

The primary digitization phase of the New England Vascular Plants project is focused on capturing images of specimens and on capturing data for a sub-set of label data fields (see Table 1). This document provides guidelines for capturing label data using a web-based data entry form created for the project.

Accessing the site

1. To access the website you will need a username and a password. To obtain login credentials email patrick.sweeney@yale.edu with (for each user):
 - a) First and Last Name
 - b) email
 - c) name of institution
2. To access the site visit <http://data.nevp.org> and supply your username and password (will be provided to you).

Guidance for entering records

1. To enter a new record click the **Data Entry Form** link.
2. Scan the QR code into the **QR Code field**, if your institution uses QR codes.
 - a) Click the **Reuse QR Code** toggle if you want to retain the QR code data for subsequent specimens (e.g., all specimens in a folder).
3. Scan barcode into **Barcode** field (required field).
4. If **Collection Code** is contained in QR code, leave blank
 - a) Click the **Reuse Collection Code** toggle if you want to retain Collection Code for subsequent specimens (disregard if using QR code data and collection code is in QR code).
5. Entering **Scientific Name**:
 - a) If the scientific name is contained in the QR code, leave **Scientific Name** field blank
 - b) If scientific name is not in QR code, type the name and select from the auto-completion drop-down list
 - After clicking a name in the list, the **UUID** field will auto-populate
 - c) If scientific name is not in drop-down:
 - If name taxon is not a hybrid, click the **ENTER NEW TAXON** link and populate the relevant fields. When the form is submitted, the name will be added to the taxon authority table and available for subsequent records.
 - If the name is a hybrid, see the **Guidance for entering hybrids** section.
6. Entering **Collector**:
 - a) Begin typing the name of the collector into the collector list:
 - If collector name (or team) is in list, choose name; the **CollectorID** field will auto-populate.
 - If collector name (or team) is not in list, type collector name into field.
 - If typing in a team, separate individuals with a pipe (|) - e.g., "M. L. Fernald | C. C. Godfrey".
7. The **Coll Date** fields are for the earliest and latest collection dates. If only one date is provided, type it into the **Coll Date (Earliest)** field. Dates must be in the format of YYYY-MM-DD (e.g., 2000-09-25). The Coll Date fields will be processed to create a DwC compliant EventDate value.
8. Entering **Locality** fields:
 - a) The locality fields are provided with auto-completion functionality.
 - b) The fields will filter by their parent (e.g., only towns in Connecticut are available in the drop-down if the State/Province field is populated).
 - c) If town is selected from the drop-down, county will be auto-populated before insertion into

Symbiota.

9. Values entered into the **Comments** field and the flag record check box are for your internal use and are not passed on to Symbiota. Flagged specimens will not be exported to Symbiota and will remain in the data entry queue.
10. After submission of data, a message will report the status of the submission. If successful, a link will be provided whereby you can edit or delete the specimen, if desired.

Guidance for entering hybrids not in look-up table

1. If a named hybrid species (nothospecies), place elements of name in genus, species, authorship fields, prepending the specific epithet with a multiplication sign × (Unicode 00D7). Likewise for named hybrids at other ranks.
2. If a hybrid other than a named hybrid:
 - a) place the entire hybrid name including the × separator (or separators) and the authors in the scientific name field. Leave the authorship field blank.
 - b) If all constituents of the hybrid are in the same genus, place the generic name in the genus field. If more than one genus is involved, leave the genus field blank.

Do not use the letter x in place of the multiplication sign × .

Table 1. List of fields to be captured. High priority items are crucial to meeting goals of project. Medium priority fields are not crucial to goals of project, but are of significant value for QC and duplicate finding purposes.

Field Name	Darwin Core Value	Priority	Note
Barcode	dwc:catalogNumber	required	
Collection Code	dwc:collectionCode	required	can be supplied in QR code
Scientific Name	dwc:scientificName	high	can be supplied in QR code
Collector	dwc:recordedBy	medium	can be supplied in QR code
Coll Number	dwc:recordNumber	medium	
Coll Date (earliest & latest)	dwc:eventDate	high	derived from earliest & latest coll. dates
Verbatim Coll Date	dwc:verbatimEventDate	medium	important if date is ambiguous
Country	dwc:country	high	
State/Province	dwc:stateProvince	high	can be supplied in QR code
County	dwc:county	low	can be supplied in QR code or derived from state + town
City	dwc:municipality	high	
Locality	dwc:locality	medium	supply if town not provided

Editing records

Un-exported records are available for editing. Click the **Specimen Table** link (beneath the page title or on the login page) to view the **Specimen Record Table** with a table of specimens (with edit links) and a form to search for specimen to be edited. The **Specimen Record Editing** form works similarly to the **Data Entry Form**.

Exporting data for ingest into Symbiota

This should be done frequently (at most weekly). Clicking the Export button on the **Specimen Record Table** page will prepare specimen records for import into the CNH portal. Only un-flagged specimens with corresponding images on iPlant will be exported. After export, the records will no longer be available for editing within the website.

Quick date capture from (for skeletal record creation)

A form is available that allows for the capture of the folder-level QR code data and barcode. This form is available from the main menu and is located at http://data.nevp.org/data_entry_lite.php. This form can be used to create skeletal records very quickly. These records and their respective images can be imported into Symbiota where further transcription can take place from the image and using Symbiota's Occurrence Editor.