**mVACS & MIMIC Lab Protocol**

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| **Purpose** |

The collection of *C. difficile* positive stool and banana broth samples for downstream applications.

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| **Materials & Equipment** |

* Copan Diagnostics Nylon-Flocked Swab (catalog no. 23-600-959)
* Corning spatula with small spoon (catalog no. 14-245-96)
* Starstedt micro tubes with cap assembled (catalog no. NC0418367)
* Samco graduated transfer pipettes (catalog no. 22-610-171)
* Fisherbrand cryo/freezer box with 8x8 separators (catalog no. 03-395-464)

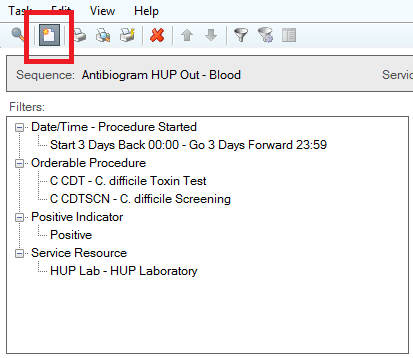
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| **Procedures** |

**Note**: Specimen collection and biobanking for mVACS is to occur twice per week and is based on reports pulled via Cerner. MIMIC specimen collection and biobanking will occur intermittently, per request, but can physically be accomplished on the same two days.

1. **Cerner Report Generation**
   1. Open Cerner and sign in. **Note**: For access-related issues, please contact your immediate supervisor and/or project manager.
   2. Select “Statistical Reports.”



* 1. Within the “Select Sequence” window that populates, select “Detailed Line Listing” under Report. Click “OK.”
  2. Right click in the Filters window and select “Modify Filters.” A window will populate that has a list of filterable options on the left and those that are automatically selected on the right.
  3. Click on the following selected filters and move them to the left: Encounter Type, Group – Client, Task Detail – Susceptibility Detail.
  4. From the list on the left of available filters, select “Positive Indicator” and move it to the right. Click “OK.”
  5. In the Filters window, right click on each individual filter and select “Modify Filter Defaults” and make the following selections:
     1. Date/Time - Procedure Started: **The appropriate window in terms of date**; note that this is selected in the number of days back from current date and number of days forward from beginning date. If report is generated on schedule, you should choose 3 days back and 3 days forward (Tuesday report) or 2 days back and 2 days forward (Friday report).
     2. Orderable Procedure: **C CDT, C CDTSCN**
     3. Positive Indicator: **Positive**
     4. Service Resource: **HUP Lab – HUP Microbiology**
  6. Your Filter window should now look like this:



* 1. Click the “Run Queue” button, highlighted in the image above in red.
  2. Your Queued Report will populate in the bottom most window. Double click on it to retrieve the report.
  3. Transcribe the applicable information from the Cerner report to the study data entry spreadsheet. This spreadsheet will be used to complete the LabVantage specimen accessioning process. Information recorded is to include:
     1. HUP accession number
     2. Patient MRN
     3. Patient last name
     4. Patient first name
     5. Specimen type (stool or banana broth)
     6. Immunoassay result (EIA pos or EIA neg)

1. **LabVantage Specimen Accessioning**
   1. Open LabVantage and sign in. **Note**: This SOP assumes basic knowledge of LabVantage. For training, see your immediate supervisor.
   2. Accession the samples according to the following specifications:
      1. Event Selector
         1. Study: ID\_mVACS OR ID\_MIMIC (whichever is appropriate)
         2. Site: UPHS
         3. Cohort: Participant
         4. General Collection, uncheck “add duplicate visit.”
         5. Collection date (the date the stool was collected from the patient)
      2. Subject Selector
         1. In the “description” field, enter the mVACS or MIMIC subject ID which is assigned in the study spreadsheets located in Box.
         2. Click “Add New Subject” followed by “Next.”
      3. Expected Samples
         1. Select the appropriate Sample Type(s):
            1. 1 Stool swab = “Stool Swab”
            2. 1 Banana Broth = “BacCellIso”
            3. 3 Stool in cryovial = “Stool”
      4. Once accessioned, select each new sample and add the immunoassay result under the “Species” attribute.
      5. Complete the accessioning process, print the generated labels and affix them to the appropriate sampling vessel.
2. **Specimen Collection**
3. Specimens are located in the HUP Microbiology lab (Gates Building, 4th floor). For the door code, please see your immediate supervisor or project manager. Note that you are required to wear a lab coat in this area and use the appropriate PPE.
4. **Stools**
   1. In the walk-in are bins labeled with each day of the week, Sunday-Saturday. Stool specimens can be found within these based on the day of the week that they were received. Collect the applicable stools in a plastic bin, marking on the container the day of the week bin from which they were removed.
   2. Take the stools to the virology lab. Hood #1 (the smallest of those in Virology) is used for stools. All supplies required for use of the hood are available nearby (biohazard waste bags and bench pads). Ready the hood for use.
   3. For each stool, take a swab sample by inserting the flocked tip into the sample and removing it once it is sufficiently soiled. Carefully place it into its tube and set aside.
   4. Using a sterile scoopula/spoon, carefully scoop the stool in up to three 2mL microtubes.
   5. After completion, remove the specimens from the hood. Remove any generated waste and wipe it down with hydrogen peroxide followed by ethanol. Tie biohazard bag shut and dispose of in the sharps bin. Turn off the hood only when everything has been removed.
   6. Return the primary stool containers to the appropriate bin within the walk-in.
5. **Banana Broths**
   1. Positive (yellow) banana broths can be found in a rack within the 4°C refrigerator in the Virology corridor.
   2. Take the broths to the virology lab. Hood #1 (the smallest of those in Virology) is used for stools. All supplies required for use of the hood are available nearby (biohazard waste bags and bench pads). Ready the hood for use.
   3. Using a transfer pipette, carefully remove ~2mL of banana broth from the tube and transfer it to an appropriately labeled 2mL microtube. Once the banana broth has been aliquoted, it can be disposed of.
   4. After completion, remove the specimens from the hood. Remove any generated waste and wipe it down with hydrogen peroxide followed by ethanol. Tie biohazard bag shut and dispose of in the sharps bin. Turn off the hood only when everything has been removed.
6. **Data Collection Finalization**
   1. Once the specimens have been collected, return to the appropriate spreadsheet in Box (mVACS\_data\_entry or MIMIC\_data\_entry) and insert “true” or “false” in the “specimen\_found\_truefalse” column according to which samples were located and biobanked.
   2. For each banana broth banked, enter “tox” or “nontox” in the ID Microbial Species attribute column in LabVantage according to spreadsheet.
      1. This information can also be found in the Cerner report.
   3. For each stool swab/stool vial collected, enter “EIA pos” or “EIA neg” in the ID Microbial Species attribute column in LabVantage according to the spreadsheet.
      1. This information can also be found in the Cerner report.
7. **Notes on MIMIC**
   1. A representative from the MIMIC study will reach out to the lab with particular patient stool samples of interest for collection. These samples are to be collected and banked in similar fashion, but should be accessioned under the MIMIC study in LabVantage and should be recorded in the MIMIC spreadsheet in Box.
   2. PI = Dr. Amanda Pebenito