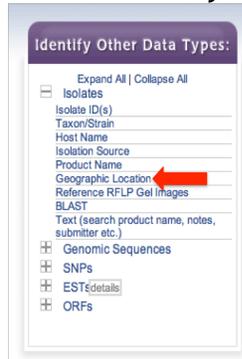


Exploring Isolate Data (Exercise 7)

7.1 Exploring isolates in *Cryptosporidium* and using the alignment tool.

Note: For this exercise use <http://www.cryptodb.org>

- a. Identify all *Cryptosporidium* isolates from Europe. (hint: search for isolates by geographic location in the “identify other data types” section).



- b. How many of these were isolated from feces? (hint: add another isolate search step).
- c. Out of those in step ‘b’, how many are unclassified *Cryptosporidium* species?
- d. How many of these originated from humans?
- e. How many of the isolates in step 2 were typed using GP15/40 (GP60)?
- f. Compare some of these isolates using the multiple sequence alignment tool (clustalw). Do you see any sequences with insertions/deletions?
- g. Take a look at the tree that was built using this alignment (guide tree). Change the isolates that you selected for alignment - how does the tree change? Do isolates from the same country cluster together?

7.2 Typing an unclassified isolate.

Note: For this exercise use <http://www.cryptodb.org>

- a. Select one of the unclassified isolates from step ‘c’ (above) that was typed using 18S small subunit ribosomal RNA (hint: Add a column for isolate product).

Geographic Location (step 1) - 2290 IsolateRecordClasses.IsolateRecordClass [Download Results](#)

First 1 2 3 4 5 Next Last Advanced Paging 1 selected: leave menu to submit Reset Columns

Isolate Id	Organism	Strain	Host	
<input type="checkbox"/> AB089284	Cryptosporidium muris	RN66	rat	<input type="checkbox"/> Isolation Source
<input type="checkbox"/> AB089285	Cryptosporidium andersoni	kawatabi	cow	<input type="checkbox"/> Description
<input type="checkbox"/> AB089286	Cryptosporidium muris	RN66	rat	<input checked="" type="checkbox"/> Isolate Product
<input type="checkbox"/> AB089287	Cryptosporidium muris	RN66	rat	<input type="checkbox"/> Is Reference
<input type="checkbox"/> AB089288	Cryptosporidium andersoni	kawatabi	cow	<input type="checkbox"/> Isolate Type
<input type="checkbox"/> AB089289	Cryptosporidium andersoni	kawatabi	cow	<input type="checkbox"/> Collected By
<input type="checkbox"/> AB089290	Cryptosporidium parvum	HNJ-1	Mammals - human	<input type="checkbox"/> Length
<input type="checkbox"/> AB089291	Cryptosporidium parvum	HNJ-1	Mammals - human	<input type="checkbox"/> Weight
<input type="checkbox"/> AB089292	Cryptosporidium parvum	HNJ-1	Mammals - human	Unknown
<input type="checkbox"/> AB089293	Cryptosporidium parvum	HNJ-1	Mammals - human	Unknown
<input type="checkbox"/> AB089294	Cryptosporidium parvum	HNJ-1	Mammals - human	Unknown
<input type="checkbox"/> AB089295	Cryptosporidium parvum	HNJ-1	Mammals - human	Unknown

- b. Copy the DNA sequence from the isolate record page.
- c. Go to search for isolates based on BLAST, select isolates and make sure only the reference isolates are selected in the target organism window.
- d. Paste the DNA sequence in the input window and select the blastn program. Click on "Get Answer".
- e. Explore your results. Based on the similarity which reference isolate is this one closest to?

7.3 Exploring isolates in *Plasmodium*.

Note: For this exercise use <http://www.plasmodb.org>

- a. Identify all isolates from Mexico.
- b. How many of those are *P. falciparum*? How many *P. vivax*?
- c. What about all of North and South America? (Hint: revise the first step in your strategy to include all countries in both continents).
- d. For these results, add columns such as isolate product and length. Sort these columns and explore your results. For example, what product is mainly used in typing *P. falciparum* isolates? What about *P. vivax* isolates?