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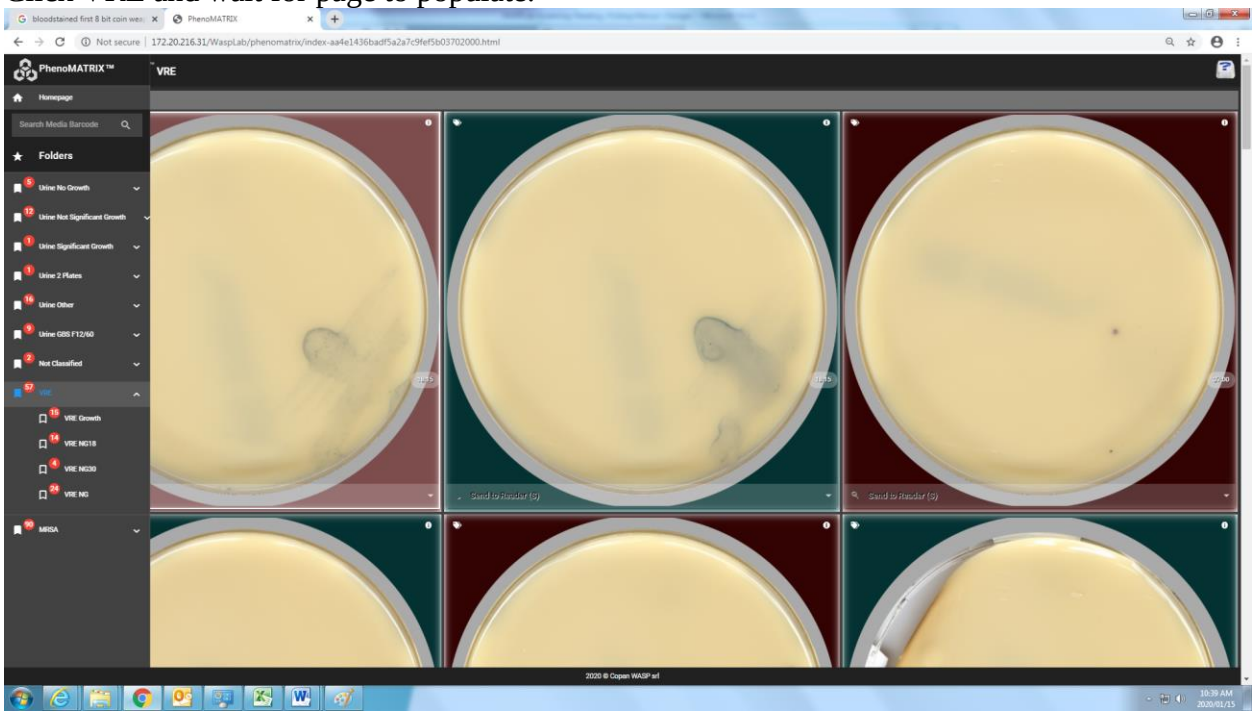
## PHENOMATRIX

PhenoMATRIX™ is an advanced system to pre-assess and group culture plates for review by a trained laboratory professional. The system does not provide any automatic verification or automatic release of culture plate. WASPLab® users read, interpret and segregate bacterial cultures with the click of a button.

Infection Control

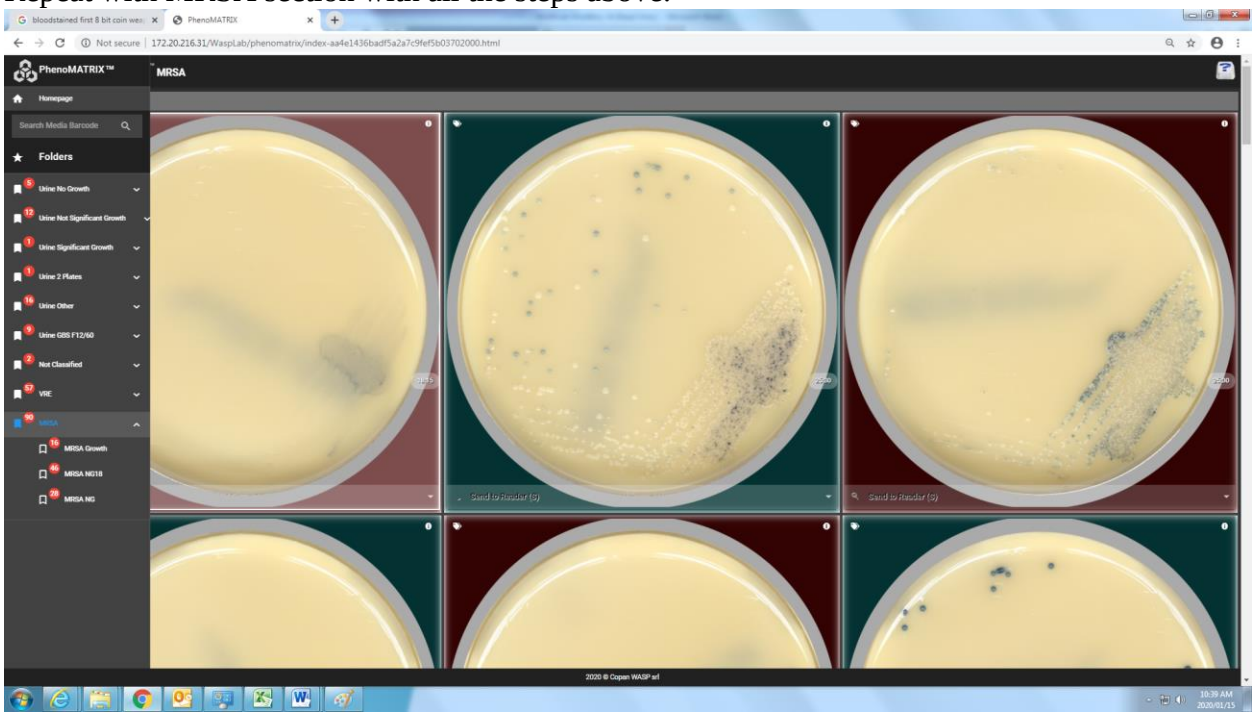
For MRSA and VRE, the plates are separated by growth and no growth along with respective time reincubation readings. The software has a predetermined result for the plate

1. Click VRE and wait for page to populate.



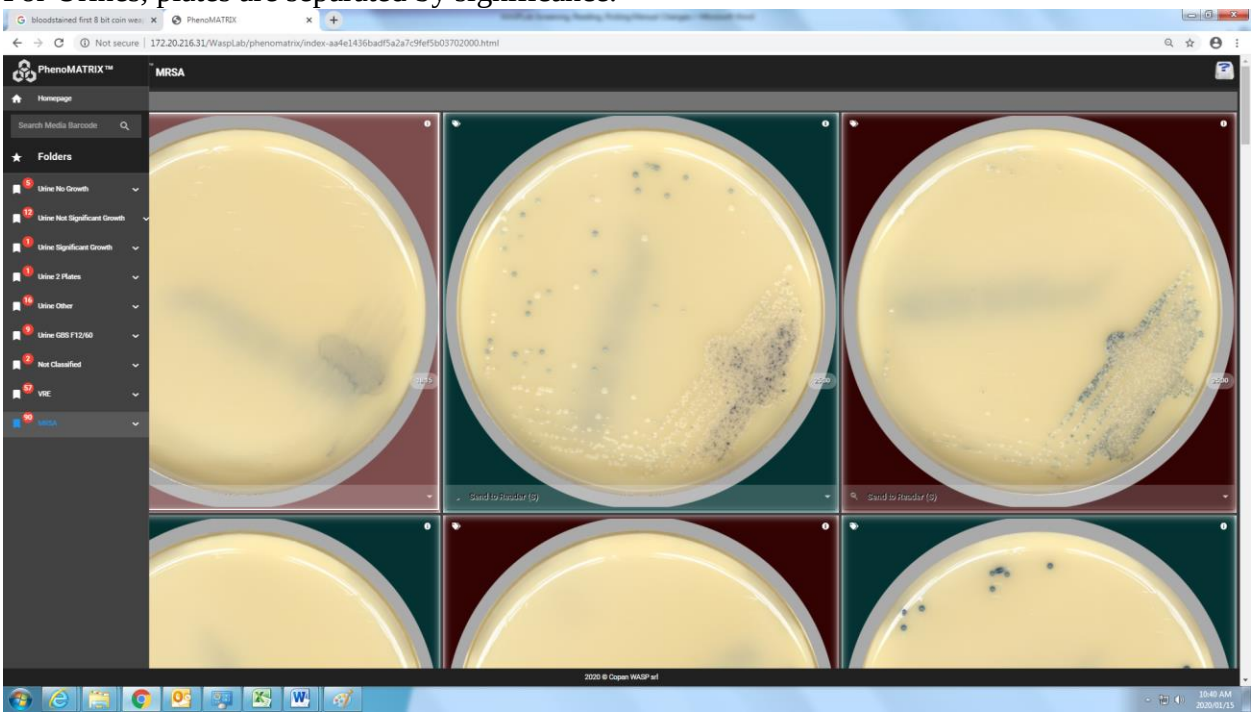

   Go through each section individually: if technologist does not agree with predetermined result given by WASPLAb, change the readings for plates using the drop down
2. Visually go through each plate under each section to ensure that correct result is being resulted
3. Ensure to scroll all the way down to populate the green SEND button on the top right hand corner of the screen
4. Samples not at their end life will continue to incubate

5. Samples at their end life that are negative will automatically go to the trash (Line 100)
6. Samples "Send to Reader" will appear on the reading page of the technologist assigned to reading for that protocol
7. Repeat with MRSA section with all the steps above.



Urine

For Urines, plates are separated by significance.




1. Click on No Growth
    - Screen through all plates to ensure all plates do not have growth
    - Ensure to scroll all the way down to populate the green SEND button on the top right hand corner of the screen
    - All No Growth will automatically go to trash (100)
2. Click Urine Non-Significant Growth (NSG)
    - If technologist does not agree with predetermined result given by WASPLAb, change the readings for plates using the drop down
        - Click the to check demographics of patient to determine if patient is female 12-60 y/o before resulting NSG
    - Ensure to scroll all the way down to populate the green SEND button on the top right hand corner of the screen
    - Samples changed to “Send to Reader” will appear on the reading page of the technologist assigned to reading for that protocol
    - All NSG will automatically go to trash (100)
3. Click Urine Mixed Growth (MG)

- If technologist does not agree with predetermined result given by WASPLAb, change the readings for plates using the drop down
  - Click the  to check demographics of patient to determine if patient is female 12-60 y/o before resulting MG
- Ensure to scroll all the way down to populate the green SEND button on the top right hand corner of the screen
- Samples changed to "Send to Reader" will appear on the reading page of the technologist assigned to reading for that protocol
- All MG will automatically go to trash (100)

4. Click on Urine BP (Ecoli's)
   - Send pure growth Ecoli's ensuring to scroll all the way down to populate the green SEND button on the top right hand corner of the screen
5. Result all other significant urines
   - Change readings for plates if necessary
     - Follow protocols for NSG and MG if changing to these readings
   - For significant growth urines requiring work up, ensure that "Send to Reader" is the result being populated in the drop down
   - Ensure to scroll all the way down to populate the green SEND button on the top right hand corner of the screen
   - Samples "Send to Reader" will appear on the reading page of the technologist assigned to reading for that protocol
   - If reading has been changed to No Growth/Non-Significant Growth/Mixed Growth, these plates will automatically go to trash (100)

## SCREENING

Screening Bloods

1. Click on Screening and then click on Explore next to Bloods
2. See Workflow of Screener/Reader for detailed breakdown of instructions
3. Select appropriate time reading for sample:
    a. Send for Work –Up: To be used when there is something significantly growing on the plate(s) where technologist will need to manually go into LIS for further work up.
    b. Same: To be used when the same set of plates are morphologically the same as the other plates in the same set and no work is needed to be done on that plate.
    c. Same worked on: To be used on plates where you have done any work on plates
    d. Same as other bottle: To be used on the full set of plates of a second set where no work up is needed to be done
4. Click Send at the end of the page and continue until all Blood culture screening is complete

Screening CRE/ESBL

1. Click on Screening and then click on Explore next to IC Screens
2. Check sample to see if CRE/ESBL is ordered

3. If No Growth:
    a. Click no CRE/no ESBL depending on what was ordered on sample
4. If any Growth:
    a. Click Send to Reader
5. Result MRSA/VRE plates in Screening as applicable

<u>Screening Stools</u>

1. Click on Screening and then click on Explore next to stools
2. Each plate will have a respective resulting line
    a. Hektoen:
        i. If no growth: Click No Growth (Prelim)
        ii. If no green or H2S seen: Click No green/H2S prelim
        iii. If ANY green or H2S seen: Leave all other plates unselected and click send to reader
    b. MacConkey:
        i. If no growth: Click No Growth (Prelim)
        ii. If no NLF seen: Click No NLF (Prelim)
        iii. If ANY NLF seen: Leave all other plates unselected and click send to reader
    c. Sorbitol MacConkey:
        i. If no growth: Click No Growth (Prelim)
        ii. If no NLF seen: Click No NSF (Prelim)
        iii. If ANY NSF seen: Leave all other plates unselected and click send to reader
    d. Campylobacter (Usually the last plate that is screened)
        i. Go into LIS to check to make sure all previous work ups have been completed
        ii. If no growth/growth that does not resemble Campylobacter AND all work up has been completed with no significant stool pathogens: Click No Campy/Neg Stool Final
        iii. If no growth and sample is still being worked on: Click No Growth (Prelim)
        iv. If growth does not resemble Campylobacter and sample is still being worked on: Click No Campy (Prelim)
        v. If ANY colonies resembling Campylobacter seen: Leave all other plates unselected and click send to reader

<u>Screening Group B Streptococcus Screens:</u>

1. Click on Screening and then click on Explore next to GBS
2. Any growth seen on plate, click ?Entero/GBS
3. If not growth on plate, click no GBS

## READING

Reading CRE/ESBL

1. Sign in to "Reading Assignment"
2. Click on Reading and then click Start Reading IC samples
3. For CRE samples
    a. NLF
        i. Isolate - choose nv Unidentified organism
        ii. Colony count – choose isolated
        iii. Work up:
            1. Choose NLF (ESBL/CRE) if there are enough colonies to make a 0.5 MF Standard
            2. Choose NLF SBPOD (ESBL/CRE) if there aren't enough colonies to make a 0.5 MF standard
    b. LF
        i. Isolate – choose nv Unidentified organism
        ii. Colony count – choose isolated
        iii. Work up
            1. Choose LF -CRE (ESBL/CRE) if there are enough colonies to make a 0.5 MF standard
            2. Choose LF - SBPOD (ESBL/CRE) if there aren't enough colonies to make a 0.5 MF standard
4. For ESBL samples
    a. NLF
        a. Isolate - choose gnb
        b. Colony count – choose isolated
        c. Work up:
            i. Choose NLF (ESBL/CRE) if there are enough colonies to make a 0.5 MF Standard
            ii. Choose NLF SBPOD (ESBL/CRE) if there aren't enough colonies to make a 0.5 MF standard
    b. LF
        a. Isolate – choose gnb
        b. Colony count – choose isolated
        c. Work up
            i. Choose LF -ESBL (ESBL/CRE) if there are enough colonies to make a 0.5 MF standard

ii. Choose LF - SBPOD (ESBL/CRE) if there aren't enough colonies to make a 0.5 MF standard

5. If there are different morphotypes of colonies be sure to select each one as a different pick point and follow respective steps
6. Result other plates that were left unselected during screening. After this you will be allowed to press "submit"

Reading MRSA

1. Click on Reading and then click Start Reading on IC Samples
2. Check history of patient in LIS and document if New/Previous <3 months under isolated comment in WASPLab
3. If enough colonies to do MS:
    a. Isolate - choose gpc
    b. Colony count - choose quantitation according to growth of plate
    c. Work up
        i. Choose MS Blue Only (MRSA)
    d. If not enough colonies to do MS/too mixed
        i. Organism - choose gpc
        ii. Choose quantitation according ot growth of plate
        iii. Work up – choose Blue sub (MRSA)
4. Result other plates that were left unselected during screening. After this you will be allowed to press "submit"

Reading VRE:

1. Click on Reading and then click Start Reading on IC Samples (or as applicable)
2. For <2+ Blue:
    a. Click the eye symbol, then click Submit
3. For <5 purple
    a. Isolate –choose nv gpc
    b. Colony count – choose Isolated
    c. Work up – choose <5 cols Purple/Royal Blue (VRE)
4. For >5 purple
    a. Check history of patient in LIS and document if New/Previous <3 months under isolated comment in WASPLab
    b. If New:
        i. Isolate – choose gpc
        ii. Colony count – choose Isolated
        iii. Work up – choose >= 5 cols Purple/Royal Blue
    c. If Previous <3 months:

i. Isolate – choose gpc
ii. Colony count – choose Isolated
iii. Work up – choose Prev Purple/Royal Blue

5. Result other plates that were left unselected during screening. After this you will be allowed to press "submit"

Reading Urines:

1. Click on Reading and then click Start Reading on Urine Samples (or as applicable)
2. For gram negative bacilli growing on Chrome Plate
    a. Isolate – choose gnb
    b. Colony count – choose quantitation according to growth of plate
    c. Work up – choose GNB from CHROME (Urine)
3. For Enterococcus growing on both sides of UTI plate
    a. Isolate – choose gpc
    b. Colony count – choose quantitation according to growth of plate
    c. Work up – choose Entero from CNA (Urine)
4. For beta haemolytic streptococcus querying Group B Streptococcus
    a. Isolate – choose gpc
    b. Colony count – choose quantitation according to growth of plate
    c. Work up – choose Grp B/BHS CAT STRGP (URINE)
5. For tiny pinpoint/alphae haemolytic colonies growing on CAN attempting to do MS
    a. Isolate – choose Unidentified organism
    b. Colony count – choose quantitation according to growth of plate
    c. Work up – choose tiny pinpoint from CNA (Urine)/tiny alpha from CAN (Urine)
6. For Staphylococcus species growing on both sides of plate
    a. Isolate – choose gpc
    b. Colony count – choose quantitation according to growth of plate
    c. Work up – choose Staph from CNA
7. For yeast
    a. Isolate – choose yeast
    b. Colony count – choose quantitation according to growth of plate
    c. Work up – choose Yeast from CNA
8. For Sterile Urines
    a. Following steps 2-7 for specific WASPLab entries
    b. For different morphotypes, ensure to have different pick points for each one
    c. For second plate associated with Sterile Urine
        i. Isolate – leave blank
        ii. Colony count – leave blank
        iii. Work up – choose Same as pickpoint plate (Urine)

d. If burgundy pink E-coli is one of the morphotypes
    i. Isolate – choose esccol
    ii. Colony count – choose quantitation according to growth of plate
    iii. Work up – choose Ecoli from Chrom (Urine)

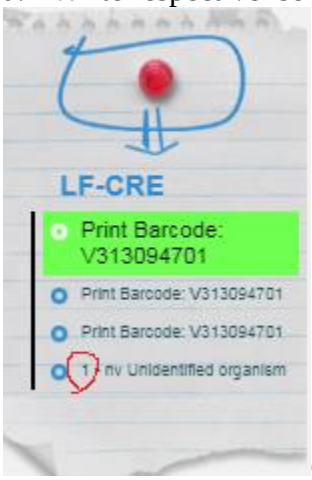
Reading Stools

1. Click on Reading and then click Start Reading on Stool Samples (or as applicable)
2. Each plate will have a different reading pattern
    a. Hektoen:
        i. If enough colonies available for testing:
            1. Isolate – choose gnb
            2. Colony count – choose isolated
            3. Work up – choose ?Green and/or H2S from HEK (STOOL)
        ii. If not enough colonies available for testing
            1. Isolate – choose gnb
            2. Colony count – choose isolated
            3. Work up – choose ?Green and/or H2S Sub Hek (STOOL)
    b. MacConkey
        i. Isolate – choose gnb
        ii. Colony count – choose isolated
        iii. Work up – NLF from MAC (STOOL)
    c. Sorbitol MacConkey
        i. Isolate – choose gnb
        ii. Colony count – choose isolated
        iii. Work up – NSF from MAC (STOOL)
    d. Campylobacter
        i. Isolate – choose gnb
        ii. Colony count – choose isolated
        iii. Work up – ?Campy (STOOL)
3. Result all other negative stool plates as necessary

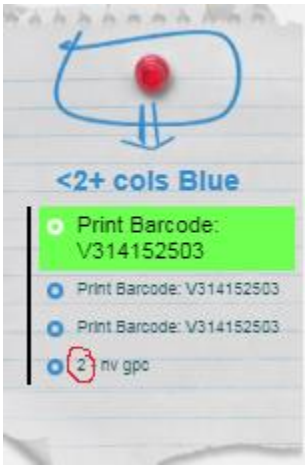
**PICKING**

Picking IC Screens/Urines/Stools

1. Click on Picking and scan plate in hand using barcode reader
2. Print labels for plate ensuring to make note of the isolate number associated with the colony
    a. Write respective isolate number onto printed labels



e.g. this is Isolate 1



e.g. this is Isolate 2

3. Ensure to match isolate number with associated plate and colony
4. Stick labels onto plate and place into “to be MS rack” if MS is not immediately done
5. If no MS is needed, prelim plate(s) and place in working rack (e.g. CRE and SBVRE)
6. For green/H2S/NLF/NSF/?Campy Stools and NLF CRE/ESBL
    a. Perform Oxidase on respective plates, document into LIS, and prelim/final samples as needed. Follow respective SOP for further work up of plates

Picking Bloods:

1. Obtain plate from Stacker 103
2. Individually scan each plate into LIS
3. Under the respective media line and using the keypad:
    a. Input appropriate incubation time
    b. Input appropriate colony description
    c. Input units for MS
4. Follow Picking Workflow for detailed picking information in regards to Blood Cultures.

## ***Record of Edited Revisions***

**Manual Section Name:** WASPLab Screening, Reading, Picking Manual

| Page Number / Item | Date of Revision | Signature of Approval |
|---|---|---|
| Annual review | November 06, 2019 | Dr. T. Mazzulli |

**Full document review included in all updates. Bi-annual review conducted when no revision had been made within 2 years.**

| Page Number / Item | Date of Revision | Edited by: |
|---|---|---|
| Updated various steps | January 21, 2021 | Dorna Zareianjahromi |
| Minor formatting change | April 11, 2021 | Jessica Bourke |
| Biennial Review with no change | February 27, 2023 | Jamaal Pratt |
| Minor formatting change | November 22, 2023 | Jamaal Pratt |
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