Barcoding and Preliminary Data Capture

What follows is a description of the procedure we are using at NHA (University of New Hampshire) for barcoding and creating a "skeletal" database record for each specimen. Feel free to contact us for suggestions on adapting it for your collection. The macroalgal collection at NHA had not been barcoded or databased before the NSF ADBC project started. Overall, we are working through the collection cabinet by cabinet, cubby by cubby, folder by folder. This work is being done by undergraduate students.

Keep in mind that the goal here is to barcode the specimens and to create a skeletal record for each specimen that will be completed later after the specimen has been imaged and the image and skeletal record have been uploaded to the macroalgae project portal (macroalgae.org). There are a number of tools on the portal that simplify transcription of the rest of the label information. For example, when the skeletal data is uploaded, the genus, species and any infraspecific epithet are checked against the AlgaeBase and the authors of the taxon name and higher taxonomy (family, etc.) are automatically filled in. The portal also has OCR capabilities that work very well on type labels and saves a lot of typing. There is also a built in link to GeoLocate that can interpret locality information and return latitude and longitude directly into the specimen record. There are more details on transcribing labels and georeferencing localities in other documents

Materials and Equipment: Computer with MS Excel, the BarcodeTemplate.xlsx worksheet (from macroalgae.unh.edu), a barcode reader (optional), barcodes (see below for ordering info), drop tags.

Step by Step

1. We started by numbering the cabinets and cubbies to make it easier to return the folders to their original spots.
2. Beginning with cubby #1 in the first cabinet, all of the folders in the cubby are moved to a work table. After checking that the folders are in the proper order (generally, this is alphabetical by genus and species), the folders are numbered with the cabinet, cubby and folder number. Again, this is just to make it easier to return them to their correct spots.
3. One folder at a time, a barcode is attached to the first specimen. We attach the barcode just above the primary specimen label to make it easy to see later in the specimen image when zoomed in on the label. If there is no space above the label, we attach it vertically to the left of the specimen label.
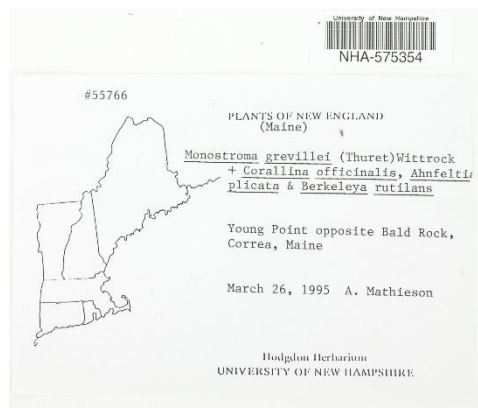
4. The barcode is scanned (or typed) into the "catalognumber" field of the first blank row of the Excel template. The genus, and specificEpithet that the specimen is filed under is typed into the corresponding fields in the Excel row. Any other fields that will not change from sheet to sheet (e.g. the "recordEnteredBy" field) are also typed in. You don't need to fill in all of the fields at this stage. At NHA, we also fill in the country, state and county only because our collections is organized geographically within each taxon. So if, for example, we have 9 specimens of *Monostroma grevillei* from Hancock County, Maine, USA, they will all be together in the same folder. When we enter the genus, species, county, state and country for the first *Monostroma grevillei* specimen, we can just copy it to the next 8.
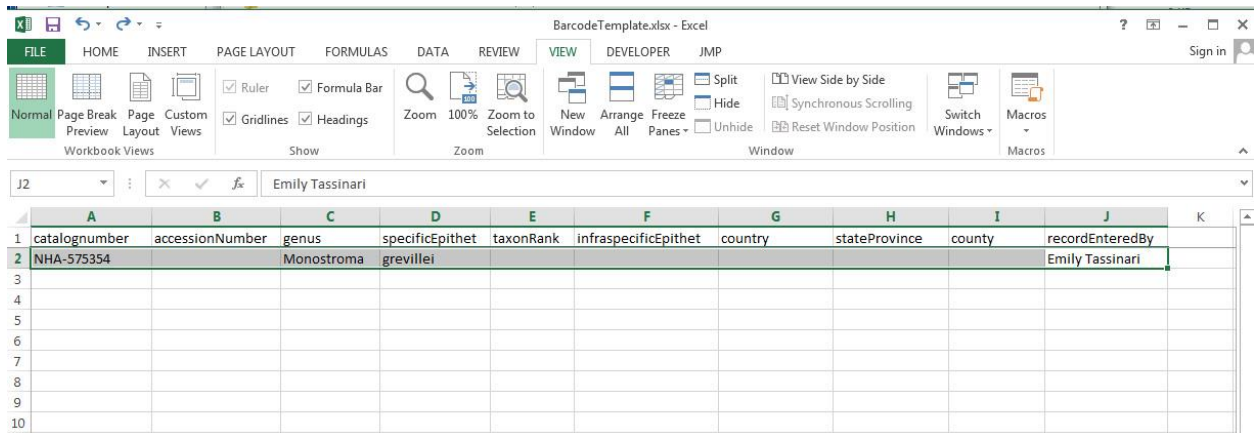
5. Barcodes are attached in sequential numeric order to the rest of the sheets in the folder (with the same taxon name).
6. The first row for the taxon in the Excel worksheet is copied down the worksheet to as many rows as there are specimens of that taxon. Do this by selecting the cells from column A through J in the first row of the taxon and then dragging the tiny square that appears at the bottom of the cell in column J down the worksheet. By doing it this way, the barcode number will be automatically incremented for each row. Note that if your specimens were previously barcoded
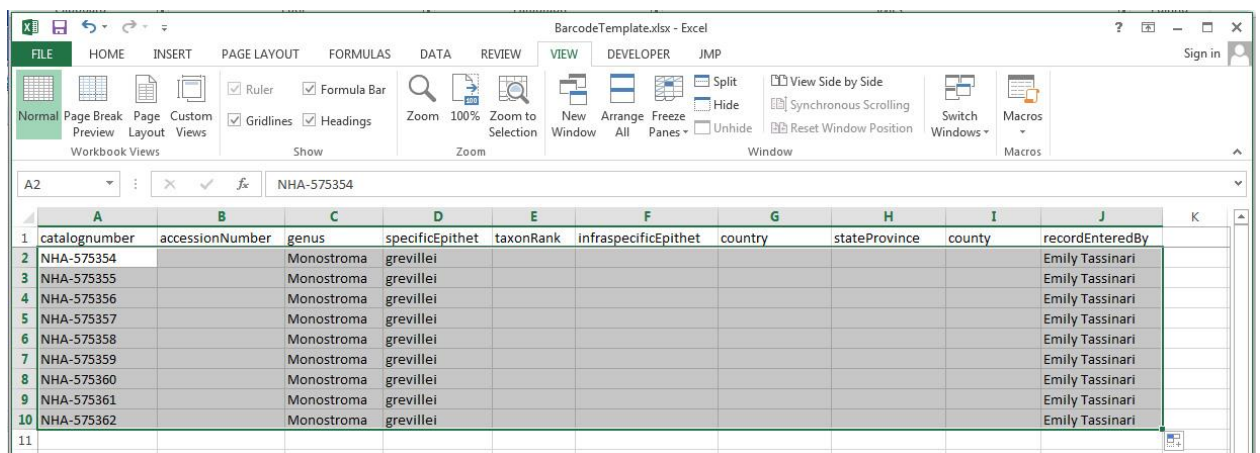
and are not in numeric order, you can still copy the taxon name, but you will need to use the barcode reader to enter the barcode for each row.

7. When all of the folders from a cubby have been barcoded and logged in the Excel worksheet, they are returned to the cubby and a drop tag that says "Barcoded Above Here" is tucked under the bottom folder.
8. We put a sticky note on the front of the cabinet so that the next person barcoding knows which cabinet we're working on.
9. We backup the file daily and when we have around a thousand records, we save the Excel worksheet as a .csv file and upload it to the portal and start a new Excel file.

Special Considerations:

a. For specimens that take up more than one sheet, we use only one barcode (attached near the primary label) then later we image each of the sheets and give each image the same name, but with a _1, _2, _3 sufffix. Eg. NHA-123456_1, NHA-123456_2, etc. That way when you bring up the record for the specimen on the portal, all of the images will come up together. If you give each sheet a separate barcode, they will be treated as different specimens.
b. If a sheet has two or more different specimens, each with its own label, give each specimen its own barcode. Position it next to the label for that specimen. Later, when you image the sheet, image the entire sheet multiple times (once for each barcode) and name the first image for the first barcode and the second image for the second barcode, etc.

Order Information for Barcode Labels

Most herbaria use barcodes that start with the herbarium acronym followed by a 6 or 7 digit number. For example, we use NHA-123456 as our format. There are a number of places to get barcode labels. We have been using these: