Hidden Microbiome of Infection Surveillance Culture Program and the Living µBiome Bank

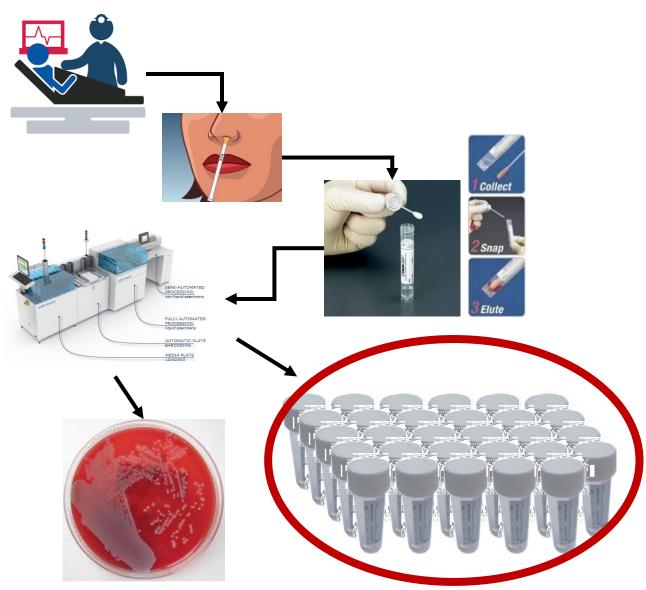
Alexander V. Alekseyenko^{1,2} and Jihad Obeid²

¹Program for Human Microbiome Research ²The Biomedical Informatics Center (BMIC) Medical University of South Carolina



MUSC Hospital Active Infection Surveillance culture program

- Every inpatient admitted to the hospital is subject to the program
- Swabs for MRSA and VRE are obtained as soon as possible after admission
- Samples are processed within 24-48 hours to determine colonization
- BD auto-streaking instrument is used to minimize bias
- 75% of the specimen volume remains in excess and is discarded within a week of collection



Number of specimens processed by MUSC Diagnostic Microbiology Lab (DML) in a typical month

N/month	Specimen description
2,584	Urine in BD preservation tubes* or sterile containers
2,472	MRSA surveillance Eswabs**
2,379	VRE surveillance Eswabs**
501	Wound Eswabs**
364	Lower respiratory specimens in sterile containers
170	Vaginal/rectal Eswabs** for Group B Streptococcus
160	Stool submitted for C. difficile PCR in sterile containers
147	Stool submitted for G.I. PCR Panel in sterile containers
105	Tissues, frozen at -70C for 1-2 months
52	Sterile body fluids

Vision: The surplus materials from active infection surveillance program will be used for translational research at MUSC



Why focus on infection surveillance culture program specimens?

Sampling uniformity

- Only a few trained nurses are assigned to collect the swabs, minimizing the collection bias.
- Sample handling is automated, minimizing handling bias.

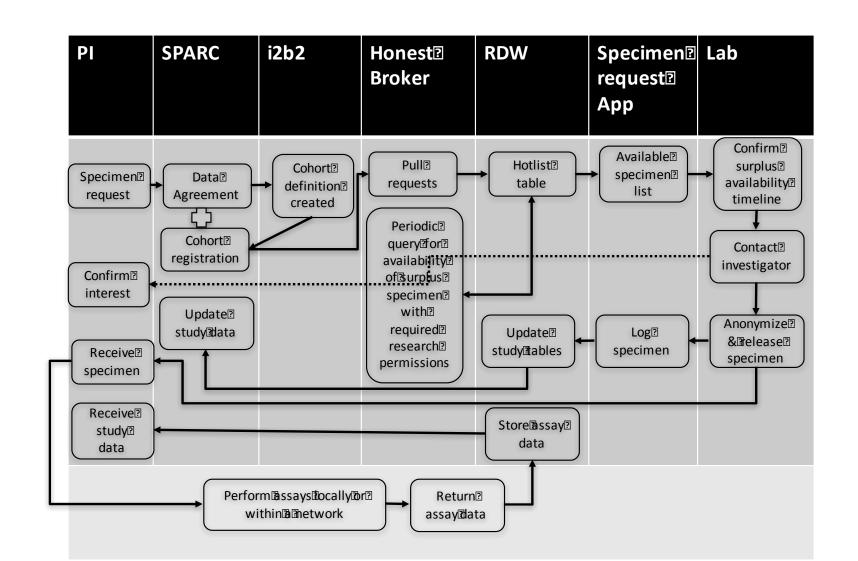
Participation reach

- All subjects are subject to the program.
- MRSA swabs are collected from almost every subject.
- VRE swabs collected from select units (surgery, etc.)

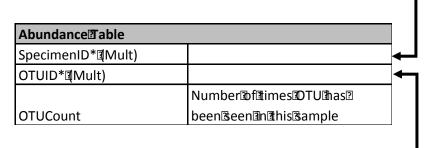
Impact potential

- Specimens are collected early in the course of providing care.
- Specimens are collected throughout care provision timeline.

Preliminary Living µBiome Bank Workflow



Preliminary RDW schema for microbiome



Sample Data Table		
ResearchID** (Mult)	Alpha/Numeric	
SpecimenID**¶Mult)	Alpha/Numeric	
BatchID*	Sequencing@nalysis@batch	
CollectionDate	Date	
ProcessingDate	Date	
Body s ite	Text(e.g.@Nasal	
LabdD	textawhoatollectedaheasample)	
TestType	Text MRSA/VRE	
TestOutcome	positive, an egative, anconclusive	
	ResearchID** Mult) SpecimenID** Mult) BatchID* CollectionDate ProcessingDate Body ite Lab ID TestType	

Batch Table				
BatchID*				
ExtractionProtocol				
SequencingType	WMGS,116S			
BatchDate	Date			
FileRef	Location in far aw is equences			

OTUIDTable	
OTUID**	
NCBITaxaID*	
	Exacts equence representing 2
RefSeq	this®DTU®

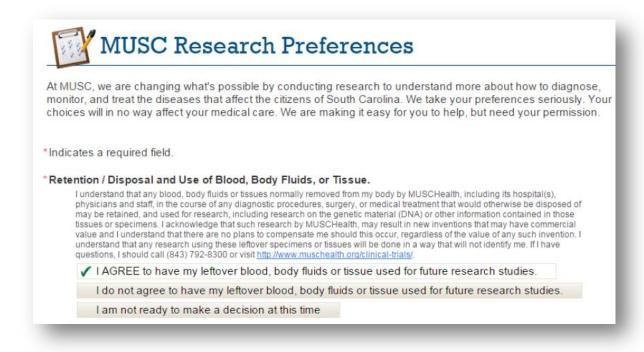
	NCBITaxa@able			
>	NCBITaxaID**	Unique Identifier Ifor Ithe Itaxon		
	Domain	e.g. ® acterium		
	Phylum	e.g. rmicutes		
	Class	e.g. ® acilli		
	Order	e.g. ® acillales		
	Family	e.g. ß taphylococcaceae		
	Genus	e.g. ß taphylococcus		
	Species	e.g. @ Aureus		
	Strain	N/A		
	Isolate	N/A		

Immediate Goals

- Goal 1: Determine the suitability of surplus surveillance testing material for microbiome analysis.
- Goal 2: Determine feasibility of obtaining the excess specimens from DML in a de-identified way.
- Goal 3: Establish the infrastructure for storage of massive amounts of patient microbiome data in RDW.
- Goal 4: Perform proof of principle pilot research studies on these specimens.
- Goal 5: Provide a system for ordering de-identified microbiome specimens from precisely defined patient cohorts within and outside MUSC.
- Goal 6: Determine the utility of microbiome biomarkers in predicting patient visit health outcomes.

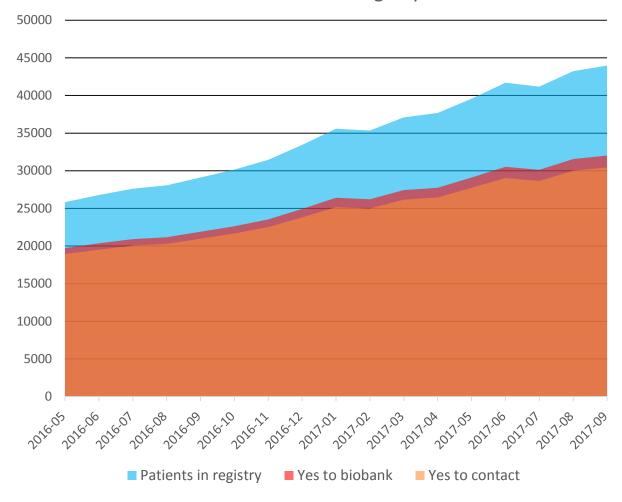
Consent challenges

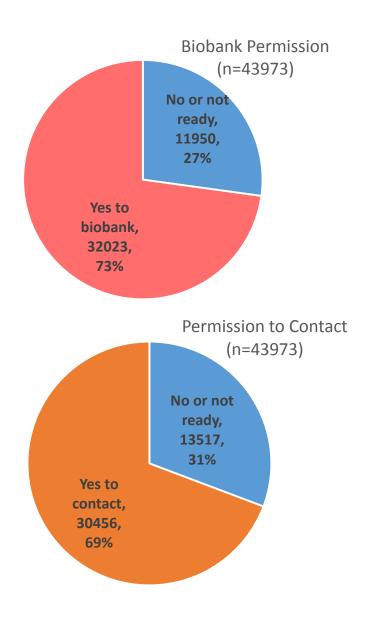
- We will use research preferences collected routinely in EHR
- Patients are invited either via Patient Portal or during encounter
- However there are limitations...



Research Preferences

Research Permissions Registry: Trend

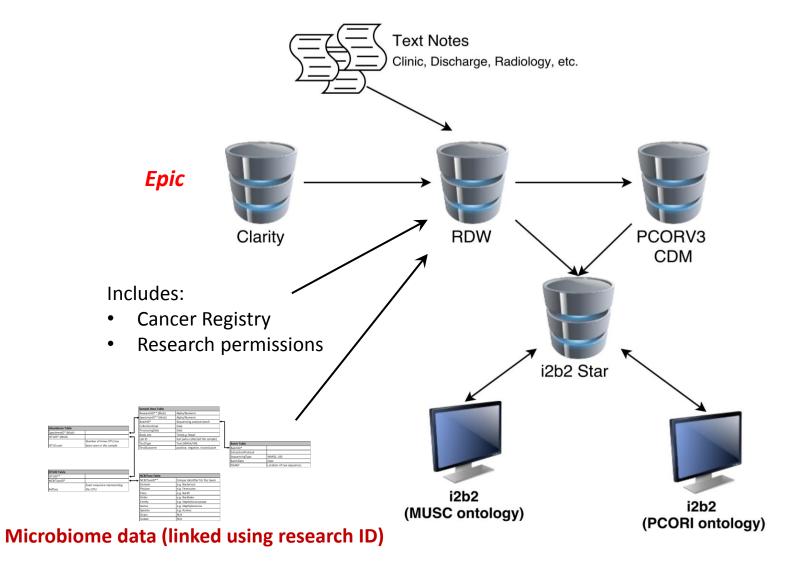




Consent challenges (continued)

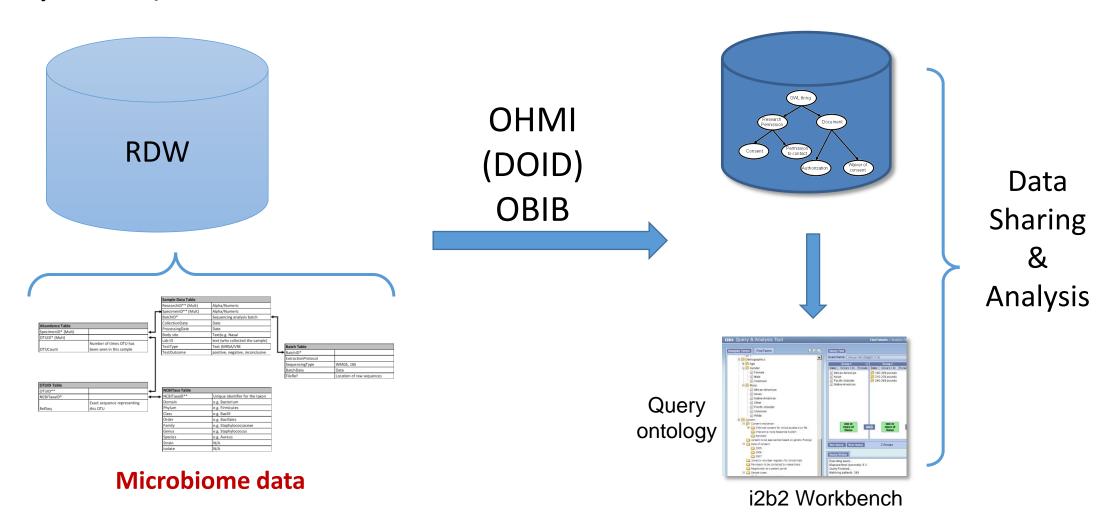
- Less than 15% of patients have answered the MUSC Research Preferences questionnaire
- We will exclude those who do not agree to have their leftover specimens for future research studies
- What about the other 85% of patients who have not answered the questionnaire?

Research Data Warehouse





Microbiome data repository (in RDW and beyond)



Acknowledgments

- Leslie Lenert, Chief Research Information Officer
- Cassy Salgado, Director Infectious Diseases
- Lisa Steed, Director Microbiology Diagnostic Lab
- Bashir Hamidi, Statistical Analyst & IRB specialist
- Katharine Patterson, MSHI Capstone Student

Grant #s: The project described was supported in part by the NIH National Center for Advancing Translational Sciences (NCATS) through Grant Number **UL1TR001450** and MUSC College of Medicine Enhancing Team Science (COMETS) award to AVA.

