

## TRAINING UPDATE

**Lab Location:** SGAH and WAH  
**Department:** Field Operations

**Date Implemented:** 8/23/2016  
**Due Date:** 9/15/2016

### DESCRIPTION OF PROCEDURE REVISION

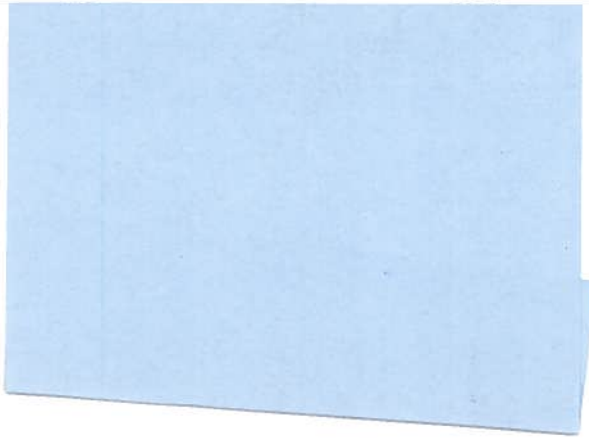
<b>Name of procedure:</b>
FES, Processing Microbiology Orders
<b>Description of change(s):</b>
<ol style="list-style-type: none"><li>1. Procedure was reformatted and updated to make steps clearer and easier to understand.</li><li>2. When performing FES, you must scan plates/specimens for one patient at a time. Specimens must be labeled PRIOR to moving to the next patient's plates/specimens.</li><li>3. When placing the FES label, you must compare the patient name on the FES label to the patient name on the plate/specimen BEFORE applying the label. Do not label the specimen/plate if the names do not match.</li><li>4. Labels should be applied in a way that allows the patient name on BOTH the FES label and the lab/hospital label to be viewed at the same time.</li><li>5. After the "BATCH END" label prints, verify the number of specimens processed on the "BATCH END" label matches the number of specimens being sent (ie, count the number of specimens being sent to ensure it matches the number on the bath label).</li></ol>

Non-Technical SOP

<b>Title</b>	<b>FES, Processing Microbiology Orders</b>	
<b>Prepared by</b>	Leslie Barrett	Date: 10/2/2009
<b>Owner</b>	Samson Khandagale	Date: 10/2/2009

<b>Laboratory Approval</b>		
<b>Print Name and Title</b>	<b>Signature</b>	<b>Date</b>
<i>Refer to the electronic signature page for approval and approval dates.</i>		
<b>Local Issue Date:</b>		<b>Local Effective Date:</b>

<b>Review:</b>		
<b>Print Name</b>	<b>Signature</b>	<b>Date</b>



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### 1. PURPOSE

This procedure describes the steps to electronically submit microbiology orders to the Quest Chantilly and print the required labels.

The Front End System (FES) with Off Site Accessioning (OSA) extensions allows electronic orders to be processed and associated specimens labeled before the specimens are delivered to Chantilly. The LIS (Sunquest) function ROB must be performed prior to FES as this electronically transmits orders to the Quest Chantilly FES system. Refer to Related Documents for FES Process Map.

### 2. SCOPE

This procedure applies to microbiology orders and specimens submitted to Quest Chantilly for testing.

### 3. RESPONSIBILITY

All staff must understand and adhere to this procedure when processing microbiology specimens for submission to the Quest Chantilly laboratory.

### 4. DEFINITIONS

**A. FES:** Front End System refers to the software system used to transmit order/receipt information into the Quest Diagnostics Nichols Institute-Chantilly Laboratory Information System (LIS) from a remote site (SGMC/WAH). Additional FES terms are described in addendum B.

**B. OSA:** Off-site accessioning

**C. Tandem:** Name of Quest Diagnostics Nichols Institute, Chantilly, VA. laboratory information system

**D. Sunquest:** Laboratory Information System (LIS) at SGMC and WAH

**E. Client ID Number:** Chantilly client number to denote facility


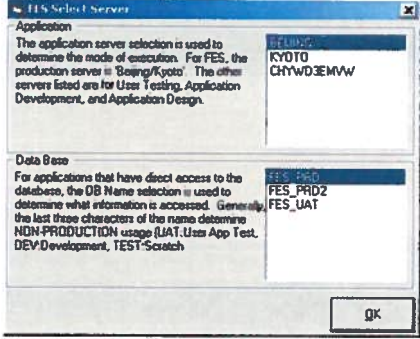

a. SGMC microbiology account number is 23495

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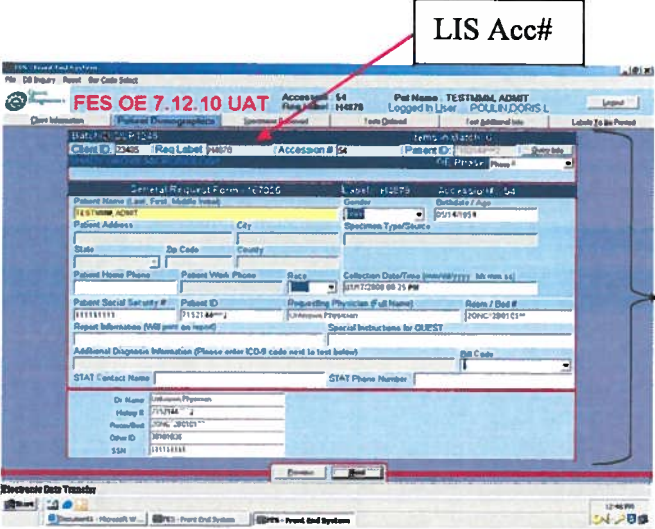
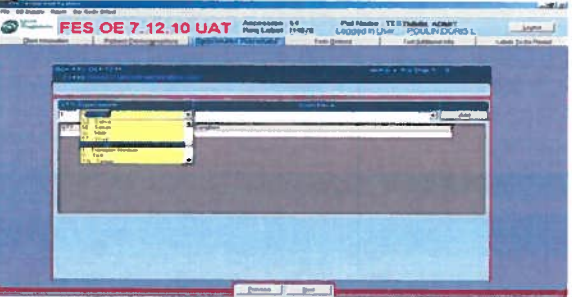
- b. WAH microbiology account number is 23494
- c. PH&R (ARH) microbiology account number is 23495
- F. Facility ID Code:** code utilized in FES to denote facility
  - a. SGMC facility ID is 42.
  - b. WAH facility ID is 43.
  - c. PH&R (ARH) facility ID is 42.
- G. HID:** Hospital Identification, code utilized in Sunquest to denote facility
  - a. **WAH** = Washington Adventist Hospital
  - b. **SGAH** = Shady Grove Medical Center
  - c. **ARH** = Physical Health and Rehabilitation
  - d. **ABH** = Adventist Behavioral Health

**5. PROCEDURE**

Step	Action
1	When specimens for microbiology culture arrive in the laboratory, they are received per normal process and routed to microbiology where technical staff will plate and incubate the specimens per procedure.
2	Specimens that will be referred to the Quest Chantilly laboratory will be placed in the appropriate bin in the microbiology area. Specimens/plates must be separated by hospital location (SGMC/WAH, PH&R, ABH).
3	Using ROB, create a manual batch by location (hospital, PH&R, or ABH) for department MC. <ul style="list-style-type: none"> <li>A. Send only one HID per batch. DO NOT create an automatic batch or you will accession specimens for more than one site.</li> <li>B. Scan the barcode of each specimen to add the accession number to the batch. You MUST scan the accession number on the plate/tube/specimen.</li> </ul> Verify that the number of specimens in the bin is the same as the number of specimens listed on the ROB list.
4	After ROB is complete, pull the ROB pending logs for each site (hospital, PH&R, and ABH) and provide them to microbiology.
5	Queue the ROB batch(es) for transmission.
6	Log into FES and choose a facility. <ul style="list-style-type: none"> <li>A. Enter the following information into FES.                             <ul style="list-style-type: none"> <li>a. Tech name = tandem tech code for the employee</li> <li>b. Password</li> <li>c. Facility ID                                     <ul style="list-style-type: none"> <li>i. 42 = SGMC, PH&amp;R (either site), or ABH (either site)</li> <li>ii. 43 = WAH</li> </ul> </li> </ul> </li> </ul>

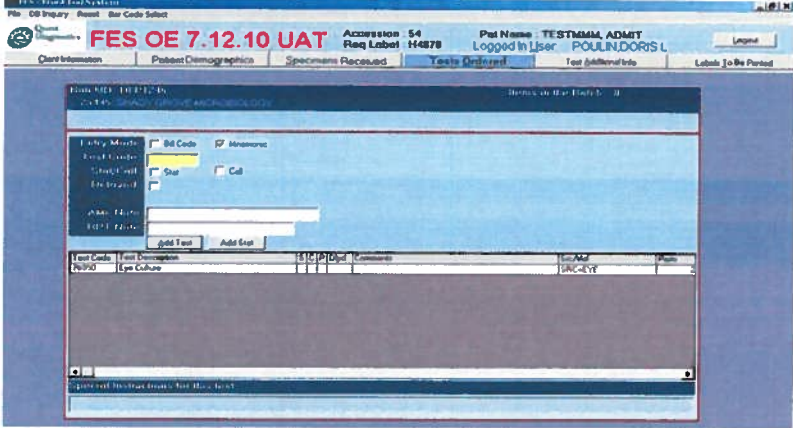
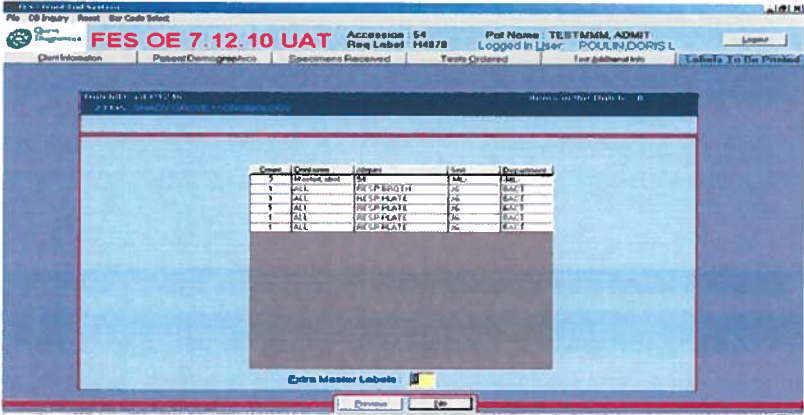
Step	Action
6 Cont	<p>B. Click the “login” button or press “enter.”</p> 
7	<p>Select the FES server if prompted.</p> <p>A. Click “OK.”</p> <p>B. <b>Do not change the defaults of BEIJING and FES_PRD.</b></p> 
8	<p>Enter the client number on the “Client Information” screen then press “enter” twice to validate the client number.</p> <p>A. 23495/0 = SGMC, PH&amp;R, or ABH</p> <p>B. 23494/0 = WAH</p> 
9	<p>Two “batch start” labels will print.</p> <p>A. The batch code will consist of your tech code and the current time.</p> <p>B. Place one label on the Sunquest ROB batch list, and place the other on the FES courier list.</p>
10	<p>Scan the specimens into FES.</p> <p>A. In the “Req Label” field, use the barcode scanner to scan in the LIS accession number from the specimen.</p> <p>B. The LIS accession number will appear in the “Req Label” field.</p> <p>C. The demographic information for the order will autofill.</p> <p>D. Verify that the patient name and ID on the screen match the patient name and ID on the specimen.</p> <ol style="list-style-type: none"> <li>If the identifiers match, press “enter.”</li> <li>If the identifiers are discrepant, resolve any discrepancies before moving forward.</li> </ol>

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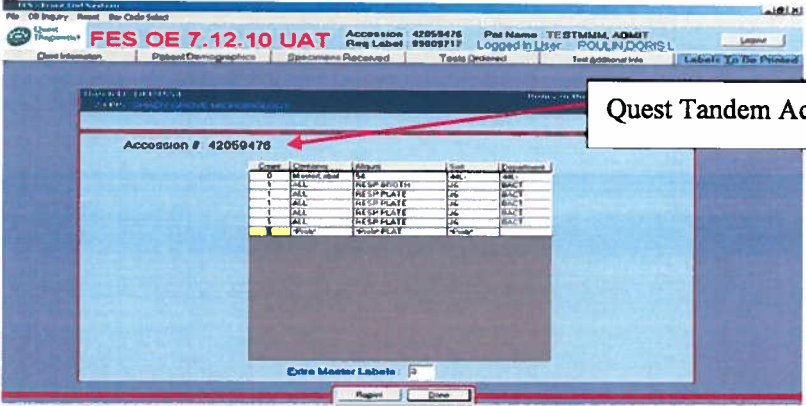
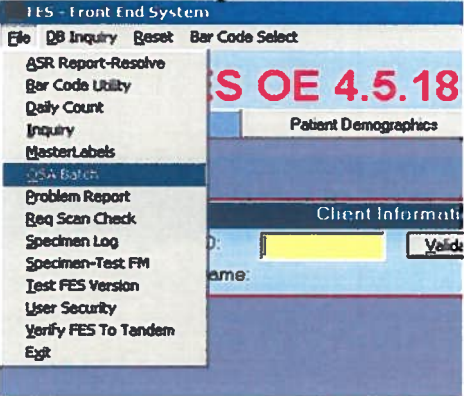
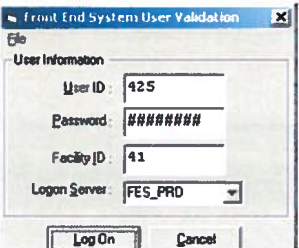
Step	Action
<p>10 Cont</p>	<div style="text-align: center;">  </div> <p>E. If the “No Order On File” message appears, in the lower, left-hand corner of the screen,</p> <ol style="list-style-type: none"> <li>Confirm that the ROB batch has been queued. Queue or re-queue if indicated.</li> <li>Verify the correct hospital ID is displayed.</li> <li>Verify the correct facility ID is displayed.</li> <li>Verify the correct client ID is displayed.</li> <li>Contact LIS support if you cannot resolve the issue.</li> </ol> <p>F. If the “Object or With Block Not Set” message displays, contact Chantilly Operations at 703-802-7600, ext. 7129.</p>
<p>11</p>	<p>The system will prompt you for a specimen type.</p> <ol style="list-style-type: none"> <li>Use the Sunquest ROB batch list to obtain the source.</li> <li>In the “Specimen” field, select the appropriate specimen type from the dropdown menu or type the first couple of letters (i.e. type “SW” for “swab”) and press enter.</li> <li>In the “Condition” field, select an appropriate source from the dropdown menu or type the source when prompted. This will occur for fluid, wound, tissue, and miscellaneous cultures.</li> <li>Refer to Addenda A for additional guidance.</li> <li>You will get a green screen if you fail to enter a specimen type in the specimen field.</li> </ol> <div style="text-align: center;">  </div>



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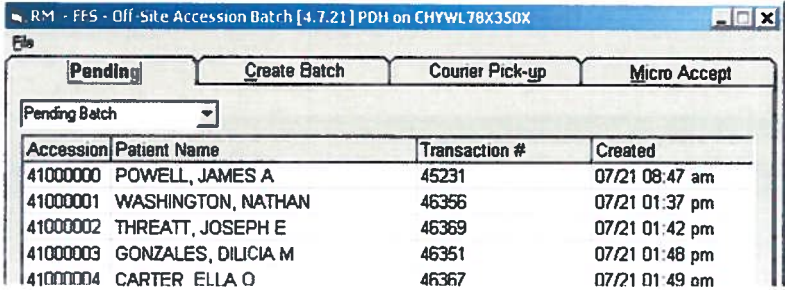
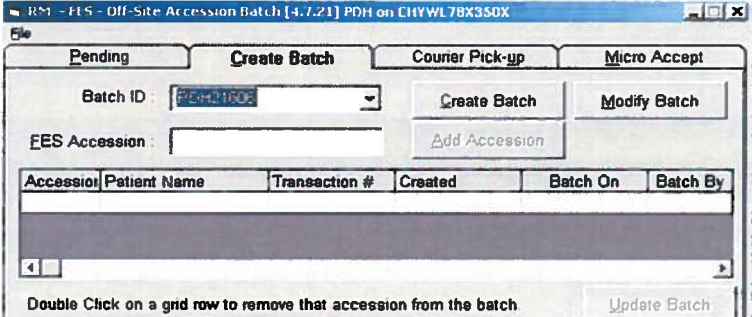
Step	Action
12	<p>A “Test Ordered” screen will appear and display the Quest Tandem order code, test description, and source of the culture. Press “enter.”</p> 
13	<p>The following screen will appear to show the number of labels that will print when you press “enter.”</p> <ol style="list-style-type: none"> <li>Change the count of the “Master Label” row to zero “0” then press “enter.”</li> <li>If you see an “A” or “P,” go back to the previous screen. You entered the incorrect source or condition for this order.</li> </ol> 
14	<p>Label the current plates before moving to the next specimen and click “done” to move to the next specimen.</p> <ol style="list-style-type: none"> <li>Compare the patient name on the FES label to the patient name on the microbiology label to ensure they match exactly. Resolve any discrepancies before moving forward.</li> <li>Place the first label on the specimen. This is the label that contains the specimen source (ie SRC = EYE and RESP BROTH). The label is placed with the tube top facing your right.</li> <li>Place the plate labels on each plate and broth specimen. Do not cover the name on the original label when adding the new label.</li> <li>Return the specimens to the biohazard bag.</li> <li>Place irretrievable samples in a purple biohazard bag.</li> <li>Place any extra labels in the pouch of the biohazard bag.</li> </ol>

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Step	Action
15	<p>The accession screen will display. Scan the next LIS accession into the “Req Lab” field.</p>  <p>Continue steps 10-15 until all specimens have been scanned.</p> <p>Enter and label one specimen at a time. <b>DO NOT</b> remove all specimens/plates from their biohazard bags simultaneously and line them up on the counter to label.</p>
16	<p>When all samples have been scanned and labeled, click the “File” button.</p>
17	<p>Create the FES batch list.</p> <p>A. From the “File” option, select “OSA Batch.”</p>  <p>B. Enter the appropriate facility ID and click “Log On.”</p> <p>A. 42 = SGMC, PH&amp;R, or ABH</p> <p>B. 43 = WAH</p> 



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Step	Action
17 Cont	<p>C. The “Off-Site Accession Batch” screen will appear.                      Note: OSA will automatically set the Caps Lock and Number Lock status.</p>  <p>D. Select the “Create batch” tab.                      The system will automatically create a batch ID. This is a combination of the user’s initials followed by the last digit of the day-of-month and then the hour and minute component of the current time.</p>  <p>E. Click on the “Create Batch” button.                      F. Add the accessions to the batch by scanning the FES barcode accession number (not the LIS accession number) into the “FES accession” field.                      G. Notes:</p> <ol style="list-style-type: none"> <li>a. There should be a one-to-one match for every specimen being sent to Chantilly.</li> <li>b. A maximum of 15 samples should be included in each batch.</li> <li>c. If the accession is already on the packing list, a message box is displayed noting the position of the accession on the list.</li> <li>d. If the accession is not pending for the packing list (i.e. the accession is not on the list of pending accession from the first tab), an error message is displayed.</li> <li>e. An accession can be removed from a batch by double-clicking on the accession in the list of accessions on the batch.</li> </ol>

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Step	Action
17 Cont	<p>f. No changes are made to the batch until the Update Batch button is selected. If changes are made to the batch and the user attempts to leave the screen before saving them, a message box is displayed allowing the user to save the batch before losing the changes made.</p> <p>H. Once all accessions have been added, click the "Update Batch" button.</p> <p>I. Wait for the screen to clear after updating the batch.</p> <p>J. Click the "Pending" tab to transmit the orders on the OSA batch.</p>
18	<p>Click on the "Pending" tab to see if there are any other orders pending. If orders are pending, you MUST modify the batch that was created to add them.</p> <p>The pending tab must be empty until the next ROB is queued from Sunquest.</p> <p><b>Pending Tab (Informational):</b> This tab shows information about pending actions for OSA. There are three (3) actions that can be pending:</p> <p>A. Pending Batch</p> <ol style="list-style-type: none"> <li>a. This is a list of accessions that have been entered in FES but have not yet been assigned to a Courier Pick-Up batch.</li> <li>b. <i>You must always go back to the Pending Tab after creating a batch. The Pending Tab should NOT have any orders pending once a batch is created.</i></li> <li>c. If you have patients in the Pending Tab which are greater than one day:             <ol style="list-style-type: none"> <li>i. Check in Sunquest and if canceled, notify lead tech or supervisor.</li> <li>ii. If not canceled in Sunquest, YOU MUST troubleshoot the problem.</li> </ol> </li> </ol> <p>B. Pending Pick-Up</p> <ol style="list-style-type: none"> <li>a. This is a list of batches created that have not yet been picked-up by the courier.</li> <li>b. This will generally have only one entry.</li> <li>c. If there are batches older than 24 hours, check to see if specimens have been picked up and if so, contact Quest Chantilly Micro to resolve pending samples.</li> </ol> <p>C. Pending Accept</p> <ol style="list-style-type: none"> <li>a. This is a list of batches that have been picked-up by the courier but not yet accepted by the Chantilly Lab.</li> <li>b. This will have multiple entries only if multiple batches are created for courier pick-up.</li> <li>c. If there are batches older than 24 hours, you need to contact Quest Chantilly Micro to resolve pending.</li> </ol> <p>For any pending batch that is greater than one (1) week old, notify a supervisor or lead tech who will contact Chantilly IT to resolve.</p>

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Step	Action
19	<p>Print the courier packing list.</p> <ol style="list-style-type: none"> <li>A. Access the “Courier Pick Up” tab.</li> <li>B. Highlight the batch you are working with.</li> <li>C. Enter either “SGAH” or “WAH” in the courier name field.</li> <li>D. Click the “Print” button to print a sufficient number of copies of the batch report in order to place on in each micro bag.</li> <li>E. Verify that the specimen/plates and orders match.</li> </ol>
20	<p>Log out of FES.</p> <ol style="list-style-type: none"> <li>A. A “Batch End” label will automatically print.</li> <li>B. Place this label on the Sunquest ROB packing list and on the FES courier list.</li> <li>C. Highlight the number of specimens processed from the FES batch label.</li> <li>D. Verify that the number of specimens processed matches the number of specimens actually being sent.                             <ol style="list-style-type: none"> <li>a. Note the number of specimens on the ROB list may differ from the number of accession numbers for XIDS and XIDSN. These tests share an accession number in the Sunquest system but have different accessions in Tandem.</li> <li>b. If AER and ANA blood cultures have the same accession on the ROB list, verify they have separate FES numbers. You should never have more than 5 plates with the same FES number.</li> </ol> </li> </ol>
21	<p>Place one copy of the FES/Courier packing list in each microbiology biohazard bag (bag with wide yellow stripe).</p>
22	<p>Staple the following documents together and maintain onsite for 1 month.</p> <ol style="list-style-type: none"> <li>A. ROB batch list on top.</li> <li>B. Followed by the ROB packing list.</li> <li>C. Followed by the FES packing list.</li> </ol>
23	<p>Place the specimens in the incubator until the courier arrives.</p>
24	<p>The courier will deliver the samples directly to the microbiology department in Chantilly. At that time, Chantilly microbiology personnel will accept the samples in the computer system.</p>

**FES Problems**

Refer to FES Troubleshooting Process Map (see Related Documents) for steps to investigate problems or issues with the FES application.

**Downtime Processes**

If the Hospital cannot access FES or orders are not in FES, then the specimens will remain on site stored in the hospital's incubator.

- Do NOT send specimens to Quest if the orders have not gone through FES.
- If there are questions on whether samples can be sent, contact Group Lead Tech / TIC / Supervisor on site.
- If downtime is to exceed 8 hours, notify Group Lead / Supervisor on site, Administrator On Call, LIS On Call and Chantilly Micro who will determine if specimens are to be sent without accessioning in FES.

**6. RELATED DOCUMENTS**

ROB - Creating Batch for Microbiology Send outs  
 FES Password, Specimen Processing procedure  
 FES Process Map (AG.F355)  
 FES Troubleshooting Process Map (AG.F356)

**7. REFERENCES**

None

**8. REVISION HISTORY**

Version	Date	Reason for Revision	Revised By	Approved By
		Supersedes SOP S006.006		
000	8/14/12	Section 4: Add Maximum batch size, revise courier list retention time, add SOP to FES access code Section 5: Clarification of placing FES Batch end label on ROB Batch list and verifying specimens processed, changes to Print courier packing list Section 6: Update document titles	R. Master  L. Barrett	S. Khandagale
001	12/4/13	Section 4: Add Client ID, Facility ID, HID, WAH, SGAH and new locations ARH, ARHT, ARHR; add explanation to zero out extra labels Section 5: Specify separating by HID, add pulling pending logs for each HID to see orders qualified before performing ROB, add Client ID for micro orders for ARH , samples for WAH, SGAH, and ARH must processed separately. Revised working with one sample at a time Footer: version # leading zero's dropped due to new EDCS in use as of 10/7/13	N. Maskare	S. Khandagale

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2	6/15/16	Section 4: FES terms removed Section 5: Clarified basic steps, re-format into process sections and table format Section 6: Add process maps Section 9: Add addenda B	M. Sabonis L. Barrett	S. Khandagale
3	8.18.16	Header: Add WAH Section 5: Updated format and order of steps for clarity.	S. Codina	S. Khandagale

**9. ADDENDA AND APPENDICES**

- A. LIS Micro Orders and Quest Tandem Order Number
- B. FES Terminology and Descriptions

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**Addenda A**

**LIS Micro Orders and Quest Tandem Order Number**

Culture	Quest Order Code	LIS Code	Sunquest Source(SDES)	Specimen	Condition (Free Text)	Plates	Broth	SGAH/VAH Default # Plates
AFB Culture and Smear	5202	XAFBC1	Fluid	FL	Source of Fluid	0	0	0
AFB Culture and Smear	5202	XAFBC1	Urine	UC	Leave it blank	0	0	0
AFB Culture and Smear	5202	XAFBC1	Tissue	TIS	Container	0	0	0
AFB Culture and Smear	5202	XAFBC1	Sputum	MI	SP	0	0	0
AFB Culture and Smear	5202	XAFBC1	Bronch Wash	MI	BRON	0	0	0
AFB Culture and Smear	5202	XAFBC1	Aspirate Tube	MI	Aspirate Tube	0	0	0
AFB Blood Culture	8518	XAFBL1	Blood	BL	Leave it blank	0	0	1 bottle
AFB Smear	268	XAFSM1	Fluid	FL or SW	Source of Fluid	0	0	0
AFB Smear	268	XAFSM1	Urine	UC	Leave it blank	0	0	0
AFB Smear	268	XAFSM1	Tissue	TIS	Leave it blank	0	0	0
AFB Smear	268	XAFSM1	Sputum	MI	Leave it blank	0	0	0
AFB Smear	268	XAFSM1	Bronch Wash	MI	BRON	0	0	0
AFB Smear	268	XAFSM1	Aspirate Tube	MI	Aspirate Tube	0	0	0
AFB Blood Culture	8518	XAFBL1	BL	BL	Leave it blank	0	0	1 bottle
Anaerobic Culture	15871	XANAC	any source	FL or SW	Source of Fluid	5		3
Blood Culture / Aer	18100	XIDS	BL	BL	Leave it blank	4		4
Blood Culture / Anaerobe	18101	XIDSN	BL	BL	Leave it blank	5		5
Fungus Blood Culture	14701	XBLF1	BL	BL	Leave it blank	0	0	1 bottle
CSF Culture (and Gm Stain)	127350	XCSFC	CSF	CS	Leave it blank	4	1	5
Cath Tip Culture	78352	XCTIP	Cath	MI	Leave it blank	1		1
Ear Culture	76951	XEAR	Ear	SW or EAR	Leave it blank	4		4
E Coli O157	4221	XECOL	Stool	ST	Leave it blank	1		1
Environmental Culture	6320	XENVR	any source	WATER	Source of culture	1		1
Eye Culture	76950	XEYE	Eye	EYE	Leave it blank	4		4
Fungus Culture (hair,skin, nail)	7998	XFHSN	Hair, Skin, Nail	MI	Hair, Skin, or Nail	0	0	0
Fluid Culture	1273	XFLC	any source	FL	Source of Fluid	4	1	5
Fungus Smear	270	XFSMR1	any source	MI or SW	Leave it blank	0	0	0
Fungus Culture	105	XFUNC1	any source	MI or SW	Leave it blank	0	0	0
Group B Strep Cult Screen	14537	XGBSC	source	SW	Leave it blank	0	1	1
GC Culture Screen	657	XGCS	source	SW	Leave it blank	2		1
Genital Culture	778	XGENC	source	SW	Leave it blank	4		4
Millipore Water	4120	XH2O	source	WA	Leave it blank	1		1
MRSA Screen	752	XMRSA	source	any source	Leave it blank	1		1
MRSA PCR	17656	XMRSA	Nose	SW	Leave it blank	0		0
Respiratory Culture	769	XRESP	source	MI	SP	4		4
Stool Culture	15292	XSTLC	Stool	ST	Swab/Container	0	1	6
Group A Strep Cult Screen	6470	XSTPAS	Throat	SW	Leave it blank	1		1
Surgical Culture	78353	XSURG	any source	TIS	Leave it blank	5		5
MTB Complex TMA Non Resp	18006	XTBNR	any source	MI	Leave it blank	0		0
MTB Complex TMA Resp	6931	XTBRP	any source	MI	Leave it blank	0		0
Throat Culture	5870	XTC	Throat	SW	Leave it blank	2		2
Tissue Culture (and GS)	78350	XTISC	any source	TIS	Leave it blank	5		5
Urine Culture	URINEX	XURN	Urine	UC	Leave it blank	2		2
Urine Culture (Sterile, bladder, I/O, Suprapubic)	URINEX	XURN	Urine	UC	Source of Urine	4		4
VRE Culture	8557	XVRE	any source	ST	Leave it blank	1		1
Wound Culture	78351	XWDAC	any source	SW	Leave it blank	4		4
Would Culture (with Gm Stain)	783	XWDCG	any source	SW	Leave it blank	4		4

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**Addenda B**

**FES Terminology and Descriptions**

<b>FES Access code</b>	A user must be assigned a TECH ID and PASSWORD for FES remote order entry. Refer to procedure 'FES Password' for process to request ID and password, and how to re-set a password when it expires.
<b>Specimen</b>	Specimen type as such as BL (Blood Culture), CS (CSF), SW (Swab), MI (Miscellaneous for any specimen, which is not found in the drop menu), TIS (Tissue) UA (Urine), UC (Urine Cup).
<b>Condition</b>	Condition is used to define the source of the culture, such as SP (Sputum) when MI is used for specimen. Refer to addendum A. For most orders, you will leave condition blank.
<b>Master Label</b>	The first time you log in to accession the specimens, you will have a Master Label with a number, zero out the number. You will have to do this only for the first accession number. To zero out the number simply erase the existing master label number and enter "0".
<b>"P" label</b>	If you have a P label, you need to review your specimen from the previous Specimen screen to make sure you have entered the correct specimen.
<b>"A" label</b>	If you have an A label, you need to review your specimen from the previous Specimen screen to make sure you have entered the correct specimen.
<b>Extra Label</b>	Zero out the extra labels by entering "0"
<b>Enclose in Bag</b>	Zero out this label. <b>(Do NOT use this for ANA bags)</b>
<b>Blood Culture</b>	<ol style="list-style-type: none"> <li>1. Enter BL as the specimen but you will only be sending plates.</li> <li>2. Tandem will split Culture into 2 Tandem Accession Numbers for the Aero and Anaerobic cultures.</li> <li>3. If you have more than 5 plates for any single accession, there is an error. Stop and correct the problem.</li> </ol>
<b>One specimen, multiple orders</b>	You must have a specimen for every order. If QNS to split, call nurse or physician to cancel test.
<b>Biohazard Bag</b>	One patient specimen or plates from one specimen/accession per Biohazard Bag. Do NOT put plates from multiple patients or multiple accessions in a single Biohazard Bag. If extra labels were printed, place in the outside pouch.
<b>Plates</b>	Check to be sure all plates are taped closed. If lids are not taped to plates, add tape before proceeding.
<b>Batch Size</b>	Maximum batch size is limited to 15 accessions.
<b>ROB</b>	ROB is the Reference Batch List created by the LIS (Sunquest). Place the Batch Start and Batch End on this document.
<b>Courier List</b>	List to be included in every yellow bag being sent to Chantilly. Generate as many copies as needed by changing the # of copies when printing the courier list. Site keeps the courier list for 1 month.
<b>Green screen</b>	If you do not enter a specimen or plates at the Specimen Screen, you will get a Green Screen. The only way to exit is to CTL/ALT/DEL to log off FES.
<b>Problems</b>	Refer to "FES troubleshooting Process Map"

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