Remote Databasing in Specify7

For UMMZ Insect Collection

SPECIFIC INSTRUCTIONS FOR ENTERING OUR DATA:

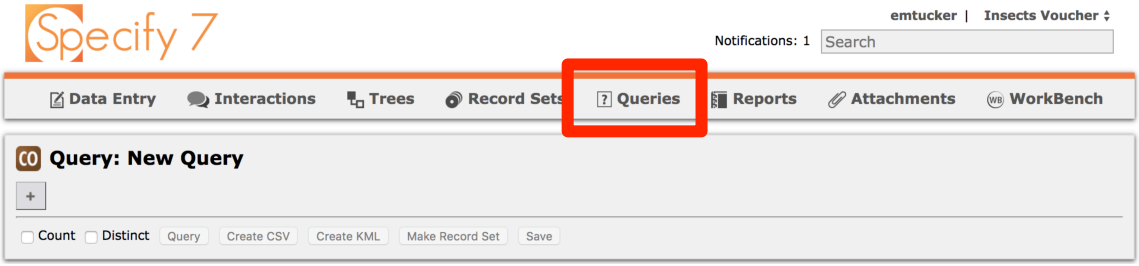
LET ME KNOW IF YOU HAVE ANY QUESTIONS!! It is much easier to enter it right the first time then to fix errors introduced!

Pick a group to work on transcribing:

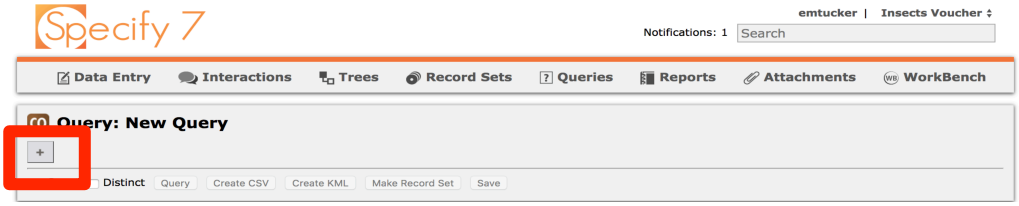
- Go to the shared Google Spreadsheet **"Remote Specimen Transcription TPT"**
- Pick a taxonomic group to work on and enter your name under "Assigned to" so that we don't duplicate efforts

Create a query and record set for your group:

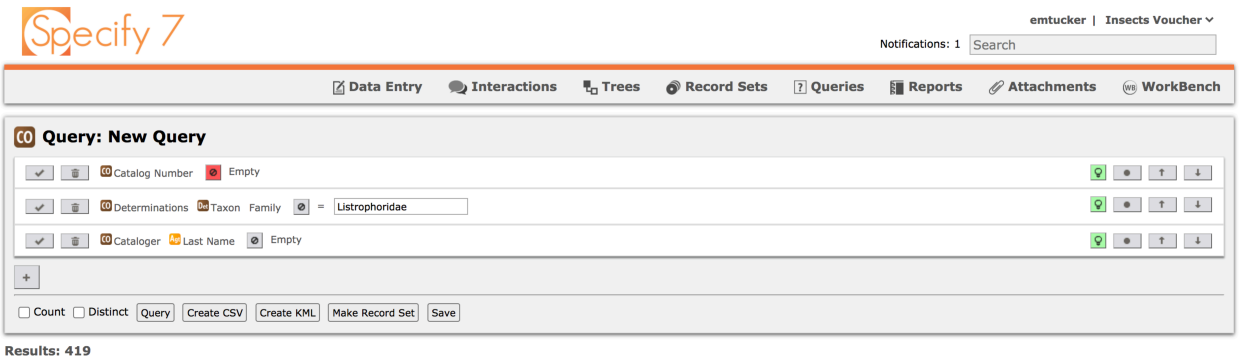
- Click "**Queries**" at the top of the page



- Click "**new**" when the pop up box asks
- Choose "**Collection Object**" for the type of query
- Click the **"+"** to add a field



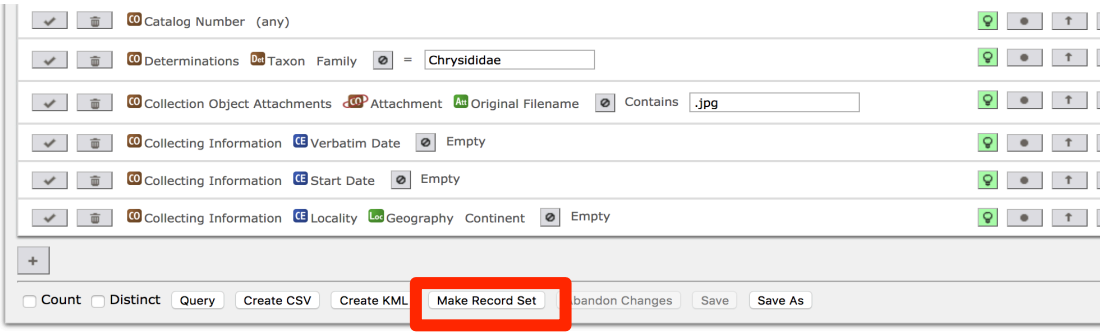
- Select "**Catalog number**", then select "**=**"
- Select "empty" from drop down options
- Then click not equal to **"≠"** button (so it only shows entries with catalog numbers)
- Click the **"+"** button again to add another line
- Add "**Determinations**" → "**Taxon**" → "**Family**" → Select **"="** → enter your family name from the Google spreadsheet (alternatively this could be an order or genus if that is the group you choose – just enter order or genus instead of family under taxon above). There may be additional instructions for certain taxon groups in the spreadsheet.
- Add another line
- "**Cataloger**" → "**Last Name**" → "**Empty**" (this should make sure you don't pull up any records already transcribed)
- Your finished query should look like this (except the family name will be different):



- Click the **"Save As"** button at the bottom so you don't need to do this again except for changing the family name when you move to another group on the spreadsheet
- Give this query a name - I called mine "Mites to Transcribe", but you can name it anything you want.

Create a record set to work with:

- Click "**Query**" at the bottom of the page if you still have the query page up (this may take a little while depending on the number of records it finds)
    - If you are no longer on the query page: Click the big "**Queries**" button on the top of the page, select the query you saved when it asks, then click the "Query" button on the bottom of the page
- Wait until the query finishes. There will be a long list of records and it will say "Results: ####"
- Click the "Make Record Set" button

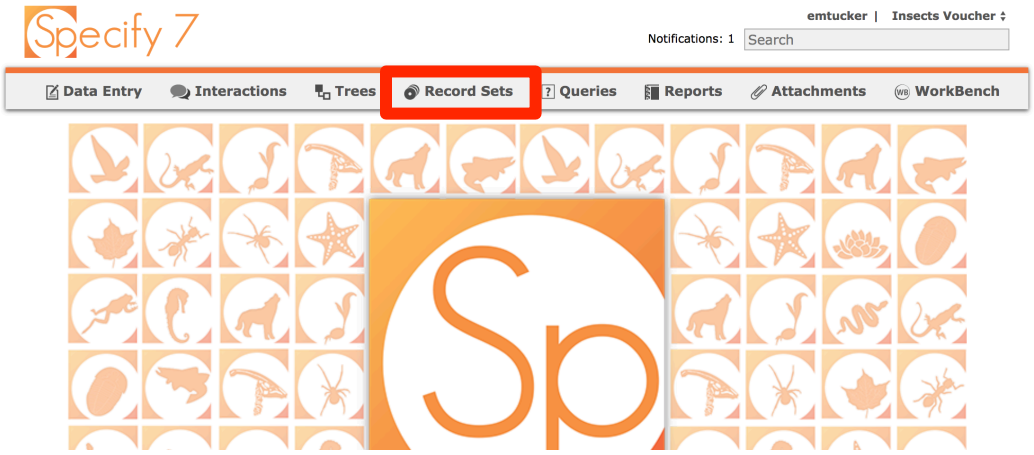


- Give this record set a name that is meaningful to you (maybe something like "Mite Family – Your Name", but it can be anything i.e. "dataset 1" etc.)

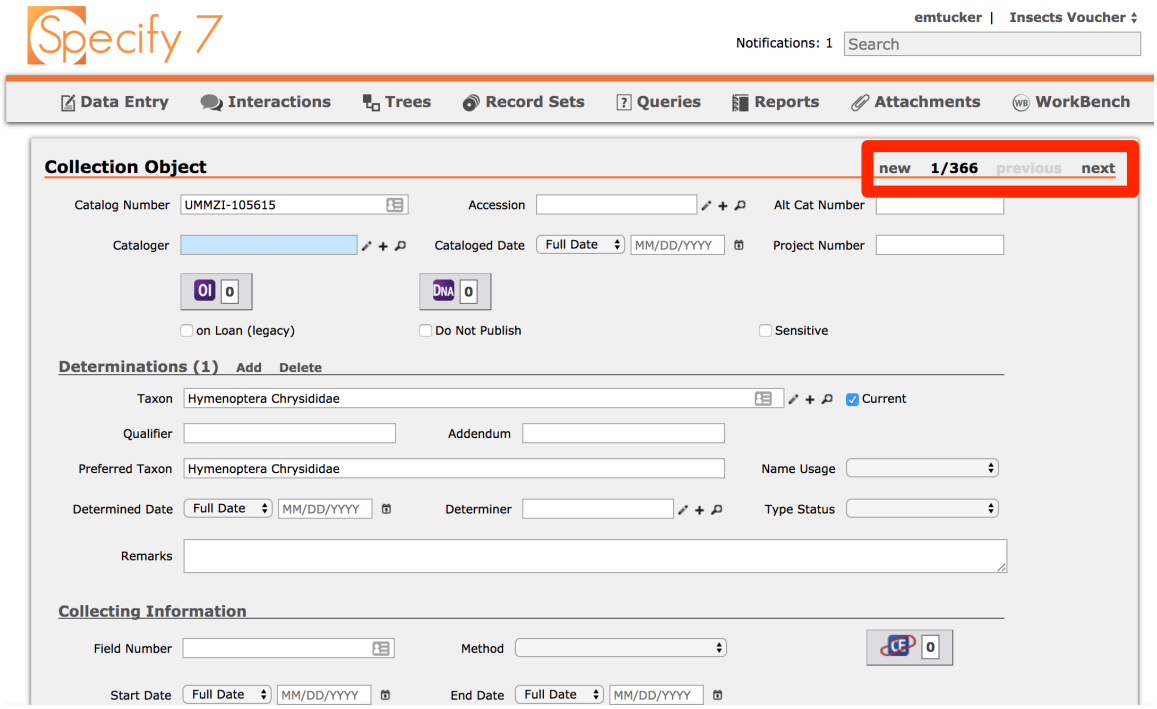
- Save
- When prompted, you can click “yes” if you are going to work on data transcription and entry now, or “no” if you want to work on data entry later.

Entering data from a record set:

- On the main Specify page click the “Record Sets” button at the top of the screen (skip this step if you clicked yes after creating the record set)



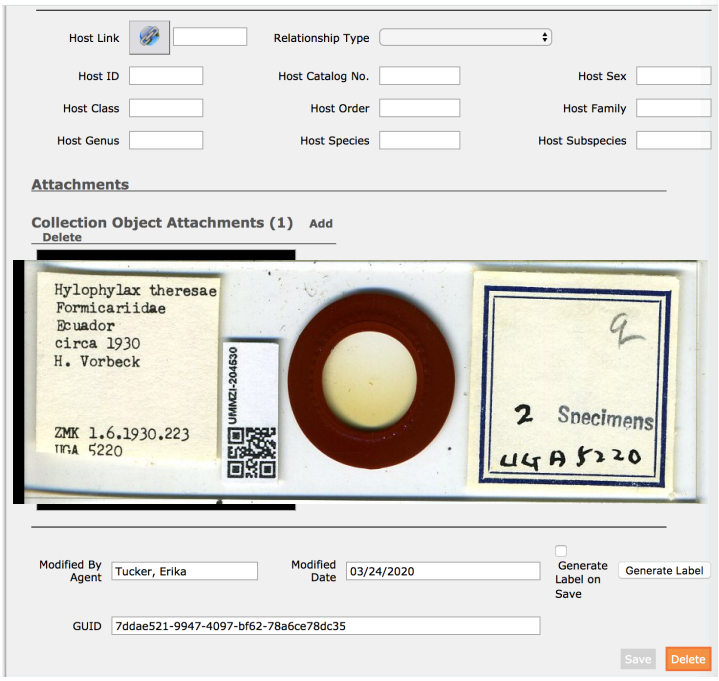
- Choose the record set you want to work on
- You should see a screen similar to this:
- Note the “new 1/366” at the top. This shows you how many records are in your record set and the “next” button allows you to navigate between records in your record set.



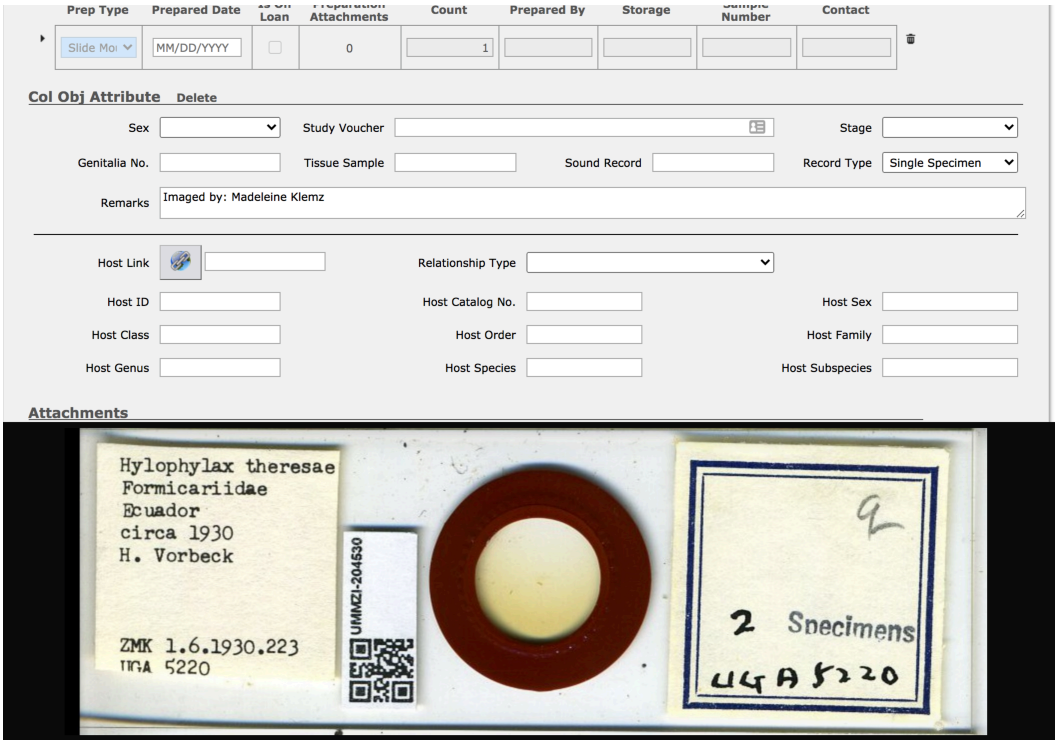
- ***TIME SAVING NOTE*** If you are working on a very large dataset and already transcribed a bunch of records, you can go back to your saved query, re-query the data you want to work on, and create a new record set that will no longer include the records you already transcribed. This will save you clicking through many, many, pages of already transcribed records to get to the empty ones.

Data entry:

- The "cataloger" is you. Start to type in your last name and a dropdown menu should appear that contains your name (the more you type of your last name the more accurate the dropdown list of options becomes). You will not be able to save if you do not enter a cataloger.
- Enter "**NSF TCN: Terrestrial Parasite Tracker**" in the "**Project Number**" box (under the "Alt Catalog Number" near the top)
- Scroll to the bottom of the page where the image is

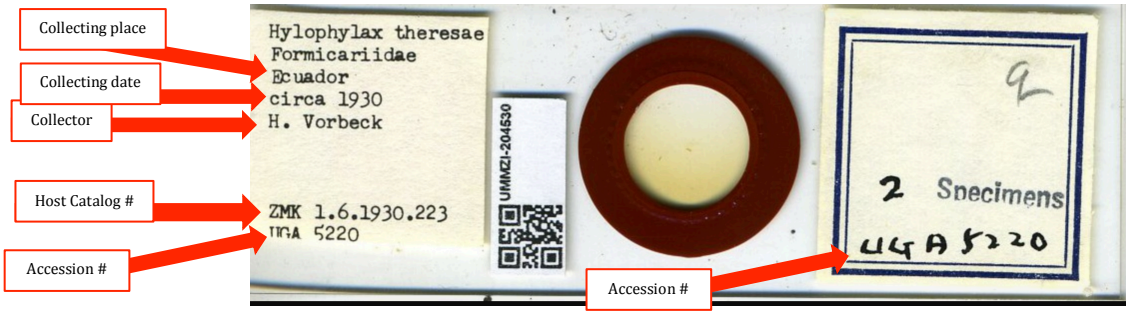


- Open the image in another window (either be right clicking or other means) and arrange the two Internet windows (one with image, one with data entry) next to each other so you can see both (or above and below). If you have multiple browser capable devices at home you could also put one image on your TV or ipad etc. while the data entry widow is on you computer.



- Zoom in on the label data – you will need to be able to read this
- If your specimen has a UGA ###, BMOC ###, CKP ###, etc. (*not* the UMMZI-####), this is the specimen "accession number" and there is likely already data in the database that you can copy and paste into this record.
    - If you specimen has what looks like an accession number on it, create a Specify query in a new browser tab or window (don't close your current window/tab)
    - Go to "Query", select "Collection Object" query, then add "Accession"→ Accession Number" → "=" and enter accession number on your specimen image.
    - Click on any result (if there is one) and copy and paste information from the already entered record into the record you were starting to work on.
- If there is no corresponding accession number already in the database with information you can copy, proceed to enter all new data.
- **GOOGLE ALL TAXON NAMES AND LOCATIONS** before entering them in database to make sure you are spelling them correctly. Cut and paste is your friend!
    - Check VertNet for the host information if there is something that looks like a "host catalog number" (see image below)
    - Windows shortcut keys:
        - copy = "ctrl c"
        - paste = "ctrl v"
    - Mac short cut keys:

- copy = "command c"
- paste = "command v"

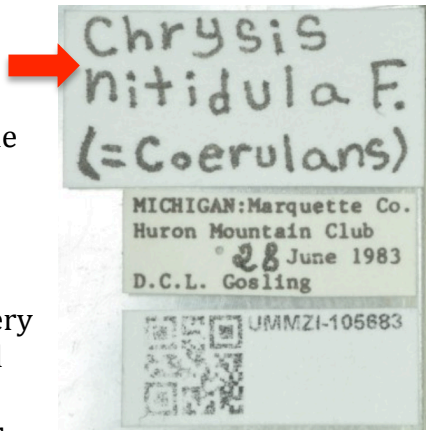


- **Ask me and/or Barry if you have questions about anything on the specimen labels!**
  - There is also a separate document Barry and I made with common label markings for our slides in the shared Google drive for this project:
    - "1. Label codes, terms, meanings, etc."

More General Specify Information for UMMZ Insect Collection:

Determinations Section

- Start with Googling the taxonomic name and making sure the complete taxonomic name is in the database (this is actually a very bad example as the name copied from our unit trays is totally incorrect – Bombus balteatus is a type of bumble bee not a Chrysididae/cuckoo wasp)
- Do not change the taxonomic information in the database to a clearly incorrect taxon. If you Googled the name Bombus you would have found it is in the family Apidae, not Chrysididae (the family being used in this example)

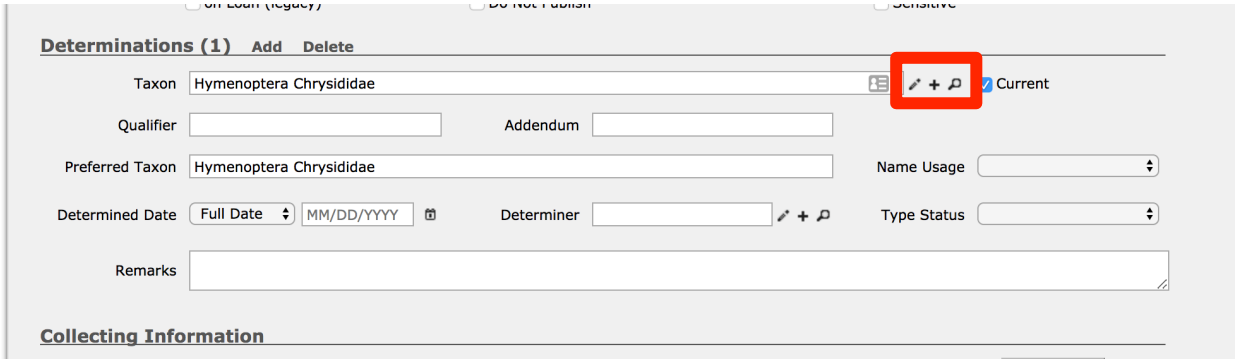


- Chrysis nitidula is a type of Chrysididae
- The "F." (or "Dahlbom" in the Bombus label) indicates the original authority. The person who very first discovered this is a new species and described it. This is different from the determiner. The determiner usually has something like "det. Tucker 2019" and indicates that Tucker identified the specimen (not described this as a new species).
- The "(=coerulans) is indicating that another species (Chrysis coerulans) was synonymized under Chrysis nitidula. You do not need to worry about that right now.
- Now that you have checked the proper spelling and made sure the name does belong in the family Chrysididae, **search the taxon** name to see if it is in our database. The taxon names are in a hierarchical/tree type of table. In order for a species name to exist, first a genus needs to exist. In order for a genus to exist,

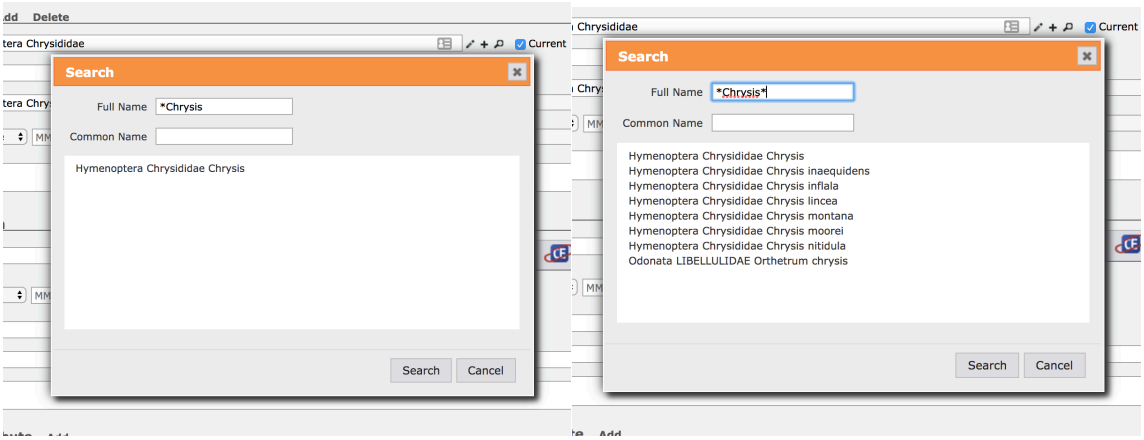
first a family needs to exist. And so on. The common hierarchal levels are as follows (there are also may in-between level, but we'll start with these):

- **Order** - often ends in "ptera", although not always. Things like Hymeno**ptera** or Ortho**ptera**). Order name is always capitalized.
- **Family** – always ends in "idae". Like Chrysid**idae** or Ap**idae**. Family name is always capitalized.
- **Subfamily** – always ends in "**inae**".
- **Genus** – has a variety of endings. Chrysis and Bombus are genus names in the above example. Always capitalized.
- **Species** – variety of endings. Usually the gender of the name matches the genus gender if based on Latin or Greek words. NEVER CAPITALIZED. The name nitidula or balteatus in the above examples.

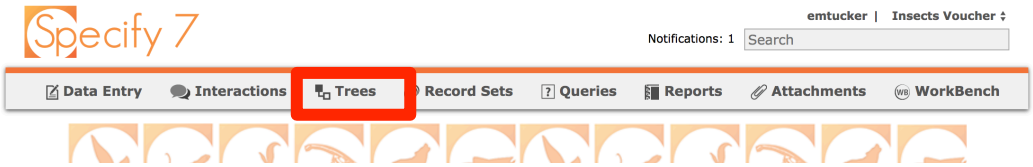
- There are two ways to look for a taxon name in the database
- Click the magnifying glass button to search (do not use the pencil – this actually will change other records than the one you are working on)



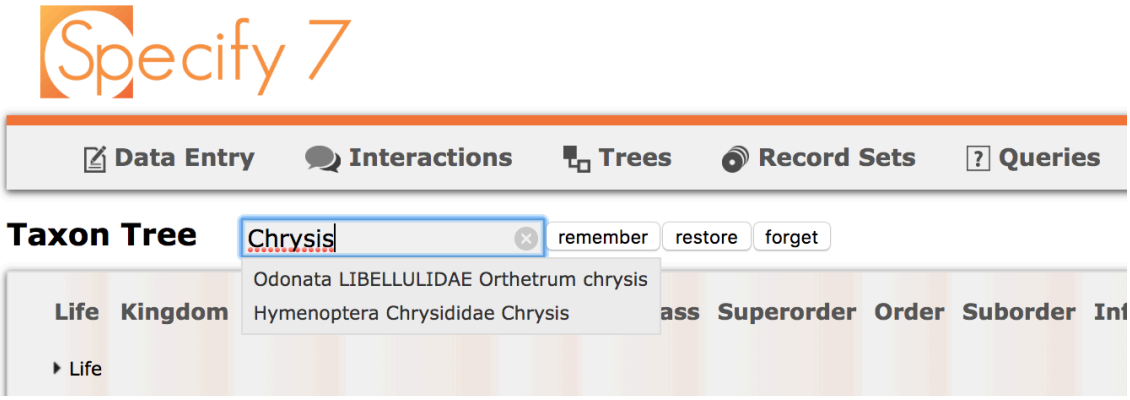
- In the search box that pops up add and "*" before the genus name so that you do not need to type out "Insecta Hymenoptera Chrysididae Chrysis". The asterisk acts as a wildcard and can be used before and/or after the name you are searching. Remember the species name won't be in the database unless the genus is already there.
- Searching with an asterisk in front vs in front and after brings up different results.



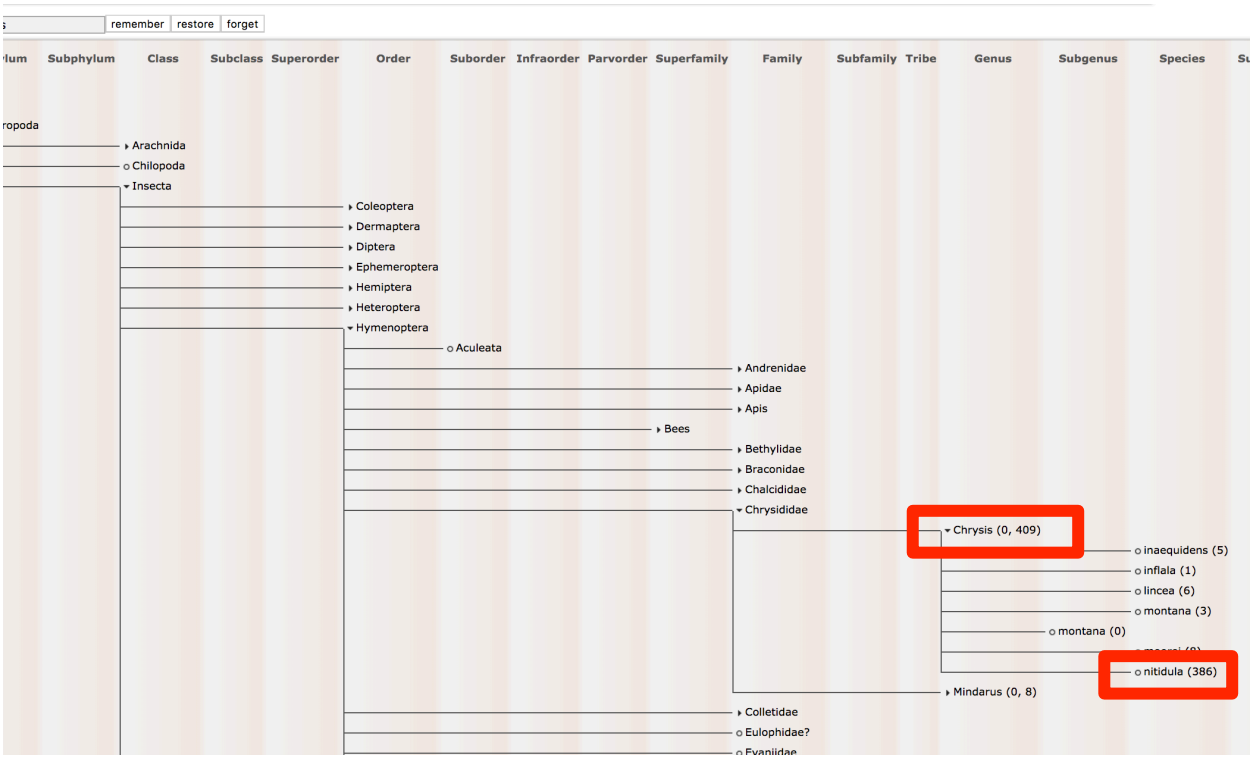
- If the species (or other taxonomic level) you need is on the list you can just click the one you want and it will auto fill the taxon box for you.
- If it is not on the list, you will need to add it. I find the easiest way to add new taxa (or geographic places when we get to that) is through the tree function in the database
- To search for a taxon in using the tree feature, open an other tab, go to specify, and click the "**Trees**" button at the top



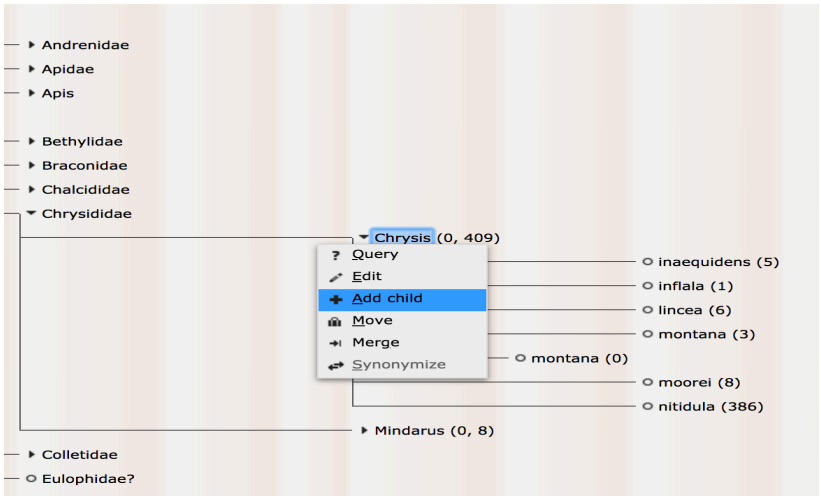
- Select "**Taxon**" from the list
- Enter the taxon name you want to look for in the search box at the top left. A drop down menu should appear as you start to type. You must select from this list, or not. You cannot just type it in and search.



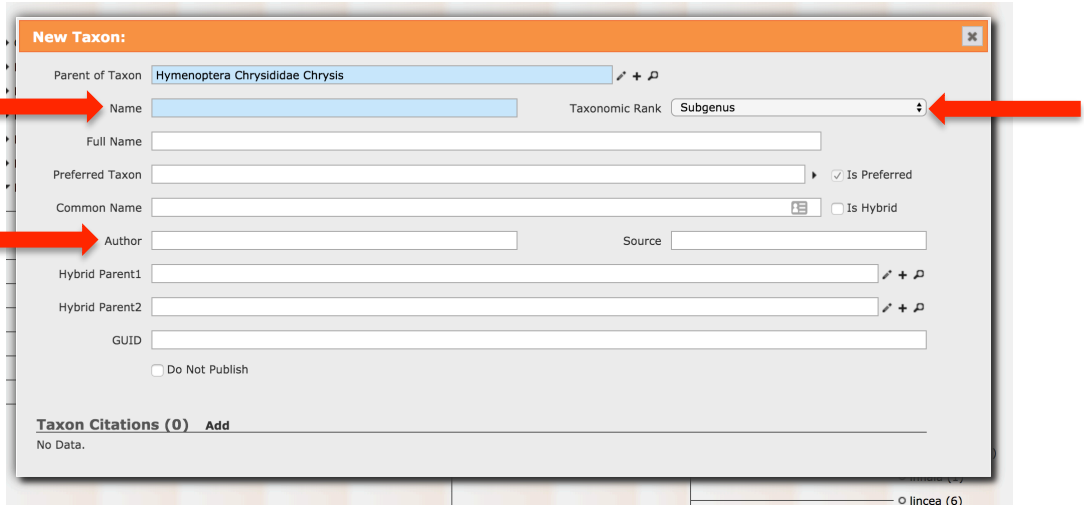
- When you click the name you want the tree will automatically expand until the group you selected is shown. You can manually do all this by clicking the little triangles next to each name to expand a group.



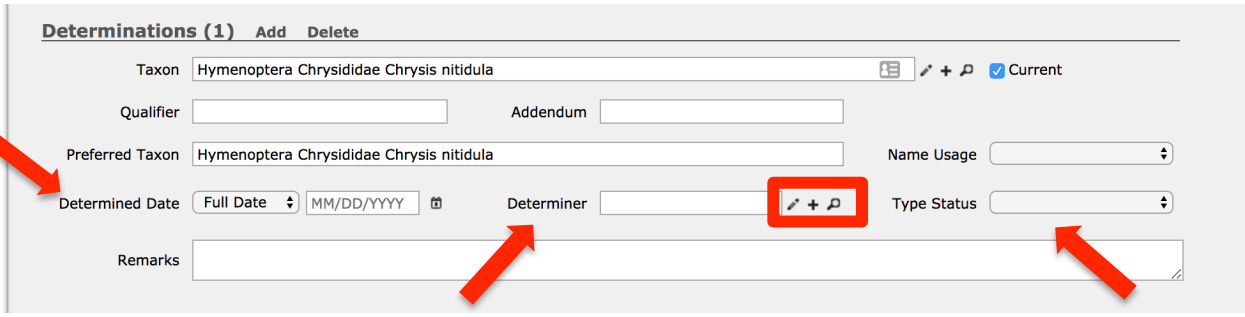
- In this case the genus and species we need are both already available. If they were not, we can add a new taxon by right clicking the level above what we need to add, otherwise known as the parent taxon, and clicking add child. So, if we wanted to add another **species** of Chrysis, we would right click Chrysis and select add child



- This will bring up the new taxon box. Enter the species name in “Name” and make sure you **select the correct taxonomic rank.** If you have the original authority name enter that (and associated date) in the “Author” box



- Click save when you are sure you filled this out correctly.
- It make take a few moments after saving, but once it finished, you can immediately see where you placed the new species in the tree.
- Once the species (or other taxon) you need is in the tree go back to the data entry page and search the taxon box again (*remember to use asterisks*). Select the taxon you need in the search results.
- After you enter the taxon, check to see if there is a determiner listed. In this case there is not, but if there were it would be on the same label as the taxon name and often have a date associated with it. Determiner information usually looks something like: Det. Tucker 2019 or Leg. F.M. Gonzalez 5/1994.

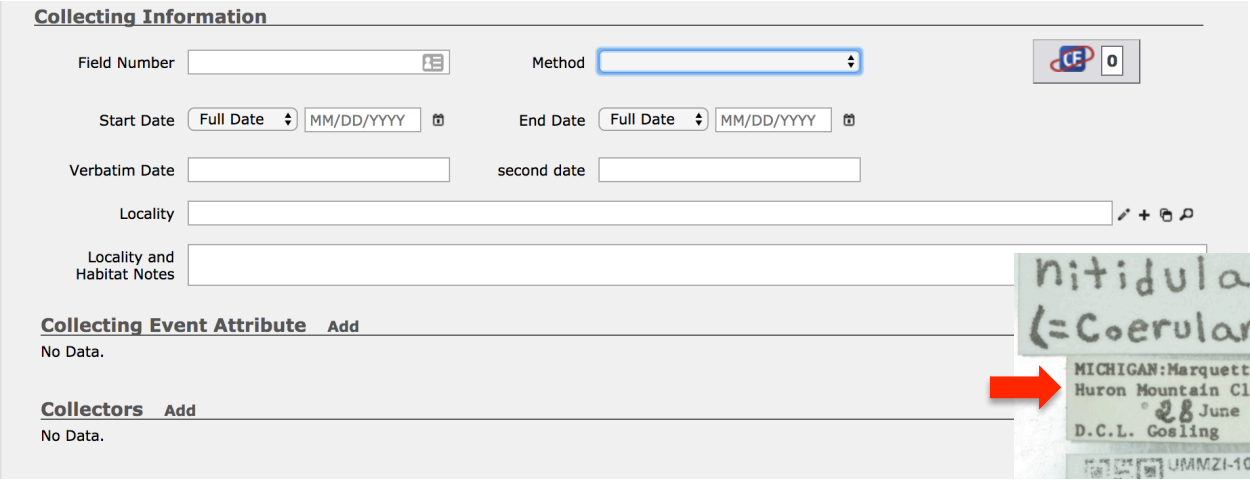


- The determined date can be changed to month/year or just year depending on what information is available. For the determiner (if listed) start typing in the last name and a drop down menu of options will appear. If it is not on the list you can search for a name by clicking the magnifying glass button and using asterisks like with the taxon names. If the name is just not there, you can add the name by clicking the "**+**" next to the magnifying glass.
- The type status can usually be left blank. However, sometimes you will find a determination label that says something "Holotype", "Paratype", "Typus", etc. If the label says something like that select the matching term from the "Type Status" dropdown menu.

Collecting Information Section

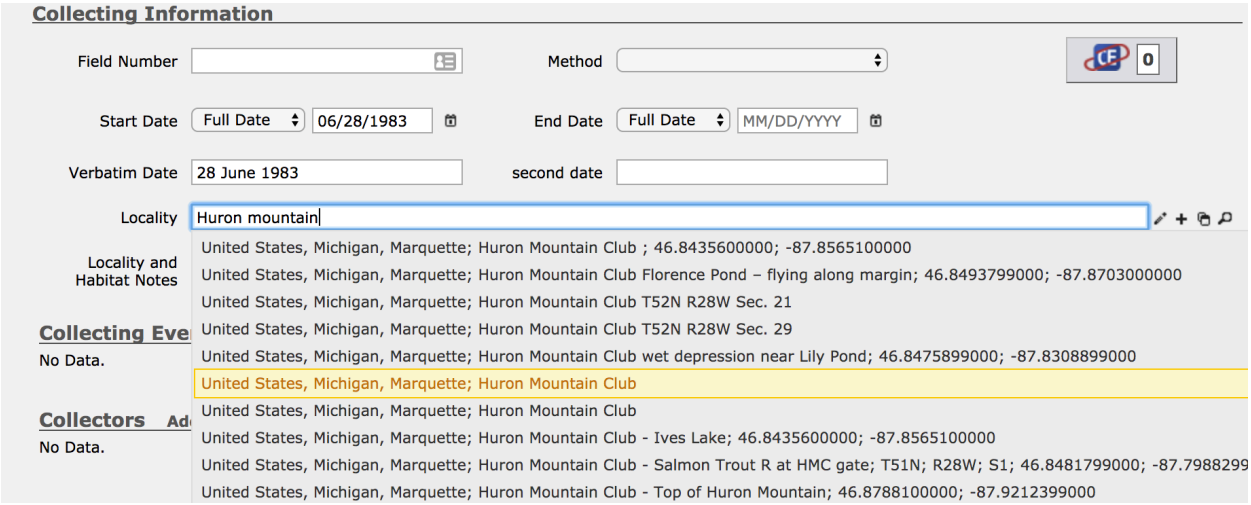
This information is always on a separate label from the determination information and contains information about where, when, who, and how a specimen was collected.

- The "**Field Number"** is often somewhat ambiguous on labels. If it is given, its usually a short string of letters or numbers (e.g, site 123, plot xyz-2, etc.). Our ample label does not have a field number.
- **"Method"** is sometimes given for how a specimen was collected. This is a dropdown menu you can select from. Often says something like malaise trap, pit fall trap, or on flower (=hand caught). No collection method is given for our example. If you come across a method not on the list, let me know and I will add to the list.

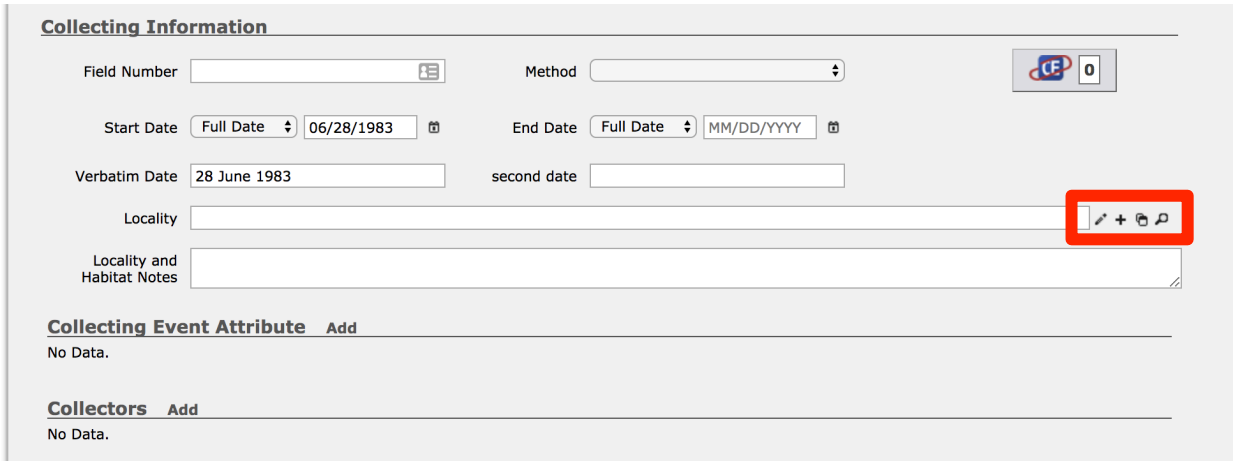


- The "**Start Date**" is the first (sometimes only) date given on the label. This should be entered in the standard format mm/dd/yyyy. If there is only a month/year or just a year, click the "Full Date" dropdown next to "Start Date" and change it for the date information you have. In our example the Start Date is 06/28/1983
- If there is a second date, or the date is part of a series, but the last part of the date in "**End Date**". Insects are often collected passively in traps that can be left out for days, weeks, sometimes even months. If this were the case you would usually see sometime like: Malaise Trap, June 1-July 7 2019. There is no end date in our example.
- The "**Verbatim Date**" is for entering the date *EXACTLY* as it reads on the label with no formatting. In our example you would put "28 June 1983" in the verbatim date. This is important because depending on how confusing the label is, sometimes the start date can be misinterpreted and it is important to have the verbatim date to check it against. This example is pretty easy, but insect labels often have roman numerals included in the date (e.g., 28.vi.1983) and many of the older ones are hard to read. If there is something unclear or totally illegible in the date, put it in hard brackets (e.g., [2?]8 June 1983 if you couldn't tell for sure that is says 28)

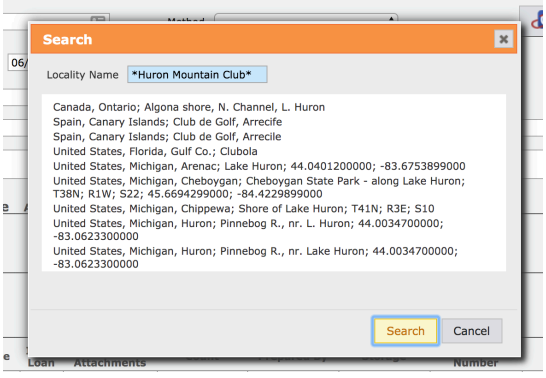
- Filling in the “Locality” box is similar to filling in the taxon box. First Google the location to make sure you are spelling it correctly.
- You can start typing the last part of the location name into the locality box and it will produce a drop down menu for you to select from

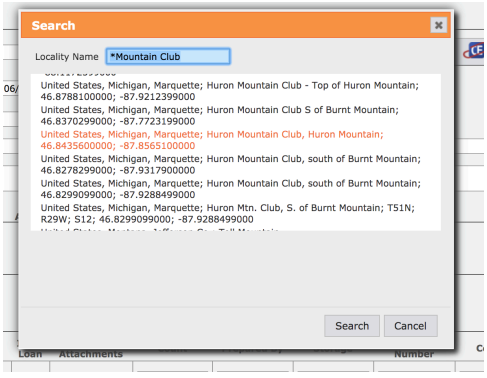


- This one appears pretty quickly in the dropdown menu. If it is not in the list, then click the magnifying glass to search for the location.

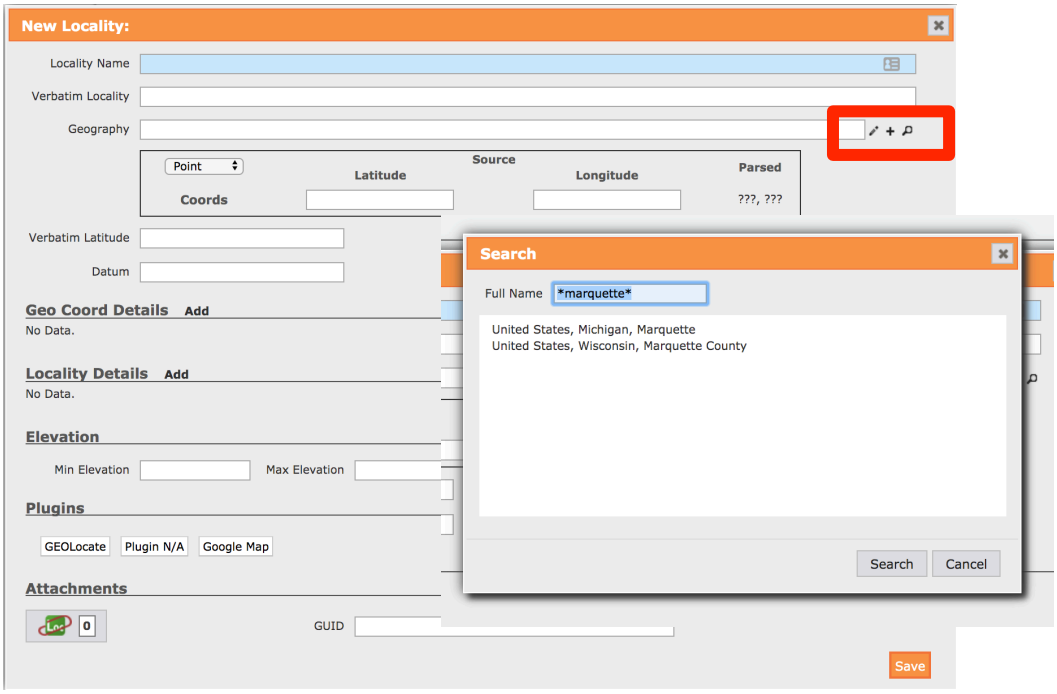


- In this case we will look for the “Huron Mountain Club”. Remember to use asterisks before and after. You can also try searching just parts of a name. The first search does not appear to have what we need, but a second search with just “*mountain club” brings up a lot more similar results (the search is often very finicky about how things are entered – do not ask me why)

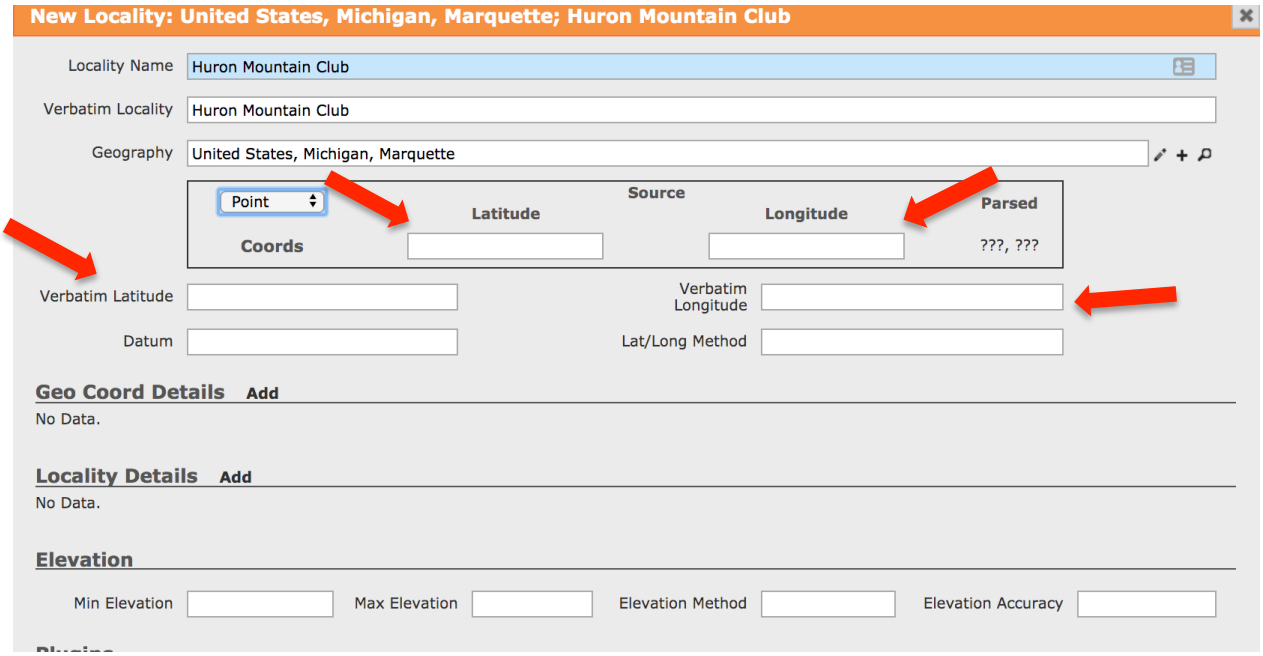




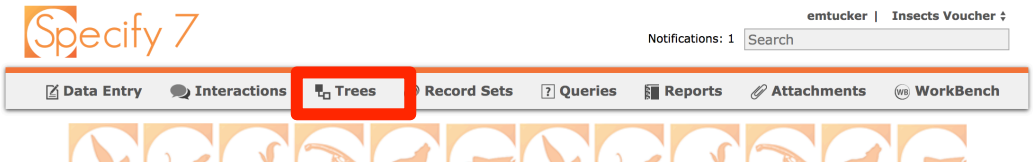
- The result in the search box, while similar, has geographic coordinates listed when our label does not. So we are going to choose from the original drop down menu that appeared when we started typing because that had an option for the huron mountain club without coordinates.
- If the location you need to enter is not on any of these lists/searches then you would need to add a new location. To add a new location click the **"+"** at the end of the locality box. This will bring up a "New Locality" box to fill in.
- Adding a new locality is similar to adding a new taxon. You have to have the higher level added before you can add a lower level. For example, a state must exist before you can add a county, a county must exist before you can add a city, a city needs to exist before you can add a place or address in that city.
- To add Huron Mountain Club as a location (if it wasn't already in the available lists), first search for the where the location that the club belongs to in the geography box (i.e., the club is located in Marquette County). You can do this by starting to type in the box, or by searching with the magnifying glass and asterisks.



- Select the place you need, then type in the "Locality Name" and "Verbatim Locality". In this case the verbatim is the same as the standardized locality.

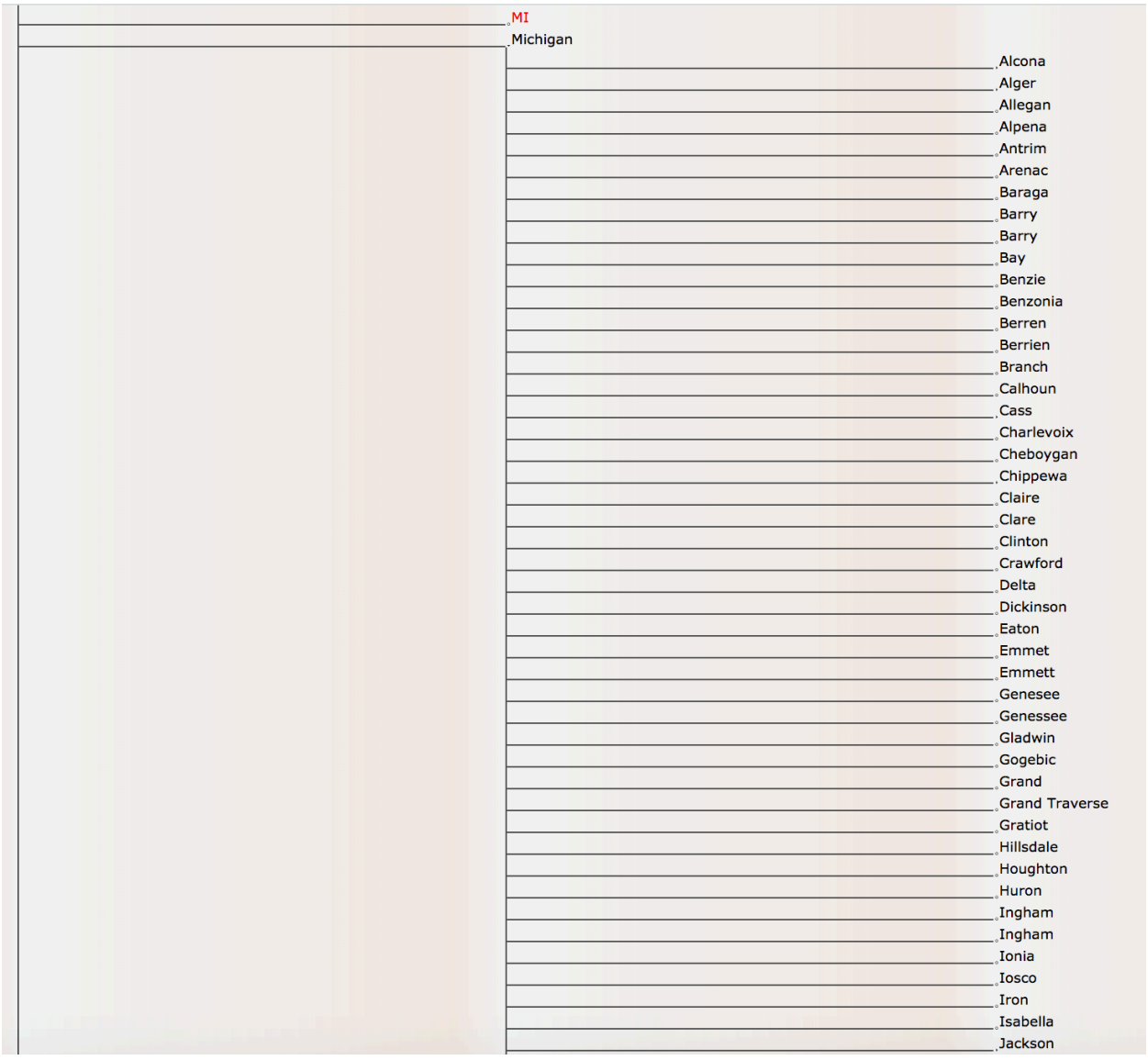


- This box is also where you would add coordinates if there were any on the labels. "**Verbatim Latitude**" and "**Verbatim Longitude**" would be where you put the coordinates from the label *EXACTLY* as they were written, the "**Latitude**" and "**Longitude**" box above would be where you put the standardized or corrected coordinates (e.g., if your verbatim corrdinates were in minutes, seconds, degrees, you could translate them to decimal degrees and put them in the standardized boxes, or if you looked up the coordinates but they were in the middle of the ocean instead of in Michigan, you could entry the fixed coordinates in the standardized coordinate boxes).
- If an elevation is given that goes in this box as well (usually it looks something like 340', 340ft, 340m) under "**Min Elevation**". If there is a second elevation listed put in in "**Max Elevation**".
- Hit save at the bottom of the box when you are done entering the new location.
- You can also search and add new locations through the "Trees" button like you did with the taxon tree. Open a new tab and click "Trees", then select "Geography" from the list

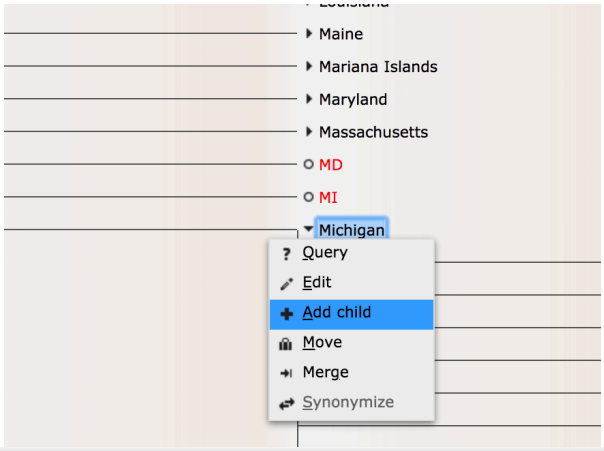


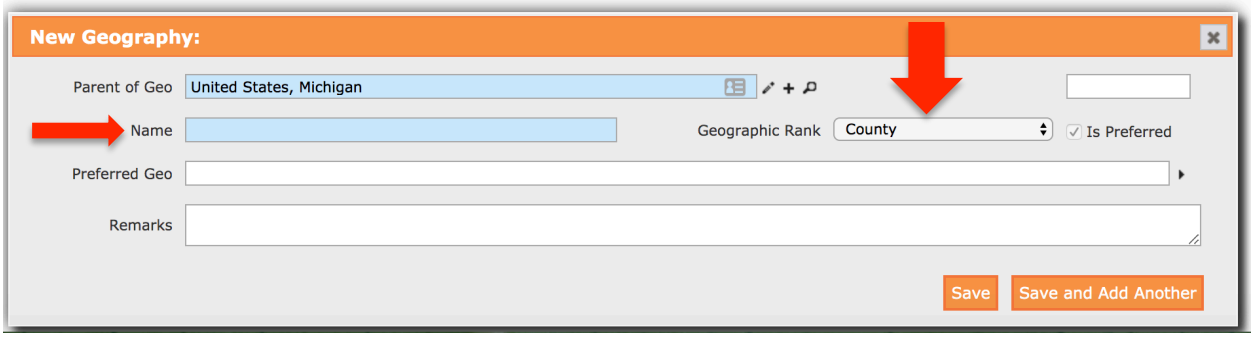
- You can start to type in the place you are looking for in the search box and select it when it pops up or navigate through the arrows on the tree.

- This tree only goes down to the City/Town level. It works great for adding most geographical levels like cities, counties, states, and countries, but when you need to add the specific location (like a club or street) you will need to add that through the locality box as we went over above.

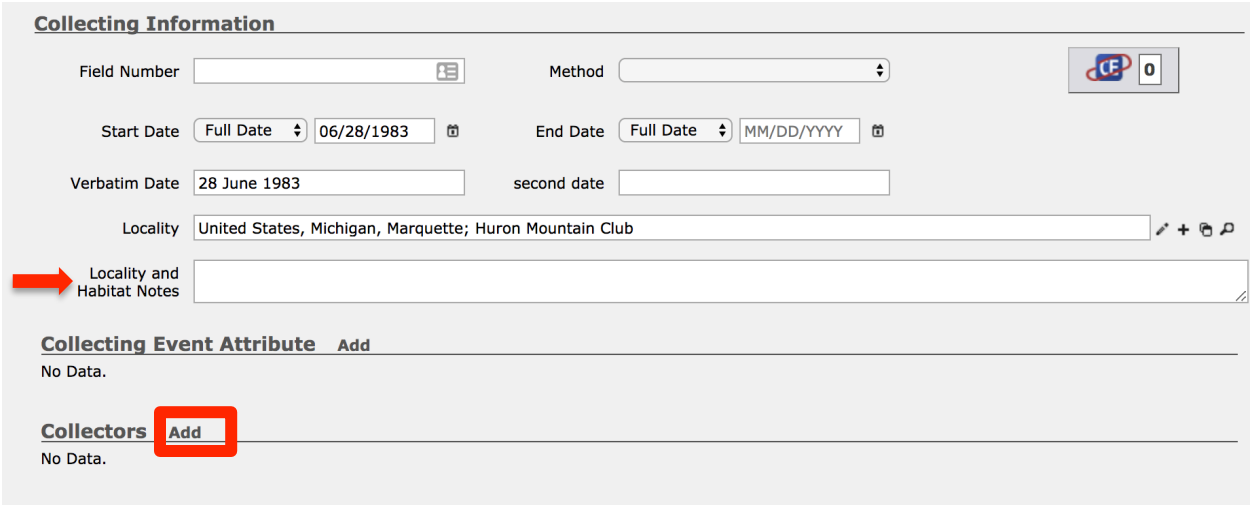


- To add a new a new level to the tree, right click what you want to add it under (the containing geography) and click add child



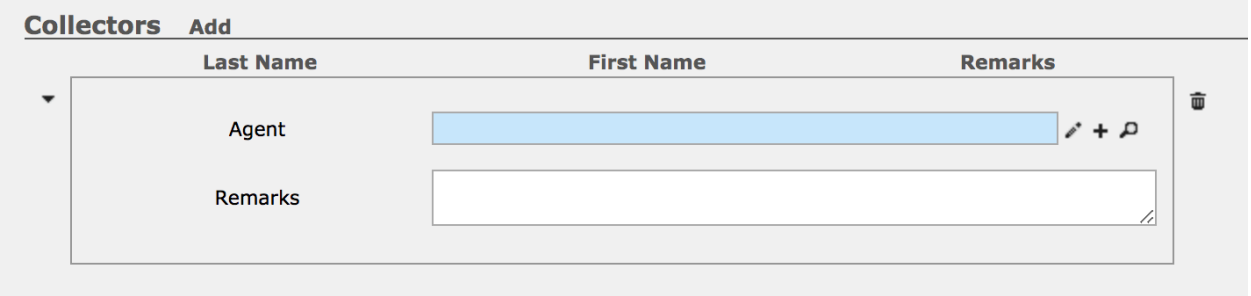


- Then fill in the location name. Make sure you select the correct "**Geographic Rank**"! Hit save when done. You will be able to see immediately where the new location is in the tree
- Go back to your data entry page.

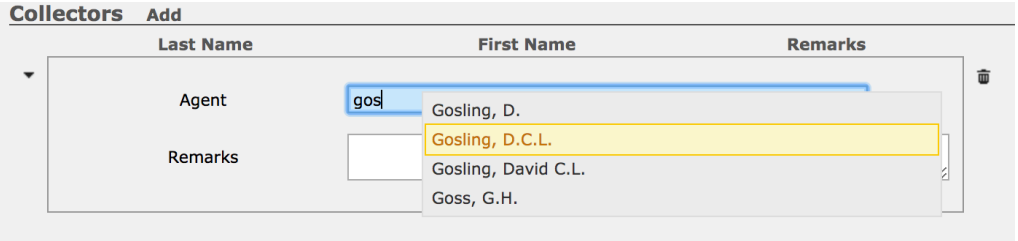


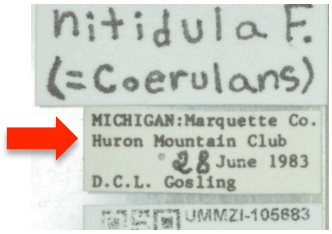
- The "**Locality and Habitat Notes**" is where you would put information from the label like "meadow habitat" or "on log" or "attacking fly". This is also a good place to put any other information that doesn't fit into one of the other boxes.

- Click the "Add" button next to "**Collectors**" if there is a collector given on the label. This will bring up a new entry field for entering the collector(s). It works just like the determiner and cataloger boxes.

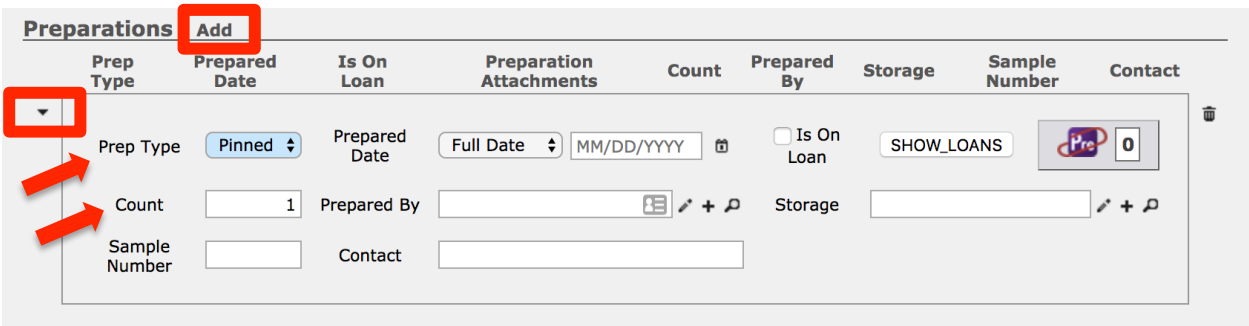


- Start to type in the collector's last name in the "Agent" box and select from the dropdown menu. If not in the dropdown menu, use the magnifying glass to search (with asterisks) or add a new agent/collector if the name is not in either list.
- The collector in our case is Gosling and is on the list



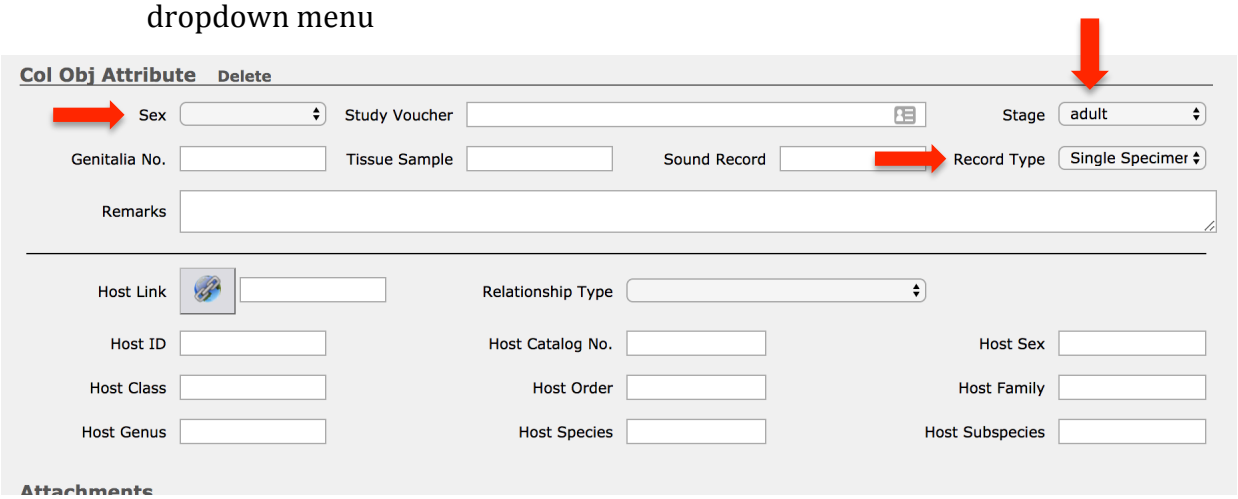


- The "**Preparation**" section should be partially filled out already, but please double check it.
- Both the "**Prep Type**" and the "**Count**" should be filled in. Click the little arrow button under "**Preparation**" to expand the details. If there is no information in the section already click the "**Add**" button next to "**Preparation**"



- Most specimens you'll be working with are pinned, but sometimes you'll get something else like in vial or in an envelope, or a nest. Select the appropriate "**Prep Type**" for your specimen from the dropdown menu.
- "Count" should always be "1". This refers to the number of specimens. 1 pinned specimen, 1 vial of specimens (even if there are multiple bugs on the pin or vial). Sometimes this number changes to zero if the specimen is out on loan or destroyed for some reason, but you should always put "1".

- The "**Col. Obj. Attribute**" section is for additional information about the specimen or its host (if information is provided).
- If the "**Sex**" is noted on the specimen label select the correct sex from the dropdown menu



- Most of the specimens are adults, but if you have a larva, or pupa, or something change the life "**Stage**" from the dropdown menu
- You will also want to check the "**Record Type**". Normally this is a single specimen on a pin or a single specimen in a vial. Sometimes though there may be multiple specimens on a pin, or in a vial ("lot"). Select the appropriate "**Record Type**" from the dropdown menu
- If you have a parasite specimen or a pollinator there may be additional information about what the specimen what found on. This goes in the host information section. If the specimen was found on a squirrel, put "squirrel" in the "**Host ID**" (=common name). Then google what family or other taxonomic unit squirrels are and fill out "**Host Family**" or appropriate taxon level. Same thing if a bee was collected on a "bull thistle". Put "bull thistle" in "**Host ID**" and then google it to find out what the genus/species is for "bull thistle". Put genus in "**Host Genus"** and species in "**Host Species**".
- Going back to the top of the page again, besides filling in the "**Cataloger"** (you), there is our "**Catalog Number**" which should already be filled in (=unique number, barcode number). There is also an "**Alt Cat Number**". This is often a combination of numbers and letters similar to our own UMMZI-####, but from a different museum or project (e.g., USNM 2119, INHS 1009, HIC 15879, etc.).
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