Beginner's Instructions for new Participants of the Consortium of North American Lichen Herbaria

by **F. Bungartz**, Collections Manager of Lichens and Digital Data, Arizona State University

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Welcome to the Consortium of North American Lichen Herbaria (http://lichenportal.org/)!

As the Portal Administrator I recently created a new live collection for your institution and we are all excited that you will contribute to this biodiversity data portal, sharing your specimen data with the international lichenological community.

The instructions below provide some general basic information how to manage your specimen data live inside CNALH. If you are familiar with any other Symbiota Portal (e.g., SEINet, the Consortium of North American Bryophyte Herbaria, etc.) you will likely already know your way around and skip this beginner's guide.

If you are a student or volunteer and have been assigned editor for data entry into an already existing collection you can skip the part about reviewing the metadata of a newly created collection.

When getting started, any newly created collection is typically empty. It is possible to batch-upload specimen records from a spreadsheet and to get you started it is quite possible that I already uploaded some of the records you sent me. However, from now on you should familiarize yourself with the system and use the data entry tools provided to manage your existing collections and enter new occurrence (= specimen) records.

OK, here we go ...

Log-out and then log back again into your account (to refresh your user priviledges)

1. Go to "My Profile"
2. If some of the Collection Metadata for your collection that I entered is erroneous, please change it via the "Administrative Control Panel - Edit Metadata and Contact Information", else, if you are not managing a newly created collection...
3. Select the "Specimen Management" tab
4. Under "Collection Management" select "NAME OF THE COLLECTION (Acronym)" (this is of course a dummy name; only the collections that you actually have access to will show up in this *Specimen Management* tab here)
5. In the "Data Editor Control Panel" select "Add New Occurrence Record" if you want to enter new records from scratch or choose "Edit Existing Occurrence Records", if you want to check out the data I uploaded.
6. If you select "Edit Existing Occurrence Records" a search box will open, where you can define the records you want to edit; if you leave everything blank and hit "display table" a table with all records already entered will show [e.g., your data that I just uploaded ...].
7. In the table hit the SymbiotaID to access the editor for that record
8. Alternatively: if you selected "Add New Occurrence Record" that editor will automatically pop up with all fields left blank.

9. At the top of the page are small arrows |< <<| x of y |>> >| which allow you to navigate through the specimens entered or via the loupe you can modify the search criteria and get to the table display again.

10. The first tab is for entering occurrence data (= specimen records), the second tab allows you to enter a determination history of annotations for each specimen (for newly created collections, I entered an example); the third tab allows you to upload images manually, then there is a tab to link resources, or you can transfer and delete records from the admin tab.

11. One thing I often notice when batch-uploading data into a newly created collection: many collection that just got started are often NOT using catalog numbers, but the specimens are then typically identified only by the combination "Collector+Collector's Number". I would strongly recommend that you think about using unique catalog numbers, ideally barcodes. These catalog numbers should be unique to your collection, ideally are barcodes with a fixed number of digits, for example GAM005678 (I strongly recommend you use barcodes with your herbarium acronym and a fixed, even number of digits, i.e., leading zeros, no spaces; if you want to put emphasis on the different collections, add an "L" for lichens: GAML005678); the collector field and collector number in combination also uniquely identify a specimen. **Since your collection is a live data set the Symbiota GUIDs are also unique numbers that identify your specimens; they are generated automatically and *cannot* be modified**.

12. Also again: since your data are **live** you should from now on **manage all your data only inside the portal**. All changes you make outside (e.g., in the spreadsheet that you just sent me) will not show up online. Therefore: **manage all data inside the portal !** (the only exception might be that you are traveling to remote places without internet access; in that case it is possible to download a backup and edit these records and later upload the changes; this, however, only works if nobody else in the meantime modifies any data; if you absolutely have to do this we must coordinate this)

13. When you enter new records, under "Latest Identification" you can select a name from CNALH taxonomic thesaurus by starting to type, for example "*Acarospora socialis*". The system will fill in author and family. If a name does *not* occur in the drop-down and author and family are not filled in automatically, it means that the name is *not* (yet) part of CNALH's taxonomic thesaurus. You can contact me to add any name that has been published, but generally *unpublished* names (i.e., *nominae nudae*, nom. nud.) should not be added to the thesaurus. Sometimes it may be necessary to quickly enter a name that is not in the thesaurus and it is even possible to enter any kind of working name without necessarily adding it to the thesaurus. However, please be careful! Unless necessary you should try to avoid adding to much "nonsense" that will be piling up, names not in CNALH's thesaurus. Ideally every name that you enter should be a published, accepted name.

14. Most of the other fields are pretty self-explanatory and the small green "?" explain what kind of content should be entered into each field. I suggest you use a standardized way to enter collector and determiner name, for example always "Bungartz, F." or "Frank Bungartz" or "F. Bungartz" (the system allows you to enter this any way you like, but it still makes sense to be somewhat consistent).

15. I suggest you use the "Processing Status" field to design yourself a data entry workflow, you can use the categories in that field to mark specimens data entry progress.

16. If you need to print any labels for your specimens, there is a field called "Label Project" under "Curation". You can create a new Label Project by simply entering a name here. From the Data Editor Control Panel you can then select "Print Specimen Labels" and there Select the Label Project that you just created from the dropdown, so that you print only labels for the specimens that you want.

17. Finally, with "Go to New Occurrence Record" you will be presented a new blank record unless you decide to check the option to carry over the locality data from one record to the next.

18. There are tutorials at http://symbiota.org/docs/symbiota-introduction/symbiota-help-pages/
19. There is lots more buried under the hood, like loan management, printing labels, etc. - but this should get you started ...

All the best. In know this is just the start. Please don't hesitate to contact me, if you have any questions.