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| Microbiology Send Out Reporting | | | | | | | |
| **Purpose** | | This procedure provides instruction for resulting Microbiology send-out tests. | | | | | |
| **Principal and Clinical Significance** | | In an effort to reduce turn-around times and improve patient care, send-out reports need to be resulted daily. | | | | | |
| **Policy Statements** | | This procedure applies to Microbiologists who perform culture set-up and plate reading. | | | | | |
| **Test Codes** | | ANAC (Anaerobic Culture for Fastidious Organisms),  CHLP (Chlamydia pneumonia DNA PCR),  FUNG (Fungus Culture),  LEGC (Legionella Culture),  NCUL (Nocardia Culture)  AFBB (Smear and Culture for AFB) are send-out tests to Mayo Medical Labs (MML), and results are auto-filed. Please refer to [MCVI 5.4 Acid Fast Bacilli Reporting and Susceptibility Add On](MCVI%205.4%20Acid%20Fast%20Bacilli%20Reporting%20and%20Susceptbility%20Add%20On.docx)  VRESP (Viral Respiratory Culture) is a send out test to Mayo Medical Labs (MML) and results are auto-filed.  VIRNR (Viral Culture, non-respiratory) is a send out test to Mayo Medical Labs (MML) and results are auto-filed.  VHSV (Herpes Culture on neonates) is a send out test to Mayo Medical Labs (MML) and results are auto-filed. | | | | | |
| Procedure | | 1. Report reference lab results daily. 2. **Critical**: Verify correct patient and test code when entering results. 3. Call completed worksheets using worksheets MICSO, MCSO2, LEGC2 and FUNG2. 4. Place competed reports in the scanning slot of the black stacking file in the Reception area. There is a slot for Children’s patients to scan into Cerner and a slot for clinic patients (PIP, NEPED, etc…) that will be scanned to the G: drive. 5. Do not scan results in autopsies (MCAL/SCAL). These do not get entered into Cerner. 6. File preliminary reports from MDH only in the folder located in the Micro send out file. 7. Check and resolve the overdue pending logs. Check with Send Outs for overdue Fairview Outreach UMP Labs missing results. The Send Outs staff use the Atlas interface and can print out results. If not resolved, call UM lab for results. MDH and LabCorp must be phoned for missing results. | | | | | |
| **Results Reporting** | | 1. Record results in Sunquest Function Micro Result Entry 2. Enter patient report using accession number. 3. Verify patient name, collect date, test code and source of the specimen. 4. Use MRN inquiry function in Sunquest if accession number is not available. 5. Enter result. 6. Place performing reference lab code after result    1. **MDH** for MDH (no key for MDH)    2. **UM** for Fairview Outreach UMP Labs (key **B**)    3. **RUM4** for LabCorp. 7. When ready to Final, enter comment **SCAND** using (key **V**)**.** 8. Verify the document for correct collect date, change as needed. The collection time MUST be added if not on the document for scanning. 9. Final result using forward slash. (/). 10. Deliver reports to be scanned (not autopsies reports) to Lab front room and place into the Cerner scanned reports slot and clinic scanned report slot in the black stacking file. 11. If culture requires a correction, the code **CORR (**corrected report) must be used in CULTURE RESULTS. Refer to the procedures [MCVI 5.0 Micro Ordering and Receiving](MCVI%205.0%20Micro%20Computer%20Training.docx), [MCVI 5.1 Mislabeled / Unlabeled Specimens](MCVI%205.1%20Labeling%20Errors-Specimen%20Mix-up.docx) 12. If growth should occur or additional testing should be requested after the culture has been finalized, remove the final status and send out a supplementary report using the code **SRPT** in SREQ or CULTURE RESULTS. Re-final the culture when identifications and /or testing are complete. | | | | | |
| **Acid Fast Bacilli**  **Smear/Culture** | | Mayo Medical Laboratories will call Positive smear and Positive culture results to Children’s: | | | | | |
|  | | 1. **Critical Value**: All positive smear and culture results will be reported by Children’s immediately by telephone to the physician or the patient’s nurse. Fill out a blue “Verbal Results” slip with the person called and date/time to document the call. | | | | | |
|  | | 1. Access a hard copy of results in MayoACCESS. Refer to [MCVI 5.4 Acid Fast Bacilli Reporting and Susceptibility Add On.](MCVI%205.4%20Acid%20Fast%20Bacilli%20Reporting%20and%20Susceptbility%20Add%20On.docx) | | | | | |
|  | | 1. Result the preliminary result in MEM at the CTB1P prompt. Refer to [MCVI 5.4 Acid Fast Bacilli Reporting and Susceptibility Add On.](MCVI%205.4%20Acid%20Fast%20Bacilli%20Reporting%20and%20Susceptbility%20Add%20On.docx) | | | | | |
|  | | 1. Susceptibility can be added to existing accession number. Refer to [MCVI 5.4 Acid Fast Bacilli Reporting and Susceptibility Add On](MCVI%205.4%20Acid%20Fast%20Bacilli%20Reporting%20and%20Susceptbility%20Add%20On.docx) | | | | | |
|  | | 1. Turn-around time is approximately 9 weeks. | | | | | |
| **Fungal Culture** | | 1. Report daily updates-**Negative** reports 2. Line 1: **NFTD** (key **zero**)–No Fungus isolated to date 3. Line 2: **UM**- (key **B**) ---Performed by Fairview Outreach UMP Labs, for additional information see separate report. 4. UMP preliminary reports do not need to be saved. Recycle them in shred-it bins. 5. Example as follows:   CULTURE RESULTS  1. NO FUNGUS ISOLATED TO DATE  2. Performed by Fairview Outreach UMP Labs, for  additional information see separate report.     1. Fungal cultures are held for 4 weeks. 2. **Final reports:** replace line 1 with code **NGUM**- Culture negative after 4 weeks incubation. **(Key A)** 3. Check collect time and add **SCAND** comment. **(Key V)** 4. Example as follows:   CULTURE RESULTS  1. CULTURE NEGATIVE AFTER 4 WEEKS INCUBATION  2. Performed by Fairview Outreach UMP Labs, for  additional information see separate report.  3. A scanned image is available.   1. **Positive reports:** 2. Report organism with by looking up code for organism using ellipses  **…** look up ASPE   b. Example: [aspe ASPF for Aspergillus fumigatus  c. Example as follows:  CULTURE RESULTS  1. ASPERGILLUS FUMIGATUS ISOLATED  2. CANDIDA ALBICANS ISOLATED  3. PENICILLIUM SPECIES ISOLATED  4. Performed by Fairview Outreach UMP Labs, for  additional information see separate report.  5. A scanned image is available.   1. Final results may have additional comments. Enter these results after the reference lab on line 3.    1. **Key F** – **NOAD**- No additional fungus cultured after 4 weeks incubation.   CULTURE RESULTS  1. ASPERGILLUS FLAVUS ISOLATTED  2. Performed by Fairview Outreach UMP Labs, for  additional information see separate report.  3. NO ADDITIONAL FUNGUS CULTURED AFTER 4 WEEKS INCUBATION.  4. A scanned image is available.   * 1. **Key S** – **UTH**-Unable to hold for culture for 4-week incubation due to overgrowth of fungus.   CULTURE RESULTS  1. ASPERGILLUS FLAVUS ISOLATED  2. UNABLE TO HOLD CULTURE FOR 4 WEEK INCUBATION DUE TO  OVERGROWTH OF FUNGUS.  3. Performed by Fairview Outreach UMP Labs, for  additional information see separate report.  4. A scanned image is available.   1. **Critical Value**: Isolation of Zygomycetes: *Mucor sp. Rhizopus, Cryptococcus neoformans, Coccidioides immitis, Histoplasma capsulatum, Blastomyces dermatitidis, Sporothrix schenkii*, and other fungi in significant body sites will be reported immediately by telephone to the physician or the patient’s nurse. Document in the computer the person called and the date/time of the call. 2. Check with Send outs for overdue Fairview Outreach UMP Labs missing results. Send out staff uses the Atlas interface and can print out results. If not resolved, phone UMP lab for results at 612-273-7838 or the Mycology Department with culture questions at 612-273-3415. 3. **There is a charge for identification**. Bill only codes need to be added on the Sunquest billing tab. 4. Refer to [MCVI 5.31 Add on micro UM bill codes](MCVI%205.31%20Add%20on%20micro%20UM%20bill%20codes.%202015.xlsx), the UM bill only spreadsheet for charge codes. 5. Turn-around time is approximately 4 weeks. 6. Report Negative cultures with No Fungus to Date, do not use “No Growth After 8 Days”   Result the positive Fungal cultures as soon as a result is received so that the culture will post in Cerner. | | | | | |
| **Chlamydia Pneumoniae by PCR** | | 1. Negative Culture: NCPP -No Chlamydia pneumoniae DNA detected by PCR. 2. Line 2–RUM4-Performed by Lab Corp. 3. Check collect time and enter SCAND comment. (KEY V) 4. Example as follows:   CULTURE RESULTS  1. NO CHLAMYDIA PNEUMONIAE DNA DETECTED BY PCR  2. Performed by Lab Corp.  3. A scanned image is available.  5. The code for a Positive result is PCP.  6. Call LabCorp at 1-888-522-2677, client # 22900172, account # 22330890 for missing reports and questions.  7. Turn-around time is 1 week. | | | | | |
| **Legionella Culture** | | 1. **Negative Culture: NOLEG---** Culture for Legionella pneumophila is Negative. Check for data base change=Legionella species not isolated 2. Line 2– **MDH-** Performed at MDH. 3. Check collect time and add SCAND comment. **(KEY V)** 4. Example as follows:     CULTURE RESULTS  1. CULTURE FOR LEGIONELLA PNEUMOPHILA IS NEGATIVE.  2. Performed by the MN Dept of Health For additional  information see separate report.  3. A scanned image is available.   1. **Positive** **Culture:** Use ellipses **…** legion . Code **LPN** for Legionella pneumophila. 2. Call MDH at 651-201-5073 with missing reports or questions. 3. Turn-around time is 2 weeks. | | | | | |
| **Anaerobic Culture** | | 1. **Negative Culture: NOAN-** No Anaerobes isolated. 2. Line 2– **UM- (key B) --** Performed at Fairview Outreach UMP Labs, for additional information see separate report. 3. To result the gram stain, at MDE tab enter **;HIDE**  to hide the gram result, turns into <<Do Not Report> 4. Example as follows:   GRAM SMEAR: 1. <<DO NOT REPORT>  CULTURE RESULTS  1. NO ANAEROBES ISOLATED  2. Performed by Fairview Outreach UMP Labs, for  additional information see separate report.   * 1. A scanned image is available.  1. **Positive** **Culture**: Use the ellipses to look up **…** the code for PROPI   code PACN =Propionibacterium acnes   1. **Bill only codes need to be added** on the Sunquest billing tab.   Refer to [MCVI 5.31 Add on micro UM bill codes](MCVI%205.31%20Add%20on%20micro%20UM%20bill%20codes.%202015.xlsx), the spreadsheet for charge codes.   1. Check with Send outs for overdue Fairview Outreach UMP Labs missing results. Send out staff uses the Atlas interface and can print out results. If not resolved, phone UMP lab for results at 612-273-7838 or the Microbiology Department with culture questions at 612-273-3665. 2. Turn-around time is 2 weeks. | | | | | |
| **Nocardia Culture** | | 1. **Negative** **Culture**: **NNOC** -No Nocardia isolated after 4 weeks incubation. 2. Line 2 -**UM** (**key B)---**Performed at Fairview Outreach UMP Labs, for additional information see separate report. 3. Check collect time and add **SCAND** comment **(Key V)**     CULTURE RESULTS  1. NO NOCARDIA ISOLATED AFTER 4 WEEKS INCUBATION  2. Performed by Fairview Outreach UMP Labs, for  additional information see separate report.  3. A scanned image is available.   1. **Positive** **Culture:** Use the ellipses **…** to find code. NOCARDIA NOCR= Nocardia species 2. Check with Send outs for overdue Fairview Outreach UMP Labs missing results. Send out staff uses the Atlas interface and can print out results. If not resolved, phone UM lab for results at 612-273-7838 or the Mycology Department with culture questions at 612-273-3415. 3. Turn-around time is 4 weeks. | | | | | |
| **STOOL**  **Results from MDH** | | **Salmonella**--  Isolates will be sent to MDH following MDH Reportable rules and for typing. MDH will report serotypes using whole genome sequencing within 7 days. Culture should remain open until MDH results are received. Add comment **WGS** after typing result   1. **Preliminary report:** Report Salmonella species on line 1-**SALM-ISOL-SENT** 2. **Final report**: After whole genome sequencing results are received, add code **WGS** to result. 3. Add SCAND comment (KEY V) 4. Final culture.   If preliminary report from MDH is Salmonella typhi, change result in Sunquest and notify provider. Scan report.  **Campylobacter/Shigella/E coli 0157—**   1. Append the code SENNR **-** (sent to MDH per reporting rules, no further report). 2. Verify results. Do not scan. Results may be recycled.   **Shiga toxin testing by PCR—**  Verify results. Do not revise report. Save results in EHEC file. Do not scan. | | | | | |
| **Strep pneumo typing** | | **Strep pneumo typing is reported by MDH due to frequent requests and our patient population.**  **MDH types referred isolates for epidemiologic purposes and reports are sent back to our lab.**   1. Report *Streptococcus pneumoniae* on line 1 2. Final culture. 3. When typing results are received, reopen culture, use code SRPT and add typing results. Append code TYPM. | | | | | |
| **Supplementary susceptibility requests** | | If additional susceptibility testing is requested and cannot be performed in our lab, the test is sent to UM Fairview Medical Center or Mayo Medical Laboratories [MCVI 5.5 Isolate Sendout to MML](MCVI%205.5%20Isolate%20Sendout%20to%20MML%20Procedure.docx)   1. Fill out and bring the form U of M Microbiology Referral Request to send outs to specify which referral testing is needed. MC 5.21 [U of M Microbiology Referral Request](MCVI%205.21%20U%20of%20M%20Microbiology%20Referral%20Request.docx). 2. Their test code is IDREFER (referred susceptibility). The method is Etest, and we will be billed for each drug individually. 3. When initiating the send-out—**UM bill-only codes need to be charged** on the Sunquest billing tab in Micro Result Entry. Refer to [MCVI 5.31 Add on micro UM bill codes](MCVI%205.31%20Add%20on%20micro%20UM%20bill%20codes.%202015.xlsx), for the codes. Each drug is charged separately. 4. When results come back, enter as for any other send-out, using Susc Keyboard MIC. 5. Add the comment for: Drug name Susceptibility testing- UM. Example: (free text) Minocylcline Susceptibility testing – Performed at Fairview Outreach UMP Labs, for additional information see separate report (UM code) in the body of the report, and SCAND comment. 6. Put faxed UM result out at front desk for Cerner scanning. | | | | | |
| **Fungal Susceptibilities** | | 1. Fill out and bring the U of M Microbiology Referral Request to send outs to specify which referral testing in needed. MC 5.21 [U of M Microbiology Referral Request](MCVI%205.21%20U%20of%20M%20Microbiology%20Referral%20Request.docx). 2. Result fungal sensitivities in **Micro Result Entry** 3. Susceptibility tab 4. Use the drop down box to choose Susc Keyboard: **FMIC** 5. **You will need to enter the interpretations that are supplied with the result.** 6. Interpretation codes are as follows: **SS, I, R, NINT** (no interpretation available). 7. Example as follows:    1. Example #1   SUSC KEYBOARD: **FMIC**  ORGANISM NO: **1** (highlight)  AMPT: 0.5-SS  F5C5:  FZOL: >32.0-R  IZOL:  KZOL  MZOL:  VORI: >32.0-R  CASP: >32.0-R  . MUCOR SPECIES ISOLATED.  -FMIC- SS: AMPT(0.5)  R : FZOL(>32.0),VORI(>32.0),CASP(>32.0)  b. Example #2:  1. CANDIDA PARAPSILOSIS ISOLATED.  -FMIC- SS : AMPT(0.09),FZOL(0.25),VORI(0.006)  NINT : CASP(0.25)   1. Add comment ‘Sensitivities were performed at Fairview Outreach UMP Labs 2. Example as follows: Free text ‘The Sensitivities were’ and then use the code **UM (key B)**   3. ;Sensitivities were-UM  The sensitivities were Performed by Fairview Outreach UMP Labs, for additional information see separate report.   1. **Charge for Sensitivities on the Sunquest billing tab:** 2. Refer to [MCVI 5.31 Add on micro UM bill codes](MCVI%205.31%20Add%20on%20micro%20UM%20bill%20codes.%202015.xlsx) for the correct bill only codes. 3. The Caspofungin result does not have an interpretation because there is no standardized CLSI method. Please free-text this comment on a result line after the vendor statement. 4. The University may also add a comment about the organism susceptibilities. Please free-text that comment also. 5. Example as Follows.   CULTURE RESULTS  1. ASPERGILLUS NIGER ISOLATED  2. Performed by Fairview Outreach UMP Labs, for  additional information see separate report.  3. There is no standardized CLSI method for the interpretation  of Caspofungin.  4. The MIC is low and suggests the organism is susceptible. | | | | | |
| **Anaerobic Sensitivities** | | 1. 1. Fill out and bring the U of M Microbiology Referral Request to send outs to specify which referral testing in needed. MC 5.21 [U of M Microbiology Referral Request](MCVI%205.21%20U%20of%20M%20Microbiology%20Referral%20Request.docx). 2. Result anaerobic sensitivities in **Micro Result Entry** 3. Susceptibility tab 4. Use the drop down box to choose: Susc Keyboard: **ANMC** 5. **You need to enter the interpretations that are supplied with the result.** 6. Example as follows:     SUSC KEYBOARD: **ANMC**  ORGANISM NO: **1** (highlight)  METR : 0.38-SS  IMP : 1.5-SS  CFT : >256.0-R  PIPT : >256.0-R    1. BACTEROIDES DISTASONIS ISOLATED.  -ANMC- SS : METR(0.38),IMP(1.5)  R : CFT(>256.0),PIPT(>256.0)   1. Add comment ‘Sensitivities were Performed at Fairview Outreach UMP Labs.   Example as follows: Free text ‘The Sensitivities were’ and then use the code **UM (key B)**  3. ;Sensitivities were-UM  The sensitivities were Performed by Fairview Outreach UMP Labs  , for additional information see separate report.   1. **Charge for anaerobic sensitivities on the Sunquest billing tab**, at the time the organism is sent. 2. Refer to [MCVI 5.31 Add on micro UM bill codes](MCVI%205.31%20Add%20on%20micro%20UM%20bill%20codes.%202015.xlsx) for the correct bill only codes. | | | | | |
| **Dr. Schlievert Testing** | | |  | | --- | | 1. Staphylococcus aureus can be sent to Dr. Schlievert (Iowa) for toxin testing. Send the   isolate on a nutrient agar slant, packaged according to Category B standards. These cultures  can be finaled with the code **TSST-“**Microorganism sent to Dr. Schlievert’s lab for TSST testing. No further report.” There will be no additional charge. | | 1. Patrick M. Schlievert   Professor and Chair  Department of Microbiology  Carver College of Medicine  3-403 BSB  Iowa City, Iowa 52242  319-335-7807 | | 1. Example as follows:   CULTURE RESULTS  1. 4+ USUAL UPPER RESPIRATORY FLORA  2. 4+ STAPH AUREUS, METHICILLIN SENSITIVE  3. Microorganism sent to Dr. Schlievert's lab for TSST  testing. No further report. | | 1. Have the Send-out department contact Dr Schlievert (Iowa) for results and questions.   Email is: patrick-schlievert@uiowa.edu. | | 1. If a hard copy is received, un-final culture and result with the comment Dr Schlievert provides. | | | | | | |
| **Haemophilus Typing Results from MDH** | | |  | | --- | | 1. Haemophilus from sterile sites will be sent to MDH for typing. 2. Haemophilus from non-sterile sites that are wet in morphology will only be sent to   MDH for typing upon request of physician and with approval from MDH. 651-201-5073   1. MDH types for group B and sends us a report within 24 hours. Please call MDH 651-201-5073   if report is not received the day after the isolate was sent.   1. Use these codes to result Haemophilus typing.   **HITA**  HAEMOPHILUS INFLUENZAE TYPE A  **HITB**  HAEMOPHILUS INFLUENZAE TYPE B  **HITC**  HAEMOPHILUS INFLUENZAE TYPE C  **HITD** HAEMOPHILUS INFLUENZAE TYPE D  **HITE** HAEMOPHILUS INFLUENZAE TYPE E  **HITF** HAEMOPHILUS INFLUENZAE TYPE F  **HITG** HAEMOPHILUS INFLUENZAE TYPE G | | 1. Append code **TYPM-**Typed at MDH- after result. | | 1. Example as follows:   a. Line 1: 2+-HITE-;(BIOTYPE II)-BLP-TYPM  b. Result looks like:  2+ HAEMOPHILUS INFLUENZAE TYPE E (BIOTYPE II) Beta lactamase positive Typed by MDH   1. Example: as follows:   a. Line 1: 2+-HFLU-;not B-BLP-TYPM  b. Result looks like:  2+ HAEMOPHILUS INFLUENZAE, not B Beta lactamase positive Typed by MDH | | | | | | |
| **Organism Identification sent to MDH** | | |  | | --- | | 1. Organism identifications are sent to MDH for molds, gram-positive rods, and Campylobacter   ID’s, and others that we are unable to identify. | | 1. After the result is entered, append the code: **IMDH**-Identified by MDH. | | 1. Example #1:    1. CAMPYLOBACTER COLI ISOLATED. Identified by MDH.    2. A scanned image is available. | | 1. Example #2:   1. SINGLE COLONY OF CLADOSPORIUM SPECIES ISOLATED. Identified by MDH.  2. A scanned image is available. | | 1. Hard copy reports are scanned into Cerner. Add code SCAND. | | 1. There is no charge for these ID’s except for molds. Add billing code FIDDH for fungal   identification. | | | | | | |
| **Emerging Pathogen Program** | | |  | | --- | | 1. Refer to the MDH poster or go to the website for current additional information.   Download and fill out the MDH fillable form to send along with the isolate. | | 1. Organisms that are sent to MDH for surveillance purposes only need to be verified in the   computer.  This includes **:**   * 1. **Bordetella pertussis,**   2. **Streptococcus pneumoniae,**   3. **Streptococcus pyogenes,**   4. **Streptococcus agalactiae**   5. **Neisseria meningitidis**   6. **Haemophilus influenzae**   7. **Listeria monocytogenes**   8. **Enteric Pathogens: Shigella, Campylobacter, E.coli 0157:H7, Yersinia** | | Do not scan. Results do not need to be saved. | | | | | | |
| **Frequently Asked Questions** | | |  | | --- | | 1. When do you leave a culture open?   Answer:  Stool cultures with Salmonella and Campy that need further identification.  Cultures with Haemophilus typing.  Cultures waiting for ID from MDH.  Preliminary FUNG cultures. | | 2. When do we Final Cultures:  Answer: Stool cultures with Shigella, Campylobacter jejuni and EC 0157can be finaled.  Cultures with Staph aureus to Dr Schlievert’s lab.  When the reference report says ‘Final Report’ | | 3. Why do we un-final a culture before entering results and then re-final?  Answer:  Cultures are sometimes “un-finaled” to enter the results and then re-finaled.  It is done this way as to not clutter up the worksheets when the results come  quick enough to not lose the report. | | | | | | |
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| **Training Plan/ Competency Assessment** | | **Training Plan** | | | **Initial Competency Assessment** | | |
| 1. Employee must read the procedure. 2. Employee will observe trainer performing the procedure. 3. Employee will demonstrate the ability to perform procedure, record results and document corrective action after instruction by the trainer. | | | 1. Direct observation. | | |
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| **Historical Record** | |  |  |  | |  | |
|  | | **Version** | **Written/Revised by:** | **Effective Date:** | | **Summary of Revisions** | |
| 1 | Susan DeMeyere | 2005 | | Initial Version | |
| 1.1 | Becky Carlson | 4/15/2009 | | Modified preliminary filing procedure. File MDH prelims only, in file folder by Virology.  Updated command prompts to Sunquest GUI format.  Added code for positive Chlamydia Pneumoniae PCR.  Added AFB susceptibility section  Changed mucoid streps to Dr Kaplan’s lab, to be finaled, not held open. BC | |
| 1.2 | Becky Carlson | 9/18/2012 | | Added instructions regarding Shigella, Campy, E0157 and Shiga toxin | |
|  | | 1.3 | Becky Carlson | 6/1/2013 | | Added the AFB3 billing code, and hyperlinks to MDH submission poster and fillable form. | |  |  |
| 1.4 | Tina Gronquist | 1/6/2014 | | Reformatted into online format | |
| 1.5 | Becky Carlson | 3/13/2015 | | Removed AFB1 billing code, updated AFB2 and AFB3.  Updated LEGC- Legionella DFA no longer performed. New resulting code NOLEG | |
|  | | 2 | Becky Carlson | 4/3/2015 | | Re-numbered from MC 107 | |
|  | | 3 | Becky Carlson | 11/20/15 | | Removed UM billing charges, refer to spreadsheet, | |
|  | | 4 | Becky Carlson | 7/20/2016 | | Removed AFB, BCAF resulting instructions | |
|  | | 5 | Becky Carlson | 12/6/2016 | | Salmonella and Strep pneumoniae typing are no longer reported back to labs from MDH. | |
|  | | 6 | Susan DeMeyere | 11/30/2017 | | Added MC 5.21 U of M Microbiology Referral Request and added hyperlinks for MC 5.31 Add on micro UM bill codes.  Added MCVI 5.4 Acid Fast Bacilli Reporting and Susceptibility Add on  Changed Strep pneumo typing that MDH will perform for Children’s | |
|  | | 7 | Susan DeMeyere | 8/30/2019 | | Updated CHLP and salmonella information. Added instruction for clinic results and autopsies.  Added Viral send outs tests. | |
|  | | 8 | Susan DeMeyere | 9/20/2021 | | Updated Haemophilus typing instructions | |