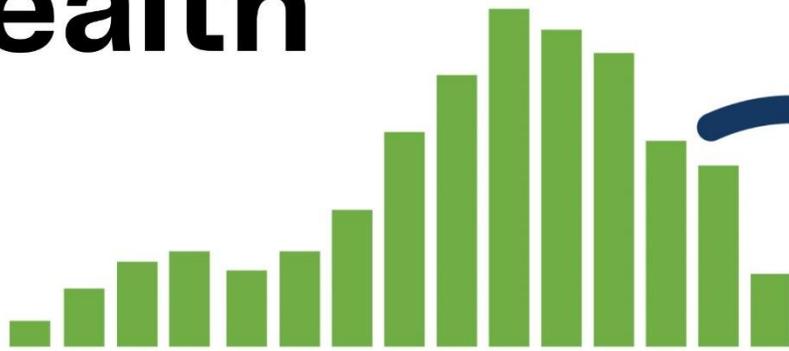


Virginia Department of Health



VIRGINIA EPIDEMIOLOGY SEMINAR

September 29, 2022

Hampton Roads Convention Center
Hampton, Virginia

VDH VIRGINIA
DEPARTMENT
OF HEALTH



In support of improving patient care, this activity has been planned and implemented by Virginia Department of Health and VCU Health. VCU Health is jointly accredited by the Accreditation Council for Continuing Medical Education (ACCME), and the American Nurses Credentialing Center (ANCC), to provide continuing education for the healthcare team.

VCU Health designates this live activity for a maximum of **4.0 AMA PRA Category 1 Credits™**. Physicians should claim only the credit commensurate with the extent of their participation in the activity.

4.0 ANCC contact hours.

This activity was planned by and for the healthcare team, and learners will receive 4.0 Interprofessional Continuing Education (IPCE) credit for learning and change.

Virginia Epidemiology Seminar Agenda
Thursday, September 29, 2022
Hampton Roads Convention Center
Hampton, VA

8:30 a.m. **Registration**

9:00 a.m. **Welcome and ‘State of Epidemiology in Virginia’**
Lilian Peake, MD, MPH
Director, Office of Epidemiology

9:15 a.m. **Welcome to Hampton Health District**
Natasha Dwamena, MD, MPH, FACOG
Health Director, Hampton & Peninsula Health Districts

SESSION 1

Moderator – Natasha Dwamena, MD, MPH, FACOG
Health Director, Hampton & Peninsula Health Districts

9:25 a.m. **Salmonellosis in a 3-Year-Old Male with Hypoxic Ischemic Encephalopathy and Resultant Gastrostomy Tube Dependence**
Krysta ‘McKenna’ Luzynski, MSc, Epidemiologist Senior
Southside Health District

By the end of this session, the participant will be able to:

- *Review disease characteristics of non-typhi, non-paratyphi serotype salmonellosis.*
- *Discuss the importance of a robust public health investigation.*
- *Describe the roles of epidemiologists in disease prevention and control.*

9:45 a.m. **Validation and Implementation of Real-time PCR for Detection of MTBC/MAC: Examining Impacts to Virginia’s Public Health Laboratory and Department of Health**

Rana Mehr, MS, Principal Scientist
Division of Consolidated Laboratory Services

By the end of this session, the participant will be able to:

- *Recognize the different mycobacterial nucleic acid amplification testing (NAAT) performed at DCLS.*
- *Identify the benefits of the DCLS TB Laboratory's newly implemented testing algorithms.*
- *Summarize the impacts of mycobacterial NAAT on individual patients and public health.*

10:05 a.m. **Missed Opportunities: An Evaluation of Reports of Latent Tuberculosis Infection (LTBI) One Month or More from Initiation of Treatment for Tuberculosis (TB) Disease, Virginia, 2020-2021**

Laura Young, MPH, CIC, Tuberculosis Epidemiologist
Division of Clinical Epidemiology, Office of Epidemiology, Virginia
Department of Health

By the end of this session, the participant will be able to:

- *Describe the differences between tuberculosis disease and tuberculosis infection.*
- *Describe the reporting requirements for tuberculosis disease and tuberculosis infection.*
- *Identify reporting and follow-up challenges and their potential impacts on tuberculosis elimination efforts.*

10:25 - 10:40 a.m. **Break and Trivia**

SESSION 2

Moderator – Stephanie Kellner, MPH

Junior Regional Epidemiologist, Division of Surveillance and Investigation, Office of Epidemiology,
Virginia Department of Health

10:40 a.m. **Differences between Urban and Rural Mothers in Virginia: An Analysis of 2016-2020 VA Pregnancy Risk Assessment System Data**

Kenesha Smith Barber, MSPH, PhD, Community Health Epidemiology
Program Manager
Division of Population Health Data, Office of Family Health Services,
Virginia Department of Health

By the end of this session, the participant will be able to:

- *Describe maternal health disparities seen in urban and rural areas of Virginia.*
- *Differentiate between adverse health outcomes that are more likely to be found among rural mothers in VA versus that of urban VA mothers.*
- *Design similar studies to examine disparities among urban and rural populations using VA data.*
- *Conclude, confirm, or revise the researcher's public health implications regarding urban/rural disparities among VA mothers.*

11:00 a.m. **Residence and Social Determinants of Health Near Hazardous Waste Sites in Virginia: Impact on Lung Cancer Clusters**

Rexford Anson-Dwamena, MPH, Epidemiologist
Office of Health Equity, Virginia Department of Health

By the end of this session, the participant will be able to:

- *Describe the proximity to superfund site and lung cancer incidence and help determine the need for action.*
- *Describe the social determinants of health indicators and lung cancer incidence.*
- *Identify lung cancer mortality hotspot areas in the state.*

11:20 a.m.

Over-the-Counter Caution: Self-Harm Hospitalizations due to Acetaminophen Poisoning among Virginia Youth, 2016-2020

Lauren Yerkes, MPH, CPH, Injury and Violence Prevention Epidemiologist
Division of Population Health Data, Office of Family Health Services, Virginia Department of Health

By the end of this session, the participant will be able to:

- *Evaluate the burden of self-harm hospitalizations due to acetaminophen poisoning among Virginia youth.*
- *Learn how acetaminophen poisoning affects health outcomes, such as liver toxicity, and how many Virginia youth are impacted over the 2016-2020 time period.*
- *Identify prevention efforts to reduce self-harm hospitalizations due to acetaminophen poisoning.*

11:40 a.m.

Using Cluster Detection and Response to Prevent the Spread of HIV in Western Virginia, 2021

Christina Martone, MPH, Cluster Detection and Response Program Coordinator

Jennifer Johnson, BS, Disease Intervention Specialist

Division of Disease Prevention, Office of Epidemiology, Virginia Department of Health

By the end of this session, the participant will be able to:

- *Describe how the HIV Cluster Detection and Response (CDR) program at VDH uses genetically related HIV infections to identify clusters of recent and rapid HIV transmission in Virginia.*
- *Recall the CDR efforts for a cluster detected in the Western region of Virginia.*
- *Recognize how to build a rapport and use motivational interviewing skills.*

12:00 – 1:30 p.m. **Lunch and Networking**

SESSION 3

Moderator- Alexandra Lorentz, PhD

Genomic Epidemiology Laboratory Liaison Lead Scientist, Division of Consolidated Laboratory Services

1:30 p.m.

Spatial Analysis of COVID-19 Incidence During the Delta (July 17- November 13, 2021) and Omicron (November 27-March 26, 2022) Waves

Cali Anderson, MPH, COVID Epidemiologist

Central Virginia Health District

Victoria Watson-Nichols, MPH, Assistant HAI Data Analyst

Division of Clinical Epidemiology, Office of Epidemiology, Virginia Department of Health

By the end of this session, the participant will be able to:

- *Identify the block groups within the Central Virginia Health District with the highest incidence of COVID-19 during both the Delta and Omicron waves.*
- *Summarize the key demographic and socioeconomic factors that influence COVID-19 incidence within these disparate block groups.*
- *Determine the best outreach strategies for future prevention of COVID-19 in these high incidence areas.*

1:50 p.m.

Piloting Wastewater-Based Surveillance of SARS-CoV-2 Variants in Virginia, 2021 - 2022

Lauren Turner, PhD, Lead Scientist

Division of Consolidated Laboratory Services

By the end of this session, the participant will be able to:

- *Describe advantages and limitations of wastewater sequencing for population-based SARS-COV-2 variant surveillance.*
- *Describe how the aggregation of surveillance data for wastewater differs from clinical testing data.*
- *Describe a laboratory workflow for wastewater sequencing and additional tests that precede sequencing analysis.*

2:10 p.m.

Differentiating Persistently Positive COVID-19 Cases from Sars-Cov-2 Reinfection Utilizing Laboratory Evidence, Virginia, 2020 – 2021

Haley Greene, MPH, CPH, Junior Regional Epidemiologist

Jenny Crain, MS, MPH, CPH, Genomic Epidemiologist

Division of Surveillance and Investigation, Office of Epidemiology, Virginia Department of Health

By the end of this session, the participant will be able to:

- *Highlight the value of conducting a real-time epidemiologic research study during an ongoing pandemic supported by genomic laboratory evidence during an ongoing pandemic.*
- *Understand the importance of whole genome sequencing (WGS) as a method for differentiating persistently positive COVID-19 cases from SARS-CoV-2 reinfection.*
- *Compare the advantages and disadvantages of using genomic sequencing paired with case-level epidemiologic interview data to monitor genetic changes in the virus, over time, through enhanced surveillance of SARS-CoV-2 variants.*

- 2:30 p.m. **COVID-19 Vaccine Scheduling Support for Phase 1B and the Federal Retail Pharmacy Program, Virginia, 2021**
Jenae Davis, MPH, Crosscutting Epidemiology Program Coordinator
Division of Surveillance and Investigation, Office of Epidemiology, Virginia Department of Health
- By the end of this session, the participant will be able to:
- *Compare the advantages and disadvantages of using REDCap scheduling for mass vaccination events.*
 - *Explain the role of both VDH and Deloitte to meet the needs of scheduling vaccinations.*
 - *List the processes of using REDCap and R-Studio to generate reports for the projects.*

2:50-3:05 p.m. **Break and Trivia**

SESSION 4

Moderator – Julia Murphy, DVM, MS, DACVPM
State Public Health Veterinarian, Division of Surveillance and Investigation, Office of Epidemiology, Virginia Department of Health

- 3:05 p.m. **Mass Rabies Exposure Event Linked to Horse Farm in Montpelier, Virginia**
Alex Neal, BS, Epidemiologist Senior
Abi Nimitz, BSN, RN, Communicable Disease Nurse
Chickahominy Health District
- By the end of this session, the participant will be able to:
- *Recognize scenarios that present unique risk factors that contribute to large rabies exposure events.*
 - *Identify educational opportunities to prevent large rabies exposure events.*
 - *Be prepared to respond to mass rabies exposure events.*

- 3:25 p.m. **Multi-strain Shiga Toxin-Producing E. Coli Outbreak Associated with Agritourism in Loudoun County, Virginia**
Kevin Embrey, MPH, District Epidemiologist
Loudoun Health District
- By the end of this session, the participant will be able to:
- *Identify three main risk factors for STEC infection in agritourism settings.*
 - *Discuss the role of whole genomic sequencing in zoonotic outbreak investigations.*
 - *Describe three disease prevention best practices for agritourism settings.*

3:45 p.m. **Cryptosporidium Parvum Outbreak Associated with Raccoons at a Wildlife Facility**

Brandy Darby, DVM, MPH, DACVPM, Veterinary Epidemiologist
Division of Surveillance and Investigation, Office of Epidemiology, Virginia Department of Health

By the end of this session, the participant will be able to:

- *Become familiar with commonly recognized animal reservoirs of Cryptosporidium parvum.*
- *Review common modes of transmission for Cryptosporidium parvum.*
- *Appreciate that raccoons might be an under-recognized source of cryptosporidiosis; human and animal healthcare providers should consider cryptosporidiosis in patients with raccoon exposures and gastrointestinal illness.*

4:05 p.m. **Closing Remarks**

Voting for People's Choice Award

Katherine McCombs, MPH

Deputy Director, Division of Surveillance and Investigation, Office of Epidemiology, Virginia Department of Health

4:15 p.m. **Award Presentations**

Grayson B. Miller, Jr., MD Award Presentation

Diane Woolard, PhD., Award Presentation

People's Choice Award Presentation

4:30 p.m. **Adjourn**

ABSTRACT
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Salmonellosis in a 3-Year-Old Male with Hypoxic Ischemic Encephalopathy and Resultant Gastronomy Tube Dependence

Presenter: Krysta 'McKenna' Luzynski, MSc, Epidemiologist Senior, Southside Health District

Background: For Southside Health District, salmonellosis has been the most commonly reported enteric disease since 2006. While common routes of transmission for non-typhi, non-paratyphi serotype *Salmonella* include ingestion of contaminated food or animal-to-human transmission, occasionally, the possible mode of transmission differs.

Case Presentation: On April 10, 2022, a three year-old male with a history of hypoxic ischemic encephalopathy and resultant spastic quadriplegia, seizure disorder, developmental delay, and gastronomy tube (G-tube) dependence was admitted to a local hospital for lethargy and diarrhea. He developed acute renal failure secondary to *Salmonella* bacteremia.

The district epidemiologist received the culture-independent diagnostic test (CIDT) positive lab report via fax on April 13, 2022, and an attempt to contact the patient's mother on April 20, 2022 was successful. During the investigation, the epidemiologist learned that the patient did not have any contact with animals or animal products; did not have any recreational water exposure; and did not consume any unpasteurized products. Per the patient's mother, the patient is exclusively fed through a G tube using formula and distilled water. The epidemiologist verified that the patient's formula was not part of any active recalls.

The patient's mother noted that both she and the patient's grandmother had experienced similar symptoms. The patient's grandmother does not live in the patient's home, but she had come to the family's home for dinner during the incubation period. The epidemiologist discovered that the patient's mother had washed the patient's G tube syringes with the wooden cutting board and knife used to cut the raw chicken that was then cooked for that dinner. This cross contamination was a possible mode of transmission. The water used for dishwashing was unfiltered, presenting an additional potential mode of transmission that could not be eliminated.

The epidemiologist provided education on the importance of hand hygiene and recommended switching from a wooden cutting board to a glass cutting board. Since the unfiltered well water could not be excluded as the mode of transmission, the epidemiologist also recommended investing in a filter, if possible. The patient recovered fully from Salmonellosis.

Discussion: This case illustrates not only the importance of a thorough case investigation, but also the value of the epidemiologist as a health educator. By identifying possible sources of exposure and providing control measures to the patient or to the patient's family, future cases of food- and waterborne diseases can be prevented.

Validation and Implementation of Realtime PCR for Detection of MTBC/MAC: Examining Impacts to Virginia's Public Health Laboratory and Department of Health

Presenter: Rana Mehr, MS, Principal Scientist, Division of Consolidated Laboratory Services

Background: In 2021, the Division of Consolidated Laboratory Services (DCLS) Tuberculosis (TB) Laboratory validated a rapid, cost effective laboratory-developed test for the detection of *Mycobacterium tuberculosis* complex (MTBC) and *Mycobacterium avium* complex (MAC) DNA by real time polymerase chain reaction (PCR) for direct testing of sputum specimens and culture isolates. Previously, MTBC nucleic acid amplification testing (NAAT) performed by DCLS was limited to the Cepheid Xpert MTBC/Rifampin (RIF), which was restricted for use on first-time Fluorochrome smear positive specimens from patients not on anti-tuberculosis therapy. In 2021, this testing algorithm resulted in 17.5% of TB cases being detected by NAAT within 2 days of specimen receipt, versus the Healthy People 2030 benchmark of 77%. The adoption of a new multiplexed, real-time PCR assay provides an alternative method for NAAT on direct sputa and improves DCLS' NAAT reporting benchmark to further align with goals for rapid diagnosis of MTBC.

Methods: DCLS utilized the New York State Department of Health, Wadsworth Center's Detection of MTBC and MAC DNA by real-time PCR standard operating procedures as the reference method with in-house modifications. The laboratory used a phased approach for implementation of the assay, starting with isolate testing in January 2022 to replace GenProbe Accuprobe testing. Direct sputa testing was implemented in April 2022 after outreach and education was provided to local health departments.

Results: Implementation of real-time PCR testing allowed for sputa specimens to be tested within 2 days of receipt, regardless of Fluorochrome smear result. Specimens with MTBC DNA detected that meet Xpert MTB/RIF criteria are reflexed for rapid detection of rifampin resistance. Specimens that do not meet Xpert MTB/RIF criteria are shipped to the Centers for Disease Control and Prevention (CDC) for Molecular Detection of Drug Resistance (MDDR) testing as requested by VDH TB Control. Cultures with mycobacterial growth are also tested by real-time PCR to confirm or rule out MTBC and/or MAC. Tuberculosis patients who submit multiple specimens under TB Control patient management have varied testing algorithms that were established in conjunction with reference standards to ensure efficient testing and reporting practices.

Conclusions: Implementation of the MTBC/MAC DNA by real-time PCR assay ultimately benefits public health intervention efforts and provides a rapid, cost-effective method for patient diagnosis. This improved testing algorithm has allowed DCLS to successfully perform NAAT on 57.7% of sputum specimens within 2 days of receipt.

Missed Opportunities: An Evaluation of Reports of Latent Tuberculosis Infection (LTBI) Three Months or More From Sputum Collection for Evaluation for Tuberculosis (TB) Disease, Virginia, 2020-2021

Presenter: Laura Young, MPH, CIC, Tuberculosis Epidemiologist, Division of Clinical Epidemiology, Office of Epidemiology, Virginia Department of Health

Background: LTBI became reportable in Virginia in November of 2018. The majority of reports are received via electronic laboratory reporting (ELR) of positive interferon-gamma release assays (IGRAs), which indicate infection with TB. Patients may be tested for LTBI in the community and either never be fully evaluated or never be treated for LTBI at that time. Some of these patients go on to develop active TB disease. Since 2019, VDH has received over 20 thousand reports of at least a positive test for TB infection, often with little or no additional information.

Methods: Examine counted TB cases from 2020 and 2021 (n=329) and match with any existing LTBI reports available in the Virginia Electronic Disease Surveillance System (VEDSS). Examine the following variables from the TB investigation: date of report, date of sputum smear collection, date therapy started, disease site, primary reason evaluated for TB, tuberculin skin test at diagnosis result, interferon gamma release assay at diagnosis result, HIV status at time of diagnosis, additional TB risk factors. Examine the following variables from the LTBI report: date of report, reporting organization, additional clinical information if available.

Results: Twenty-three patients with counted TB disease had at least one positive IGRA collected since LTBI became reportable, 90 days or more prior to their work up for active disease. The earliest date of sputum collection captured in the TB investigation was used as a proxy for work up for active disease.

Conclusion: There is missed opportunity for treatment of LTBI which can prevent progression to active TB. There is also likely missed opportunity for earlier entrance into care of patients with active disease, which could reduce severity of illness, degree of infectiousness, and thus the potential for additional exposures of contacts. Increased staffing and ability to follow-up on LTBI reports could reduce TB morbidity and improve TB outcomes in Virginia.

Differences between Urban and Rural Mothers in Virginia: An Analysis of 2016-2020 VA Pregnancy Risk Assessment System Data

Presenter: Kenesha Smith Barber, MSPH, PhD, Community Health Epidemiology Program Manager, Division of Population Health Data, Office of Family Health Services, Virginia Department of Health

Background: Significant and persistent racial and income disparities in birth outcomes exist in the United States, and this holds true for Virginia. Health disparities are seen across urban and rural areas, where inner city and rural residents seem to have poorer health outcomes when compared to suburban residents. Due to the geographic diversity of Virginia, this study seeks to examine whether maternal behaviors and adverse birth outcomes differ by urban–rural status.

Methods: VA Pregnancy Risk Assessment Monitoring System (PRAMS; 2016-2020) data were used for this secondary data analysis. A chi-square (Wald F) test of differences of association was used to determine differences between urban and rural mothers. Outcomes examined included: preterm birth, pregnancy intention, maternal disease diagnoses, breastfeeding, healthcare provider visits, and other maternal experiences.

Results: A total of 4,763 mothers participated in 2016-2020 VA PRAMS. Of those, 9% (n=370) resided in rural areas of Virginia. Rural women were significantly less likely to be breastfeeding at discharge (90% vs. 76%; $\chi^2= 13.30$; $p= 0.0003$), to continue breastfeeding for 2-6 months (64% vs. 43%; $\chi^2= 18.79$; $p< 0.0000$), and to receive adequate prenatal care according to the Kotelchuck index (81% vs. 74%; $\chi^2= 3.04$; $p=0.0277$), compared to urban mothers. Rural mothers were also found to be significantly more likely to have an unintended pregnancy (24% vs. 31%; $\chi^2= 4.97$; $p=0.0070$), to experience depression during pregnancy (11% vs. 20%; $\chi^2= 6.16$; $p=0.0131$), to smoke during pregnancy (5% vs. 12%; $\chi^2= 6.88$; $p=0.0088$), and to be enrolled in the WIC program (22% vs. 44%; $\chi^2= 26.41$; $p<0.0000$), compared to urban mothers. Urban and rural mothers were not found to have statistically significant differences regarding preterm birth, diabetes, hypertension, postpartum depression, and other examined Maternal and Child Health (MCH) outcomes.

Conclusions: Mothers residing in rural areas were less likely to participate in maternal behaviors, such as breastfeeding and attending healthcare visits, and were more likely to be enrolled in supplemental programs and to participate in risky pregnancy behaviors, such as smoking. When examining birth outcomes, no statistically significant differences were found. Future research should examine these relationships among a larger population to potentially increase statistical significance, and should seek to explore if racial disparities exist within urban versus rural regions. Additionally, social support programs should be examined in rural areas to assess pre- and post-pregnancy behaviors. Examining contributions of individual or area-level factors to health disparities can lead to cross-sector collaborations in taking a population health and equity focus on reducing MCH disparities.

Residence and Social Determinants of Health Near Hazardous Waste Sites in Virginia: Impact on Lung Cancer Clusters

Presenter: Rexford Anson-Dwamena, MPH, Epidemiologist, Office of Health Equity, Virginia Department of Health

Background: Understanding the spatial patterns of lung cancer near hazardous waste sites in a population provides insight to their causes and controls.

Methods: Data for lung cancer from 2009-2018 from Virginia Cancer Registry for adults 35 years and older were abstracted. Spatial-scan statistical software (SaTScan) was used to spatially and temporally detect lung cancer clusters near hazardous waste sites near the U.S. Environmental Protection Agency (U.S. EPA) National Priority List (NPL) sites in Virginia. Mortality rates were modeled with Health Opportunity Index indicators using regression analysis.

Results: Incidence rate of lung cancer for clusters with proximity from superfund sites less than 1.5 miles was higher (133.44) compared to that of more than 2 mile (118.77), while mortality rate (for areas less than 1.5 miles) was 91.08 and for areas more than 2 miles distance (80.84). Income inequality index, job participation index, affordability and education index ($p < 0.000$) emerged as significant predictors.

Conclusions: This study presents suggestive evidence of an association between proximity to superfund sites and lung cancer. Living in low-socioeconomic status (SES) areas was associated with higher total lung cancer incidence, and higher total cancer mortality. After accounting for individual age and race, living in lower-SES areas remained associated with higher lung cancer incidence, and higher total cancer mortality. Increasing access to screening and healthcare in high priority areas will reduce mortality.

Over-the-Counter Caution: Self-Harm Hospitalizations due to Acetaminophen Poisoning among Virginia Youth, 2016-2020

Presenter: Lauren Yerkes, MPH, CPH, Injury and Violence Prevention Epidemiologist, Division of Population Health Data, Office of Family Health Services, Virginia Department of Health

Background: Self-harm remains an important public health issue among Virginia youth. Acetaminophen is a common medication for over-the-counter pain relief and a frequent drug used for self-harm. This study analyzes self-harm hospitalizations due to acetaminophen poisoning (SHA) of youth and young adults aged 10-24 years in Virginia from 2016-2020 and the association between selected demographics and acute hepatotoxicity (AH) and self-harm history in young Virginians hospitalized for SHA.

Methods: Data are inpatient SHA hospitalizations of Virginians 10-24 years from 2016-2020 (n=1,055). A Mann-Kendall test was used to determine if there was a temporal trend, and three multivariate logistic regression models were used to assess relationships between demographic characteristics and hospitalization for SHA, AH, and self-harm history.

Results: The trend of SHA hospitalizations from 2016-2020 was not significant (Kendall tau=0.60, p=0.14). Youth 15-19 years had 33% higher odds of being hospitalized for SHA than youth 20-24 years [adjusted odds ratio (AOR): 1.33; 95% confidence interval (CI), 1.14-1.56]. Females were hospitalized for SHA at 62% higher odds than males (CI, 1.38-1.90). People of other race(s) were 1.82 times the odds of being hospitalized for SHA than people who were white (CI, 1.49-2.22). Poisonings involving more than one drug had 48% higher odds of being hospitalized than acetaminophen only (CI, 1.28-1.72). Seventy-six SHA hospitalizations had an AH diagnosis. Males had 93% higher odds of AH than females (CI, 1.17-3.19). Youth from medium metro areas were 2.30 times the odds of an AH diagnosis than large fringe metro areas (CI, 1.18-4.46). Poisonings with more than one drug had lower odds of AH than acetaminophen only (AOR: 0.45, 0.25-0.79). Over one-third (34.7%) of SHA hospitalizations had a history of self-harm coded. Males (AOR, 0.73; CI, 0.53-0.99) and Black youth (AOR, 0.64; CI, 0.45-0.91) had lower odds of having recorded history of self-harm.

Conclusions: Although not significant, there is an increase in the number of SHA hospitalizations from 2016-2020. Being an older teenager, female, and using more than one drug are associated with increased risk of SHA hospitalization. Among youth hospitalized with SHA, being male and from a less urban area is associated with increased risk for AH, and being male and Black is associated with lower odds of having a self-harm history. Limiting access to over-the-counter medications and immediate transport to and receipt of medical care are key to preventing SHA and AH. Coding self-harm history should be standard practice for patients at risk.

Using Cluster Detection and Response to Prevent the Spread of HIV in Western Virginia, 2021

Presenter: Christina Martone, MPH, Cluster Detection and Response Program Coordinator and Jennifer Johnson, BS, Disease Intervention Specialist, Division of Disease Prevention, Office of Epidemiology, Virginia Department of Health

Background: Cluster Detection and Response (CDR) is a tool that uses HIV genotypes to identify groups of related HIV infections. CDR was used to identify an HIV cluster in Western Virginia and those data were used to intervene and prevent further growth of the cluster.

Methods: Laboratories reported HIV genotypes to the Virginia Department of Health (VDH). VDH analyzed these genotypes using Secure HIV Trace software to identify genotypes that are genetically related. Identifying HIV clusters of concern included finding five or more people with genetically related genotypes that have been diagnosed within the previous 12 months. A Disease Intervention Specialist (DIS) contacted individuals in the cluster to provide support with treatment and prevention options.

Results: VDH identified an HIV cluster in Western Virginia in April 2020 consisting of eight people with genetically related infections. In 2021, 17 more people were genetically linked to the cluster. Cluster response efforts led to the identification of four additional named partners living with HIV and 11 additional named partners who were HIV negative. Additionally, DIS completed two initial partner services interviews and nine re-interviews, 14 people received HIV testing, and four people received pre-exposure prophylaxis (PrEP) referrals. Cluster growth decreased after these efforts. A total of nine people were identified as being virally unsuppressed at the time of cluster detection, of whom eight achieved viral suppression within six months after cluster identification.

Conclusion: Cluster detection highlights gaps in care and delivery of services. Detecting this cluster allowed VDH to offer tailored services to people living with and not living with HIV. We provided HIV testing and PrEP referrals in an effort to stop the spread of HIV. Conducting numerous partner services interviews led to discovering new named partners and allowed us to offer services to more people. As a result of these efforts, the cluster growth decreased in the fall of 2021, and by the winter of 2021, we were able to discontinue rapid response efforts. One limitation of CDR is that only about 60% of newly diagnosed individuals have a genotype test performed, limiting the ability to detect additional possible genetic linkages. For this reason, it is important to include field services in concert with the data analysis component of CDR to identify any named partners who may be connected to the cluster.

Spatial Analysis of COVID-19 Incidence During the Delta (July 17-November 13, 2021) and Omicron (November 27-March 26, 2022) Waves

Presenter: Cali Anderson, MPH, COVID Epidemiologist, Central Virginia Health District and Victoria Watson-Nichols, MPH, Assistant HAI Data Analyst, Division of Clinical Epidemiology, Office of Epidemiology, Virginia Department of Health

Background: The Central Virginia Health District within the Commonwealth of Virginia comprises Lynchburg City and the counties of Amherst, Appomattox, Campbell, and Bedford. Demographics vary widely within the district, particularly between the City of Lynchburg and its more rural counties. There are multiple factors that directly influence health outcomes in the population that vary per locality, including access to healthcare, poverty, racial disparities, environmental influences, and social factors.

Methods: Data on reported COVID-19 cases were gathered from the Virginia Electronic Disease Surveillance System (VEDSS) database during the district's Delta and Omicron variant waves from July 17, 2021 - November 13, 2021 and November 27, 2021 - March 26, 2022, respectively. Specific date ranges were selected based on an epidemiologic curve of case data from the district. These final data were cleaned utilizing Microsoft Excel 2016 © and spatially analyzed through ArcGIS Pro 2.9.2 ©.

Results: Heat maps were generated to depict disease incidence between census block groups, which revealed variation between the Delta and Omicron variant waves. Due to the increased transmissibility of Omicron in comparison to Delta, Omicron incidence surpassed Delta by approximately ten thousand cases (45%) and affected a larger number of census block groups. Nevertheless, both maps reveal overlapping block groups that were impacted more severely by both COVID-19 variants within the district. Localities that experienced high Omicron and Delta incidence include Goodview, Huddleston, Goode, Altavista, Brookneal, Central Appomattox, and Northern sections of Amherst, all areas that are rural in composition and mostly comprised of white senior citizens and middle-aged adults with low vaccination uptake. High incidence was also shown in an inner city block group of Lynchburg City where the demographics skew younger, with a primarily African American composition and a median household income roughly \$20,000 less per year than the rural communities.

Conclusion: Based on these findings, several block groups within the district were disproportionately affected by both the Delta and Omicron variants, which can inform future outreach efforts to these target areas. Such efforts should include community-specific vaccination and COVID-19 mitigation messaging targeting an older, white, conservative population in the rural areas and a young, African American population in inner city Lynchburg. These groups are two disparate populations that require distinctly different messaging to effect community-level change.

Piloting Wastewater-Based Surveillance of SARS-CoV-2 Variants in Virginia, 2021 – 2022

Presenter: Lauren Turner, PhD, Lead Scientist, Division of Consolidated Laboratory Services

Background: Wastewater systems aggregate biological waste for thousands to hundreds of thousands of individuals at a single location and can signal SARS-CoV-2 infection surges, as viral copies are an indicator of positive COVID-19 cases, new hospitalization, and admission to Intensive Care Units. Wastewater variant surveillance may provide an early warning system for the emergence of high-risk variants in communities. Beginning in September 2021, DCLS participated in a procedural pilot study with the VDH Division of Water and Wastewater Services and the US FDA to identify sequencing methods and software tools to assess data quality and lineage classification of SARS-CoV-2 in wastewater samples.

Methods: Two Northwest Virginia utilities were selected as pilot sites with the intent of sampling up to two times weekly for a 6 month period. 24-hour composite samples were shipped to DCLS for digital droplet PCR analysis (ddPCR) to enumerate SARS-CoV-2 viral copies. Nucleic acid extracts with SARS-CoV-2 viral copies close to or above the limit of detection for the ddPCR assay were selected for sequencing. DCLS used primer enrichment to improve resolution of SARS-CoV-2 variants by creating PCR amplicons to cover the entirety of the viral genome prior to next-generation sequencing. Sequence quality was evaluated with DCLS-developed and FDA bioinformatics pipelines. The Scripps Research Institute Freyja pipeline was used to estimate the abundance of SARS-CoV-2 lineages.

Result: Wastewater samples were collected for 41 consecutive weeks at Site 1 (September 2021 – June 2022), and 16 consecutive weeks at Site 2 (March – June 2022). Retrospective sequencing of positive samples was performed on 23 samples across 17 weeks from Site 1 (November 2021 – April 2022), and 9 samples across 5 weeks (March – April 2022) from Site 2. More than 88% of the samples attempted met the interim data quality requirements proposed for the FDA project. Lineage estimates by Freyja proportionally reflected the shift in predominant variant strains from Delta to Omicron (WHO designations) observed in clinical cases in the same time frame. Sequencing surveillance also provided more discrete information about a shift in predominant Omicron sub-lineages, from BA.1 to BA.2, between March and April 2022.

Conclusion: Wastewater testing over time can provide trend data indicating a rise in COVID-19 cases and sequencing of samples can indicate shifts in predominant viral variants in communities. This is an important monitoring tool for emerging variants with increased transmissibility and severity.

Differentiating Persistently Positive COVID-19 Cases from Sars-Cov-2 Reinfection Utilizing Laboratory Evidence, Virginia, 2020 – 2021

Presenter: Haley Greene, MPH, CPH, Junior Regional Epidemiologist and Jenny Crain, MS, MPH, CPH, Genomic Epidemiologist, Division of Surveillance and Investigation, Office of Epidemiology, Virginia Department of Health

Background: Previously there was no national consensus regarding classification of a SARS-CoV-2 reinfection as a new case; therefore, Virginia only counted a case once during 2020. While the 2021 national surveillance Coronavirus Disease (COVID-19) case definition recommends re-enumeration of patients with multiple molecular amplification tests (MATs) >90 days apart, classification of reinfection cases also depends on the availability of Whole Genome Sequencing (WGS) SARS-CoV-2 variant lineage results. Given this limiting factor, more commonly available MAT data may be used to rule-out persistent infection.

Methods: A subset of COVID-19 cases (March 2020 – December 2021), with two positive MAT specimens collected >90 days apart, were stratified into three cohorts based on intervening test results: 1) Persistently Positive (PP) cases with additional confirmatory results, 2) Reinfection cases with two intervening negatives, or 3) Excluded cases with insufficient laboratory data. WGS data matched with epidemiological cohort data was utilized to assess genetic differences among multiple SARS-CoV-2 variants isolated from the same person. Descriptive statistics were performed on Virginia Electronic Disease Surveillance System data using Microsoft SQL Server Management Studio and MS Excel. Phylogenetic trees were created using Nextstrain to differentiate between persistent infection and true reinfection.

Results: Of 1,116,282 confirmed cases in Virginia, 10,057 also tested MAT positive >90 days later; however, only 39 possible reinfections had at least one WGS result (preliminary data). When examining cohorts classified by MAT results alone, the dataset contained 33 PP cases and 6 reinfections. Alternatively, cohorts classified by variant lab evidence revealed 10 PP and 29 reinfection cases, based on predominantly circulating variants and specimen collection dates. PP cases had a shorter interval between infections (mean = 179.4 days) as compared to reinfections (mean = 329.3 days); the overall range was 90-505 days. Delta was the most common SARS-CoV-2 variant in this dataset.

Conclusions: These data suggest that differentiating persistent infection from multiple reinfections over time by genetically distinct variants has become exceedingly difficult through routine public health surveillance. Intervening MAT labs indicate viral infection clearance in the absence of WGS results, but this case classification method has less utility as the SARS-CoV-2 virus continuously evolves and seroprevalence increases. This underscores the importance of conducting WGS on MAT positive specimens collected from patients with a history of COVID-19. Additional prospective studies of epidemiological data paired with WGS results from separate COVID-19 episodes in the same person are needed to understand persistent infection and to characterize SARS-CoV-2 reinfection.

COVID-19 Vaccine Scheduling Support for Phase 1B and the Federal Retail Pharmacy Program, Virginia, 2021

Presenter: Jenae Davis, MPH, Crosscutting Epidemiology Program Coordinator, Division of Surveillance and Investigation, Office of Epidemiology, Virginia Department of Health

Background: In February 2021, VDH worked with federal partners and retail pharmacies to implement the Federal Retail Pharmacy Program and provide free COVID-19 vaccines to residents who met the phase 1B criteria of Virginia's vaccination strategy. VDH and Deloitte assumed scheduling responsibility for sites that could not ensure enrollment of residents meeting phase 1B criteria. The Cross-Cutting Epidemiology team built an ad-hoc REDCap vaccine scheduling project as a temporary solution while a more robust IT solution was developed.

Methods: Beginning February 23, 2021, Deloitte shared a retail pharmacy vaccination site list along with the amount of appointments per event per day. VDH designed a temporary REDCap system where call center agents were able to mass schedule individuals that met phase 1B criteria. VDH developed and ran an R script that generated hourly reports of appointments made by event and removed time slots in real time as they reached maximum appointments. Reports were sent to each retail pharmacy to track anticipated incoming volume, and this process was maintained Monday-Friday 9AM-8PM until VDH finalized its VASE+ system (Vaccine Appointment Scheduling Engine).

Results: Using the temporary system created in two days with REDCap, Deloitte was able to schedule over 16,500 Virginia residents for their 1st doses of the COVID-19 vaccine between February 23rd and March 22nd prior to the implementation of VDH's longer term scheduling system, VASE+. We scheduled over 25 mass vaccination events in the early stages of the COVID-19 vaccination rollout. The number of appointments that were scheduled varied by event and capacity, and we scheduled up to 86 (5 minute) time slots a day with up to 7 appointments per time slot. After individuals appeared for their first dose, the second dose was scheduled in person.

Conclusion: A high priority, low turnaround time scheduling system was designed and implemented using REDCap to schedule over 16,500 Virginia residents for their 1st dose of a COVID-19 vaccine between February 23rd and March 22nd. This demonstrated the flexibility of REDCap to act as a stopgap measure for vaccine scheduling during a rapid roll out event.

Mass Rabies Exposure Event Linked to Horse Farm in Montpelier, Virginia

Presenter: Alex Neal, BS, Epidemiologist Senior and Abi Nimitz, BSN, RN, Communicable Disease Nurse, Chickahominy Health District

Background: A local veterinarian contacted Chickahominy Health District (CHD) on April 6th, 2022 to report they were submitting a deceased pygmy goat for rabies testing. The infant goat was located on a working farm in Montpelier, VA that taught horseback riding to children. The caller wanted to notify the LHD in advance because there was potential for a large number of exposures.

During the preceding week there was a children's riding camp in session with approximately 20 children staying on the farm, in addition to children coming in for routine lessons. The goats were housed in a large pen away from the horses. On March 31st the infant goat was noted to be limping and a large jagged gash was observed on the goat's buttocks. The goat became increasingly weak and unable to feed and was taken to the veterinarian where OG tube feedings were initiated. For the next several days the owner of the farm, her daughter, and many children and parents associated with the riding program cared for the goat, including dropping the OG tube and trying to initiate feedings and administer medications.

Methods: On April 7th CHD received the goat head for testing and on the following day CHD was notified of a positive result. The farm owner compiled a list of all individuals who could have potentially been exposed during the exposure window and on April 11th an investigation began.

Results: Seventy three people from approximately 25 different families were interviewed by the district Epidemiologist and the Communicable Disease Nurse as potential exposures. Seventeen individuals were determined to be exposed by the LHD and recommended for rabies post-exposure prophylaxis (PEP) and three received rabies PEP on their own volition out of an abundance of caution. PEP was completed for all individuals by April 27th.

All animals on the farm were examined and none were found to have noticeable wounds. In consultation with the State Public Health Veterinarian, the LHD recommended that the mother of the infant goat be quarantined for six months and that all other goats in the pen be quarantined for one month.

Conclusion: A "perfect storm" of circumstances – including the adorable nature of the goat, the large number of people involved in its care, the initiation of tube feedings, the lack of PPE and the lack of recognition that rabies could be a possible cause for the goat's illness– led to this mass exposure event. Greater awareness and increased public education surrounding rabies are needed to prevent similar events in the future. Rapid response was critical in protecting those who were exposed.

Multi-strain Shiga Toxin-Producing *E. Coli* Outbreak Associated with Agritourism in Loudoun County, Virginia

Presenter: Kevin Embrey, MPH, District Epidemiologist, Loudoun Health District

Background: In early April 2022, The Loudoun County Health Department (LCHD) identified a cluster of Shiga toxin-producing *E. coli* (STEC) among individuals who interacted with baby goats at Farm X in Loudoun County prior to illness.

Methods: A collaborative investigation was undertaken by LCHD, Virginia Department of Health (VDH), Virginia Division of Consolidated Lab Services (DCLS), and the Virginia Department of Agriculture and Consumer Services (VDACS). Using the VDH Enteric Case Report Form, LCHD communicable disease staff interviewed reported cases and those identified through a REDCap survey designed to enhance case finding and assess potential risk factors for exposure. VDH Veterinarian Epidemiologists and LCHD Epidemiologists conducted a site visit to Farm X to collect fecal samples from goats, environmental swabs, and to evaluate surroundings. Specimens from human cases were forwarded to DCLS, where laboratory testing and whole genome sequencing (WGS) were conducted for both human and goat samples.

Results: After initial cases were determined to be epidemiologically linked to the farm, LCHD recommended that public interactions with goats at the farm be suspended for the remainder of the spring season. Thirty-five cases, from 23 households, met the outbreak case definition. Twenty cases (57%) were nine years of age or younger. Thirty (86%) were Virginia residents and five (23%) were out-of-state. A risk factor analysis was performed using survey data; results were not statistically significant. DCLS cultured seven human specimens and isolated STEC serotypes O111:H8 and O103:H2 in five and two specimens, respectively. Additionally, twelve isolates were obtained from six of nine pooled goat feces samples from the farm. STEC Serotype O111:H8 was identified in 7 (58%) and O103:H2 in 5 (42%) of the isolates from animal specimens. WGS was conducted on all isolates. Sequencing results showed high genetic similarity between the human and animal isolates from each serotype. STEC was not isolated from environmental swabs. Recommendations to minimize communicable disease risk to the public were provided to the owners of Farm X.

Conclusion: While agritourism provides the public many opportunities to experience farming and animal husbandry, some agritourism activities present a risk for zoonotic transmission of disease to humans. A farm site visit was an important investigative step in developing recommendations. WGS provided key evidence linking human cases to interactions with farm animals. Recommendations developed and implemented during this investigation could help reduce the risk of illness while allowing farms and the public to continue enjoying the benefits of agritourism.

Cryptosporidium Parvum Outbreak Associated with Raccoons at a Wildlife Facility

Presenter: Brandy Darby, DVM, MPH, DACVPM, Veterinary epidemiologist, Division of Surveillance and Investigation, Office of Epidemiology, Virginia Department of Health

Background: *Cryptosporidium parvum* is a parasitic zoonotic pathogen responsible for diarrheal illness in humans and animals worldwide. We report an investigation of a cryptosporidiosis outbreak in raccoons and wildlife rehabilitation workers at a Virginia facility.

Methods: A retrospective cohort study was designed to better understand clinical illness and possible exposures; a questionnaire was developed and distributed to all 49 facility personnel. Probable cases were defined as people who worked or volunteered at the facility and experienced gastrointestinal illness (diarrhea and abdominal cramping, vomiting, or anorexia) occurring after June 6, 2019; confirmed cases had additional laboratory evidence of *Cryptosporidium* infection. Stool specimens from sick humans and raccoons were collected and tested for gastrointestinal pathogens. Water samples from pretreatment taps inside and outside the building were tested for bacterial indicators of fecal contamination

Results: Fifteen (31%) of 49 facility personnel experienced symptoms meeting the case definition, including four laboratory-confirmed cases. Seven juvenile raccoons were reported to have diarrhea; six had laboratory-confirmed cryptosporidiosis. *Cryptosporidium parvum* of the same molecular subtype (IIaA16G3R2) was identified in two human cases and six raccoons. Raccoon illness preceded human illness by 11 days, suggesting possible zoonotic transmission from raccoons to humans.

Conclusion: This appears to be the first report of a human cryptosporidiosis outbreak associated with exposure to raccoons infected with *C. parvum*. Raccoons might be an under-recognized reservoir for human *C. parvum* infections. Further study is needed to explore the prevalence of cryptosporidial species in raccoons and their role as a wildlife reservoir.

Notes

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Special thanks to Donald Moore for coordinating the 2022 Virginia Epidemiology Seminar.

Awards

The People's Choice Award

For the first time this year, you will have the opportunity to vote on the presentations. Please go to the link when provided on your phone or computer and choose the one presentation from the day that you think was the best overall. You can only choose one presentation.

Diane Woolard, PhD Award

Dr. Diane Woolard served as a leader in applied public health epidemiology for over 30 years. She served as the Director of the Division of Surveillance and Investigation within the Virginia Department of Health's (VDH) Office of Epidemiology in Richmond. Throughout her tenure at VDH, Dr. Woolard has provided calm, sound leadership throughout countless disease surveillance and investigation efforts that protect the health of Virginians. Dr. Woolard's expertise and extensive experience in disease reporting requirements and the use of disease surveillance data helped transform disease reporting in Virginia. A teacher and mentor, her commitment to training future epidemiologists has helped produce public health leaders both nationally and internationally. The Diane Woolard award is presented to the recipient that best demonstrates collaboration with public health partners, information sharing, and leadership in public health.

Grayson B. Miller, Jr., MD Award

Dr. Miller received his undergraduate degree from Duke University in North Carolina and his medical degree from the Medical College of Virginia. He completed a residency in internal medicine and a fellowship in infectious diseases at MCV, becoming certified in both. He was an officer with CDC's Epidemic Intelligence Service from 1974-1976, stationed at the Pennsylvania Health Department. He served as the State Epidemiologist for Virginia from 1977-1997. He was the director of the Crater Health District from 1997-2002. After his retirement in 2002, he came back into the VDH central office as a part-time medical consultant with Emergency Preparedness and Response, the Office of Epidemiology and Community Health Services until he decided to fully retire in 2006. Dr. Miller set an example for the epidemiologists who followed him, teaching us how to focus on using the proper scientific methods while also understanding the practical realities of the context of the situations. He taught by example, demonstrating the importance of working collaboratively and with a sense of humor. He still lives in Richmond and, along with his wife, Nancy, has enjoyed many travel and learning adventures during his retirement. The Grayson B. Miller award is presented to the recipient that best demonstrates dedication to the field of public health practice, use of epidemiology methods, and advancements in knowledge of public health.

The judges for the award are the Director of the Office of Epidemiology, the Division of Surveillance and Investigation and the previous year's winner of the award.

