

MEDSS – Guide for Team D

General Information-----

- MEDSS is an electronic disease surveillance system that allows public health officials in Minnesota to receive, manage, process, and analyze disease-related data. MEDSS is a person centric database; all disease events for an individual are connected to their identity in MEDSS. The MEDSS security environment displays only the data someone needs and is authorized to see (e.g., if you work in foodborne diseases, you will not see measles disease events).
- The main MEDSS page can be found at: <https://apps.health.state.mn.us/medss/login.do> and can be accessed through Internet Explorer or Firefox.
- Passwords and login names are case sensitive. If you enter your password incorrectly 3 times, the system locks you out and you need to call IS&TM to reset it.
- An “**event**” in MEDSS is a disease linked to a person at a single point in time – what we might sometimes call a “case” or an “isolate”.
- A “**workflow**” is a queue of events grouped by pending tasks or common features (ex: Physician Follow-Up Needed, Data Entry Pending)
- The “**dashboard**” is where you work with and find information for a single event/case

In the foodborne unit, we enter several disease events in MEDSS:

Parasitic diseases, including *Cryptosporidium* and *Cyclospora*

Bacterial diseases, including *Campylobacter*, *E. coli* O157 and non-O157 shiga-toxin producing *E. coli*, Enterotoxigenic *E. coli*, *Listeria*, *Salmonella*, *Shigella*, *Vibrio*, and *Yersinia*

Data is transmitted to the CDC FoodNet program at least once per month. Data is merged with data from other FoodNet sites across the country to provide a picture of foodborne disease trends nationwide. If you would like to learn more about FoodNet and see summaries of data, go to the FoodNet website: <http://www.cdc.gov/foodnet/>

We also use data in PHLIS to look at statewide incidence rates and trends, as summarized in the annual Communicable Disease Summary of the MDH Disease Control Newsletter:

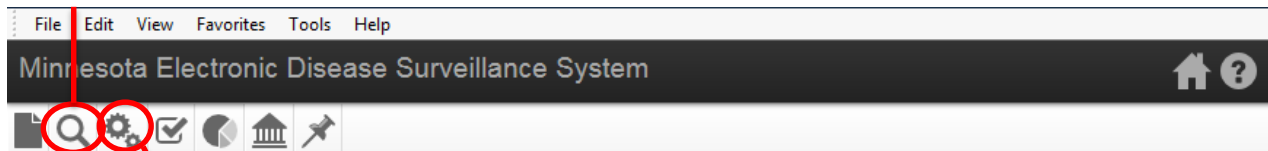
<http://www.health.state.mn.us/divs/dpc/ades/pub.htm#DCN>

Every year we enter more than 2,000 cases in MEDSS.

Data Entry Tips-----

- The MEDSS system logs you out if you are inactive for a time and your changes won't be saved! Also, if you exit a screen without pressing "SAVE", nothing will be saved!
- You should not need to enter new cases into MEDSS, only update existing cases.
- CRF = case report form

Search for an event



Go to Workflows

Foodborne disease case definitions-----

New event or case – a person with an infection that is not previously recorded in MEDSS and/or hasn't been recorded in MEDSS in the last 30 days. If an event exists in MEDSS within 30 days prior to the event you are searching for, the most invasive source (e.g. blood is more invasive than stool) should be the event saved in MEDSS. Other events within 30 days are simply merged together in MEDSS and paper copies are not kept.

Duplicates – a duplicate is a case or event that occurs ≤ 30 days of an existing case or event of the exact same disease in MEDSS. Example: Jane Doe has *Campylobacter jejuni* isolated from a stool specimen collected on June 5, 2011. Then we get another case report saying that the same individual had *Campylobacter jejuni* isolated from a stool sample collected on July 2, 2011. We will NOT enter any information from that second report into MEDSS, because that is considered a duplicate. However, if Jane Doe had a positive *Campylobacter jejuni* with a specimen collection date of June 5, 2011 and a positive *Campylobacter coli* (or *Salmonella*, or some other FoodNet pathogen) collected July 2, 2011, that report would be entered in MEDSS and counted as a new event or case.

Carriers – a carrier is someone who has a specimen positive for a pathogen >30 days but <365 days after an earlier specimen was positive for the same pathogen. A common scenario may be a daycare attendee with an STEC infection who submits multiple stool samples over several weeks or months until they have two negative stools. If that child was first positive on February 3, 2011 and had subsequent positive stools on February 11, February 24, and March 10, you would consider the February 11 and February 24 specimens "repeats/duplicates" and not enter any data on them in MEDSS. However, the March 10 specimen was collected over 30 days after

the original sample, so you would consider the March 10 specimen a “carrier” specimen, and enter that information in MEDSS as a carrier.

Steph keeps track of carriers so that we can account for them in our annual case counts. We want to document these specimens and the length of time that these cases shed their pathogen, yet we do not want to count them as incident or “new” cases.

How to enter dailies into MEDSS-----

1. The yellow sheet is your starting point. Every case has a yellow sheet in the beginning, but most yellow sheets will be missing some required information. You will need to compile the necessary information from several sources including the MEDDS database, the report card (if provided), and/or from calling the clinic directly. Recording all the information you acquire on the yellow sheet is helpful before entering into MEDDS and creating a Case Report Form (CRF).

2. Search for the Event

Click on the magnifying glass on the dashboard. A search screen opens.

The screenshot shows the MEDSS search interface. The search criteria form is open, and the search results table is empty. The search criteria form includes the following fields:

- Type: Normal
- Event ID: [Yellow background]
- Last Name: [Text input]
- First Name: [Text input]
- Maiden/Other Name: [Text input]
- Birth Date: [Date input]
- Gender: [Dropdown menu]
- State: [Dropdown menu]
- Disease: [Dropdown menu]
- From Date: [Date input]
- To Date: [Date input]
- NETSS ID: [Text input]
- Legacy ID: [Text input]
- State ID: [Text input]
- Alias: [Text input]
- Home phone: [Text input]
- Mobile phone: [Text input]
- MDH Lab ID: [Text input]

The search results table is empty, showing 0 to 0 of 0 entries. The table has the following columns: Event ID, Name, Birth Date, Status, Disease, Create Date, Effective From, and External ID.

Search for the first and last name of the case – matches will appear on the right. If there are multiple events for cases, they will be listed there. Look at the dates and the disease for each event to find the one that matches the CRF. If you think there are duplicate or carrier cases, let Steph, Amy, or Theresa know. We will deduplicate/merge them. You can also find cases in the Clinician Follow up workflow.

3. Compiling required information

Look in the blue report card folder to see if the clinic submitted a report card. If the report card does not contain the necessary information or if a report card was not submitted, check the Persons tab and Lab Results tab in MEDDS. The **Persons tab** in MEDSS often contains demographic information such as name, address, gender, and date of birth. The **Lab Results tab** often contains submitter, lab, and patient status information. If the report card, Persons tab, or Lab Results tab does not contain all the required information needed to complete the CRF, make a note of what is missing on the yellow sheet, and proceed to calling the appropriate clinic.

****Note:** If antibiotic information is the only information missing, you do not need to call the clinic and can move on to entering the data into MEDDS (step 4).

Call the clinic –

Refer to yellow sheet for physician name and phone number and call phone the number provided.

- If you're calling a hospital, ask to speak with Infection Control (ICP)
- If you're calling a clinic, ask to speak to the nurse or assistant of the physician

If the phone number is not provided, refer to the Rolodex and look up the phone number for the appropriate clinic/hospital. If unable to reach a clinician or ICP, leave a detailed message. Remember to provide patient name, DOB, and all the missing information that we need.

4. Enter information from yellow sheet into MEDSS --

If you do not still have the dashboard open: Either search for the person with the magnifying glass, or find the person in the "Clinician Follow-Up Needed" workflow and click on the blue Event ID to open the case on the dashboard.

When entering any data in MEDSS, Capitalize first letters of proper nouns like first/last names, clinic names, and capitalize letters in the state lab ID number – try to stick to normal rules of capitalization since some information in MEDSS may be used for mailings or other purposes.

5. Update address and phone –

Click on the "Persons" tab, click on the "Edit Person" button, and enter the address and phone information. Make sure to use proper address standards so MEDSS can geocode the location. Click SAVE to go back to the dashboard.

If the case is from out of state, give the CRF to Theresa after entering all of their information into MEDSS. We do **not** interview out of state cases.

1

Persons

Name	Gender	Birth Date	Address	Status
Christopher P. Bacon	Male	04/05/1901	1234 Frying Pan Ave N., Minneapolis, MN 55555	Active

2 Edit Person

Basic Information Address Information Linked People Demographic History

Basic Information

Name: Christopher P. Bacon
 Maiden/Other Name:
 Alias:
 Birth Date: 04/05/1901
 Death Date:
 Age: 113
 Gender: Male
 External ID: PFEPLWPCNG
 Birth Certificate Number
 Death Certificate Number
 Party ID History
 Address: 1234 Frying Pan Ave N., Minneapolis, MN 55555
 County:
 Country: USA
 Home Phone: (952) 555-5555
 Mobile Phone:
 Work Phone:
 Email:
 Contact Method:

Edit Address

Address Type: Home

Start Date: 03/04/2015

End Date: 01/01/2030

Street: 1234 Frying Pan Ave N.

City: Minneapolis

State: MN

Zip Code: 55555

County: Carver County

Country: USA

Home Phone: (952) 555-5555

Mobile Phone:

Work Phone:

Email:

Contact Method:

Save Cancel Help

6. Update other CRF info using the Wizard –

Go back to the “Event Data” tab and select the appropriate wizard from the drop down menu (see selecting the appropriate wizard below). Click “View Wizard” and enter all information from

the yellow sheet into the wizard starting at the top. (If you needed to enter the address in the “Persons” tab, change the answer for “Update address at time of reporting with current address” to “yes”. When you hit save, the address will update.)

Minnesota Electronic Disease Surveillance System - Verification

Event Summary

Basic Information

Event ID: 10037520
 Disease: Salmonella (including Typhi)
 Person: Christopher P. Bacon Birth Date: 04/05/1901 (Male) Phone: (952) 555-5555
 Dates: Create Date: 03/04/2015 Effective From Date: 03/04/2015
 Type: Interactive
 Investigation Status: Open
 Linked Events/Contacts: 0 linked event(s)/contact(s) (View)
 Linked Exposure Sites: 0 linked exposure site(s) (View)
 Attachments: 0 attachment(s) (Add)
 Notifications: 1. Specimen ID:
 2. Serotype:
 3. PFGE:
 4. Interviewed:
 5. CRF Completed:
 6. International Travel:
 Case Status:
 Episode Date: null

Event Data | Lab Results | Persons | Tasks

Question Package	Person	Last Update	Updated By	Status
a.1 Administrative	Christopher P. Bacon	03/04/2015	Brandon Diessner [DiessB1_ELR]	Completed
b.1 Demographic	Christopher P. Bacon	03/04/2015	Brandon Diessner [DiessB1_ELR]	Completed
c.1 Clinical and Lab Interpretations	Christopher P. Bacon	03/04/2015	Brandon Diessner [DiessB1_ELR]	Completed
d.1 Risk History	Christopher P. Bacon	03/04/2015	Brandon Diessner [DiessB1_ELR]	Completed
d.2 UMASH Animal Exposures	Christopher P. Bacon	03/04/2015	Brandon Diessner [DiessB1_ELR]	Completed
d.3 Reptile Information	Christopher P. Bacon	03/04/2015	Brandon Diessner [DiessB1_ELR]	Completed
i. 1 CEA	Christopher P. Bacon	03/04/2015	Brandon Diessner [DiessB1_ELR]	Completed

Wizards: [Dropdown Menu]

Selecting the appropriate Wizard –

The appropriate wizard to select from the drop down menu will be the name of the case’s pathogen. For Salmonella and Campylobacter, a CEA wizard will also appear. The CEA wizard contains everything from the “pathogen wizard”, with additional CEA study questions that will need to be completed *after* the interview (step 8). Typically, Team D students do not need to concern themselves with any of the other wizards.

Event Data | Lab Results | Persons | Tasks

Question Package	Person	Last Update	Updated By	Status
a.1 Administrative	Christopher P. Bacon	03/04/2015	Brandon Diessner [DiessB1_ELR]	Completed
b.1 Demographic	Christopher P. Bacon	03/04/2015	Brandon Diessner [DiessB1_ELR]	Completed
c.1 Clinical and Lab Interpretations	Christopher P. Bacon	03/04/2015	Brandon Diessner [DiessB1_ELR]	Completed
d.1 Risk History	Christopher P. Bacon	03/04/2015	Brandon Diessner [DiessB1_ELR]	Completed
d.2 UMASH Animal Exposures	Christopher P. Bacon	03/04/2015	Brandon Diessner [DiessB1_ELR]	Completed
d.3 Reptile Information	Christopher P. Bacon	03/04/2015	Brandon Diessner [DiessB1_ELR]	Completed
i. 1 CEA	Christopher P. Bacon	03/04/2015	Brandon Diessner [DiessB1_ELR]	Completed

Wizards: [Dropdown Menu]

View Wizard

Some information in the wizard will likely be pre-populated for you. Enter any additional information in the appropriate places. Here is a breakdown of how to answer questions in each section:

Demographic Information

As stated previously, if you needed to enter the address in the “Persons” tab, change the answer for “Update address at time of reporting with current address” to “yes”. When you hit save, the address will update.

Phone, Gender, and DOB should all populate from the persons tab. If any of these fields are blank, go back to the Persons tab and populate them.

“Race” – choose a race (or unknown) from the drop down menu. If the case is multi-racial, choose the first race, hit “add new” and choose the second race. If the races are unknown, choose unknown for both the first and second race.

“Ethnicity” – choose Hispanic, non-Hispanic, or unknown.

“Age at time of episode” – this will auto-populate if Specimen collection date is filled in and saved. Do NOT fill in “Manual age entry” unless we do not have a DOB (this should be a VERY rare event – DOB and Specimen collection date are required fields – see an epidemiologist if you have problems obtaining this information).

Submitter Information

“Medical record number” – this is the number that is sometimes under “Patient ID” on the CRF.

“Specimen collection date” – this is a required field, and it is essential that it is entered correctly for each case.

“Submitting lab name and submitter code” – use the lookup menu to find the submitting lab – you should search by HFID (Health Facility ID) – the four digit number that’s printed next to the submitting lab name, or you can search by all or part of the lab name if you can’t find it by HFID.

“Treating Physician name” – please enter the physician – capitalize first and last names. Enter as last name, first name.

“Phone” – list the clinic phone number or ICP phone number.

“Clinic” – use the lookup menu to find the clinic name.

Laboratory Information

This varies by disease – see disease specific questions below.

Patient Status/Hospitalization

“Was the patient hospitalized?” - choose yes or no from the drop down menu. If the patient was hospitalized, chose the hospital name from the lookup menu (the rest of the hospital information, like address, will populate on its own) and enter the admit and discharge dates. If

the patient was hospitalized, chose yes or no for “Transferred” and “Rehospitalized”. If the patient was only hospitalized once, the “date of first admit” and “date of last discharge” fields should be the same as the “admit” and “discharge” fields – please be sure to enter these dates. “Patient Outcome” – choose alive or dead from the dropdown menu. If the patient died, date of death must be entered on the Persons tab.

If the patient was not hospitalized, the only fields that need to be filled out in this section are the “Hospitalized”, “Patient Outcome” and “Were antibiotics given”.

Patient Status/Hospitalization	
Was the patient hospitalized?	No <input type="button" value="v"/>
Date of admission	<input type="text"/> <input type="button" value="calendar"/>
Date of discharge	<input type="text"/> <input type="button" value="calendar"/>
Was the patient transferred?	<input type="button" value="v"/>
Re-hospitalized?	<input type="button" value="v"/>
Is the patient still hospitalized (at time of f/u)	<input type="button" value="v"/>
Patient outcome	Alive <input type="button" value="v"/>
Were antibiotics given? <input type="checkbox"/>	Yes <input type="button" value="v"/> Add New
Antibiotic name	Amoxicillin [Trimox] <input type="button" value="lookup"/> <input type="button" value="trash"/>
Antibiotic prescription date	<input type="text"/> <input type="button" value="calendar"/>
Specify dose	2 mL BID, x5 days

Antibiotics

“Treated with antibiotics” - choose yes or no from the drop down menu. Note that if the patient was not prescribed antibiotics, no additional antibiotic information is needed including lab results date.

“Antibiotic name” – Fill out name of antibiotic prescribed using the lookup tool for antibiotic names.

“Date Prescribed” – Fill in the date that the antibiotics were prescribed.

“Dose and Duration “ – Common abbreviations for duration are as follows: QD – once a day, BID- twice a day, TID – three times a day. (example 1 500mg tab BID x 10 days)

If multiple antibiotics were prescribed, click the ADD NEW link next to antibiotic name and proceed to fill out the appropriate information.

7. Lastly –

In the “Administrative” section of the wizard: Check “Is case report complete”=yes, enter the date and your initials, and select “Case report printed?” = yes. This moves the case out of the “clinician follow-up” workflow and into the “interview pending” (pathogen-specific) workflow.

Administrative Information	
Is case report complete?	Yes <input type="button" value="v"/>
Case report completion date	02/23/2015 <input type="button" value="calendar"/>
Initials of person completing report	BD <input type="text"/>
Case report printed	Yes <input type="button" value="v"/>
Case report received	Yes <input type="button" value="v"/>
Was case found during an audit?	No <input type="button" value="v"/>
Was specimen or isolate sent to CDC?	Unknown <input type="button" value="v"/>
Did this case occur as part of an outbreak?	No <input type="button" value="v"/>
NORS ID	<input type="text"/>
State outbreak/cluster identification number	<input type="text"/>
Other clinical comments	<input type="text"/>
Comments for Print Template	<input type="text"/>

If MDH received a report card for the case, check “Case Report Received” =yes.

“Was case found during audit?” – enter no if this is blank, if it says yes please leave it as yes.

“Was specimen or isolate sent to CDC?” - enter unknown if this is blank, if it says yes please leave it as yes.

“Did this case occur as part of an outbreak?” – enter no if this is blank, if it says yes please leave it as yes.

“NORS ID” – skip – an epidemiologist will fill this in if necessary.

“State outbreak/cluster identification number” – skip – an epidemiologist will fill this in if necessary.

“Other clinical comments” – typically we make note in this field if the person has duplicate events, does not speak English, lives in a nursing home or other facility and cannot communicate, or other important notes about the case.

Click SAVE to save the information you entered and return to the dashboard, or click SAVE & STAY to save the information you entered and stay on the current page. ****If you return to the dashboard without clicking SAVE, nothing you entered will be saved! Also, if MEDSS logs you out due to inactivity, nothing you entered since last saving will be saved.****

File Edit View Favorites Tools Help

Minnesota Electronic Disease Surveillance System - Verification

Salmonella - Christopher P. Bacon - Salmonella (including Typhi) [Jump To...]

Save Save & Stay Cancel

Expand Details

FoodNet ResultID

FoodNet PatID (Event ID): 100837820

FoodNet PersonID: PFEPZLWPWCNQ_100837820

Medical record number for patient: Not provided

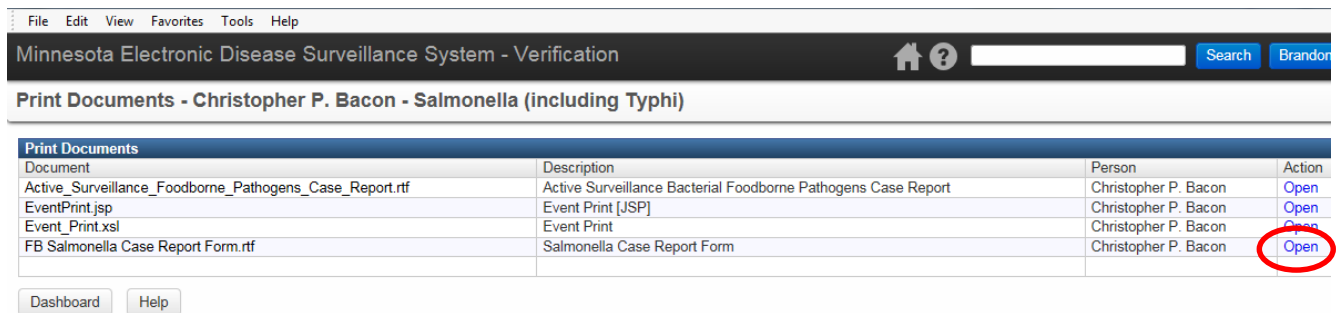
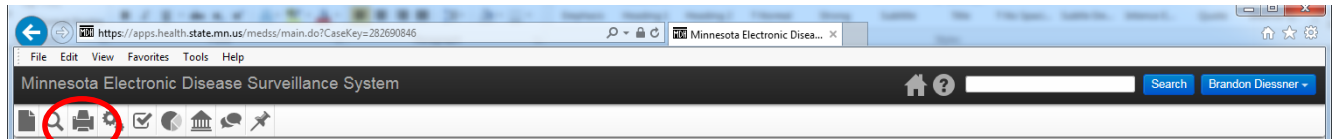
Demographic Information

Update address at time of reporting with current address No

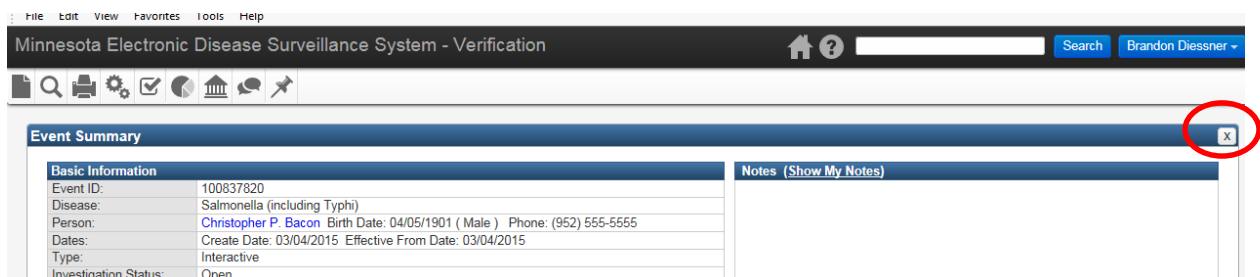
Street 1 1234 Frying Pan Ave N.

Printing the CRF

Click the printer icon in the upper left corner of the screen then open the specific pathogen's case report form. Ensure that all the relevant information is recorded on the CRF and print. You can now shred the yellow sheet and place the newly printed CRF in the appropriate to be interviewed folder.



Unload the case from your dashboard by clicking "X" in the upper right corner of the screen. Someone else cannot access the event while you have it loaded. (Actually, they can access it but it will appear as "read-only" and they will not be able to edit the event.)



8. After interview –

Search for the case (or find it in the “interview pending” workflow) and open the appropriate Wizard.

After Salmonella interviews, remember to click the “salmonella CEA” wizard and enter the items noted below, as well as the CEA questions.

Some Campylobacter interviews will also be enrolled in the CEA study. Campylobacters enrolled in the CEA study will have the appropriate interview attached with additional CEA questions. After the interview, click the “campylobacter CEA” wizard and enter the items noted below, as well as the CEA questions.

Interview data from all the other pathogens can be entered in their respective “pathogen” wizards.

Enter symptom/treatment history onset date, race/ethnicity info, and travel information.

Under “Final Foodnet Variable” section, enter the name of interviewer, date of interview, and number of attempts to contact the case, then check “Interviewed”=yes. This moves the case out of the “interview pending” workflow and into the “data entry pending” workflow.

Final FoodNet Variable	
Person Interviewed	Yes

Remember to always click SAVE or SAVE & STAY after you’ve entered new information into the wizards (noted in item #7 above).

Disease Specific Questions-----

Campylobacter

“Specimen source” - Never enter “unknown” for specimen source. The vast majority of the time it is from stool, but sometimes the specimen source is blood, urine, or something else. If it is a source that does not appear on the picklist, select “other” and type in the source.

“Specimen/isolate/plate received MDH lab” – this is typically “yes” unless Theresa notes otherwise. We should also have a received date – that’s something you can find in the lab tab or by asking an epidemiologist.

“State Lab ID #” – if we received the isolate or specimen at MDH there should be an ID number. Please capitalize any letters in the number, no space between letter(s) and number.

“Serotype/species of pathogen” – choose from the lookup tool

“Was Campylobacter isolate NAR?” – if the lab result says “NAR”, choose yes – if the lab result does not say NAR, choose no – if it says NAR unknown or the isolate was not received choose unknown

“Was isolate identified as Campylobacter (by culture)?” – if it was confirmed by culture in our lab or a clinical lab, choose yes. If it was “EIA only” or “Rapid test only”, and not confirmed in our lab, choose no.

“Confirmed by MDH lab” – choose yes or no as appropriate based on lab results

“Campylobacter species result at clinical lab” – choose from the lookup tool if known. Most of the time this will be unknown unless you see something specific listed on the lab slip for a case. If it is already answered, leave the answer as is.

“Campylobacter species result at MDH lab” – choose from the lookup tool – if it was confirmed at the MDH lab, we should know the answer for this question.

“For potential Campylobacter: what was the EIA or rapid test result at the clinical laboratory?” – Typically you won’t know this unless Theresa has made specific note of it. It should be “not tested” unless you know otherwise from Theresa or the lab slip. If it’s already answered, leave the answer as is.

“EIA result at MDH lab” – this should typically be “not tested” – if it’s anything else, Theresa or an epi will change it. If it’s already answered, leave the answer as is.

Cryptosporidium

“Specimen source” - Never enter “unknown” for specimen source. The vast majority of the time it is from stool, but sometimes the specimen source is blood, urine, or something else. If it is a source that does not appear on the picklist, select “other” and type in the source.

“Specimen/isolate/plate received MDH lab” – this is often “no” unless Theresa notes otherwise, or if there is a State Lab ID number – that is a good indication. We should also have a received date – that’s something you can find in the lab tab or by asking an epidemiologist.

“State Lab ID #” – if we received the isolate or specimen at MDH there should be an ID number. Please capitalize any letters in the number, no space between letter(s) and number.

“Cryptosporidium allele” – this will come through as a subtype update for Crypto – enter as appropriate. Typically they will start out “BGP” or “HGP” followed by a number.

“Cryptosporidium genotype” – this will also come through as a subtype for Crypto – enter as appropriate. Typically it will be I (1) or II (2).

“How was Cryptosporidium identified?” – Theresa fills this in based on submitting lab, so you can leave this alone. If it was confirmed at the MDH lab the answer is “PCR”.

“Was this an opportunistic infection?” – the answer is always “unknown”

“Confirmed by MDH lab” – Theresa would typically fill this in based on our lab information.

Cyclospora

“Specimen source” - Never enter “unknown” for specimen source. The vast majority of the time it is from stool, but sometimes the specimen source is blood, urine, or something else. If it is a source that does not appear on the picklist, select “other” and type in the source.

“Specimen/isolate/plate received MDH lab” – this is hopefully “yes” unless Theresa notes otherwise. We should also have a received date – that’s something you can find in the lab tab or by asking an epidemiologist.

“State Lab ID #” – if we received the isolate or specimen at MDH there should be an ID number. Please capitalize any letters in the number, no space between letter(s) and number.

Listeria

“Specimen source” - Never enter “unknown” for specimen source. The vast majority of the time it is from stool, but sometimes the specimen source is blood, urine, or something else. If it is a source that does not appear on the picklist, select “other” and type in the source.

“Specimen/isolate/plate received MDH lab” – this is typically “yes” unless Theresa notes otherwise. We should also have a received date – that’s something you can find in the lab tab or by asking an epidemiologist.

“State Lab ID #” – if we received the isolate or specimen at MDH there should be an ID number. Please capitalize any letters in the number, no space between letter(s) and number.

“Serotype/species of pathogen” – choose from the lookup tool – monocytogenes is not what we’re looking for (they are all species monocytogenes) – we want to enter serotype, which is typically something like 1/2A, 4B, 1, etc.

“Confirmed by MDH lab” – choose yes or no as appropriate based on lab results

Salmonella

“Specimen source” - Never enter “unknown” for specimen source. The vast majority of the time it is from stool, but sometimes the specimen source is blood, urine, or something else. If it is a source that does not appear on the picklist, select “other” and type in the source.

“Specimen/isolate/plate received MDH lab” – this is typically “yes” unless Theresa notes otherwise. We should also have a received date – that’s something you can find in the lab tab or by asking an epidemiologist.

“State Lab ID #” – if we received the isolate or specimen at MDH there should be an ID number. Please capitalize any letters in the number, no space between letter(s) and number.

“Serotype/species of pathogen” – choose from the lookup tool – examples would be Typhimurium, Newport, Enteritidis, etc.

“Salmonella group” – choose from the dropdown based upon the serotype. There are cheat sheets in Team D for this question. If a case had Salmonella II, IIIa or IIIb, IV, or VI, there is no group. If it is a Salmonella serotype that starts off “4,5,12”, it is a group B.

“Confirmed by MDH lab” – choose yes or no as appropriate based on lab results

“PFGE” – this is a subtype result that comes in from our lab – examples include TM5b, SE77, SE1B1, SH7, JAV4, etc.

Shigella

“Specimen source” - Never enter “unknown” for specimen source. The vast majority of the time it is from stool, but sometimes the specimen source is blood, urine, or something else. If it is a source that does not appear on the picklist, select “other” and type in the source.

“Specimen/isolate/plate received MDH lab” – this is typically “yes” unless Theresa notes otherwise. We should also have a received date – that’s something you can find in the lab tab or by asking an epidemiologist.

“State Lab ID #” – if we received the isolate or specimen at MDH there should be an ID number. Please capitalize any letters in the number, no space between letter(s) and number.

“Serotype/species of pathogen” – choose from the lookup tool – often sonnei or flexneri

“Confirmed by MDH lab” – choose yes or no as appropriate based on lab results

STEC

“Specimen source” - Never enter “unknown” for specimen source. The vast majority of the time it is from stool, but sometimes the specimen source is blood, urine, or something else. If it is a source that does not appear on the picklist, select “other” and type in the source.

“Specimen/isolate/plate received MDH lab” – this is typically “yes” unless Theresa notes otherwise. We should also have a received date – that’s something you can find in the lab tab or by asking an epidemiologist.

“State Lab ID #” – if we received the isolate or specimen at MDH there should be an ID number. Please capitalize any letters in the number, no space between letter(s) and number.

“Was isolate biochemically identified as E. coli?” – this is always yes if it’s E. coli O157. If it’s another type of STEC, Theresa, Carlota, or another epi will enter this information – leave blank.

“Was the isolate O157 positive?” – this is yes if it’s an E. coli O157

“O-antigen number” – only fill this in for non-O157 cases, and only if you know the answer.

“Was the isolate H7 positive?” – this is yes for E. coli O157:H7 isolates

“H-antigen number” – only fill this in for non-O157 cases, only if you know the answer.

“Was the isolate non-motile?” – if it’s an E. coli O157:H7, or if there is an answer for H-antigen number, the answer to this question is “no”. If H antigen number is not filled in and it’s not H7 positive, the answer is unknown. The answer is only “yes” if the lab result says it’s non-motile.

“EIA results at clinical laboratory?” – if EIA was done at the clinic, this should be answered.

“EIA results at MDH lab” – this is “not tested”. If another answer is already filled in, leave it as is because it may be different for special cases.

“Shiga toxin PCR results at clinical laboratory?” – this is “not tested” for every submitter except Mayo, and then a result should be entered as appropriate.

“Shiga toxin PCR results at MDH lab” – this is often pending and will be entered as an update later – it’s usually an “slt” or “stx” result – sometimes just slt-I or stx1, sometimes just slt-II or stx2, sometimes both.

“Shiga toxin PCR results at CDC?” – this is “not tested”. If another answer is already filled in, leave it as is because it may be different for special cases.

“Was E. coli shiga toxin-producing?” – you can answer this “yes” most of the time. Shiga toxin is what makes E. coli O157 and some other strains of STEC so nasty. Our lab does a PCR test to detect shiga toxin on a specimen. If the CRF says “Shiga toxin positive”, “SLT-I DNA Present” and/or “SLT-II DNA Present”, answer yes to this question. If it says SLT or Shiga toxin was not present, choose no. Otherwise choose unknown.

“Confirmed by MDH lab” – this is only yes if it was confirmed (a PCR test was done or it was biochemically identified as E. coli).

“PFGE” - this is a subtype result that comes in from our lab – examples include MN179, MN1005ECB42, MN32, etc.

Vibrio

“Specimen source” - Never enter “unknown” for specimen source. The vast majority of the time it is from stool, but sometimes the specimen source is blood, urine, or something else. If it is a source that does not appear on the picklist, select “other” and type in the source.

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“Serotype/species of pathogen” – choose from the lookup tool – often parahaemolyticus

“Confirmed by MDH lab” – choose yes or no as appropriate based on lab results

“PFGE” – this is a subtype result that comes from our lab

Yersinia

“Specimen source” - Never enter “unknown” for specimen source. The vast majority of the time it is from stool, but sometimes the specimen source is blood, urine, or something else. If it is a source that does not appear on the picklist, select “other” and type in the source.

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“Confirmed by MDH lab” – choose yes or no as appropriate based on lab results

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