that have been collected in China
- 40 records in the **Collection object** table for specimens that were collected in China.

'Muehlen*'

A search for a taxon name followed by a wildcard will return a list of all records in the **Taxon** table that begin with the search term, followed by records from the **Collection object** and **Geography** tables that contain links to the record in the **Taxon** table:

The screenshot shows a search interface with a search bar containing 'Muehlen*'. Below the search bar is a table titled 'Taxon - 24' with a single column labeled 'Full name'. The table lists various species names under the genus *Muehlenbeckia*, including *M. adpressa*, *M. australis*, *M. axillaris*, *M. coccoloboides*, *M. complexa*, *M. costata*, *M. diclina*, *M. flexuosa*, *M. florulenta*, *M. gracilimma*, *M. gunnii*, *M. horrida*, *M. monticola*, *M. platyclados*, *M. polybotrya*, *M. rhyticarya*, *M. sagittifolia*, *M. zippelii*, and *M. diclina* subsp. *diclina*. Below the table, there are buttons for 'Select All' and 'Deselect All'. At the bottom, there is a list of relationships: 'Taxon ↔ CollectionObject - 474', 'Collection Object ↔ Taxon - 708', 'Taxon ↔ Geography - 59', 'Collection Object ↔ Taxon (determined) - 703', and 'Collection Object ↔ Taxon - 721'.

Full name
<i>Muehlenbeckia</i>
<i>Muehlenbeckia adpressa</i>
<i>Muehlenbeckia adpressa</i> var. <i>rotundifolia</i>
<i>Muehlenbeckia australis</i>
<i>Muehlenbeckia axillaris</i>
<i>Muehlenbeckia coccoloboides</i>
<i>Muehlenbeckia complexa</i>
<i>Muehlenbeckia costata</i>
<i>Muehlenbeckia diclina</i>
<i>Muehlenbeckia flexuosa</i>
<i>Muehlenbeckia florulenta</i>
<i>Muehlenbeckia gracilimma</i>
<i>Muehlenbeckia gunnii</i>
<i>Muehlenbeckia horrida</i>
<i>Muehlenbeckia monticola</i>
<i>Muehlenbeckia platyclados</i>
<i>Muehlenbeckia polybotrya</i>
<i>Muehlenbeckia rhyticarya</i>
<i>Muehlenbeckia sagittifolia</i>
<i>Muehlenbeckia zippelii</i>
<i>Muehlenbeckia diclina</i> subsp. <i>diclina</i>
<i>Muehlenbeckia diclina</i> subsp. <i>diclina</i> subsp. 1 sensu Fl. Vic. 3:286 (1996)
<i>Muehlenbeckia horrida</i> subsp. <i>abdita</i>
<i>Muehlenbeckia horrida</i> subsp. <i>horrida</i>

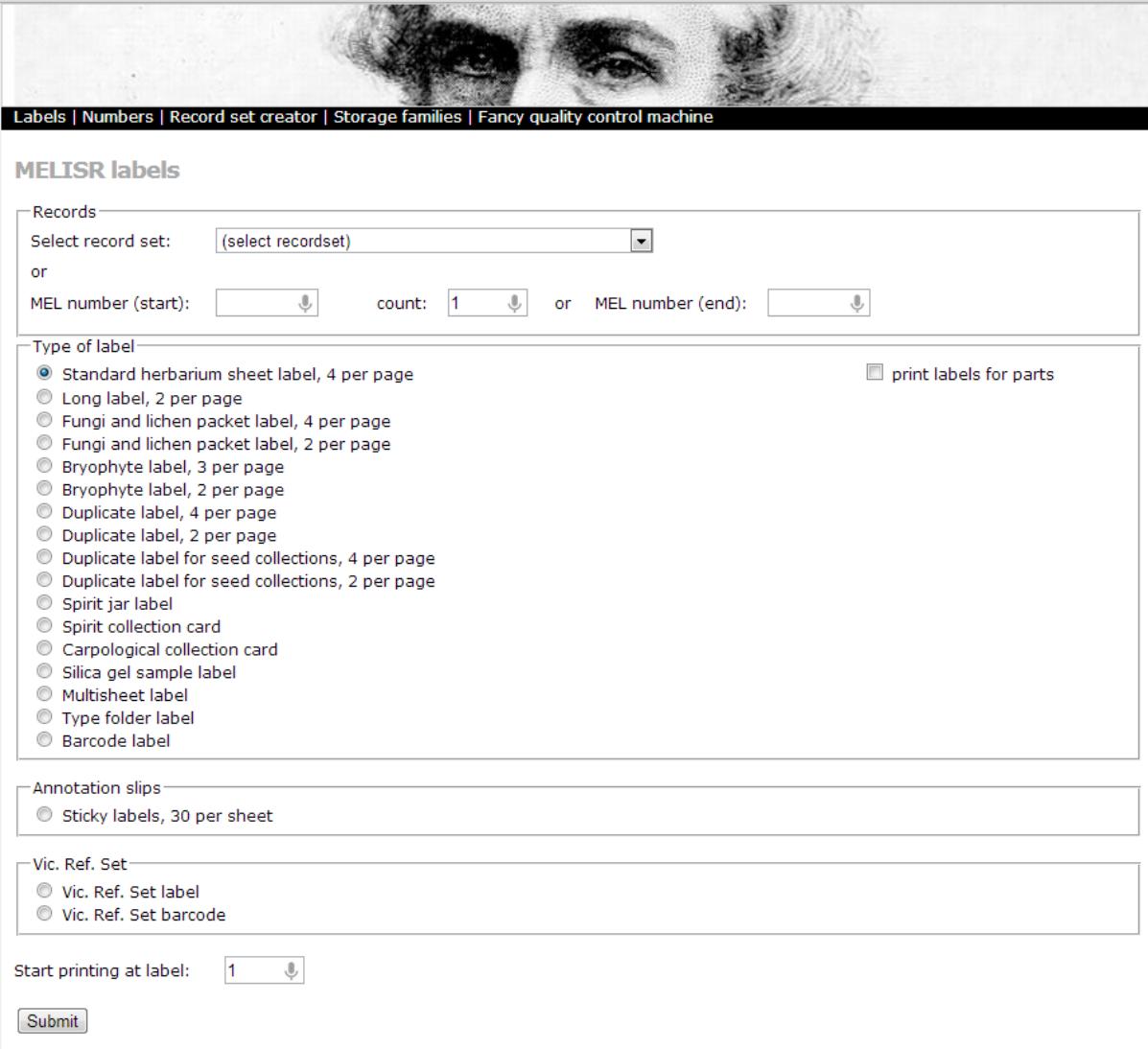
In this example there are:

- 24 records for taxon names in the **Taxon** table that start with 'Muehlen'
- 474 records in the **Collection object** table that are currently determined to a taxon name that starts with 'Muehlen' (and where the determination agent is known)
- 708 records in the **Collection object** table that contain a determination (either current or non-current) that link to a name in the **Taxon** table that starts with 'Muehlen'
- 59 records for place names in the **Geography** tree where taxa starting with 'Muehlen' have been collected
- 703 records in the **Collection object** table that are currently determined to a taxon name that starts with 'Muehlen' (and where the determination agent is either known or unknown)
- 721 **Determinations** in **Collection object** records that link to a name in the **Taxon** table that starts with 'Muehlen'.

CURATION TOOLS

Labels

The **Labels** page in the MELISR website is used to produce specimen and barcode labels.



The screenshot shows the 'MELISR labels' page. At the top, there's a navigation bar with links: Labels | Numbers | Record set creator | Storage families | Fancy quality control machine. Below the navigation is a section titled 'MELISR labels'. It contains several input fields and dropdown menus:

- Records**:
 - Select record set: (select recordset) dropdown menu
 - or
 - MEL number (start): input field with microphone icon, count: 1, or MEL number (end): input field with microphone icon
- Type of label**: A list of radio buttons for different label types:
 - Standard herbarium sheet label, 4 per page (selected)
 - Long label, 2 per page
 - Fungi and lichen packet label, 4 per page
 - Fungi and lichen packet label, 2 per page
 - Bryophyte label, 3 per page
 - Bryophyte label, 2 per page
 - Duplicate label, 4 per page
 - Duplicate label, 2 per page
 - Duplicate label for seed collections, 4 per page
 - Duplicate label for seed collections, 2 per page
 - Spirit jar label
 - Spirit collection card
 - Carpological collection card
 - Silica gel sample label
 - Multisheet label
 - Type folder label
 - Barcode label
- Annotation slips**:
 - Sticky labels, 30 per sheet (radio button selected)
- Vic. Ref. Set**:
 - Vic. Ref. Set label
 - Vic. Ref. Set barcode
- Start printing at label:** Input field with value 1 and a microphone icon.
- Submit**: A button at the bottom left.

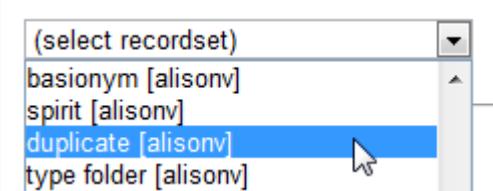
The URL for the label printing website is <http://10.15.15.99/melisr/index.php/melisrlabels/>.

Printing labels

Specimen labels and barcode labels can be printed for a record set created from a query in Specify, or you can nominate a single MEL number or a sequence of MEL numbers that you want to print labels for. For Vic. Ref. Set specimens, you can print labels by choosing a record set or MEL numbers for the specimen/s in the main collection that have Vic. Ref. Set duplicates, or you can enter the Vic. Ref. Set catalogue number.

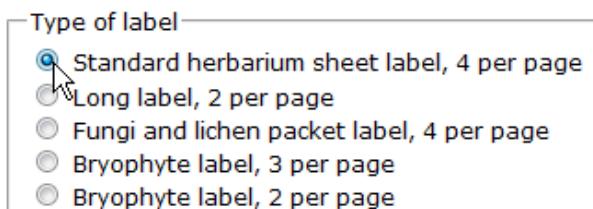
To print labels for a set of specimens:

1. In Specify, create a record set for the set of specimens you want labels for
2. In the label interface, select your record set from the drop-down list:



The Specify user name of the person who created the record set appears in brackets next to the record set name.

3. Select which type of labels you want to print:



4. Select which position on the page you want to start printing at:

Start printing at label:

5. Click the **Submit** button. A preview of your labels will appear in your browser.
6. Press **Ctrl+P** to print your labels, or use the printing controls in your PDF viewer.

To print labels for a single record:

1. In the label interface, enter a MEL number in the **MEL number (start)** field (or a Vic. Ref. Set number in the **Vic. Ref. Set number (start)** field)
2. Select which type of labels you want to print
3. Select which position on the page you want to start printing at
4. Click the **Submit** button. A preview of your labels will appear in the browser window.
5. Press **Ctrl+P** to print your labels, or use the printing controls in your PDF viewer.

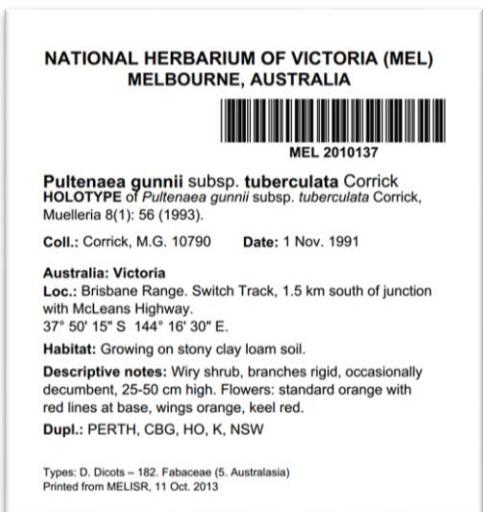
To print a sequence of numbers:

1. In the label interface, enter the first number in the sequence in the **MEL number (start)** field or the **Vic. Ref. Set number (start)** field
2. Either enter the total number of MEL numbers or Vic. Ref. Set numbers in the sequence in the **Count** field, or enter the last number in the sequence in the **MEL number (end)** or **Vic. Ref. Set number (end)** field
3. Select which type of labels you want to print
4. Select which position on the page you want to start printing at
5. Click the **Submit** button. A preview of your labels will appear in the browser window.
6. Press **Ctrl+P** to print your labels, or use the printing controls in your PDF viewer.

Type of label

Standard herbarium sheet label, 4 per page

Used for herbarium sheets.



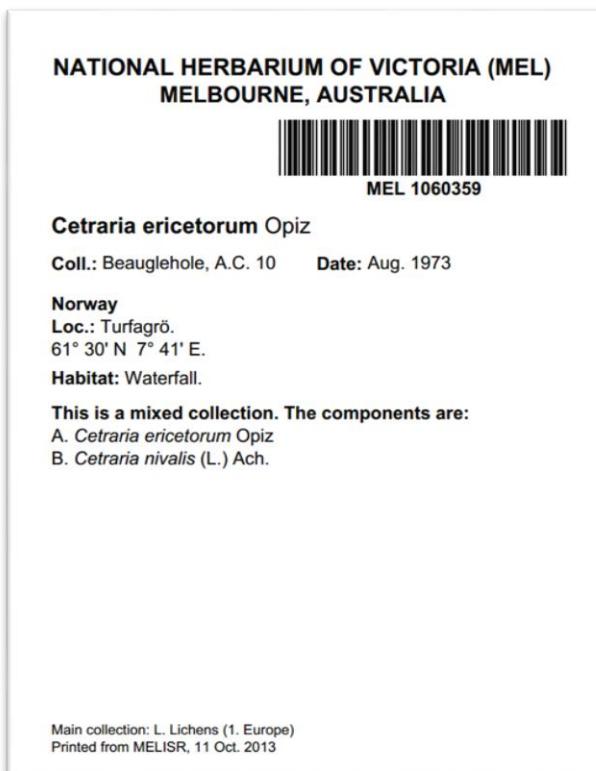
Long label, 2 per page

Used for herbarium sheets where there is too much information to fit on a 4-per-page label.



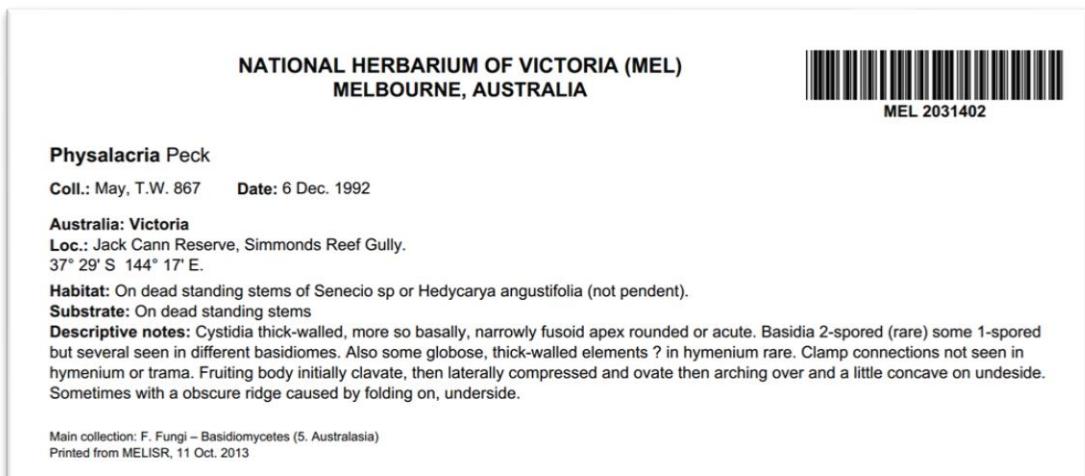
Fungi and lichen packet label, 4 per page

Used for fungi and lichen packets. The difference between this label and the standard herbarium sheet label is that the 'Storage' section appears in a set position at the bottom of the label, instead of directly below the last piece of collecting information.



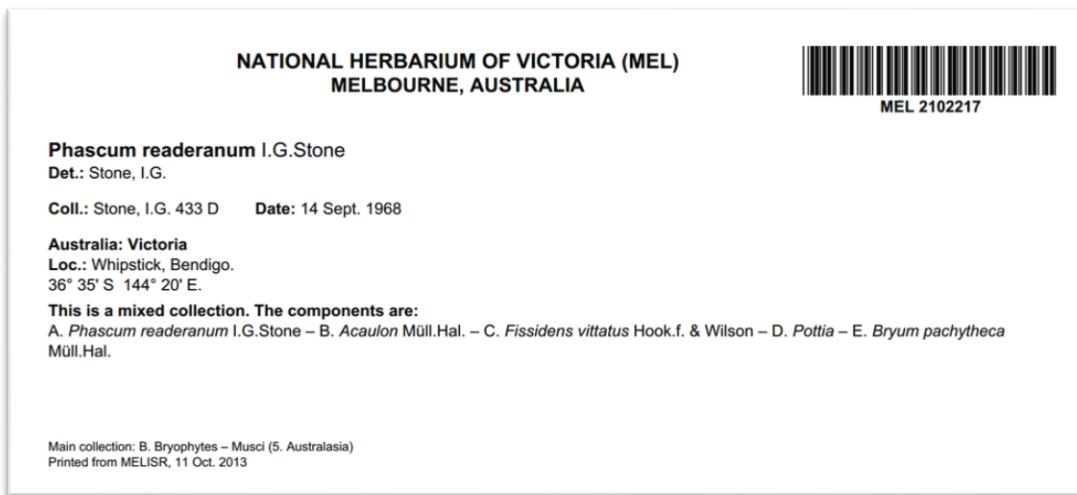
Fungi and lichen packet label, 2 per page

Used for fungi and lichen packets where there is too much information to fit on a 4-per-page label.



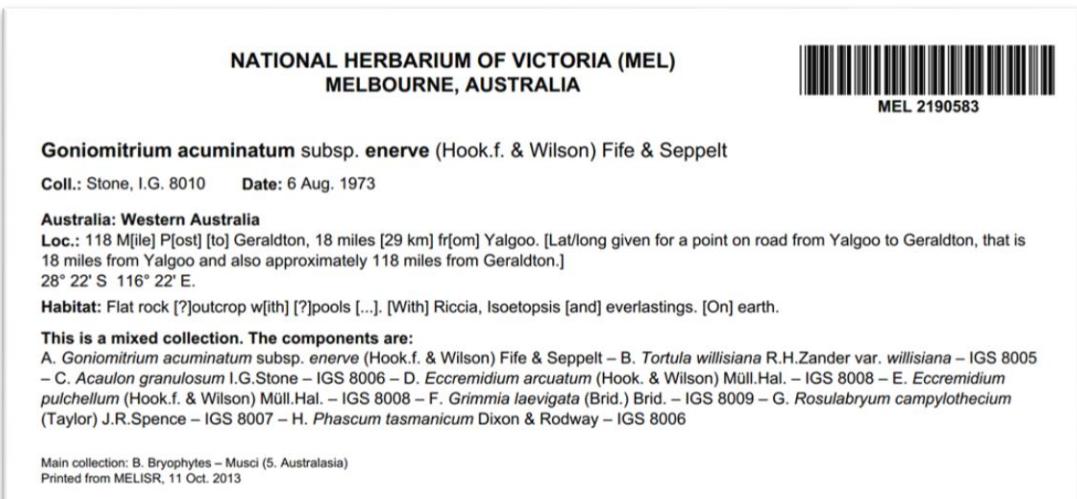
Bryophyte label, 3 per page

Used for bryophyte packets.



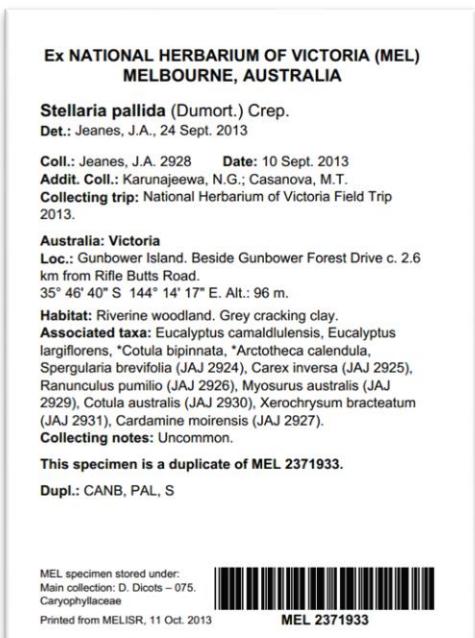
Bryophyte label, 2 per page

Used for bryophyte packets where there is too much information to fit on a 3-per-page label.



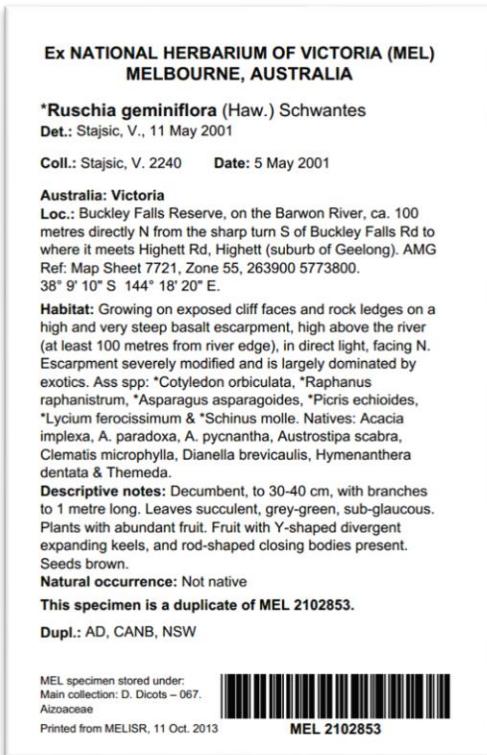
Duplicate label, 4 per page

Used for duplicate specimens. The number of duplicate labels that will be printed is determined by the **Quantity** field in the 'Duplicate' preparation.



Duplicate label, 2 per page

Used for duplicate specimens where there is too much information to fit on a 4-per-page label.



Duplicate label for seed collections, 4 per page

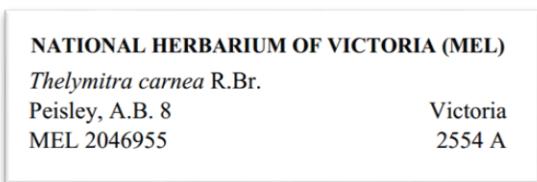
Used for duplicate seed collections, which need to be printed on adhesive paper.

Duplicate label for seed collections, 2 per page

Used for duplicate seed collections where there is too much information to fit on a 4-per-page label.

Spirit jar label

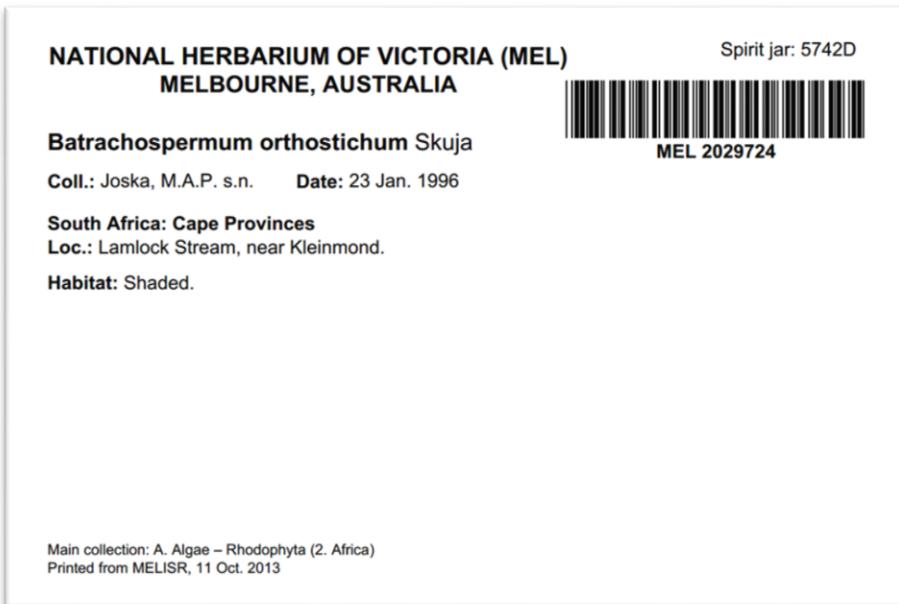
Used to label spirit jars.



Spirit jar labels should be printed on 30-per-page adhesive label sheets. You can select which position you want to start printing at by entering a number in the **Start printing at label** field in the web interface (the default position is 1).

Spirit collection card

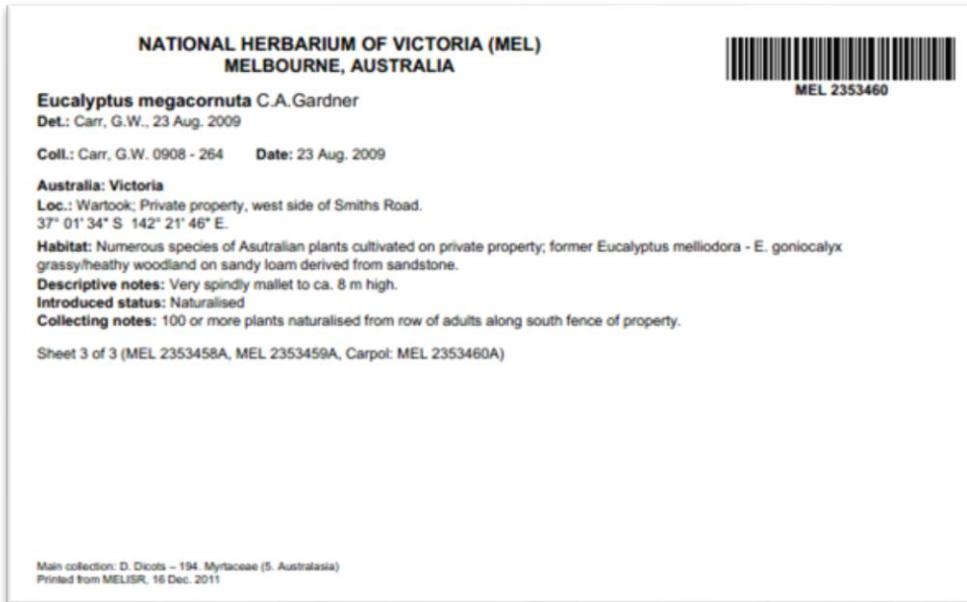
Used for spirit collection cards (rather than printing a specimen label on paper and then gluing the label to a spirit card, you can print directly onto the card):



If the label contains more information than will fit on one side of the card, it will overflow to the other side of the card.

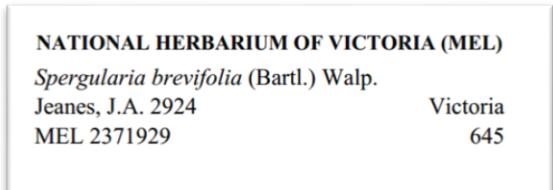
Carpological collection card

Used for carpological collection cards (rather than printing a specimen label on paper and then gluing the label to a carpological card, you can print directly onto the card):



Silica gel sample label

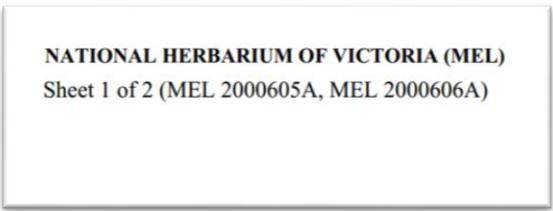
Used to label silica gel samples.



Silica gel sample labels should be printed on 30-per-page adhesive label sheets. You can select which position you want to start printing at by entering a number in the **Start printing at label** field in the web interface (the default position is 1).

Multisheet label

Used for multisheets where a full specimen label does not need to be printed.



Multisheet labels should be printed on 30-per-page adhesive label sheets. You can select which position you want to start printing at by entering a number in the **Start printing at label** field in the web interface (the default position is 1).

Type folder label

Used to label type folders.



Labels for Australian type specimens have an 'A' on the right-hand side of the label, and labels for foreign-collected type specimens have an 'F' on the right-hand side of the label. Twelve type folder labels will print on an A4 label page.

Barcode label

Used to print barcode labels for a set of databased specimens or a sequence of unused MEL numbers:



Barcode labels should be printed on 30-per-page adhesive label sheets. You can select which position you want to start printing at by entering a number in the **Start printing at label** field in the web interface (the default position is 1).

Print labels for parts

By default, labels will only be printed for part 'A' of mixed collections. If you want to print separate labels for the different components of mixed collections, tick the 'print labels for parts' box:

print labels for parts

Annotation slips

Sticky labels, 30 per sheet

Annotation slips can be printed for the current determination for each record in a record set:



Annotation slips should be printed on 30-per-page adhesive label sheets. You can select which position you want to start printing at by entering a number in the **Start printing at label** field in the web interface (the default position is 1).

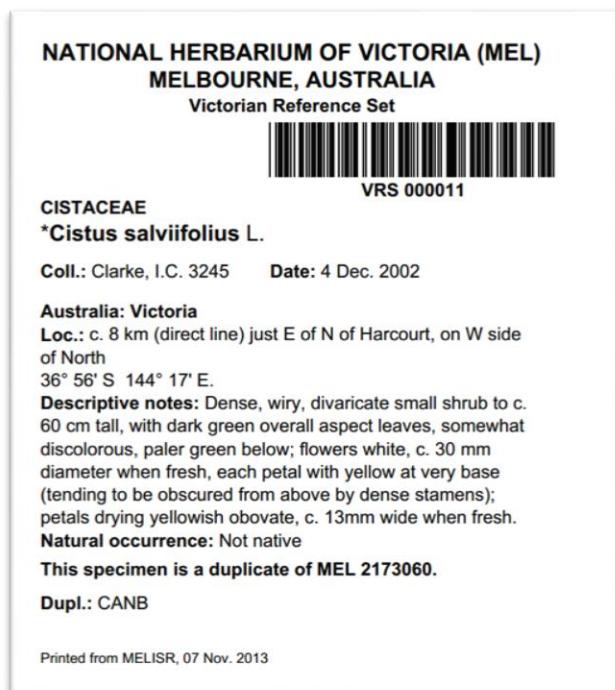
Vic. Ref. Set

There are three input options for printing Vic. Ref. Set labels:

- select a record set that includes collection object records in the *National Herbarium of Victoria* collection that have duplicates in the *Victorian Reference Set* collection
- enter a single MEL number or a sequence of MEL numbers for records that have Vic. Ref. Set duplicates
- enter a single VRS number or a sequence of VRS numbers.

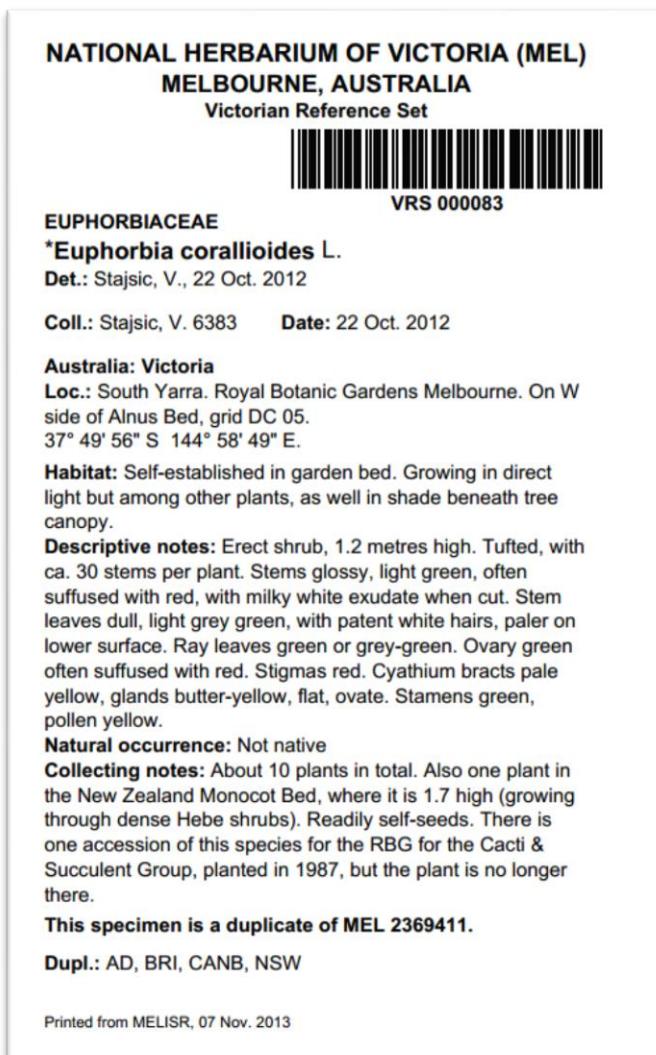
Vic. Ref. Set label, 4 per page

Used for Vic. Ref. Set specimens:



Vic. Ref. Set label, 2 per page

Used for Vic. Ref. Set specimens where there is too much information to fit on a 4-per-page label:



Vic. Ref. Set barcode

Use to print barcodes for specimens in the Vic. Ref. Set:



Barcode labels should be printed on 30-per-page adhesive label sheets. You can select which position you want to start printing at by entering a number in the **Start printing at label** field in the web interface (the default position is 1).

Numbers

The **Numbers** page in the MELISR website is used to generate sequences of MEL numbers to assign to undatabased specimens, as well as numbers for new loans and exchange records.

The screenshot shows the 'MEL numbers' section of the MELISR website. At the top, there is a navigation bar with links: Labels | Numbers | Record set creator | Storage families | Fancy quality control machine. Below the navigation bar, the title 'MEL numbers' is displayed. A search input field contains the value '100'. To the right of the input field is a microphone icon. Below the search field, there is a link 'Overview of assigned MEL numbers'. Further down, there is a section titled 'Spirit jar, microscope slide and silica gel sample numbers' with three buttons: 'Spirit jars', 'Microscope slides', and 'Silica gel samples'. A red-bordered box contains the text: 'Sample numbers for spirit collections, microscope slides and silicagel samples are now automatically created in Specify, so you don't need to look them up anymore.' Below this section, there is another titled 'Loan and exchange numbers' with two buttons: 'Loans' and 'Exchange'.

The URL for the **Numbers** website is <http://10.15.15.99/melisr/index.php/numbers>.

MEL numbers

To generate a batch of MEL numbers to assign to undatabased specimens:

1. Enter the number of MEL numbers that you need in the box (the default is 100 numbers), and click the **MEL number** button:

A screenshot of a web form. It features a button labeled 'MEL numbers' with a small cursor icon pointing at it. To the right of the button is an input field containing the number '300'.

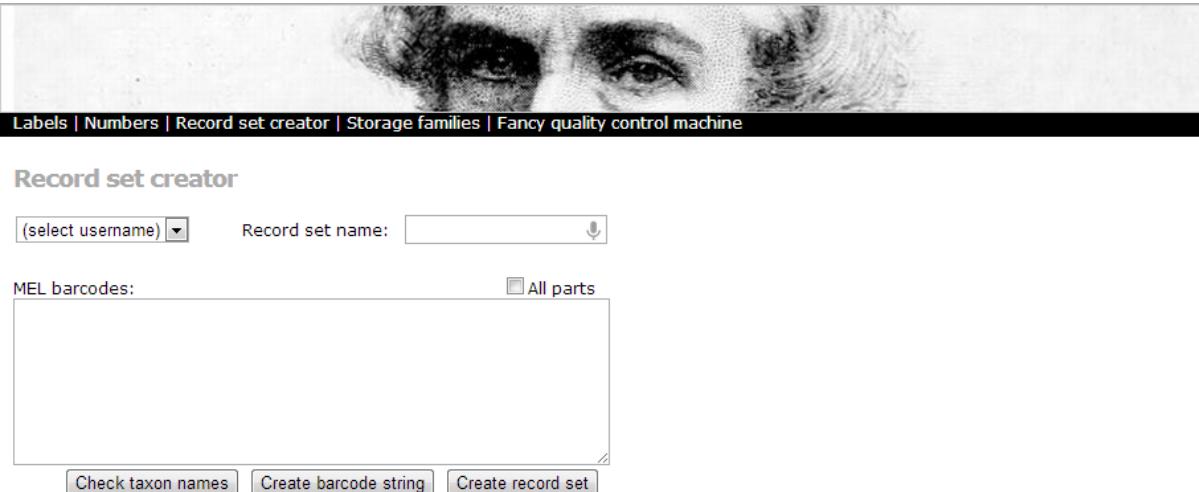
The range of numbers will be displayed.

2. Enter your name in the **Name** field (please enter both your first name and your last name), and click **Accept**
3. Either print a list of the MEL numbers (in Excel format) by clicking **print list**, or use the **MELISR Labels** web page to print barcode labels for the MEL numbers.

To see a list of who has been assigned which MEL numbers, click on the **Overview of assigned MEL numbers** link.

Record set creator

The **Record set creator** page allows curation staff to create record sets by scanning specimen barcodes. You can also create a barcode string to use for querying the database, and check the taxon names of the records in the record set.



The screenshot shows the 'Record set creator' page. At the top, there is a navigation bar with links: Labels | Numbers | Record set creator | Storage families | Fancy quality control machine. Below the navigation bar is a large image of a person's face. The main area is titled 'Record set creator'. It contains a dropdown menu '(select username) ▾', a text input field for 'Record set name:' with a microphone icon, and a text area labeled 'MEL barcodes:' with a checkbox 'All parts' and a 'Scan' button. At the bottom of the page are three buttons: 'Check taxon names', 'Create barcode string', and 'Create record set'.

The URL for the **Record set creator** is <http://10.15.15.99/melisr/index.php/recordset>.

To create a record set:

5. Select your Specify user name from the drop-down list
6. Enter a name for your record set in the **Record set name** field
7. Scan barcodes into the **MEL barcodes** text box. Note that each MEL number needs to be on a separate line. If your barcode scanner is not configured to append a carriage return after scanning, use the barcodes on page 164 to change the scanner settings.
8. Click on **Create record set**. When you next open Specify, your record set will be saved in the side bar.

To create a string of barcodes to use in the **Query builder**:

1. Scan barcodes into the **MEL barcodes** text box. Note that each MEL number needs to be on a separate line. If your barcode scanner is not configured to append a carriage return after scanning, use the barcodes on page 164 to change the scanner settings.
2. Click on **Create barcode string**
3. Copy and paste the barcode string into the **Barcode** field (in the **Collection object** table) in the **Query builder**. Remember to use the 'In' operator with your query.

To check the taxon names in your record set:

1. Scan barcodes into the **MEL barcodes** box
2. Click on **Check taxon names**. A table displaying the MEL number and corresponding taxon name will appear on the page.

PLUGINS

Specify works with the GEOLocate and Google Earth web services to assist with georeferencing and visualising specimen records. GEOLocate and Google Earth can be accessed via the **Locality** form for individual records, or via the **Plugins** module for record sets.

GEOLocate

GEOLocate uses the **Locality** description and geography to find latitude and longitude coordinate data for specimen records.

Using GEOLocate in the Locality form

To georeference a specimen record in the **Locality** form:

1. Complete the **Geography** and **Locality** fields:

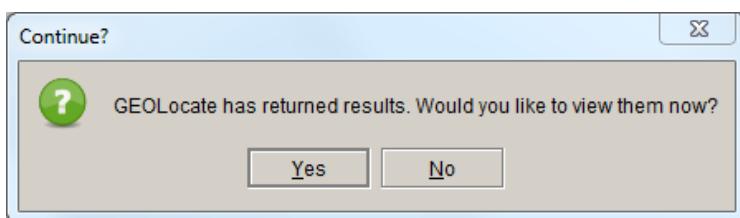
A screenshot of a software interface showing the Locality form. The 'Geography' field contains the text 'Sulawesi, Indonesia, 4. Asia-Tropical'. The 'Locality' field contains the text '20 km E of Makassar'.

Note that the **Geography** field must contain at least a country name; GEOLocate will not work if only a continent name is entered.

2. Save the **Locality** form then re-open it by clicking on the Edit symbol
3. Click the **GEOLocate** button at the bottom of the **Locality** form:



A dialogue window will indicate whether or not GEOLocate has returned results:



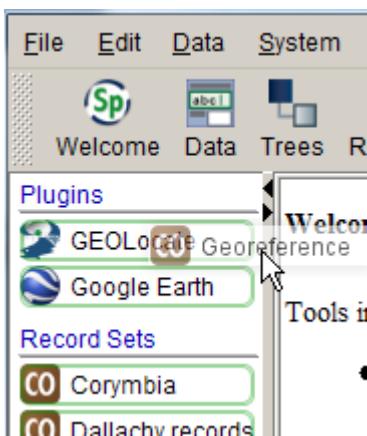
4. If there are no results, click **OK** to return to the **Locality** form. If there are results, click **Yes** to view them in the **GEOLocate results window**.

Using GEOLocate in the Plugins module

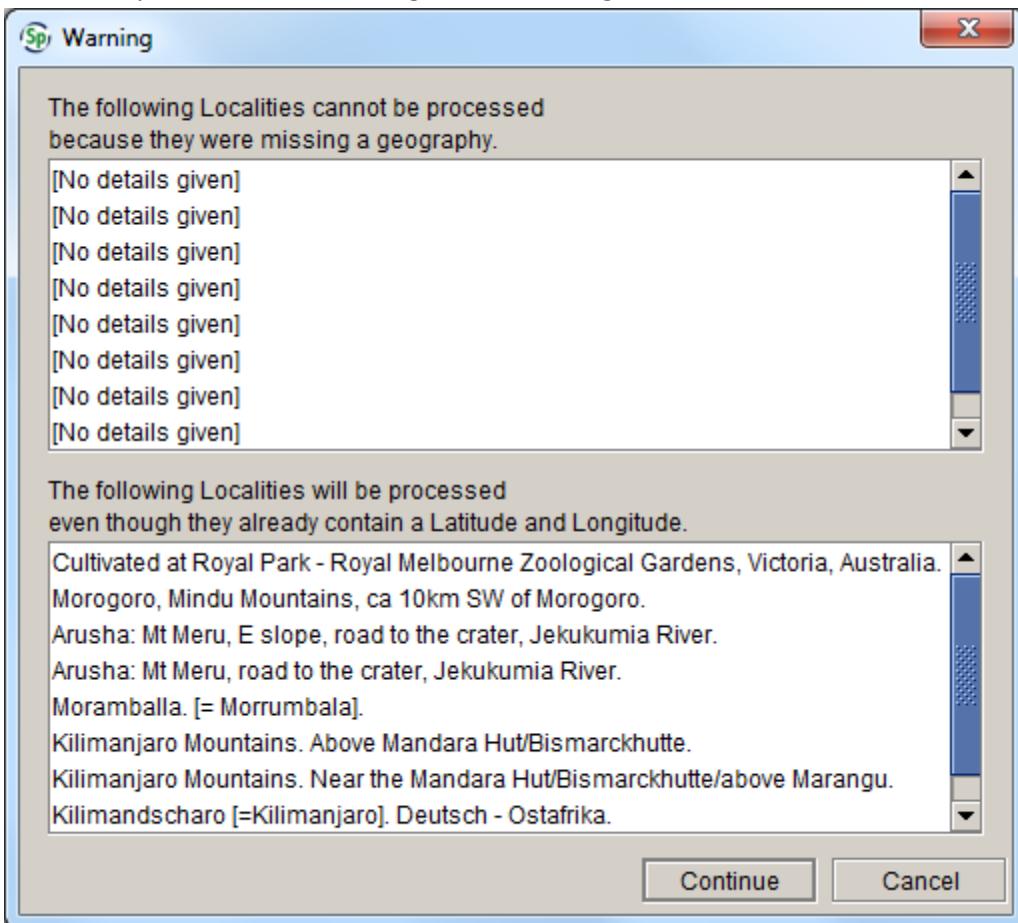
GEOLocate can be used to quickly georeference batches of records. To launch GEOLocate from the **Plugins** module:

1. Open the **Plugins** module by clicking on the **Plugins** button in the task bar

- Click and drag a record set on to the **GEOLocate** icon in the side bar:

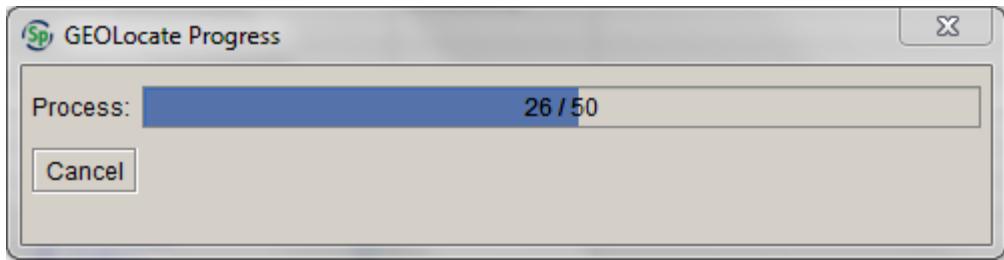


If the record set contains records that do not have **Geography** information and/or records that already have latitude and longitude, a warning will be issued:



Click **Continue** if you want to continue the georeferencing process regardless, or **Cancel** if you want to change the record set first. Do not click **Continue** unless you want to overwrite the existing latitude and longitude values.

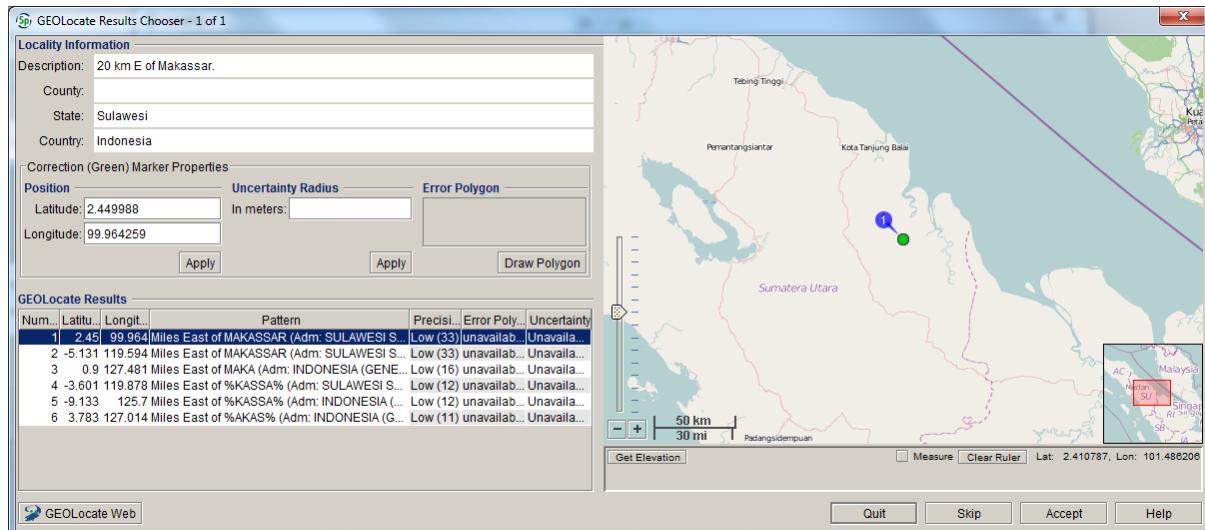
The GEOLocate progress window will indicate how many of the records in the record set have been georeferenced:



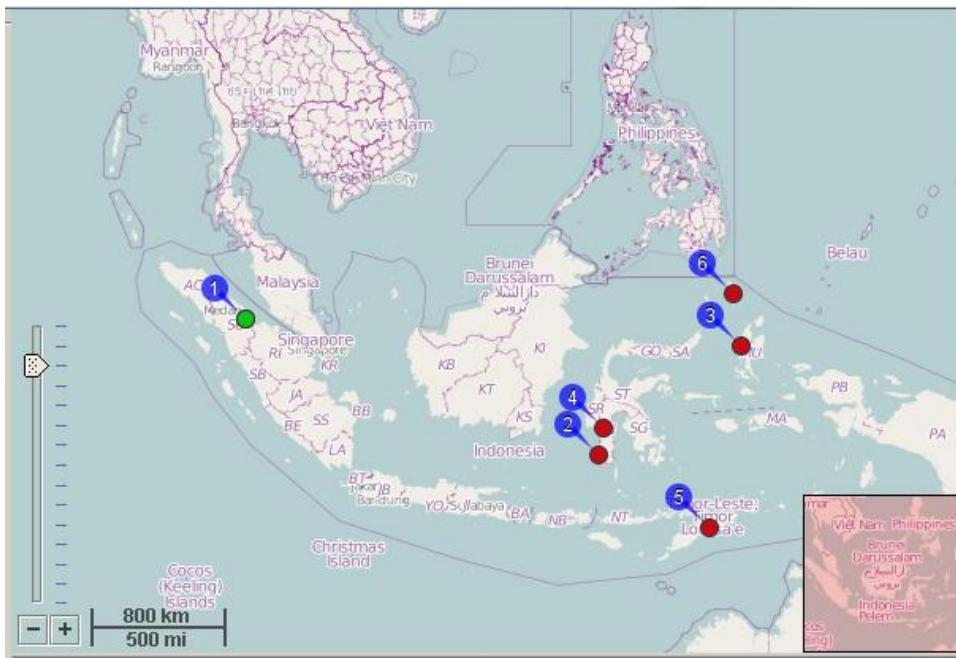
A dialogue window will indicate whether or not GEOLocate has found any matching localities.

- If there are no results click **OK** to return to the **Plugins** screen. If there are matching records, click **Yes** to view them in the **GEOLocate results window**.

GEOLocate results window



- If there is more than one result, you can scroll through the list of results to view their locations on the map. The first result in the list is not always the correct one: in the example above, the first result is on Sumatra, not Sulawesi.
- You can zoom in and out to get a more detailed view or a better overview by clicking the + and – buttons, moving the pointer in the zoom scale, or scrolling your mouse wheel. It can be useful to zoom out until you see the place marks for all the results so you can compare them easily. You can also pan the map by holding the left-hand mouse button down and dragging the map into the desired position. The result that is highlighted in the list (the first result in the above example) will have a green place marker; the other results will have red place markers:



- You can adjust the georeference by clicking on the place marker of the highlighted record (i.e. whichever one is green), holding the left mouse button down and dragging the marker to the desired position:



- The new latitude and longitude of the green dot will appear under **Position** in the **Correction (Green) Marker Properties** box (there is no need to click the **Apply** button):

Correction (Green) Marker Properties		
Position	Uncertainty Radius	Error Polygon
Latitude: <input type="text" value="-5.320705"/> Longitude: <input type="text" value="119.575195"/>	In meters: <input type="text"/> <input type="button" value="Uncertainty Radius"/>	<input type="button" value="Draw Polygon"/>
<input type="button" value="Apply"/>		

(The latitude and longitude displayed under the map are the mouse position, not the position of the green marker.)

- You can make the green marker jump back to its original position by clicking on the original red marker. The other fields in the **Correction (Green) Marker Properties** box have not been implemented in Specify, so any data entered in there won't be stored in the database.
- To save the geocode, click the **Accept** button at the bottom of the form. When using GEOLocate from the **Locality** form, the GEOLocate window will be closed; when using GEOLocate in the **Plugins** tab, the GEOLocate results window will display the results for the next record in the record set.

Caution!

If GEOLocate results are accepted, they will overwrite any existing data in the **Latitude and longitude** fields.

Other controls

- Clicking the **GEOLocate Web** button will transfer the result of the GEOLocate query to the GEOLocate website. The GEOLocate website will display exactly the same information as the plugin in Specify, but uses Google Maps as the base map, which might give more map detail. Changes you make on the GEOLocate website will not be stored in the database, so it is a safe option if you need to play around a bit to determine the correct geocode.
- Clicking the **Help** button will open **Specify Help**
- When GEOLocate is used in the **Locality** form, clicking **Skip** will close the GEOLocate window; when GEOLocate is used in the **Plugins** tab, clicking **Skip** will get you to the results of the next record in the record set
- Clicking the **Quit** button closes the GEOLocate window.

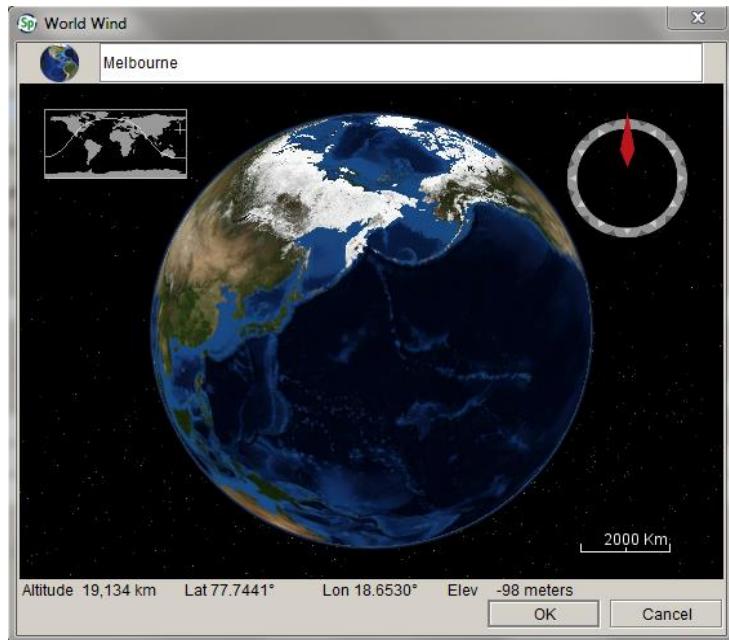
Note

GEOLocate will populate **Latitude and longitude**, **Datum**, **Source** and **Protocol**. **Uncertainty** still has to be entered in the **Locality** form.

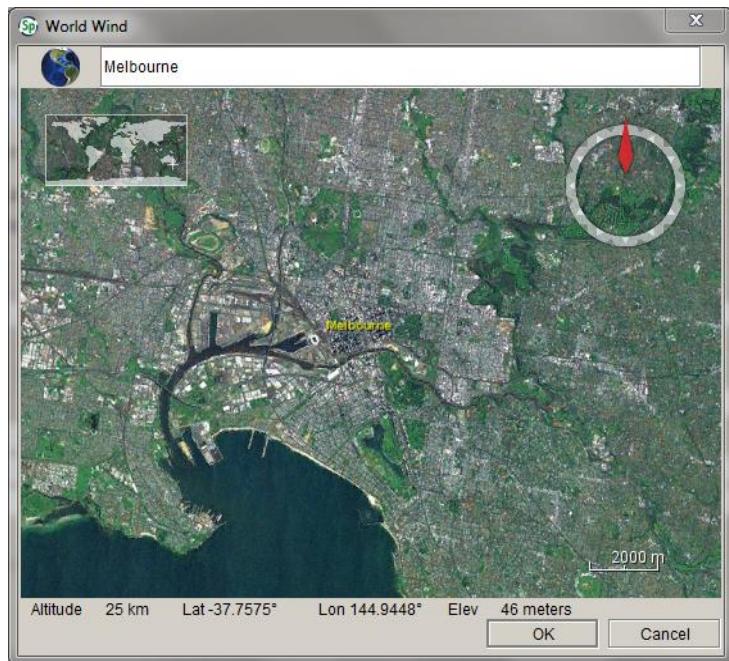
World Wind

World Wind is an open-source, 3D, interactive world viewer. It can be used in Specify to display the locality of **Collection object** records, or to map localities during data entry.

Clicking the **Display in World Wind** button will open the NASA World Wind application. A text box at the top of the World Wind window allows latitude and longitude or a locality name to be entered:



Press **Enter** after typing the locality name. The location is then displayed on a World Wind map:



If the **Collection object** has been geocoded, or if there is a locality in the **Locality** form, World Wind will automatically plot the location on the map once the button is clicked. **Never close the window by clicking the OK button unless you want to change the geocode in the Locality record.**

The following mouse controls operate in World Wind:

For a mouse with a scroll wheel:

Pan	Click and drag the left mouse button to pan in all directions
Zoom	Use the scroll wheel on the mouse or click and drag the left and right mouse buttons to zoom in and out
Tilt	Click and drag the right mouse button up and down, or press the PgUp and PgDn keys to tilt the map.
Rotate	Click and drag the right mouse button left and right to rotate the map. <i>Note:</i> crossing the top and bottom half of the screen while rotating will change the rotation direction.
Stop	Press the spacebar to stop the map
Reset heading	Press N to reset the heading
Reset all	Press R to reset all settings

For a mouse with a single button:

Pan	Click and drag the left mouse button to pan in all directions. Click the left mouse button once to center the view.
Zoom	Press and hold the Ctrl key on the keyboard and click and drag the left mouse button up and down to zoom in and out
Tilt	Press and hold the Shift key on the keyboard and click and drag the left mouse button up and down to tilt the map
Rotate	Press and hold the Shift key on the keyboard and click and drag the left mouse button to rotate the map left and right.
Stop	Press the spacebar to stop the map
Reset heading	Press N to reset the heading
Reset all	Press R to reset all settings

Google Earth

The Google Earth plugin is used as a means of visualising **Collection object** records from Specify in Google Earth. The full version of Google Earth 4.3 (or higher) must be installed on the local computer for the Specify Google Earth plugin to work.

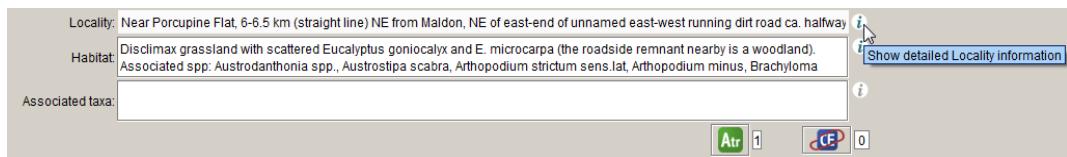
Specify plots **Collection object** records in Google Earth based on the latitude and longitude provided in the **Locality** form. Google Earth can either be launched in the **Locality** form, or by dragging and dropping a record set onto the Google Earth icon in the **Plugins** module.

Before plotting specimen records using **Google Earth**, make sure that all records in the record set contain latitude and longitude values.

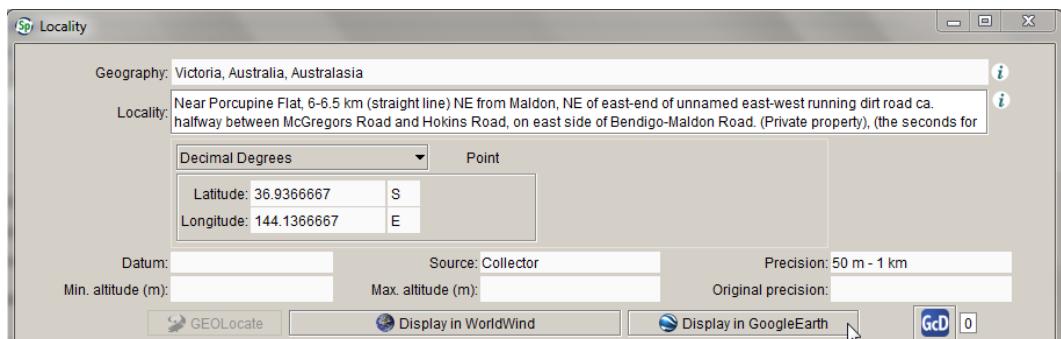
Using Google Earth in the Locality form

To launch Google Earth from the **Locality** form:

1. Open a **Collection object** record and click on the **Locality** information symbol to view the **Locality** form:



2. Click the **Display in Google Earth** button at the bottom of the **Locality** form:



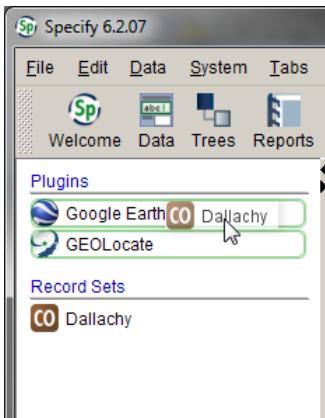
- Google Earth will open, and the **Collection object** record will be mapped:



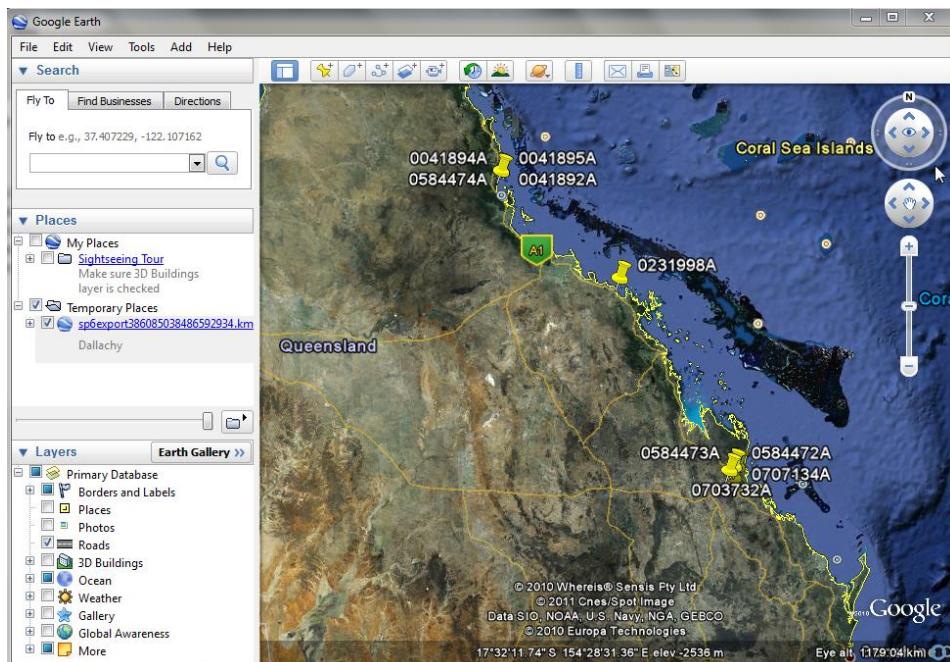
Using Google Earth in the Plugins module

To launch Google Earth from the **Plugins** module:

1. Open the **Plugins** module by clicking on the **Plugins** button in the task bar
2. Click and drag a Record set on to the **Google Earth** icon in the side bar:



- Google Earth will open, and the **Collection object** records in the record set will be mapped:



- Collection object information is shown in the Google Earth information window:



APPENDICES

1. Abbreviations

Term	Abbreviation
approximately	approx.
avenue	ave
boulevard	bvd
circa	ca. or c.
circuit	cct
close	cl.
court	ct
crescent	cres.
degrees	deg. or °
drive	dr.
east	E
esplanade	esp.
feet	ft or '
freeway	fwy
heights	hts
highway	hwy
inch	in. or "
Island/Islands	I./ls
junction	jnc.
kilometres	km
metres	m
mile	mi.
minutes	min. or '
more or less	+/-
Mount	Mt
National Park	NP
north	N
parade	pde
place	pl.

point	pt
reserve	res.
road	rd
seconds	sec., s or "
south	S
street	st
terrace	tce
track	trk
west	W
yard	yd

Note that Road, Street, Track etc. should only be abbreviated for named places, and not for general use, e.g.:

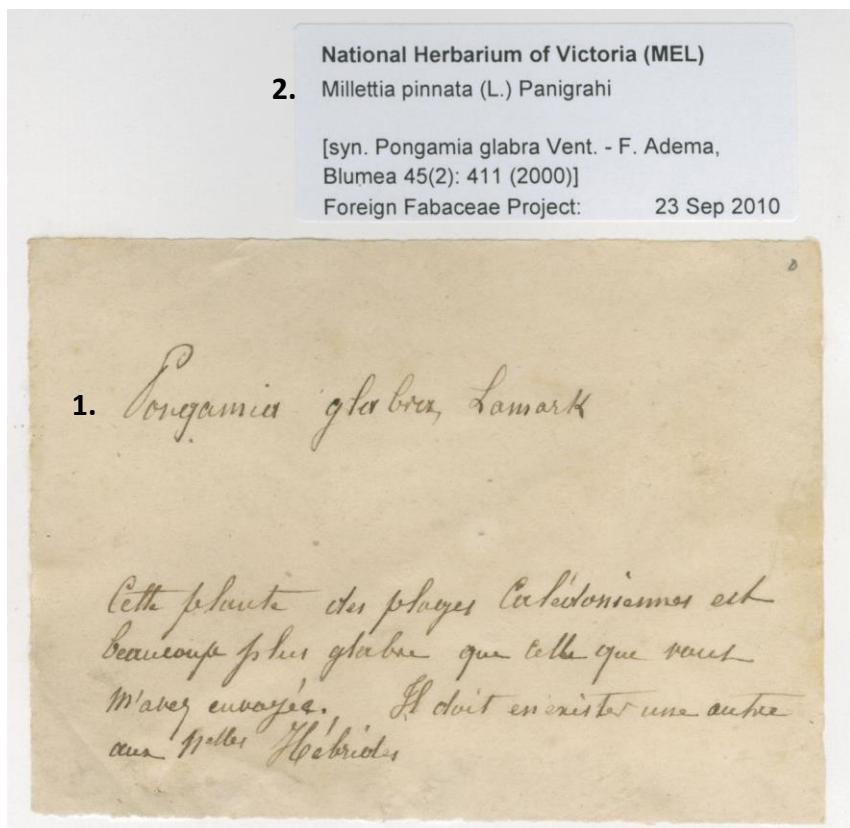
- 5 km along the Daylesford–Malmsbury **Rd** ...
- BUT
- 5 km along the **road** to Daylesford from Malmsbury ...

2. Examples of determination records

The following examples demonstrate how a range of determinations should be entered into MELISR. Because the **Current** check box is automatically ticked when you add a new determination, it is easier to enter the determinations in chronological order.

MEL 2088758

This sheet has one old label bearing a name and author combination that appears to be an error, plus one MEL annotation from the Foreign Fabaceae Project.



1. The author of *Pongamia glabra* is Vent.; *Pongamia glabra* Lamarck is not listed in Tropicos, and it is not clear whether it is a homonym, an isonym or an error. Because we know that *Pongamia glabra* Vent. is a synonym of the name to which the specimen is currently determined, *Millettia pinnata*, it's fairly safe to assume that 'Lamark' is just an error. *Pongamia glabra* Vent. can be entered as the **Taxon name**, and *Pongamia glabra* Lamarck should be entered in **Det. notes** to record what is actually written on the label:

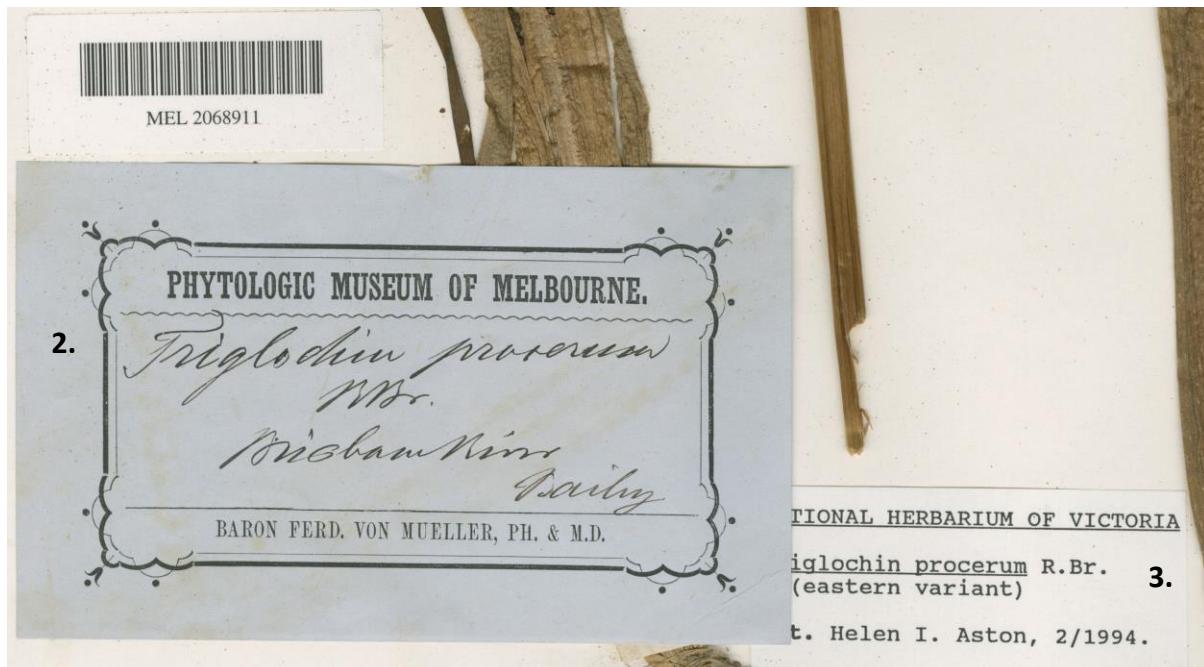
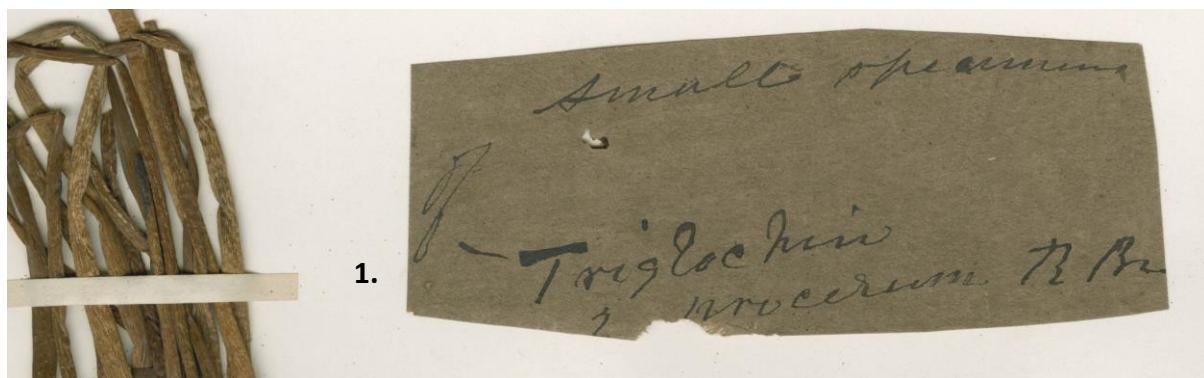
Determinations + -

Det. type: Det.	Determiner: <input type="text"/>	Date: Full Date DD/MM/YYYY <input checked="" type="checkbox"/> Current
Taxon name: Pongamia glabra	Addendum: <input type="text"/>	
Alternative name: <input type="text"/>	Determiner inferred <input type="checkbox"/>	
Qualifier: <input type="text"/>	Qualifier rank: <input type="text"/>	Addendum: <input type="text"/>
Type status: <input type="text"/>	Type qualifier: <input type="text"/>	Stored under this name <input type="checkbox"/>
Extra information: <input type="text"/>	Basis: <input type="text"/>	
Flora: <input type="text"/>	Grid ▾	
Det. notes: Pongamia glabra Lamarck	◀ ▶ 2 of 2 ▶ ▷	

2. Annotations for special projects, such as the Foreign Fabaceae Project, should be entered with 'Annot.' in the **Det. type** field and the project name as the determiner:

MEL 2068911

This specimen has three labels that bear names: the original collecting label bearing a taxon name written in F.M. Bailey's hand; an old MEL label with the same name in Mueller's handwriting; and a more recent determination on a MEL det. slip that includes extra information about the taxon concept. Even though Bailey and Mueller have given the same name to the specimen, their determinations may be of historical interest and should both be recorded.



- Enter 'Bailey, F.M.' as the determiner, and tick the **Determiner inferred** box to indicate that the determiner was inferred from the label:

The screenshot shows the 'Determinations' input form. The 'Det. type' dropdown is set to 'Det.'. The 'Determiner' field contains 'Bailey, F.M.'. The 'Taxon name' field contains 'Triglochin procerum'. The 'Alternative name' field is empty. Under the 'Qualifier' section, the 'Determiner inferred' checkbox is checked. The 'Extra information' field contains 'eastern variant'. The 'Det. notes' field is empty. The status bar at the bottom indicates '3 of 3'.

Note that, if you didn't recognise the handwriting on the original collecting label, and the taxon name is the same as one of the later determinations, there's no need to enter it as a separate determination.

- Mueller's determination can be entered in the same way as Bailey's determination:

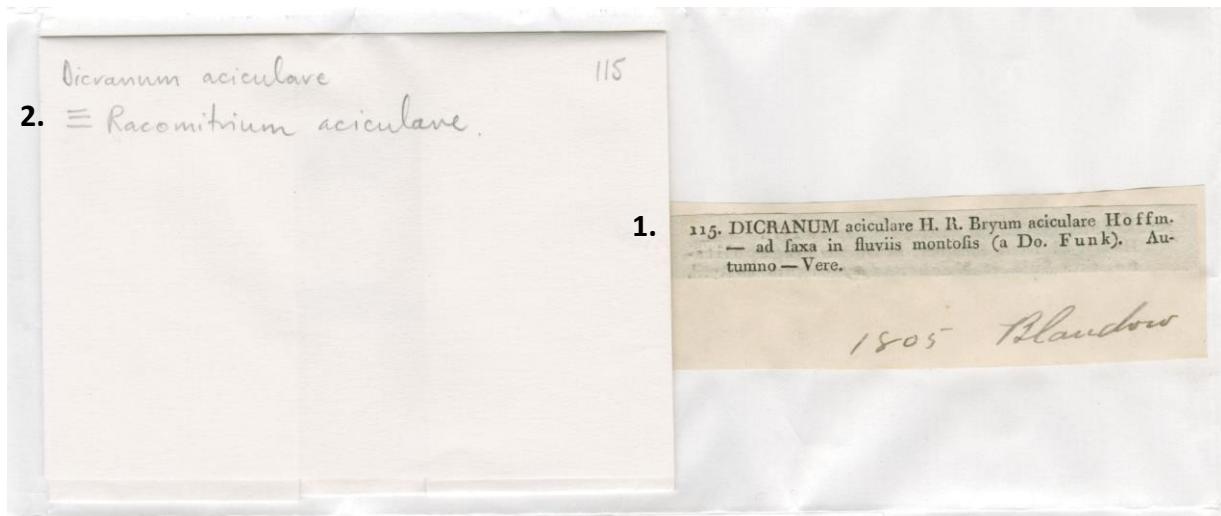
The screenshot shows the 'Determinations' input form. The 'Det. type' dropdown is set to 'Det.'. The 'Determiner' field contains 'Mueller, F.'. The 'Taxon name' field contains 'Triglochin procerum'. The 'Alternative name' field is empty. Under the 'Qualifier' section, the 'Determiner inferred' checkbox is checked. The 'Extra information' field is empty. The 'Det. notes' field is empty. The status bar at the bottom indicates '2 of 3'.

- For Helen Aston's determination (which is partly obscured in the image above), 'eastern variant' should be entered in the **Extra information** field:

The screenshot shows the 'Determinations' input form. The 'Det. type' dropdown is set to 'Det.'. The 'Determiner' field contains 'Aston, H.I.'. The 'Taxon name' field contains 'Triglochin procerum'. The 'Alternative name' field is empty. Under the 'Qualifier' section, the 'Determiner inferred' checkbox is unchecked. The 'Extra information' field contains 'eastern variant'. The 'Det. notes' field is empty. The status bar at the bottom indicates '1 of 3'.

MEL 2040511

This specimen has an older, typed label that appears to have been taken from a list of exsiccata specimens, plus a name change written directly on the moss packet.



1. 'Dicranum aciculare' on the typed label can be treated as the first determination. The author on the label (H. R.) differs from the author given in Tropicos (Hedw.), and a synonym is also given. *Dicranum aciculare* Hedw. should be selected from the **Taxon name** list, and both names and authors on the original label should be entered in **Det. notes**:

Determinations

Det. type: Det. Determiner: Date: Full Date DD/MM/YYYY Current

Taxon name: Dicranum aciculare

Alternative name:

Qualifier: Qualifier rank: Addendum: Determiner inferred

Type status: Type qualifier: Stored under this name Basis:

Extra information:

Det. notes: Dicranum aciculare H. R. Bryum aciculare Hoffm.

Grid

2. The current determination has not been attributed to a person or a project, so only the **Taxon name** field (and the **Current** box) need to be filled in:

Determinations

Det. type: Det. Determiner: Date: Full Date DD/MM/YYYY Current

Taxon name: Racomitrium aciculare

Alternative name:

Qualifier: Qualifier rank: Addendum: Determiner inferred

Type status: Type qualifier: Stored under this name Basis:

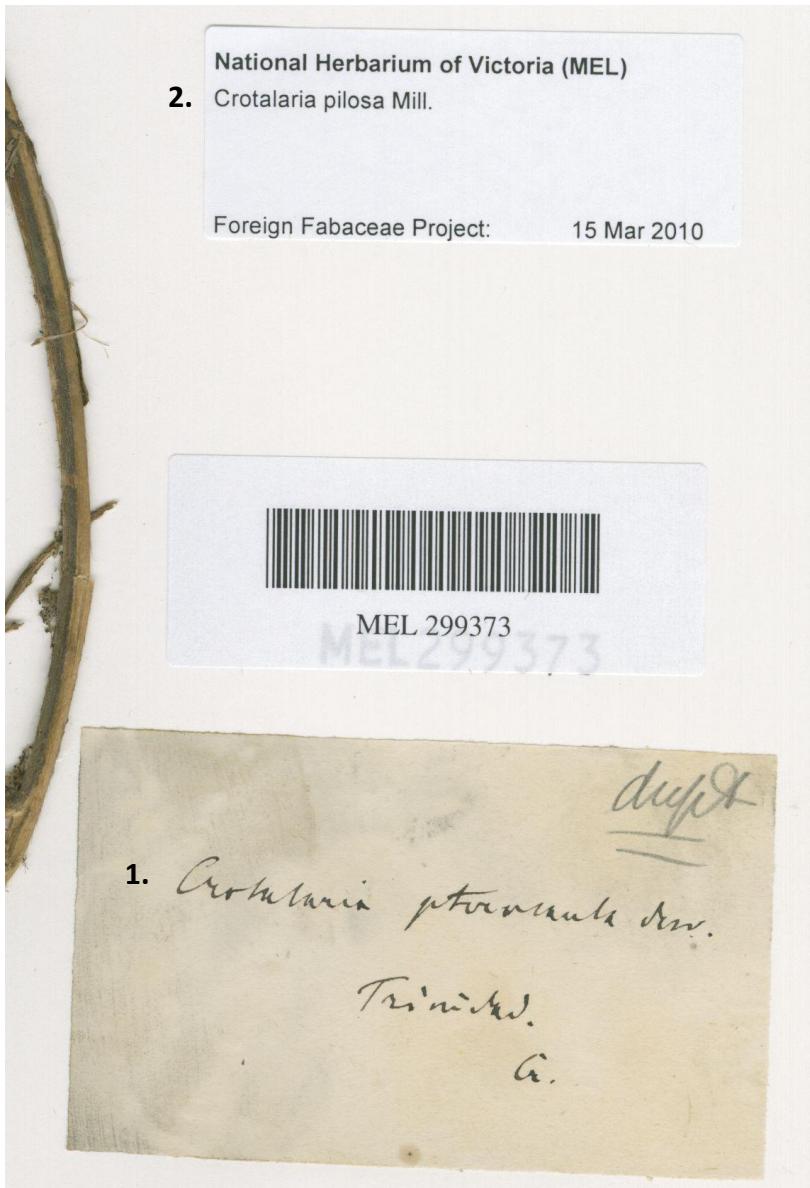
Extra information:

Det. notes:

1 of 2 Grid

MEL 299373

This specimen bears two names: *Crotalaria pterocaule*, which was not in the **Taxon** table, and a recent MEL annotation from the Foreign Fabaceae Project.



1. *Crotalaria pterocaule* is a validly published name, so it can be added to the **Taxon** table, and the determination can be entered without a **Determiner**.

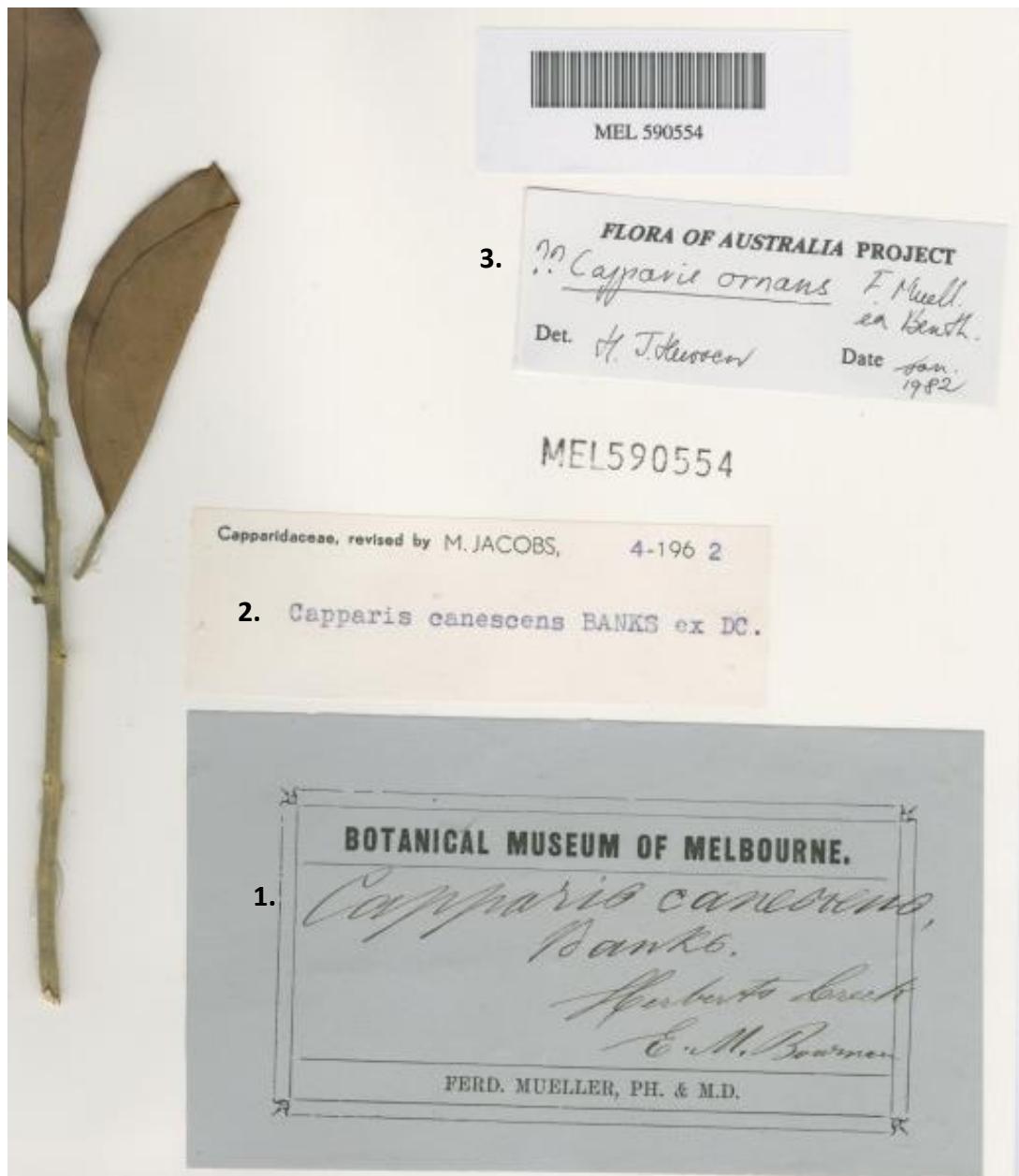
A screenshot of a software interface titled "Determinations". The form includes fields for "Det. type" (set to "Det."), "Determiner" (empty), "Taxon name" (set to "Crotalaria pterocaule"), "Alternative name" (empty), "Qualifier" (empty), "Qualifier rank" (empty), "Addendum" (empty), "Determiner inferred" (unchecked), "Type status" (empty), "Type qualifier" (empty), "Stored under this name" (unchecked), "Basis" (empty), "Extra information" (empty), "Flora" (empty), and "Det. notes" (empty). At the bottom, there are navigation buttons for "2 of 2" and "Grid".

If you are familiar with the handwriting, you could choose to enter the determiner's name and tick the **Determiner inferred** box.

2. The current annotation is straightforward:

MEL 590554

This specimen has three labels: an old MEL label with a taxon name in Mueller's handwriting; an annotation slip with the same name as the blue MEL label, and an uncertain redetermination.



- Enter 'Mueller, F.' as the determiner, and tick the **Determiner inferred** box to indicate that the determiner was inferred from the label:

Determinations

Det. type: Det. Determiner: Mueller, F. Date: Full Date DD/MM/YYYY Current

Taxon name: Capparis canescens

Alternative name:

Qualifier: Qualifier rank: Addendum: Determiner inferred

Type status: Type qualifier: Stored under this name Basis:

Extra information: Flora:

Det. notes:

3 of 3 Grid

- 'Capparidaceae, revised by M. Jacobs' should be entered in the **Det. notes** field, as it provides useful information about the determiner's knowledge of the family:

Determinations

Det. type: Det. Determiner: Jacobs, Marius Date: Mon / Year 04 / 1962 Current

Taxon name: Capparis canescens

Alternative name:

Qualifier: Qualifier rank: Addendum: Determiner inferred

Type status: Type qualifier: Stored under this name Basis:

Extra information: Flora:

Det. notes: Capparidaceae, revised by M. Jacobs

2 of 3 Grid

- Hewson's determination has a qualifier before the taxon name. By default, the **Qualifier rank** will be set to the lowest rank to which the specimen has been determined. Because the qualifier on this det. slip appears before the genus, not the species epithet, you need to select 'genus' from the **Qualifier rank** pick list:

Determinations

Det. type: Det. Determiner: Hewson, H.J. Date: Mon / Year 01 / 1982 Current

Taxon name: Capparis ornans

Alternative name:

Qualifier: ? Qualifier rank: genus Addendum: Determiner inferred

Type status: Type qualifier: Stored under this name Basis:

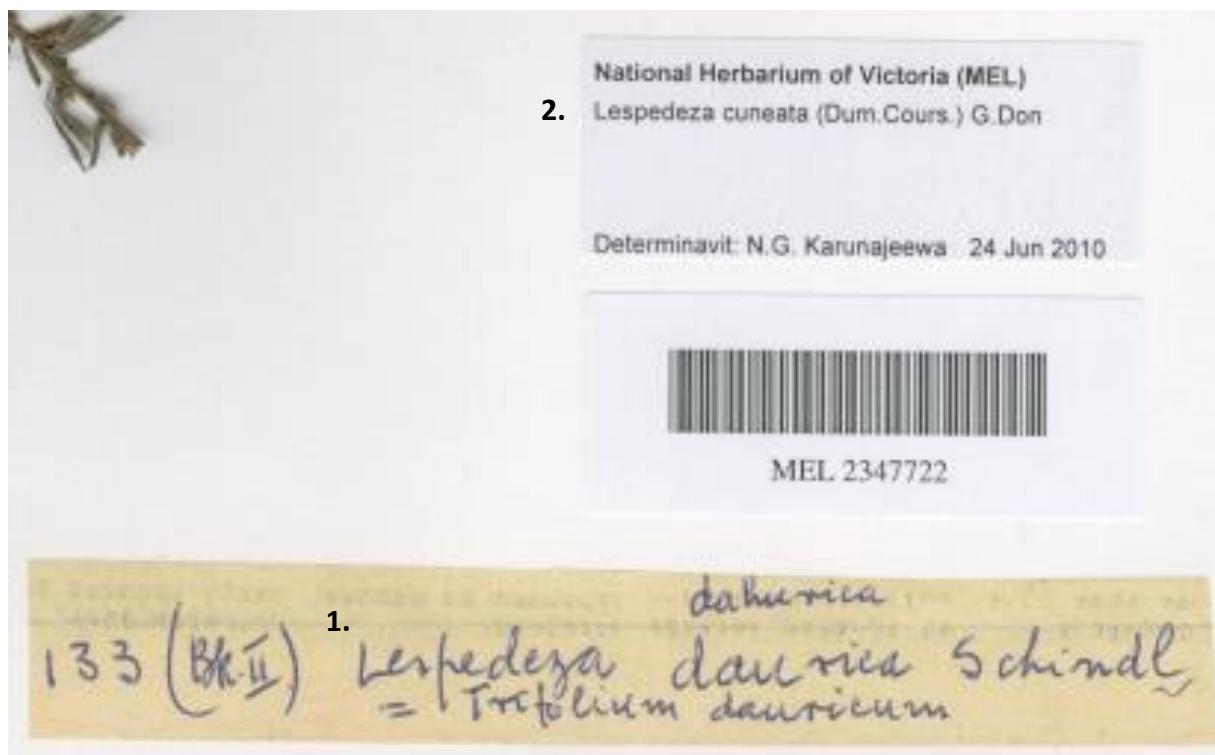
Extra information: Flora: Flora of Australia

Det. notes:

1 of 3 Grid

MEL 2347722

This specimen has one label in the collector's handwriting that bears two synonyms, and a recent MEL determination slip.



1. If there is more than one name on a single label, and they are written in the same handwriting, they can be treated as a single determination. In this case, it is not clear whether the name being applied to the specimen is *Lespedeza davurica* or *Trifolium dauricum*. Unless there is reason to think otherwise, assume that the first (and in this case, more prominent) name is the name the specimen is being determined to. On this label, there are two spellings of the species epithet *davurica*, both of which are incorrect. The correct spelling should be selected from the **TAXON NAME** drop-down list. Enter all the names in the **DET. NOTES** field to record exactly what appears on the label:

If you were familiar with the collector's handwriting, and knew that the label was written by him, you could choose to enter him as the determiner and tick the **Determiner inferred** box.

2. The current determination is straightforward:

Determinations

Det. type: Det. Determiner: Karunajeewa, N.G. Date: Full Date 24/06/2010 Current

Taxon name: Lespedeza cuneata

Alternative name:

Qualifier: Qualifier rank: Addendum: Determiner inferred

Type status: Type qualifier: Stored under this name Basis:

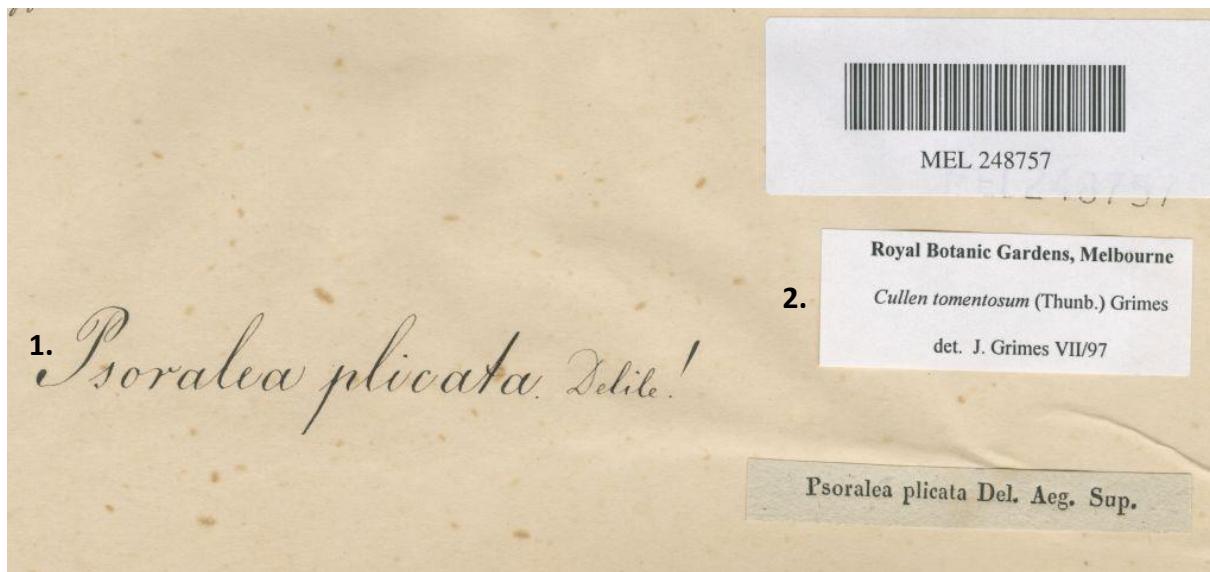
Extra information: Flora:

Det. notes:

1 of 2 Grid

MEL 248757

There are three taxon names on this sheet: one written directly on the sheet in Steetz's hand; a small, typed label reading '*Psoralea plicata* Del. Aeg. Sup.'; and a more recent determination on a MEL det. slip.



1. A taxon name written on the sheet in Steetz's hand can be treated as a determination. 'Steetz, J.' should be entered as the determiner, and the **Determiner inferred** box ticked:

Determinations

Det. type: Det. Determiner: Steetz, J. Date: DD/MM/YYYY Current

Taxon name: Psoralea plicata

Alternative name:

Qualifier: Qualifier rank: Addendum: Determiner inferred

Type status: Type qualifier: Stored under this name Basis:

Extra information: Flora:

Det. notes:

2 of 2 Grid

2. The current determination is straightforward. Note that, if known, the determiner's full initials should be entered in the **Determiner** field, even if only one initial is given on the det. slip:

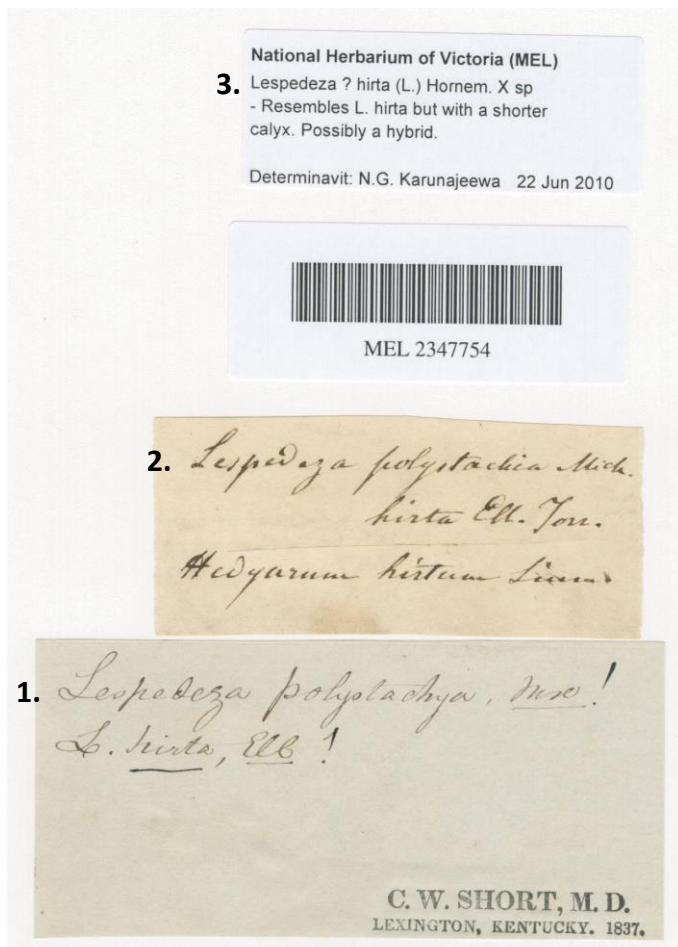
The screenshot shows a software window titled 'Determinations'. It contains fields for 'Det type' (set to 'Det'), 'Determiner' (set to 'Grimes, J.W.'), 'Taxon name' (set to 'Cullen tomentosum'), 'Date' (set to 'Mon / Year 07 / 1997'), and a checked 'Current' checkbox. There are also fields for 'Alternative name', 'Qualifier', 'Qualifier rank', 'Addendum', 'Determiner inferred' (unchecked), 'Type status', 'Type qualifier', 'Stored under this name' (unchecked), 'Basis', 'Extra information', 'Flora', 'Det notes', and navigation buttons ('1 of 2', 'Grid').

The '*Psoralea plicata* Del. Aeg. Sup.' label relates to one of Steetz's collections and should not be treated as a determination. 'Aeg. Sup.' can be entered in the **Original collection** field:

Original collection: Aeg. Sup.

MEL 2347754

This specimen has three labels with taxon names. Although the first taxon name on the bottom two labels is the same, they should be entered as separate determinations because they contain different nomenclatural information.



- Because we treat the first name on a label as the name the specimen was determined to (unless there is reason to interpret the label differently), this determination would have *Lespedeza polystachya* in the **Taxon name** field, and both names on the label entered in **Det. notes**:

The screenshot shows the 'Determinations' dialog box with the following fields filled:

- Det type: Det.
- Determiner: [empty]
- Date: Full Date
- Taxon name: Lespedeza polystachya
- Alternative name: [empty]
- Qualifier: [empty]
- Qualifier rank: [empty]
- Addendum: [empty]
- Determiner inferred:
- Type status: [empty]
- Type qualifier: [empty]
- Stored under this name:
- Basis: [empty]
- Extra information: [empty]
- Flora: [empty]
- Det. notes: Lespedeza polystachya Mx! L. hirta Ell!

At the bottom, it says '2 of 3' and has a 'Grid' button.

- The second label would be entered in the same way (i.e. with the correct spelling of *L. polystachya* in the **Taxon name** field, and the full list of names in **Det. notes**):

The screenshot shows the 'Determinations' dialog box with the following fields filled:

- Det type: Det.
- Determiner: [empty]
- Date: Full Date
- Taxon name: Lespedeza polystachya
- Alternative name: [empty]
- Qualifier: [empty]
- Qualifier rank: [empty]
- Addendum: [empty]
- Determiner inferred:
- Type status: [empty]
- Type qualifier: [empty]
- Stored under this name:
- Basis: [empty]
- Extra information: [empty]
- Flora: [empty]
- Det. notes: Lespedeza polystachya Mich. hirta Ell. Jon. Hedyarum hirtum Linn.

At the bottom, it says '3 of 3' and has a 'Grid' button.

- The current determination would be entered as follows:

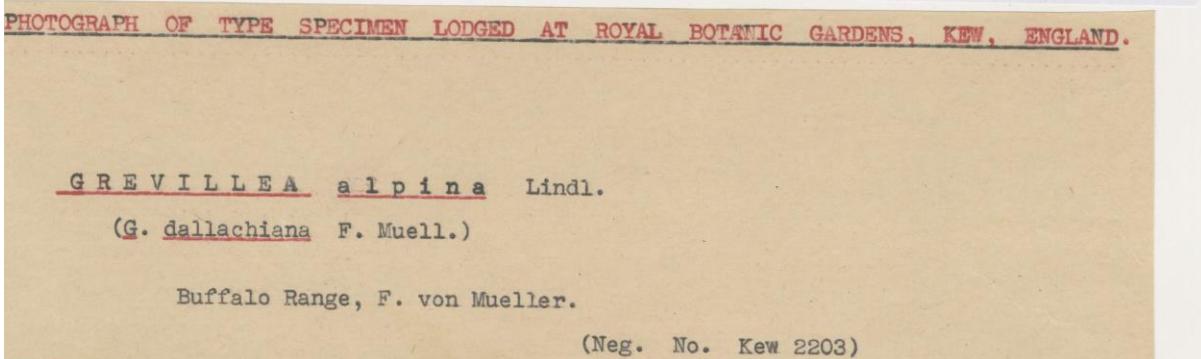
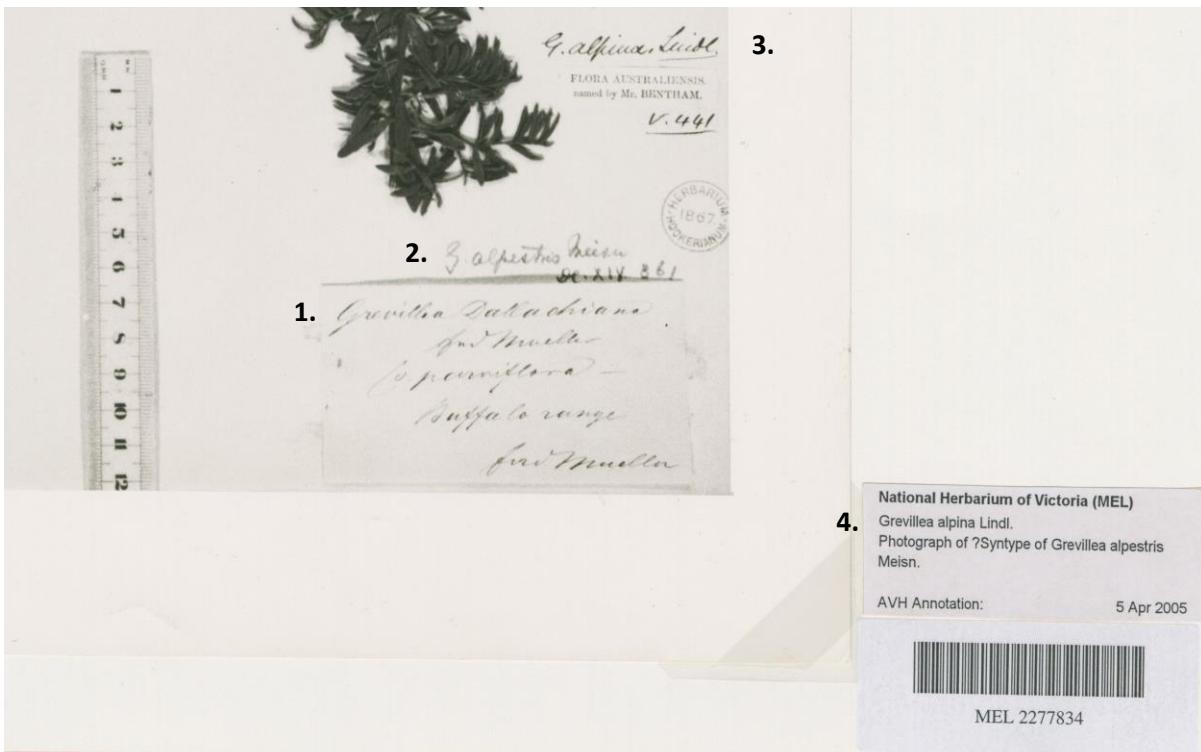
The screenshot shows the 'Determinations' dialog box with the following fields filled:

- Det type: Det.
- Determiner: Karunajeewa, N.G.
- Date: Full Date
- Taxon name: Lespedeza hirta hybrid
- Alternative name: [empty]
- Qualifier: ?
- Qualifier rank: species
- Addendum: [empty]
- Determiner inferred:
- Type status: [empty]
- Type qualifier: [empty]
- Stored under this name:
- Basis: [empty]
- Extra information: [empty]
- Flora: [empty]
- Det. notes: Lespedeza ? hirta (L.) Hornem. X sp - Resembles L. hirta but with a shorter calyx. Possibly a hybrid.

At the bottom, it says '1 of 3' and has a 'Grid' button.

MEL 2277834

This specimen has four separate determinations. The large, yellowish label at the bottom of the label looks like a herbarium label of sorts, so the names on that label wouldn't be considered determinations. The oldest determination is on the label in Mueller's hand, directly above which is a redetermination in someone else's handwriting. To the right of the specimen is a redetermination by Bentham, and the most recent annotation is a MEL det. slip that indicates the type status of the specimen.



1. Mueller's determination should be entered with 'Mueller, F.' as the determiner, and the **Determiner inferred** box ticked. Mueller has written '*Grevillea dallachiana* Ferd. Mueller [...] *parviflora*' on the label. No infraspecific taxa of *G. dallachiana* have been published, and Mueller listed *G. dallachiana* and *G. parviflora* as distinct taxa in an 1853 report. The best option in this situation is to enter *Grevillea dallachiana* in the **Taxon name** field and enter the names as they appear on the label in the **Det. notes** field:

Determinations

Det type: Det Determiner: Mueller, F. Date: Full Date DD/MM/YYYY Current
Taxon name: Grevillea dallachiana Alternative name:
Qualifier: Qualifier rank: Addendum: Determiner inferred
Type status: Type qualifier: Stored under this name Basis:
Extra information: Flora:
Det. notes: Grevillea dallachiana Ferd. Mueller [...] parviflora

14 | 3 of 4 | 15 | Grid

2. 'G. alpestris Meisn.' is written directly above the first determination. This should be entered as a separate determination, with only the **Taxon name** field filled in:

Determinations

Det type: Det Determiner: Date: Full Date DD/MM/YYYY Current
Taxon name: Grevillea alpestris Alternative name:
Qualifier: Qualifier rank: Addendum: Determiner inferred
Type status: Type qualifier: Stored under this name Basis:
Extra information: Flora:
Det. notes:

14 | 4 of 4 | 15 | Grid

3. The determination bearing the name *G. alpina* indicates that Bentham provided the name, so he can be entered as the determiner. The note below the name should be entered in **Det. notes**:

Determinations

Det type: Det Determiner: Bentham, G. Date: Full Date DD/MM/YYYY Current
Taxon name: Grevillea alpina Alternative name:
Qualifier: Qualifier rank: Addendum: Determiner inferred
Type status: Type qualifier: Stored under this name Basis:
Extra information: Flora:
Det. notes: Flora Australiensis named by Mr Bentham, V. 441

14 | 1 of 4 | 15 | Grid

4. The most recent det. slip is an AVH annotation that repeats the current name and provides the type status. There is no need to include the current name from the AVH annotation as a separate determination, as it doesn't add any information; it is better to keep Bentham's determination as the current one, because it is more informative. The type determination needs to be added with the **Det. type** as 'Type status' rather than 'AVH annot.', and the **Type status** and **Type qualifier** fields filled in. Where the specimen is stored under the typified name, tick the **Stored under this name** field (type specimens are stored under the most recently published name of which the specimen is a type). Make sure that the **Current** box is not ticked for 'Type status' determinations:

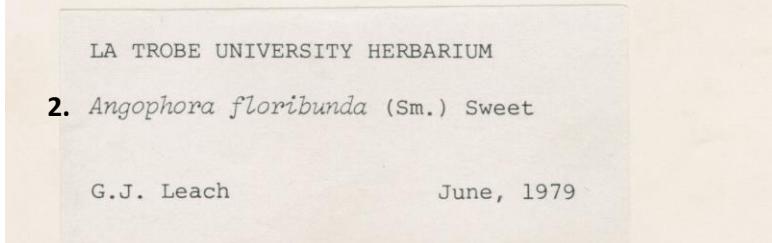
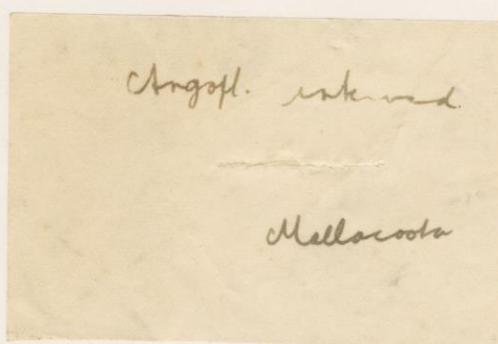
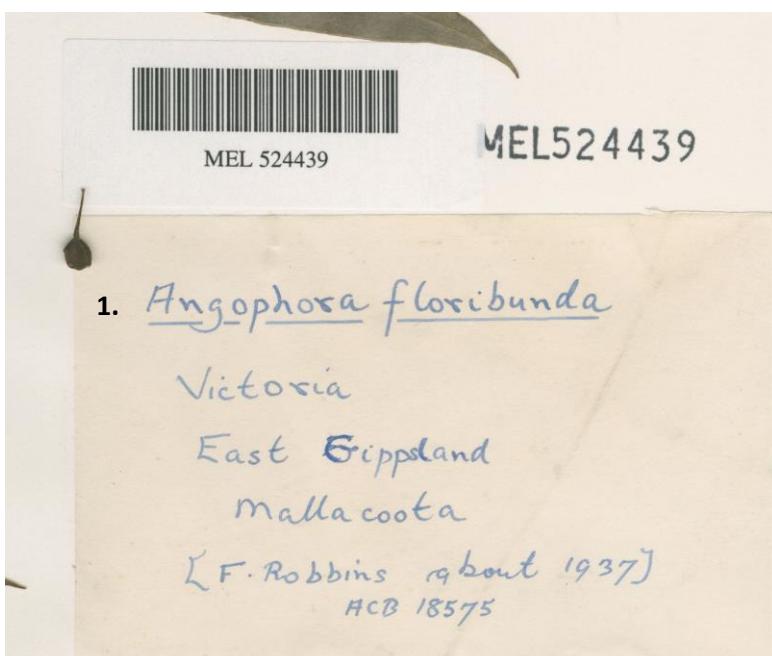
Determinations

Det type: Type status Determiner: Date: Full Date 05/04/2005 Current
Taxon name: Grevillea alpestris Alternative name:
Qualifier: Qualifier rank: Addendum: Determiner inferred
Type status: Syntype Type qualifier: ? Stored under this name Basis:
Extra information: Flora:
Det. notes:

14 | 2 of 4 | 15 | Grid

MEL 524439

There are three labels with names on this specimen. The middle label is very difficult to read, so there's no need to add it as a determination. The top label is written in A.C. Beaglehole's hand, and bears the same taxon name as the det. slip at the bottom of the sheet. Whether or not these should be treated as separate determinations is quite subjective. If you consider Beaglehole to be the determiner of the name on the top handwritten label then they should be entered as separate determinations, otherwise a single determination record would suffice.



1. If you are interpreting the taxon name written on the top label by Beaglehole as a determination, enter it with 'Beaglehole, A.C.' as the determiner and tick the **Determiner inferred** box:

The screenshot shows the 'Determinations' dialog box. The 'Taxon name' field contains 'Angophora floribunda'. In the 'Determiner' field, 'Beaglehole, A.C.' is entered. The 'Determiner inferred' checkbox is checked. Other fields like 'Date' (Full Date), 'Qualifiers', and 'Type status' are visible but not filled.

2. The La Trobe University Herbarium det. slip is straightforward:

The screenshot shows the 'Determinations' dialog box. The 'Taxon name' field contains 'Angophora floribunda'. In the 'Determiner' field, 'Leach, G.J.' is entered. The 'Determiner inferred' checkbox is unchecked. Other fields like 'Date' (Mon / Year), 'Qualifiers', and 'Type status' are visible but not filled.

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