NEW YORK STATE | Department of Health
Wadsworth Center

ARLABnetwork

Northeast Region Antimicrobial Resistance Laboratory Network

Wadsworth Center 2022-2023 Newsletter

New Staff:

Nicola Faraci
AR Bacteriology
Senior Lab Technician

Nicola earned an Associate of Science from Columbia-Greene Community College and is currently completing a Bachelor of Science degree in human biology at the University at Albany. Her fascination for the sciences began as a biological science aide in the Genomics Core at the U.S. Department of Agriculture (USDA). Her work involved sequencing new genetically modified orange varieties with targeted resistance to Huanglongbing, a citrus greening disease, carried by the Asian citrus psyllid. Following her time with the USDA, she worked as a research assistant at The Vaccine Gene Therapy Institute of Florida. In collaboration with the Karolinska Institute of Sweden, she supported studies of immunotherapy properties of natural killer (NK cells) cells in liver and breast cancer. Nicola joined the Wadsworth Center's Genomics Core in 2021, where she performed Sanger and Next Generation sequencing. In 2023, she accepted a position in the Antimicrobial Resistance (AR) Regional Laboratory conducting clinical testing in the detection and surveillance of antibiotic-resistant gram-negative bacteria. She has become especially interested in the outbreak surveillance system and how it is closely monitored in the United States, specifically the Northeast Region.

Mohammad Yasir Khan
AR Bacteriology
Research Scientist

Yasir earned his Bachelor of Science in biology from Stony Brook University and his master's degree in pharmacology from New York Medical College. In his master's program, Yasir worked in the lab of Dr. Jerry Nadler working with 12-lipoxygenase (12-LOX) and its role in SARS-CoV-2 infection in individuals with diabetes. During this time, Yasir was a contributing author for three papers in different scientific journals. Following this, Yasir worked at Regeneron as a quality control (QC) scientist before working at Wadsworth Center in August of 2023. He joined the Bacteriology Laboratory in the Antimicrobial Resistance Regional Laboratory as a research scientist. His work involves running polymerase chain reactions to detect the "big five" antibiotic resistance genes in isolates and swabs.

Gabrielle Todd
AR Mycology Research Scientist

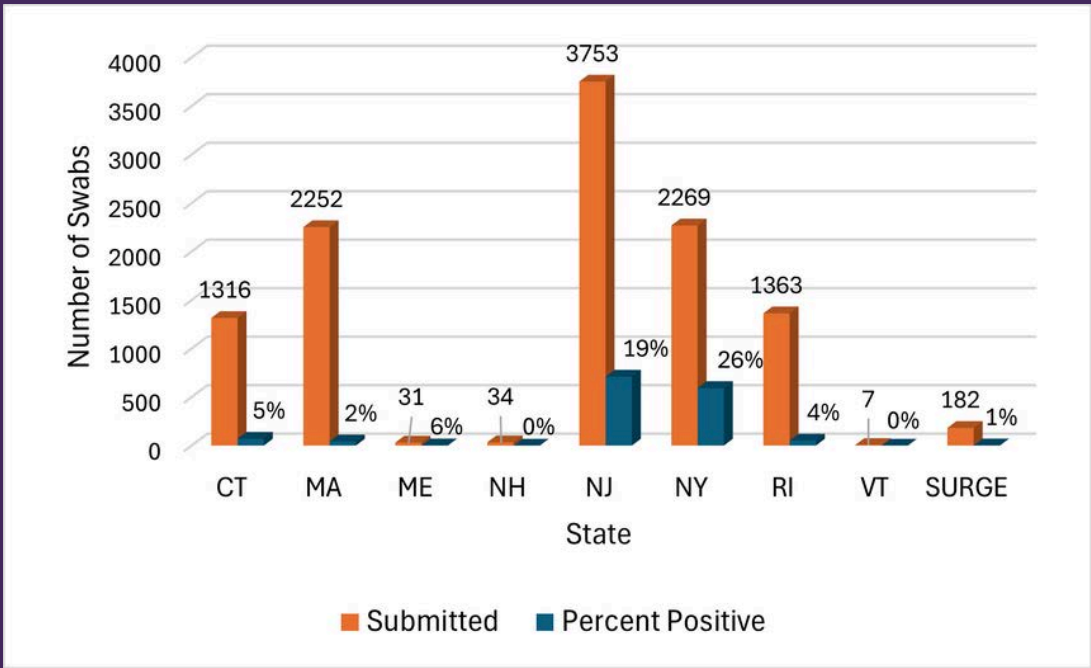
Gabrielle earned her Bachelor of Arts degree in biology from Cornell University and her doctorate in chemical biology from the University of Michigan. She then held postdoctoral researcher positions at the University of Michigan, studying the role that RNA molecules play in HIV-1 viral particle assembly, and at the RNA Institute at the State University of New York-Albany, where she worked to develop a new class of antibiotic drugs targeting conserved RNA structural motifs in gram-positive bacteria. Subsequently, she worked as a lab manager at SUNY Albany, contributing to electrophysiological and behavioral studies in mouse models of obsessive-compulsive disorder. Gabrielle joined the Mycology Laboratory at Wadsworth Center in January 2023, and her focus is to use next-generation sequencing technologies to understand the spread and drug-resistant patterns of fungal outbreaks in the Northeast United States.

Emily Cotnoir
AR Mycology Research Scientist

Emily graduated from Centre College in Danville, Kentucky with a Bachelor of Science degree in biochemistry & molecular biology, where she investigated novel antibiotics. Following her interest in drug discovery, she earned her doctorate in pharmaceutical sciences from the University of Kentucky College of Pharmacy, where she worked with chemists to develop novel antifungals. Emily joined the Wadsworth Center's Mycology laboratory in 2021 in a grant-funded Point of Care Diagnostics for *Candida auris*, followed by COVID-19, before joining the CDC-funded antimicrobial resistance program in 2023. Her focus in the laboratory is to use MALDI-TOF MS for yeast identification, and wastewater surveillance of *C. auris*.

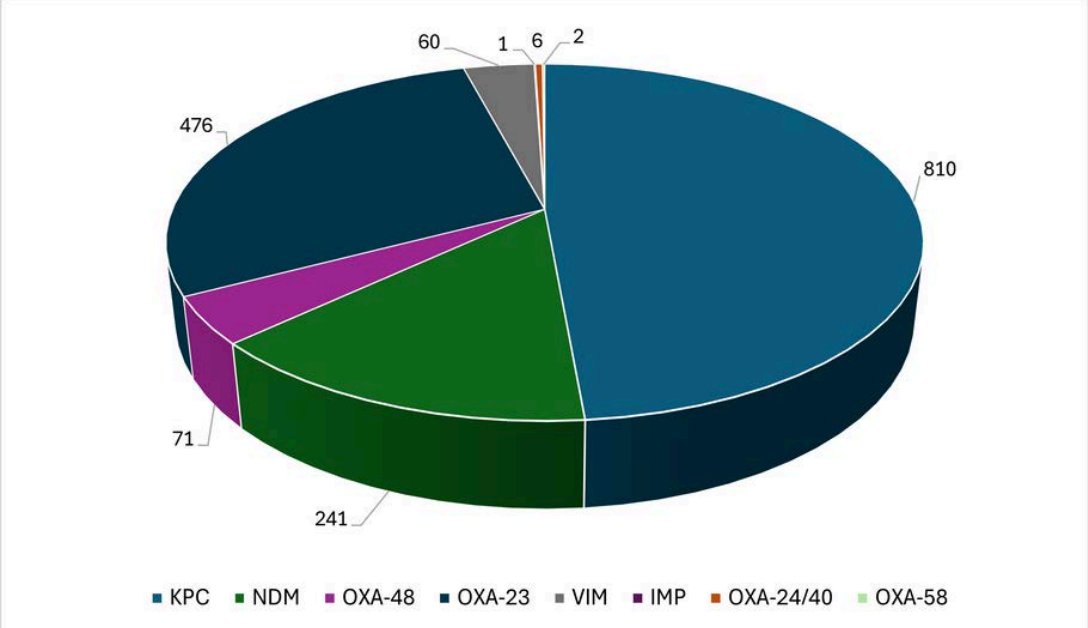
Carbapenemase-Producing Organism (CPO) Colonization Screening: 2022-2023

Figure 1: Number of swabs submitted for CPO screening by state: 2022- 2023



Note: A total of 11,207 swabs were submitted, at an average of ~15% positive overall. "Surge" states included NC, SC, and VA.

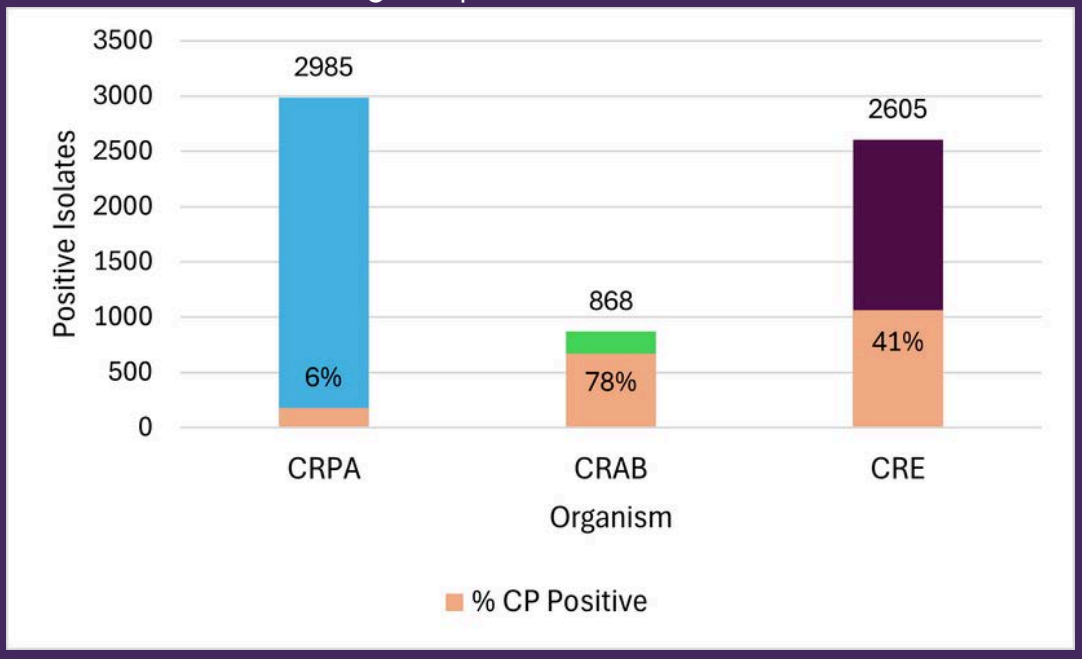
Figure 2: Carbapenemase genes detected by CPO colonization screening: 2022-2023



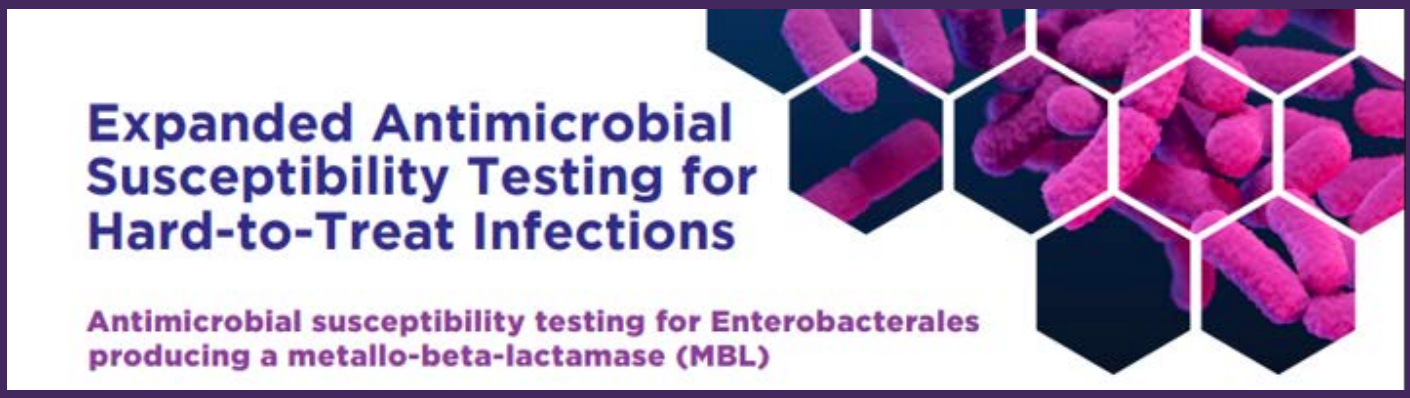
Note: There were a total of 1,667 positive colonization screening swabs with the majority KPC (49%) followed by OXA-23 (28%).

Carbapenem-Resistant Organism (CRO) Isolate Testing: 2022-2023

Figure 3: Isolates submitted to Wadsworth Center in 2022 & 2023 for carbapenem-resistance testing by organism, with percentages of carbapenemase-producing gene positive results



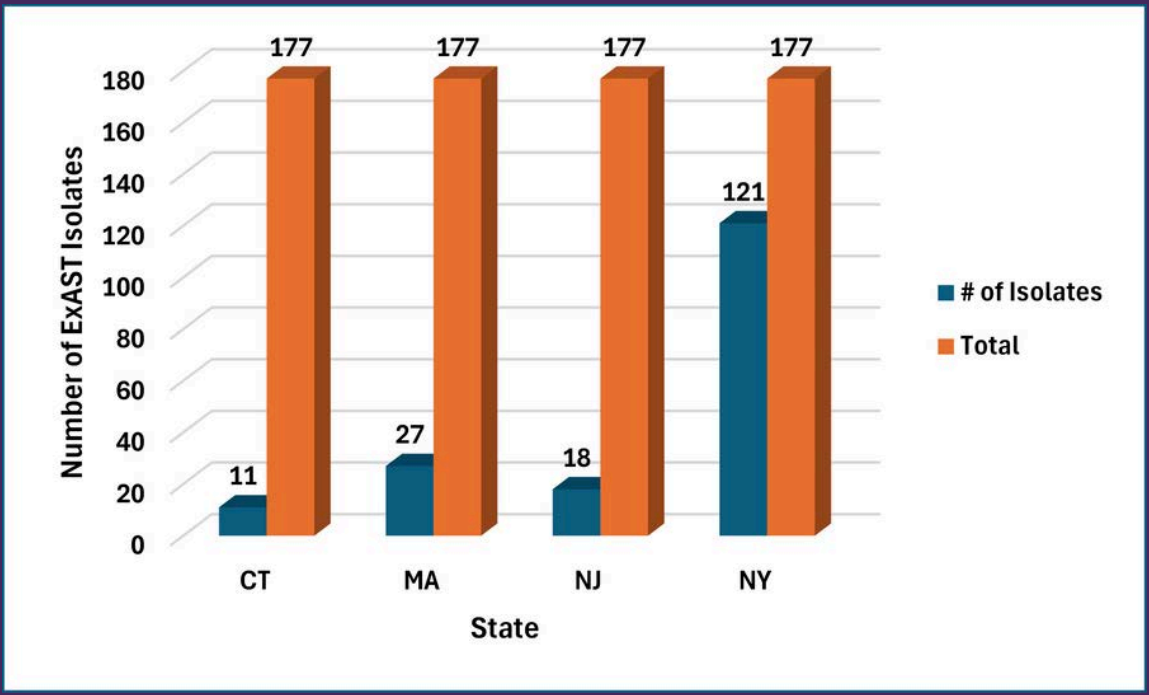
Note: CRPA: Carbapenem-resistant *Pseudomonas aeruginosa,* CRE: Carbapenem-resistant *Enterobacterales,* CRAB: Carbapenem-resistant *Acinetobacter baumannii.*



ExAST fact sheet here

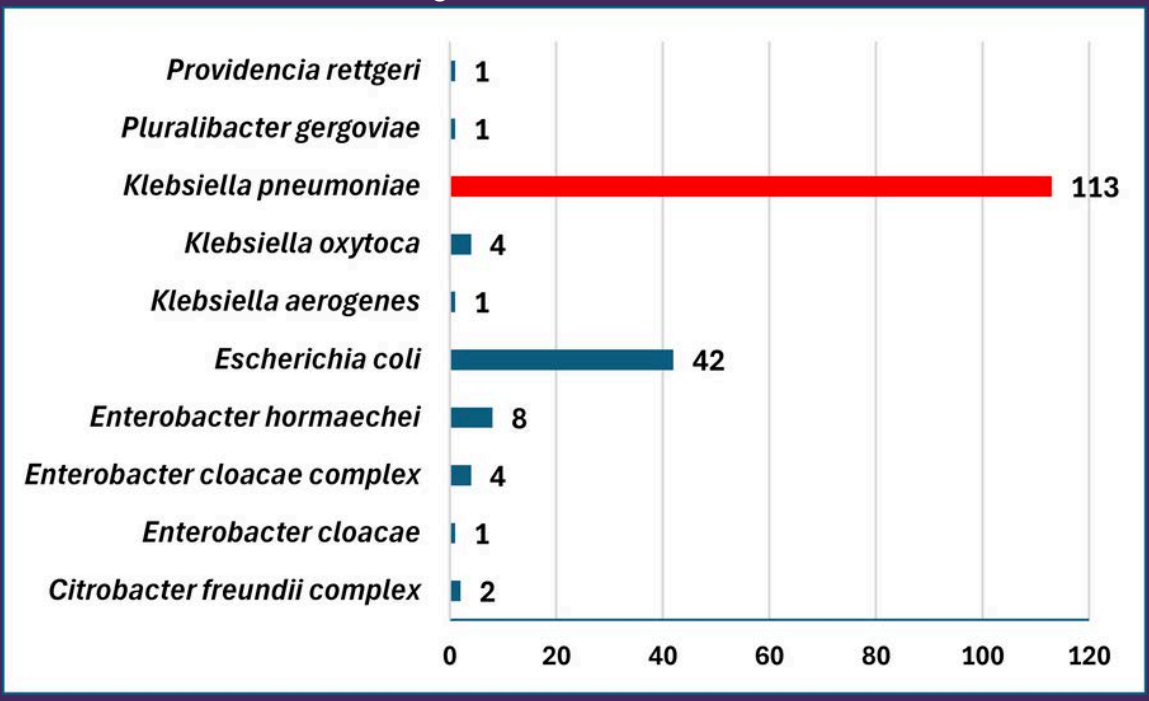
Since 2019, the Wadsworth Center has been providing expanded antimicrobial susceptibility testing for Enterobacterales producing a metallo-betalactamase (MBL) and demonstrating resistance to both aztreonam and ceftazidime-avibactam. Isolate submission requires pre-approval by contacting ARLNCORENY@health.ny.gov.

Figure 4: Number of isolates submitted for aztreonam-avibactam testing by state: 2022-2023



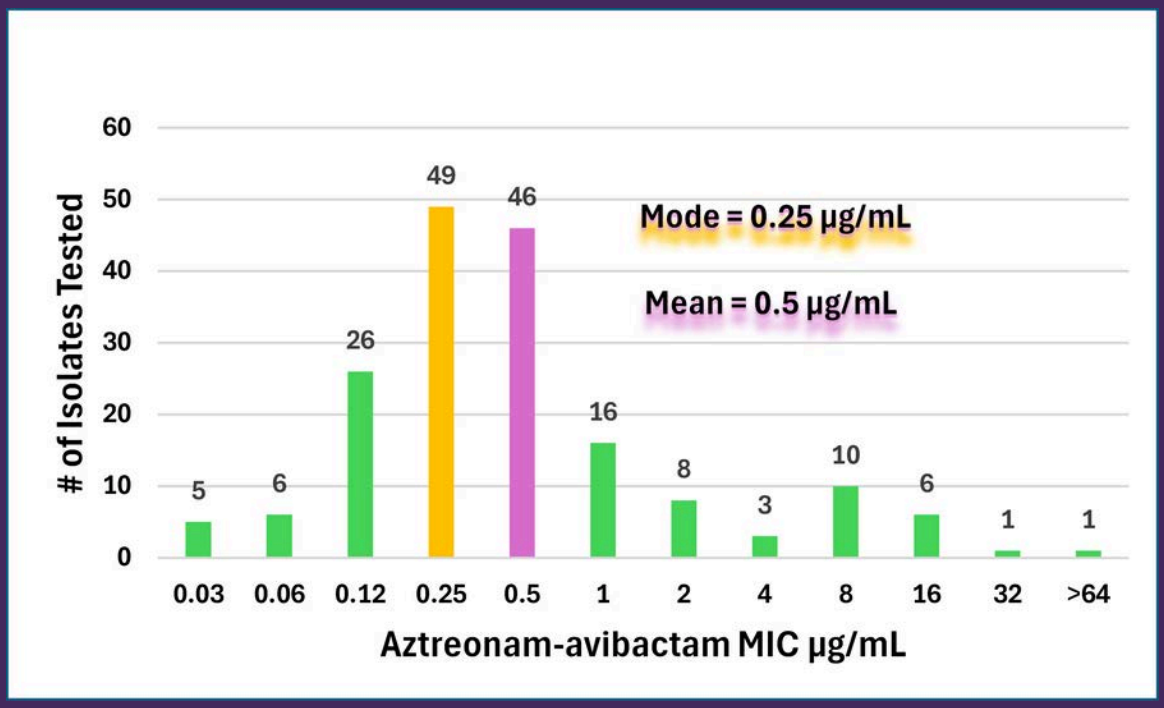
Note: All Enterobacterales isolates submitted for aztreonam-avibactam harbored the metallo-beta-lactamase, NDM. The majority of submissions (68%) were from NYS health care facilities.

Figure 5: Number of isolates submitted for aztreonam-avibactam testing by organism: 2022-2023



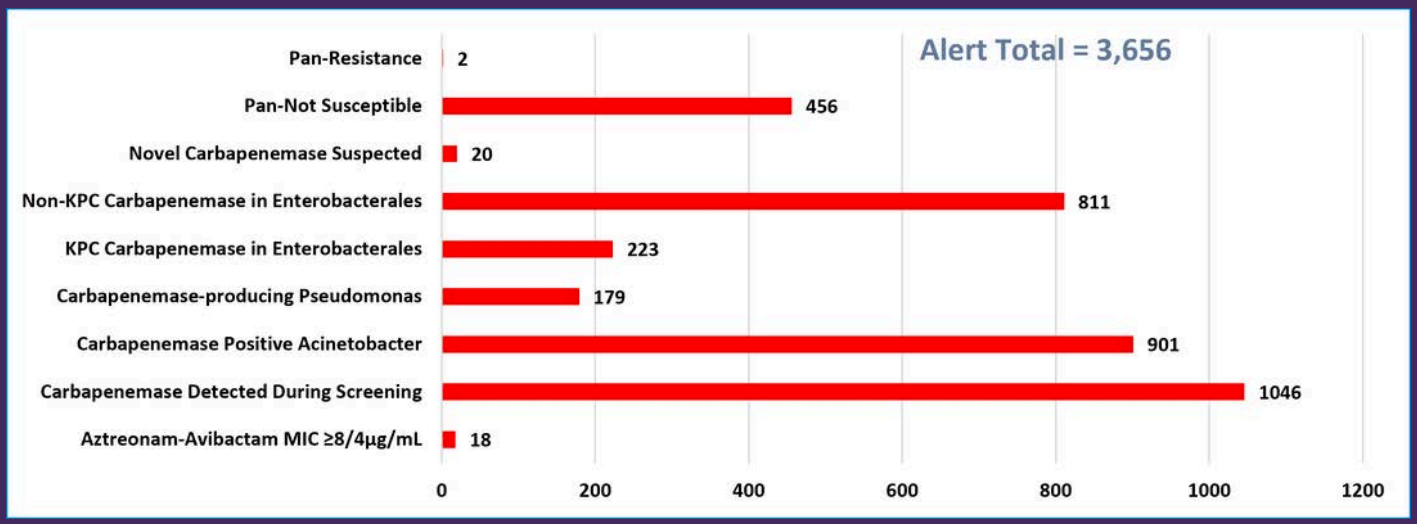
Note: The majority (64%) of Enterobacterales submitted were *Klebsiella pneumoniae* with *Escherichia coli* (24%) the second most frequently submitted.

Figure 6: Distribution of aztreonam-avibactam Minimum Inhibitory Concentration's (MICs) from Enterobacterales submitted: 2022-2023



Note: All isolates demonstrating aztreonam-avibactam MIC values ≥ 8µg/mL were *Escherichia coli* (17) and *Providencia rettgeri* (1).

Figure 7: Number of alerts reported to the Centers for Disease Control & Prevention (CDC) and State Healthcare-Associated Infection (HAI) Coordinators by the NE Regional Laboratory by alert category: 2022-2023



Note: CDC requires test results from isolates or colonization screenings that fall into "Alert Categories" be entered into the REDCap Alert database and an email notification sent to State HAI Coordinators within one day of reporting the result.

AR Whole Genome Sequencing (WGS): 2022-2023

Figure 8: Top 6 most prevalent multilocus sequence type (MLST) & carbapenemase gene variant combinations identified by WGS in CRAB isolates: 2022-2023

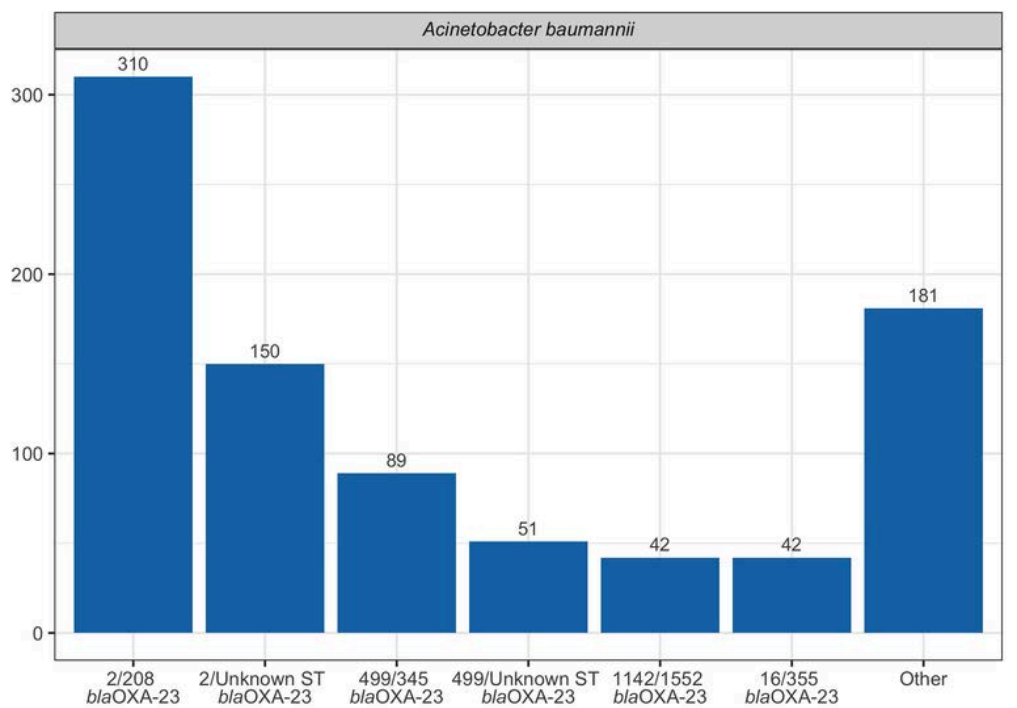


Figure 9: Top 6 most prevalent MLST & carbapenemase gene variant combinations identified by WGS in *Enterobacter cloacae* isolates: 2022-2023

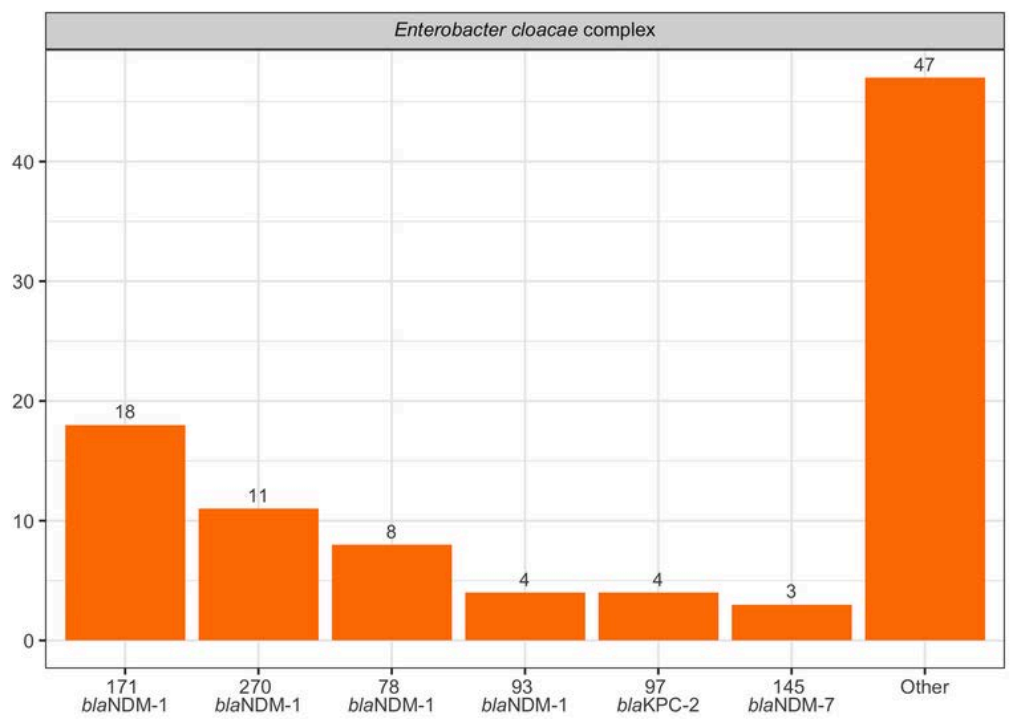


Figure 10: Top 6 most prevalent MLST & carbapenemase gene variant combinations identified by WGS in *Escherichia coli* isolates: 2022-2023

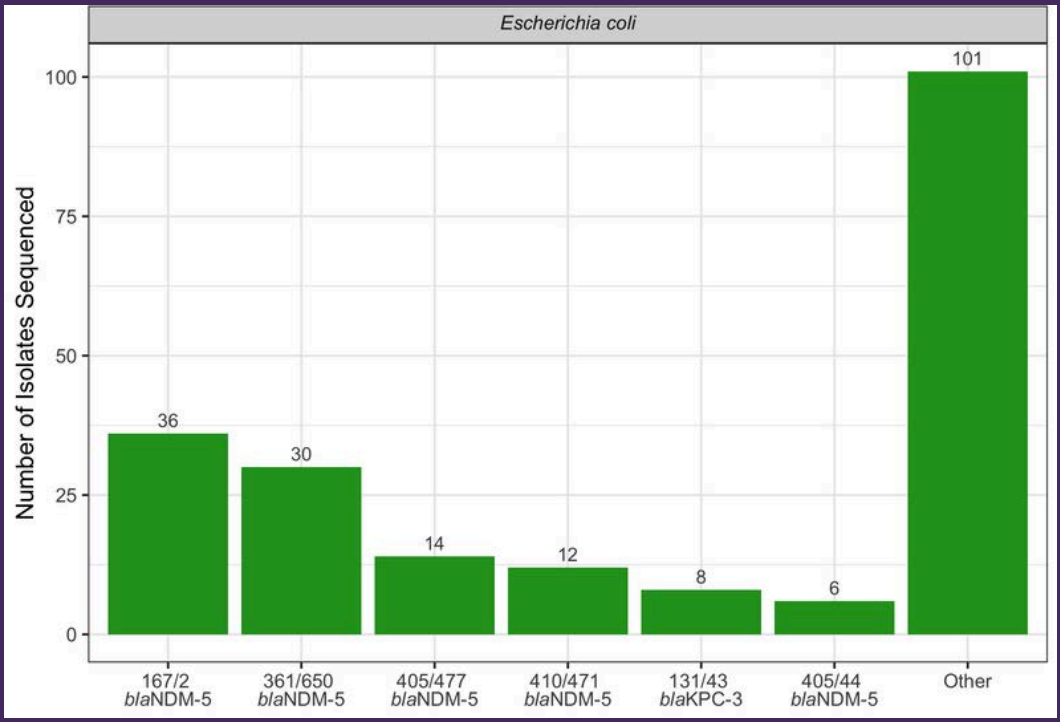


Figure 11: Top 6 most prevalent MLST & carbapenemase gene variant combinations identified by WGS in *Klebsiella pneumoniae* isolates: 2022-2023

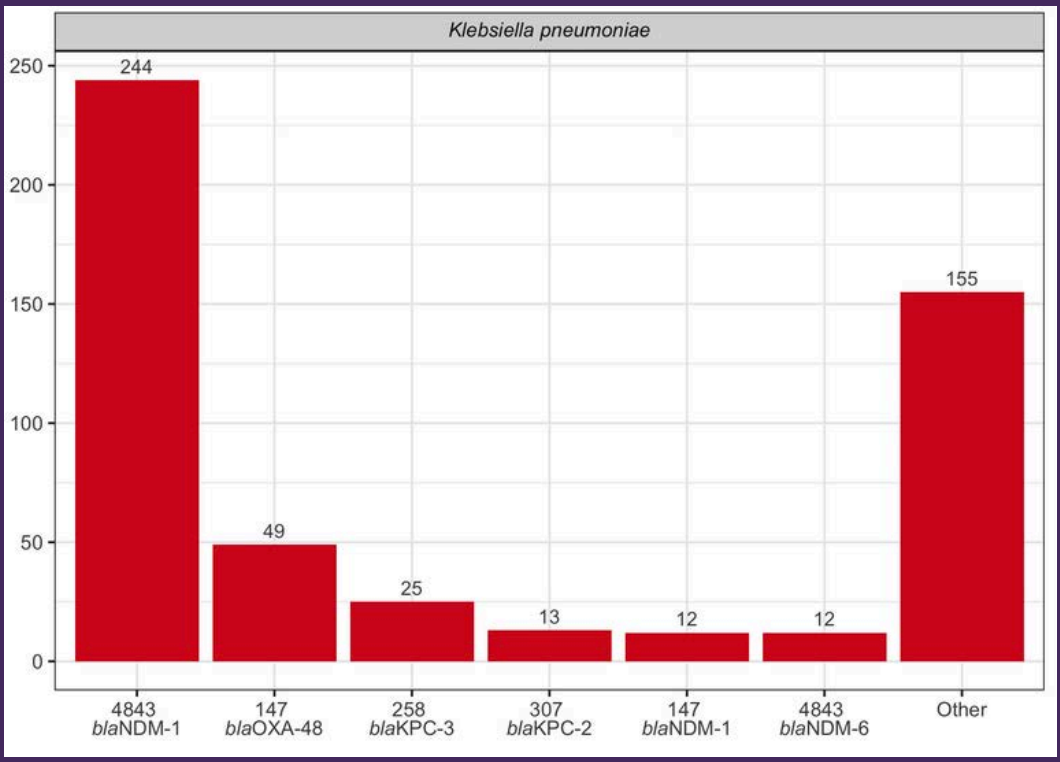


Figure 12: Top 6 most prevalent MLST & carbapenemase gene variant combinations identified by WGS in CRPA isolates: 2022-2023

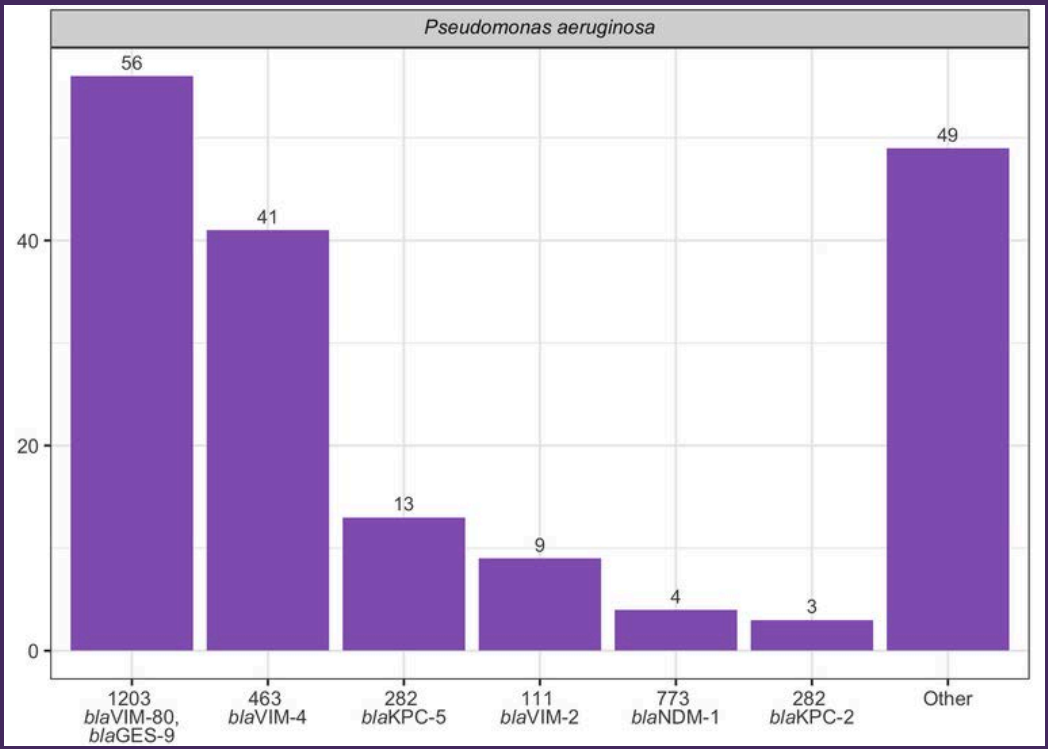
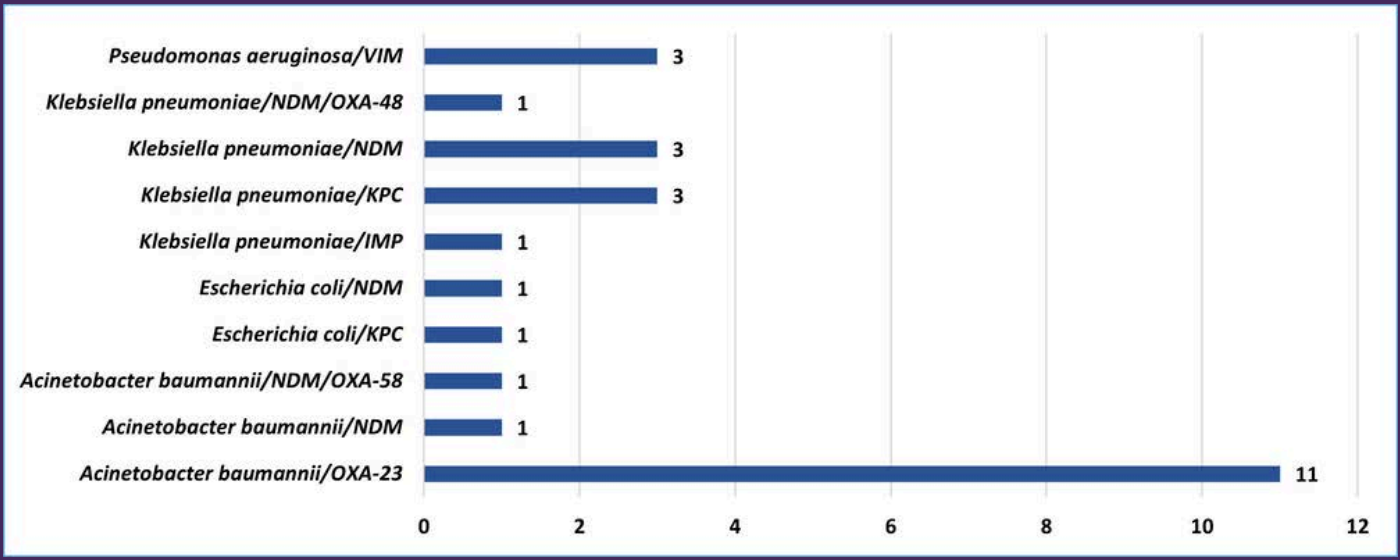


Figure 13: Number of WGS relatedness analysis requests by state: 2022-2023

Note: WGS relatedness analysis requests are performed by AR HAI request. The analysis is performed using the Wadsworth Center bioinformatic pipeline described by Haas, Lapierre, and Musser (2021) here.

Figure 14: Number of AR WGS relatedness analysis by organism and carbapenemase gene: 2022-2023



Note: The majority of AR WGS relatedness analysis requests for suspect transmission or outbreak investigation were for *Acinetobacter baumannii,* OXA-23 (42%).

Wadsworth Center AR Bacteriology News & Highlights

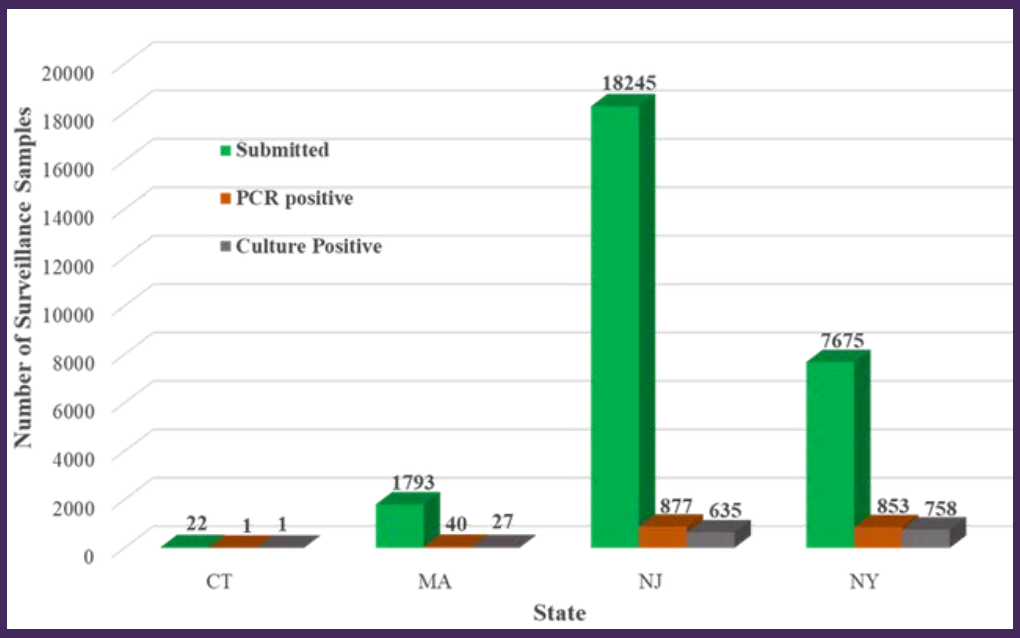
- **Events**
  - Wadsworth Center hosted the Northeast Region Antimicrobial Resistance Laboratory and Epidemiology Network Meeting at the David Axelrod Institute in Albany, NY, on May 2-3, 2023.

Note: Attendees of the Northeast Regional AR Network Meeting at Wadsworth Center in May 2023.

- **Conferences and Trainings**
  - Kim Musser and Marie-Claire Rowlinson led a discussion session on "Strategic Planning for Screening Activities" at the AR Lab Network Regional Laboratory Spring 2022 Meeting on May 16, 2022.
  - Janine Bodnar presented "Implementation of a Digital Imaging System for Reading and Interpretation of Broth Microdilution Antimicrobial Susceptibility Testing" at ASM Microbe 2022 in Washington, D.C., on June 8-13, 2022.
  - Kate Wahl presented "Comparative Analysis of Three Phenotypic Methods to Determine Metallo-β-lactamase Production in Carbapenemase-producing Enterobacterales and *Pseudomonas Aeruginosa* Isolate" at ASM Microbe 2022 in Washington, D.C., on June 8-13, 2022.
  - Kate Prussing presented "Whole Genome Sequencing for Surveillance of Carbapenem-Resistant Bacteria in the Northeastern United States" at the Eastern New York ASM Fall Symposium on September 30, 2022.
  - Kailee Cummings presented "Molecular Detection of Emerging Carbapenemases from Rectal Swab Colonization Screenings in the Northeast" at the Association for Molecular Pathology conference 2022 in Phoenix, AZ, on November 1-5, 2022
  - Christine Jacobsen presented "Implementation of a Rapid, Multiplex Immunochromatographic Assay to Streamline Culture-based Colonization Screenings for Carbapenemase-Producing Organisms" at ASM Microbe 2023, in Houston, TX, on June 15-19, 2023.
  - Liz Nazarian presented "Rise of the Resistance: Antimicrobial Resistance (AR) Laboratory Network and Enhanced Capacity for Laboratory Detection, Characterization, and Surveillance of AR Pathogens" at ASM Microbe 2023, in Houston, TX, on June 17, 2023.

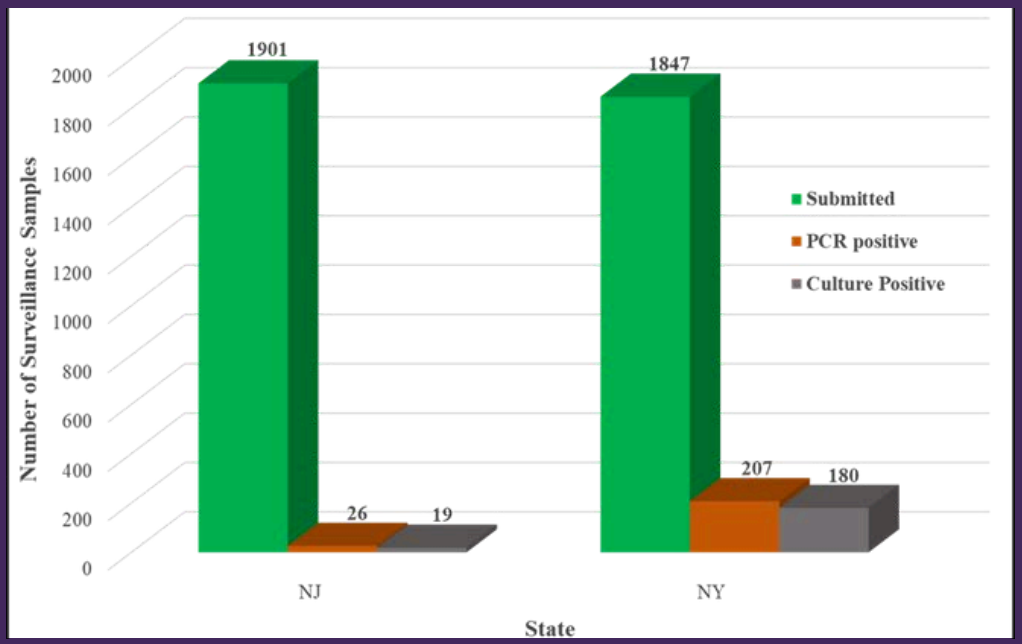
AR Mycology Lab Data

Figure 1: Number of surveillance samples submitted by states for *Candida auris* colonization screening from January 2022 to December 2023



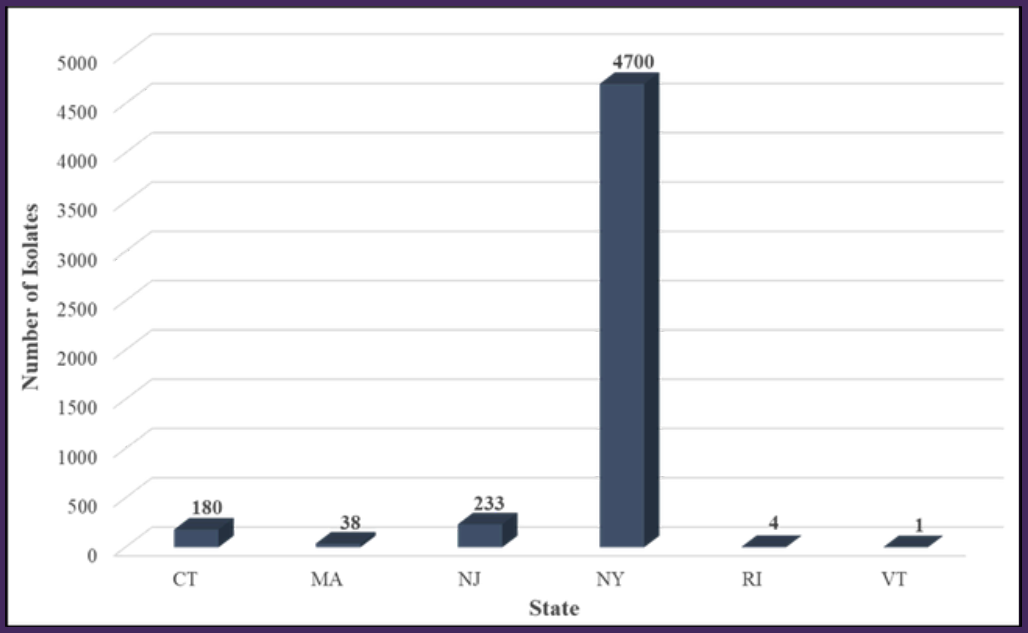
Note: The percent positivity of *C. auris* surveillance samples ranged from 2% to 11% in different states.

Figure 2: Number of admission samples submitted by states for *C. auris* colonization screening from January 2022 to December 2023



Note: Six facilities from NJ and 14 from NY adopted admission screening to control the spread of *C. auris*. The percent positivity of *C. auris* admission screening samples ranged from 1% (NJ) to 11% (NY), further emphasizing NY as a focal point of the *C. auris* outbreak.

Figure 3: Number of *Candida* and other yeast isolates submitted by states from January 2022 to December 2023



Note: A total of 5,156 isolates were submitted, predominantly from NY.

Figure 4: Number of *Candida* and other yeast isolates submitted by states for species-level identification from January 2022 to December 2023

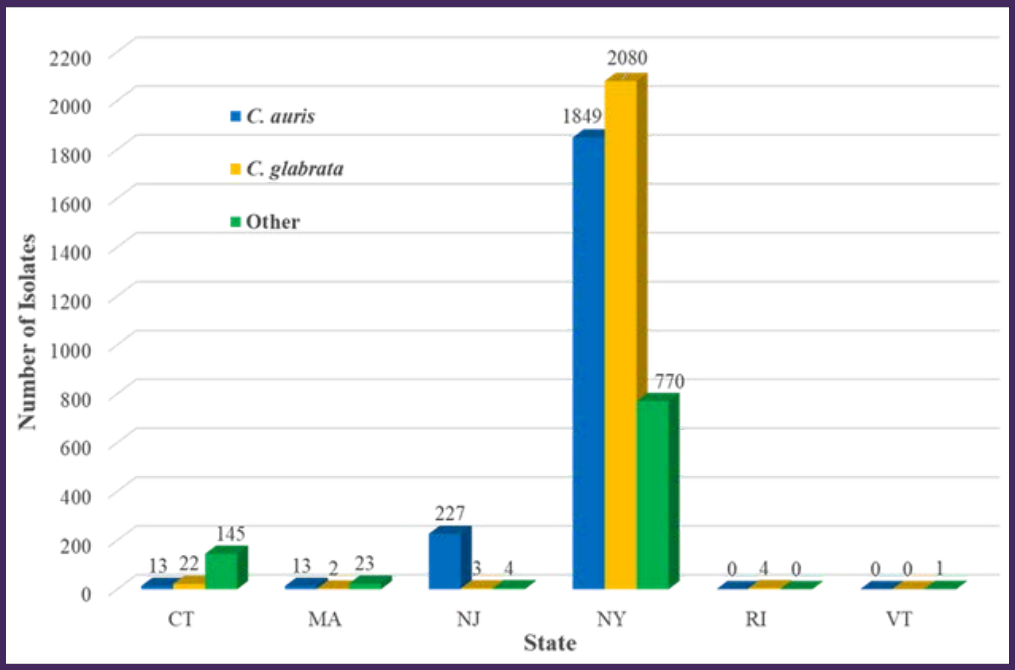
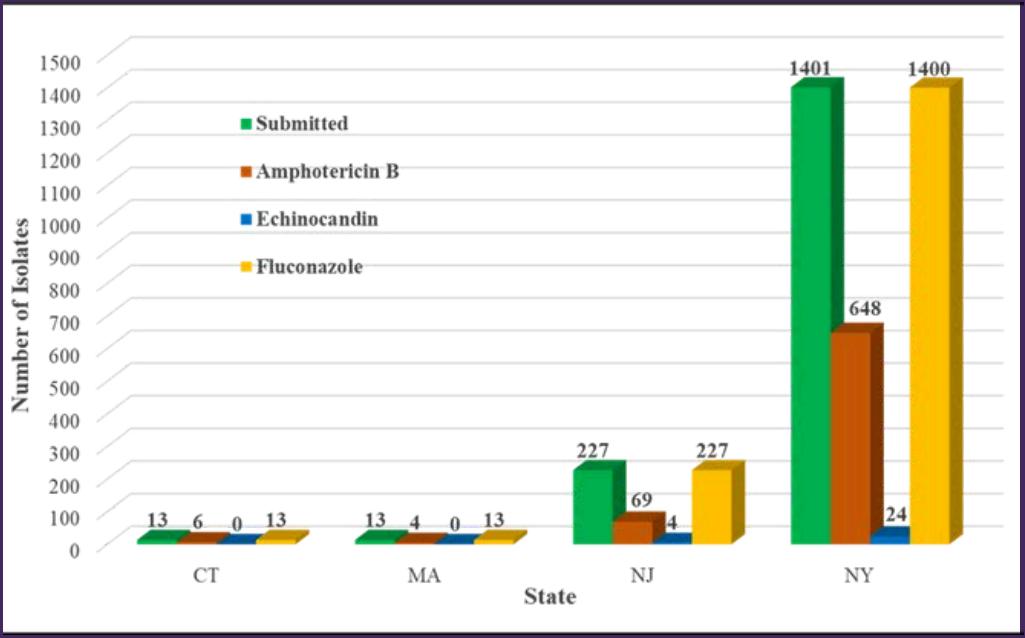
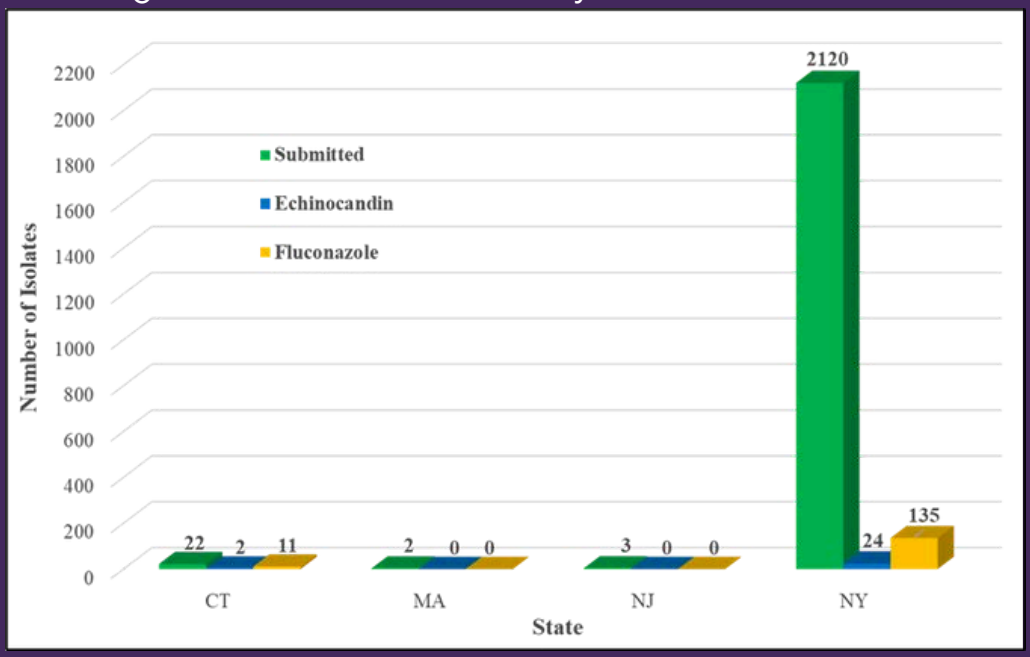


Figure 5: Number of *C. auris* isolates exhibiting resistance to various antifungals identified from January 2022 to December 2023



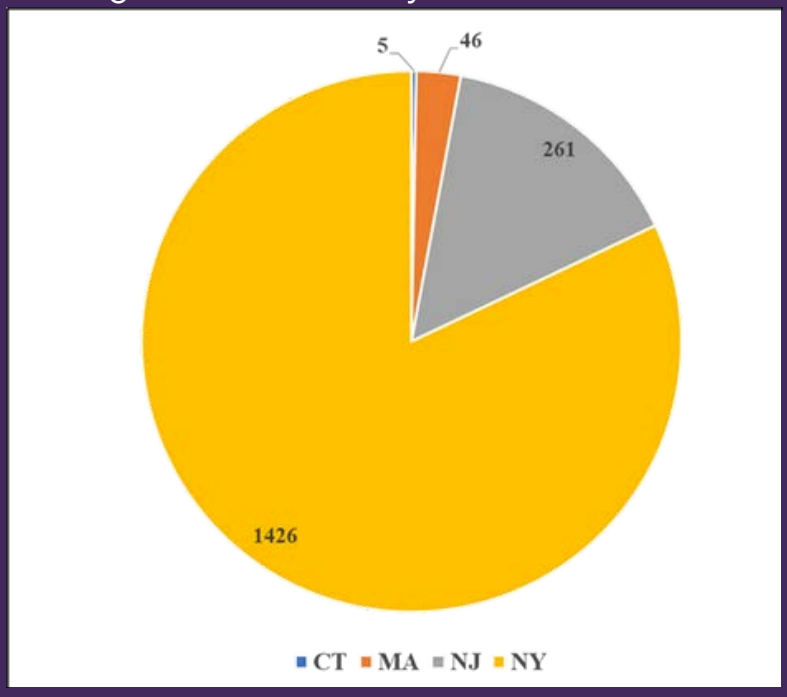
Note: Approximately 1.7% of *C. auris* isolates from NJ and NY were resistant to echinocandins.

Figure 6: Number of *Candida glabrata* isolates exhibiting resistance to various antifungals identified from January 2022 to December 2023



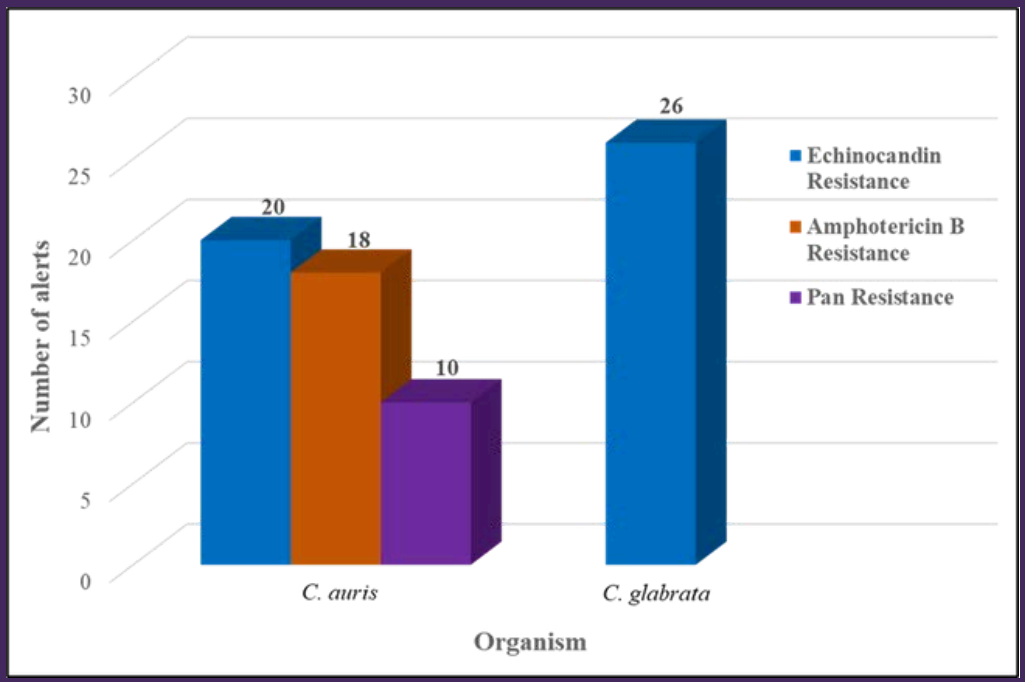
Note: Approximately 9% and 1.1% of *C. glabrata* isolates were resistant to echinocandins from CT and NY, respectively. Since CT only sends suspected resistant isolates for confirmation, the 9% may not reflect the actual resistance pattern in the state.

Figure 7: Number of REDCap alerts submitted to CDC for *C. auris* isolates from low burden regions from January 2022 to December 2023



Note: A total of 1,738 alerts were submitted to CDC during this time frame.

Figure 8: Number of REDCap alerts pertaining to antifungal resistance submitted to CDC from January 2022 to December 2023



Note: The CDC considered the Amphotericin B MIC value of 4.0 µg/mL an alert. The value ranged from 4.0 µg/mL to >32 µg/mL. Pan resistance was defined as resistance against all three major classes of antifungals, including azoles, echinocandins, and polyene.

Wadsworth Center AR Mycology Lab News & Highlights

- ***Candida auris* outbreak investigation using whole genome sequencing**
  - Effective in the summer of 2023, the Mycology Laboratory began performing whole genome sequencing (WGS) analyses of *C. auris* outbreaks in various healthcare settings in the northeast region. Our results indicated a predominance of South Asia Clade I. Our data also revealed distinct South Asia Clade I populations in different states, suggesting multiple introductions followed by clonal expansion. The WGS analysis will help elucidate the source and epidemiological link of *C. auris* outbreaks in healthcare settings.

- ***Trichophyton indotineae*: An emerging antifungal drug-resistant dermatophyte**
  - Dermatophytosis is a contagious superficial skin, hair, or nail infection caused by dermatophyte fungi. This infection has an estimated worldwide prevalence of 20%–25% and is most often due to dermatophytes of the genera *Trichophyton* (predominant U.S. genus). Antifungal-resistant dermatophytes have become common worldwide in the last decade due to the spread of a novel dermatophyte species, *T. indotineae*, formerly called *Trichophyton mentagrophytes* genotype VIII. *T. indotineae* is frequently resistant to the first-line drug, terbinafine. In early 2023, *T. indotineae* was identified in the U.S. for the first time (https://www.cdc.gov/mmwr/volumes/72/wr/mm7219a4.htm). The Mycology Laboratory provides molecular identification, antifungal susceptibility testing, and whole-genome sequencing of *T. indotineae* as part of a reference and AR Lab Network activities. If you receive any suspected cases of *T. indotineae* or *T. mentagrophytes*, please submit them to our laboratory for final identification, AFST, and WGS analyses.

- **New antifungal drug, ibrexafungerp as part of antifungal susceptibility testing panel**
  - In the summer of 2023, CDC incorporated ibrexafungerp into the antifungal microbroth panel, replacing caspofungin, due to the challenges faced while interpreting the minimum inhibitory concentration (MIC). The mycology laboratory performed internal validation of the new panel and has been offering ibrexafungerp MIC data for patient care since October 2023. Currently, interpretation for this drug is not available.

- **Conferences and Trainings**
  - Dr. Sudha Chaturvedi, Director, Mycology Laboratory, attended the APHL ID Lab Conference, Atlanta, GA, from March 12 to 15, 2023. The main conference agenda was to learn about contemporary public health microbiology issues, network with partners, explore new approaches to infectious disease testing, and understand the latest laboratory technologies, supplies, and services.
  - Dr. Sudha Chaturvedi and Ms. YanChun Zhu attended the Regional AR Lab Network Regional and Epidemiology Meeting from November 29 to December 1, 2023, in Atlanta, GA. Some of the topics discussed included the infrastructure and funding of future AR Lab networks, the role of state and clinical laboratories in testing AR pathogens, and barriers to testing and engagement in the region. The meeting also addressed the impact of COVID-19, as well as new testing needs, expansion of WGS implementation, and partnerships with clinical labs.
  - The Virtual *Candida auris* Training Series: Implementation and Validation of Culture and PCR was held from February 14, 2023, to March 7, 2023. All sessions are recorded and available through the APHL.

Image from the CDC site visit of AR laboratories at Wadsworth Center in April 2023.

Northeast Region News & Highlights

Connecticut:

Prior to 2022, Verona Integron-encoded Metallo-beta-lactamase (VIM)-type carbapenemases had never been detected in any genus or species in Connecticut. The "Index Case" was reported by an infectious disease (ID) physician at an acute care hospital- the laboratory had identified "pan-resistant" isolate collected 8-June from an immunocompromised patient; ID/Stewardship requested expanded AST from the state public health lab (SPHL) (CRPA reporting submission is voluntary). Testing at SPHL identified VIM 16-June. Additional SPHL testing confirmed isolate was susceptible only to Cefiderocol. The patient had no out-of-state medical care, but had a long COVID hospitalization in CT, and was currently inpatient at a post-acute care facility.

Upon identification of our first clinical case, we identified the patient had recent stays at two Connecticut acute care hospitals and one post-acute healthcare facility. We screened the case for *Candida auris* and performed point prevalence survey (PPS) #1 for CPOs at the post-acute healthcare facility- two additional cases were identified. When early cases were identified we screened all positive VIM cases for *C. auris*- we did not feel we had found the true "index case" and worried that there could be co-transmission. We did a lab lookback at this facility and at an inter-connected post-acute healthcare facility which identified twelve "suspicious" CRPA isolates.

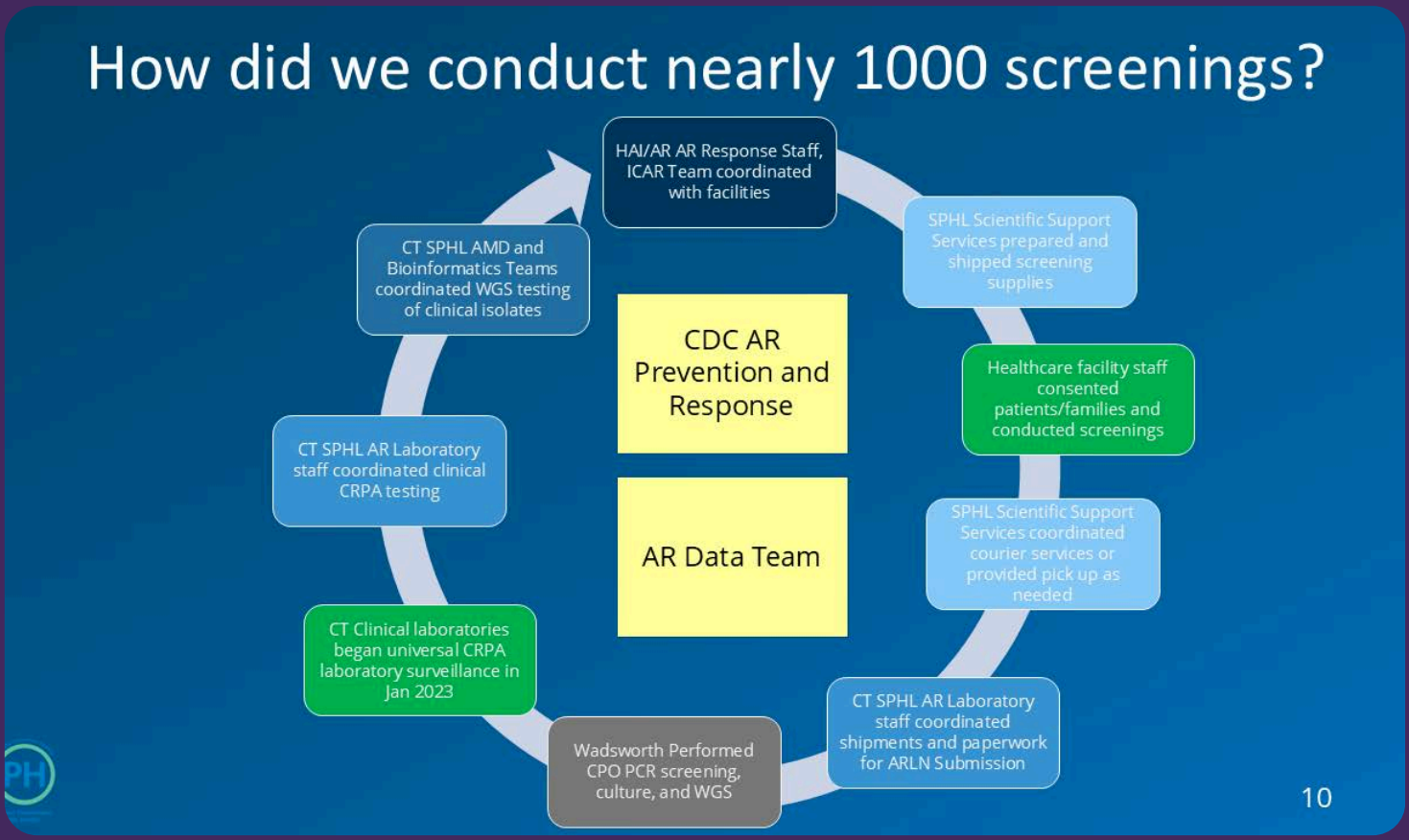
PPS #2 was targeted to the twelve suspicious isolates- five additional positives from three different units. On August 12, 2022, Whole Genome Sequencing at Wadsworth identified our initial outbreak colonization isolates from PPS as ST1203 containing VIM-2, GES-9 genes [Note VIM-80 is newly named subset of VIM-2]. On September 13, 2022, Wadsworth WGS found that the first 15 outbreak isolates differed by no more than 13 alleles, and isolates from both facilities were highly related. On September 20, 2022, CT SPHL performed WGS on a subset of clinical isolates including the index case, uploaded data to the National Center for Biotechnology Information's database.

The healthcare facility (HCF) had a strong Infection Prevention Program that had worked closely with the hospital-acquired infection (HAI)/AR Program over multiple years. The HCF's practice was to pan-culture patients (blood, urine, sputum) upon admission from all inpatient admissions. The HCF had had <5 CP-CRE cases identified since the inception of testing in 2017 (with no identified transmission), and PPS testing had not identified transmission of KPC in same time period. As of September 2022, the HCF had not had a COVID outbreak on any unit. Movement of patients between the two interconnected facilities was very rare, though some staff are shared, and a central supply and pharmacy were common.

New cases were identified in the PPS after control measures were implemented. As the investigation proceeded, our "affected" facilities expanded- to date we have had nine affected facilities.

PPS have been conducted at four locations, all using a ring strategy. Starting with a ring strategy and allowing the data to guide our action helped the facilities to manage the information they were receiving and act in stages -- this helped to overcome hesitation to colonization screening. Education and support at all stages was critical. Where a first round PPS identified no new cases, additional rounds of PPS were not conducted if the risk was not determined to be ongoing – infection control and response (ICAR) and infection prevention (IP) support were provided regardless of PPS findings. When cases were identified on PPS- we continued at two week intervals until two consecutive rounds of PPS were achieved

For facilities with multiple cases, screening has continued at increasingly expanding intervals as they gradually roll out enhanced barrier precaution (EBP) implementation- this is ongoing. Because of the unique nature of this investigation, we also conducted a specialized PPS screening of all patients with identified product exposure once the product was identified

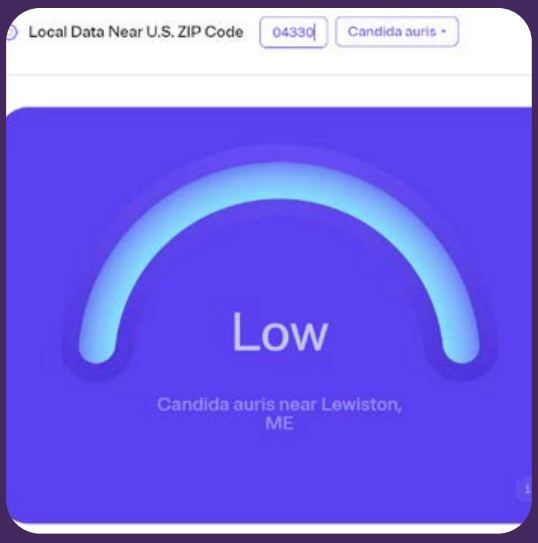


Note: Slide from Meghan Maloney's presentation on the outbreak at the 2023 Northeast Region AR Lab Network Meeting.

Maine:

Wastewater monitoring for infectious diseases excelled during the SARS-CoV-2 pandemic. Recently one company, WastewaterSCAN (www.wastewaterscan.org), has added *Candida auris* to its test menu in most states.

The public can access results in two ways. The first method is to enter a ZIP code and the infectious disease of interest. A pictograph will load with a result (Low, Medium, High) from the nearest location.The second method to view data is to create a dashboard. This allows the viewer to load several locations on a county, state, regional, or national level, displaying line chart and heat map data.



Quantitative results are provided in copies of DNA per gram of dried solid, normalized. This is achieved using Pepper Mild Mottle Virus (PMMoV), a plant virus found in peppers but rarely in animals, and at stable concentrations in the human diet without seasonal fluctuations. Using a ratio of PMMoV to *C. auris* helps to offset environmental dilution factors. As this testing is relatively new, there is not yet a direct correlation between a positive finding and prevalence in a community.

Looking to the future, it may be possible for public health HAI/AR programs to use these data to help identify outbreaks of *C. auris* in hospitals and nursing homes.While several studies describe testing and identifying *C. auris* in local wastewater during a known hospital outbreak, more research is needed to develop an actionable threshold (e.g., increase over baseline) for public health to initiate a response in healthcare settings. Until then, these data are useful to promote healthcare facility readiness.

Massachusetts:

The Massachusetts Department of Public Health (MDPH) Healthcare Associated Infections and Antimicrobial Resistance (HAI/AR) Program in the Division of Epidemiology benefits greatly from a working partnership with the MDPH Sequencing and Bioinformatics Core Division Laboratory.

The Sequencing and Bioinformatics Core Division Laboratory performs Whole Genome Sequencing (WGS) for any mCIM positive CRE or CRPA isolate submitted. For CRAB, the Lab will sequence any isolate resistant to all β-lactam antibiotics and/or all carbapenems. The Lab will inform the HAI/AR Program about any clonal isolates or those that appear closely related with few SNP differences (less than 10-20 SNP differences, depending on the organism). Case information is reviewed to determine possible links to other WGS-related cases including healthcare facility exposure(s) or overlap, procedures, risk factors, and temporal association.

Throughout 2023, the HAI/AR Program was notified by the lab of 60 isolates. Forty of these isolates comprised new WGS clusters of two or more isolates (13 total new clusters). Twenty isolates matched existing historical clusters.

While it is time-consuming to manually review patient information to look for connections, WGS information can illuminate transmission pathways that would have otherwise gone undetected and help stop further transmission. WGS information has been critical to convincing some MA healthcare facilities to perform point prevalence screenings to explore the possibility of inter-facility transmission and discover gaps in infection prevention and control.

New Hampshire:

During Autumn 2023, New Hampshire identified three cases of New Delhi metallo-beta-lactamase (NDM) producing *Klebsiella pneumoniae* (KP) in an acute care hospital. While this may not be something noteworthy or out of the ordinary for other states within New England, up until this point in NH, carbapenem resistant organisms (CRO) of this type have not been regionally significant, let alone cases that could be linked to each other.

The HAI team quickly began an investigation and realized that two of the patients had a history of being un-housed but frequented the same shelter, both patients had overlapping hospital stays at the same acute care facility, and one of the patients had previously resided in a state prison for 15 years. Additionally, there were connections with a clinic that is housed within the shelter building and a street medicine clinic.

Given the concern for transmission in the shelter setting, the NH HAI program along with the local health department requested that the CDC provide a technical assistance visit to further investigate this situation and navigate possible roadblocks with collaboration within the community. The HAI and NH PHL worked collaboratively to complete colonization screening with the Acute Care Hospital, where a third patient was identified. An ICAR was completed at all settings.

The results of this investigation resulted in improved partnerships with the infection prevention team that oversees the acute care hospital, clinic, and street medicine clinic. Lines of communication related to infection prevention and infection prevention training were established with the shelter settings and specific training is scheduled for late summer.

NH has recognized that there are opportunities to focus on health equity in these settings as well as within correctional settings. Though there were no identifiable connections between one of the patients and his residency at the state prison, there were indications that transmission may have occurred. NH HAI and NH PHL will be focusing on health equity and improved colonization screening in these under-served populations.

New Jersey:

New Jersey's AR Special Bacteriology Laboratory has been very busy with the validations of the Cepheid GeneXpert, 2 BD Max System to perform PCR on *Candida auris,* as well as the validation of Streck ARM-D kit for OXA detection in *Acinetobacter* isolate.

We are currently testing for the five carbapenem genes - KPC, VIM, OXA-48, NDM and IMP on Cepheid which cuts down on turnaround time as compared to the Streck PCR. We still keep Streck as a backup.

As of April 2024, we had three full-time employees, including the supervisor, and were in the process of hiring another full-time employee.

As a result of increased workload and decreased manpower, we are not performing testing on *Acinetobacter* or *Candida auris*. However, we are planning specimen testing in the near future, as we have completed the validation for both tests.

NJPHEL Special Bacteriology Lab is also involved in the testing of vaccine preventable diseases, organisms, and *Legionella*.

New York City

NYC has been focusing on the CRO expansion. The health code amendment was approved in October 2023 and went into effect in December 2023. NYC went from required reporting for five targeted species that were resistant to a carbapenem and/or produce a carbapenemase, to expanding to reporting all gram-negative bacteria that are resistant to a carbapenem antibiotic and/or produce a carbapenemase. This will give them the ability to detect bacteria that have previously flown under the radar (such as that pesky VIM+ CRPA). This has also given them the opportunity to resolve some longstanding reporting issues at some select labs.

At the time of this printing, most labs were on board with the expansion and have adjusted their protocols/LIS systems to accommodate the expanded reporting requirements. As of April 1st, 2024, there were only 20 labs that were still in the process of implementing the expansion. NYC's updated CRO technical guide has been provided to laboratories, instructing them exactly what and how to report. Because this is a highly technical document geared primarily to laboratories and bioinformatics staff, it is not available on the health department website. However, we welcome folks to reach out if they have any questions. The NYC Team is very appreciative to all our colleagues throughout the NYC Department of Health and Public Health Lab (PHL) for their assistance with the expansion! Nicole Burton will be reporting out on the NYC experience with the CRO expansion at NACCHO's IPC Summit in Chicago (May 7th-9th).

In April, NYC AR Unit welcomed their PHL colleagues to the Health Department to exchange ideas and information and look forward to more of in person collaborative gatherings in the future.

In addition to expanding their CRO reporting requirements, a few members of their ARU have been expanding their families with multiple babies and one fiancé "joining" the ARU team.

Posters

Posters can be viewed on the Wadsworth Center's ARLN - Publications/Presentations page here

- Bodnar, J., Nazarian, E., Jacobsen, C., Wahl, K., Musser, K.,Rowlinson, M-C. (2022, June 9-13). *Implementation of a digital imaging system for reading and interpretation of broth microdilution antimicrobial susceptibility testing.* [Poster Presentation]. American Society of Microbiology (ASM) Microbe Conference, Washington, D.C.
- Jacobsen, C., Bodnar, J., Cummings, K., Morris, S., Rose, L., Tomlin, K., Wahl, K., Nazarian, E., Musser, K., & Rowlinson, M-C. (2023, June 15-19). *Implementation of a rapid, multiplex immunochromatographic assay to streamline culture-based colonization screenings for carbapenemase-producing organisms* [Poster Presentation]. American Society for Microbiology (ASM) Microbe Conference, Houston, TX.
- Musser, K. A., Akerley, D., Dickinson, M., Haas, W., Halse, T. A., Lapierre, P., Levin, J., MacGowan, C., McGean, T., Mehta, A., Mingle, L., Mitchell, K., Morris, S., Nazarian, E., Prussing, C., Shea, J., & Rowlinson, M-C. (2023, March 13-15). *Integrating Next Generation Sequencing results into the Laboratory Information Management System to improve reporting for surveillance and outbreak investigation* [Poster Presentation]. Association of Public Health Laboratories Infectious Disease Laboratory Conference (APHL ID Lab Con), Atlanta, GA.
- O'Brien, B., Zhu, Y., Freitas, B., & Chaturvedi, S. (2023, June 15-19). *Rapid identification of molds by MALDI-TOF MS* [Poster Presentation]. American Society of Microbiology (ASM) Microbe Conference, Houston, TX.
- Prussing, C., Cummings, K., Rose, L., Morris, S., Vollmer, C., Haas, W., Mitchell, K., Nazarian, E., & Musser, K. (2023, September 12-14). *Visualization and retrospective analysis of whole genome sequencing data from carbapenemase-producing organisms in the Northeast U.S.* [Poster Presentation]. Advanced Molecular Detection (AMD) Days Conference, Atlanta, GA.
- Todd, G. C., Zhu, Y., Caplan, A. S., Jakus, J., Lipner, S. R., Acker, K. P., Morales, A., Rolón, R. M., Westblade, L. F., Manjari, S. R., Banavali, N. K., & Chaturvedi, S. (2023, September 12-14). Trichophyton indotineae: *A collaboration between clinicians, clinical, and public health laboratories is vital to prevent the spread of this drug resistant fungal pathogen* [Poster Presentation]. Advanced Molecular Detection Days, Atlanta, GA.
- Wahl, K., Nazarian, E., Bodnar, J., Jacobsen, C., Morris, S., Cummings, K., Rose, L., Musser, K., M-C. Rowlinson. (2022, June 9-13). *Comparative analysis of three phenotypic methods to determine metallo-β-lactamase production in carbapenemase-producing Enterobacterales and* Pseudomonas Aeruginosa *isolates.* [Poster Presentation]. American Society of Microbiology (ASM) Microbe Conference, Washington, D.C.

Publications

- Caplan, A. S., Chaturvedi, S., Zhu, Y., Todd, G. C., Yin, L., Lopez, A., Travis, L., Smith, D. J., Chiller, T., Lockhart, S. R, Alroy, K. A., Greendyke, W. G., Gold, J. A. W. (2023) Notes from the field: First reported U.S. cases of tinea Caused by *Trichophyton indotineae* - New York City, December 2021-March 2023. *Morbidity and Mortality Weekly Report, 72*(19), 536-37. http://dx.doi.org/10.15585/mmwr.mm7219a4
- Zhu, Y., Hager, K. M., Manjari, S. R., Banavali, N. K.,Chaturvedi, V., Chaturvedi, S. (2023) Development and validation of TaqMan chemistry probe-based rapid assay for the detection of echinocandin-resistance in *Candida auris. Journal of Clinical Microbiology, 61*(4), e01767-22. https://doi.org/10.1128/jcm.01767-22

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