VIRGINIA DEPARTMENT OF HEALTH

VIRGINIA EPIDEMIOLOGY SEMINAR

FOUNDERS INN
VIRGINIA BEACH, VA

OCTOBER 25, 2023

VDH VIRGINIA DEPARTMENT OF HEALTH

PUBLIC HEALTH PREPAREDNESS SUMMIT

Accreditation Statement

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 **4.5 AMA PRA Category 1 Credits™**. Physicians should claim only the credit commensurate with the extent of their participation in the activity.

4.5 ANCC contact hours.

This activity was planned by and for the healthcare team, and learners will receive 4.5 Interprofessional Continuing Education (IPCE) credit for learning and change.

Virginia Epidemiology Seminar Agenda
Wednesday, October 25, 2023
The Founders Inn
Virginia Beach, VA

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

9:00 a.m. **Welcome and 'State of Epidemiology in Virginia'**
Laurie Forlano, DO, MPH
Director, Office of Epidemiology

9:15 a.m. **Welcome to Virginia Beach Health District**
Caitlin S. Pedati, MD, MPH, FAAP
Health Director, Virginia Beach Health District

SESSION 1
Moderator – Caitlin S. Pedati, MD, MPH, FAAP
Health Director, Virginia Beach Health District

9:25 a.m. **Revisiting a Classic: June Wedding Post-Reception GI Illness, Virginia Beach, 2023**
Anna Barringer, BS, CPH, District Epidemiologist
Virginia Beach Health District

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

- *Describe the importance of Epidemiology and Environmental Health working together during a foodborne outbreak investigation.*
- *Identify two organisms that contribute to foodborne illness.*
- *List five best practices to prevent foodborne outbreaks.*

9:45 a.m. **Surprised by Science: The Role of Whole Genome Sequencing in Multi-Drug Resistant Organism Outbreak Management, Virginia, 2023**
Stacey Helberg, RN, Public Health Nurse III
Kristen Locklin, RN, Public Health Nurse III
Fairfax County Health Department

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

- *Review the response to when a local health department becomes aware of multi-drug resistant organism (MDRO) in high-risk facility.*
- *Highlight the value of ongoing collaboration with facility leadership and the infection prevention and control team.*
- *Discuss the role of whole genomic sequencing in multi-drug resistant organism (MDRO) investigations.*

10:05 a.m. **Apples to Apples: Using Genomic Comparison to Aid in an Outbreak Investigation**
Katelin Gali, MS, MLS, Senior Scientist
Division of Consolidated Laboratory Services

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

- *Improve understanding of whole genome sequencing (WGS).*
- *Explain how WGS can be used to assist in an outbreak of antimicrobial resistant bacteria.*
- *Demonstrate DCLS WGS surveillance and reporting system.*

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

SESSION 2

Moderator – DaShaunda Taylor, PhD, MPH
Assistant Professor, Epidemiology, College of Health Sciences, School of Community and Environmental Health, Old Dominion University

10:40 a.m. **2022-2023 Statewide Outbreak of a Rare *Neisseria meningitidis* Serogroup Y Sequence Type**
Meredith Robinson, MSc, Vaccine Preventable Disease 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:

- *Depict the clinical characteristics of meningococcal disease, including routes of transmission and methods for laboratory confirmation.*
- *Communicate the epidemiologic traits of outbreak cases, including rare findings (e.g., high case-fatality rate, lack of common risk factor).*
- *Describe methods for enhancing meningococcal disease case investigations and options for expanding access to the meningococcal conjugate vaccine for persons at increased risk during this outbreak.*

11:00 a.m. **Group A Streptococcus Outbreak Investigation in a Long-Term Care Facility, Virginia, 2023**
Clarissa Bonnefond, MPH, District Epidemiologist
Lord Fairfax Health District

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

- *List the methods used by public health to identify additional cases during a Group A Strep outbreak.*
- *Describe multiple infection control practices that are recommended by public health to prevent the spread of Group A Strep in a long-term care facility.*
- *Explain how whole genome sequencing complements the epidemiological investigation of a Group A Strep outbreak.*

11:20 a.m. **Scabies Exposure in Response to Delayed Diagnosis in an Acute Care Hospital**

Karen McGoldrick, MT(ASCP), CIC, CHOP, Infection Preventionist
Sentara Leigh Hospital

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

- *Identify the difference between normal scabies and crusted scabies.*
- *Compare what protocols need to be followed to protect staff and patients when exposed to highly contagious crusted scabies vs regular scabies.*
- *Evaluate all staff members that might be at risk of exposure to ensure prophylactic treatment in a timely manner after a crusted scabies exposure.*

11:40 a.m. **Evaluation of An Outbreak Investigation of *Candida auris* at Southside Medical Center**

E. Katrina Saphrey, MPH, District Epidemiologist
Crater Health District
Leann Carter, BSN, RN, Infection Preventionist
Ashley Cundiff, RN-BC, CIC, Infection Preventionist
Bon Secours-Southside Medical Center and Southern Virginia Medical Center

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

- *Understand etiology of C. auris transmission in an acute care setting.*
- *Recognize the importance of the collaboration between Infection Prevention Teams in an acute care settings and VDH to curve transmission of communicable diseases.*
- *Propose a novel approach to identify colonized cases during C. auris outbreak investigations.*

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

SESSION 3

Moderator- Vanessa Walker Harris, MD
Director, Office of Family Health Services, Virginia Department of Health

1:05 p.m. **Nonfatal and Fatal Firearm Injury Surveillance in Virginia**

Erin Austin, MPH, Epidemiology Program Supervisor, 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:

- *Understand current surveillance efforts by the Virginia Department of Health for firearm injury.*
- *Learn about trends for nonfatal and fatal firearm injuries in Virginia.*
- *Know how to find data about firearm injuries in Virginia.*

1:25 p.m. **Associations Between Historical Redlining and Birth Outcomes in Virginia: A 2016-2020 Study**

Ksenia Primich, MPH, a-IPC, NHSN External Data Validation Specialist,
Division of Clinical Epidemiology, Office of Epidemiology
Virginia Department of Health

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

- *Share the outline of what historical redlining is and how it affects health outcomes.*
- *Discuss the association of historical redlining and adverse birth outcomes in affected areas of Virginia.*
- *Raise important questions for new and needed research to strengthen work to understand, rectify, and prevent health inequities.*

1:45 p.m. **Disease Progression of a Chronic Mpox Case in the Crater Health District**

Courtney Ayers, BS, District Epidemiologist
Henrico County Health District

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

- *List at least three symptoms of a typical Mpox infection.*
- *Describe the steps of an Mpox investigation.*
- *Define at least one factor that can put an individual at risk for a severe Mpox infection.*

2:05 p.m. **Local Investigation of Hepatitis C Labs: An Important and Worthwhile Effort**

Shawn Harper, BSN, RN, CIC, Public Health Nurse III
Fairfax County Health Department

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

- *Correctly apply the hepatitis C case definition.*
- *Understand limitations when interpreting the hepatitis C surveillance data without universal negative lab reporting.*
- *Assess advantages and disadvantages to conducting local hepatitis C case investigations.*

2:25 – 2:40 p.m. **Break and Activity**

SESSION 4

Moderator – Ana Colón
Eastern Region Epidemiologist, Division of Surveillance and Investigation, Office of Epidemiology, Virginia Department of Health

2:40 p.m. **Impacts of Data Modernization on Rabies Exposure Reporting and Public Health Response, Fairfax County, 2023**
Kirsten Kohl Hampshire, MPH, Environmental Health Specialist
Fairfax County Health Department

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

- *Identify the advantages of collecting exposure reports electronically.*
- *Assess the dynamic needs of different reporting sources as they pertain to rabies exposure reporting.*
- *Recognize how targeted education and outreach efforts can improve rabies exposure reporting compliance and Health Department response.*

3:00 p.m. **Cryptosporidiosis Outbreak Associated with Baby Calves at a State Prison Farm**
Emilie Schweikert, MPH, CHES, District Epidemiologist
Chesterfield Health District

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

- *Identify common modes of transmission for cryptosporidium.*
- *Discuss risk factors for zoonotic disease transmission among prison farm workers.*
- *Describe disease prevention best practices for dairy and cattle farms.*

3:20 p.m. **Highly Pathogenic Avian Influenza Response in Two Commercial Flocks in Rockingham County, Virginia, 2023**
Travis Oishi, MPH, District Epidemiologist
Central Shenandoah Health District

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

- *Describe the importance of a centralized record keeping system for persons under monitoring, after exposure to an HPAI response.*
- *Identify the key players in an HPAI response.*
- *Implement specimen collection processes for Influenza testing at DCLS, either within the LHD or with providers in the community.*

3:40 p.m. **Closing Remarks**
Voting for People's Choice Award
Brandy Darby, DVM, MPH, DACVPM
Director, Division of Surveillance and Investigation, Office of Epidemiology
Virginia Department of Health

4:00 p.m. **Award Presentations**
Grayson B. Miller, Jr., MD Award Presentation
Diane Woolard, PhD., Award Presentation
People's Choice Award Presentation

4:10 p.m. **Adjourn**

ABSTRACT
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Revisiting a Classic: June Wedding Post-Reception GI Illness, Virginia Beach, 2023

Presenter: Anna Barringer, BS, CPH, District Epidemiologist, Virginia Beach Health District

Background: Within hours after the reception following a Saturday Spring wedding at a rural Virginia Beach venue, multiple attendees experienced gastrointestinal (GI) illness. After receiving calls about illness from the groom's family, the caterer for the event contacted Virginia Beach Health District Environmental Services to report the experience. An investigation was initiated immediately by environmental and epidemiology staff. Early interviews of a convenience sample of attendees indicated diarrhea and abdominal cramping as the primary symptoms, with onset beginning as soon as seven hours after the reception buffet.

Methods: The wedding reception menus and the attendees list were obtained, and a REDCap survey was prepared to obtain symptom and food histories for attendees. An environmental assessment of the foods prepared and served at the reception and an inspection of the caterer's food preparation facility were conducted. Interviews of food preparers were also conducted.

Results: Of the 61 attendees at the reception for whom responses were received, 46 (75.4%) reported diarrheal illness following consumption of food at the reception. The mean incubation period was 9.98 hours (range 7–19.5 hours), and an epi-curve demonstrated a distribution consistent with a point-source event. Survey analysis indicated pulled pork was the most likely implicated food with an attack rate of 79.63% (43 ill, 11 not ill) and a risk ratio of 1.9907 (CI: 0.6748–5.873, p-value=0.04539). The environmental assessment indicated the opportunity for improper holding temperatures, and no thermometers were observed to be available or in use for monitoring internal temperatures for cooking and cooling. Inspection of the food preparation facility indicated violations that could contribute to foodborne illness, but interviews of food handlers did not yield specific instances of potential contamination. Laboratory examination of stool ruled out norovirus and a variety of other organisms on a GI pathogens panel. However, *Bacillus cereus* enterotoxin was detected in two stool specimens and *Clostridium perfringens* enterotoxin was detected in a third specimen.

Conclusions: This was a classic outbreak of GI illness from a well-known organism. Investigation was most consistent with likely environmental contamination of a food product that was temperature abused during an event service. This event demonstrated clinical, epidemiological, and environmental elements that have been well documented to be associated with this bacterium. It represents a reminder of the importance of food handling education and of utilizing opportunities to reinforce time and temperature controls to ensure a safe food supply.

Surprised by Science: The Role of Whole Genome Sequencing in Multi-Drug Resistant Organism Outbreak Management, Virginia, 2023

Presenters: Stacey Helberg, Public Health Nurse III and Kristen Locklin, Public Health Nurse III, Fairfax County Health Department

Background: Multi-drug resistant organisms (MDROs) including carbapenem-resistant organisms (CROs) are on the rise nationally and within the Fairfax Health District. In 2023, Fairfax County Health Department's (FCHD) Acute Communicable and Emerging Diseases (ACED) program conducted two large, independent, CRO investigations: one at an acute care hospital (Outbreak A) and the second at a skilled nursing facility (SNF) (Outbreak B). In both outbreaks, epidemiological work and analysis suggested facility exposure and transmission; however, whole-genome sequencing (WGS) testing by the Division of Consolidated Laboratory Services (DCLS) supported different findings. In Outbreak A, CRE KPC transmission was suspected in an acute care hospital. Following the identification of an index case with a KPC-producing *E. cloacae*, 200 high-risk contacts were identified, and three patients were identified as positive for KPC mechanism, one of whom had *E. cloacae* organism and two with unknown organisms. In Outbreak B, transmission was suspected at a SNF after colonization screening detected NDM and OXA-48 mechanisms in the roommate of a newly admitted resident with carbapenem-resistant *Escherichia coli* and *Klebsiella pneumoniae,* both with NDM and OXA-48 mechanisms. A follow-up point prevalence survey of 17 residents in the unit resulted in an additional resident screening positive for NDM.

Methods: Containment response included case and staff interviews, contact tracing, medical record review, infection control and environmental assessment, and education. Initial laboratory testing was conducted at the acute care hospital lab and Maryland Antibiotic Resistance Laboratory Network (ARLN). DCLS performed genomic analysis which included genome assembly, species identification, single nucleotide polymorphism comparison (SNP), and AMR gene prediction using public health bioinformatician-developed bioinformatics pipelines. SNPs are the number of nucleotide differences between compared genomes. SNPs are used to determine genetic similarity with the expectation that highly similar isolates are more likely from a common source.

Results: In Outbreak A, DCLS sequenced the isolates of the index case and two of three contacts and found the isolates to be 22 SNPs apart from each other, suggesting the isolates were not closely linked genetically, and given the cases' extensive medical histories and healthcare stays, exposure likely occurred earlier in time or a different setting. The resistance gene identified for all three isolates was KPC-3. In Outbreak B**,** DCLS sequenced the isolates of the three SNF residents, and testing identified the roommates' isolates as two SNPs apart from each other, suggesting genetic relatedness indicative of a common infectious origin and confirming outbreak etiology at the SNF. The third SNF resident's isolate with NDM mechanism was determined to be from a different allele than the other two cases and therefore not included in the outbreak case count.

Conclusions: While initial laboratory testing and epidemiological analysis linked multiple CRO cases together, WGS supported and highlighted differences in the response. While the timing of WGS results does not allow for public health response actions to be modified, providing clear evidence for transmission (or lack thereof) is crucial in future understanding of the epidemiology of CRO outbreaks.

Apples to Apples: Using Genomic Comparison to Aid in an Outbreak Investigation

Presenter: Katelin Gali, M.S., MLS(ASCP), Senior Scientist, Division of Consolidated Laboratory Services

Background: Bacterial pathogen whole-genome sequencing (WGS) can enhance the identification of clusters of related organisms and potential outbreaks through high-resolution pathogen genome comparison. Genomic data can also indicate pathogen attributes, including specific antimicrobial resistance (AMR) gene prediction. DCLS has expanded genomic testing to include Carbapenem-resistant organisms (CROs) to support outbreak investigations and public health surveillance of possible illness clusters. In 2023, DCLS assisted the Fairfax County Health Department with an investigation of suspected healthcare facility CRO transmission. The index case (patient one) had traveled internationally prior to hospitalization and had two OXA-48 and NDM PCR-positive isolates, a *Klebsiella pneumoniae* and an *Escherichia coli,* from peritoneal fluid specimens. Patient two, a close facility contact, also had an OXA-48 and NDM positive *K. pneumoniae* isolate submitted to DCLS. A third NDM PCR-positive patient (patient three) received colonization screening testing in Maryland. All four isolates were sequenced by DCLS or Maryland due to the suspicion of an outbreak.

Methods: Short-read WGS was performed on an Illumina MiSeq System. Genomic analysis included genome assembly, species identification, single nucleotide polymorphism comparison (SNP), and AMR gene prediction using public health bioinformatician-developed bioinformatics pipelines.

Results: *K. pneumoniae* isolates from patients one and two differed by an estimated two SNPs, suggesting they were very similar and likely related to a common source or transmission event. In contrast, patient three's *K. pneumoniae* isolate differed by >25,000 SNPs from the other two patients' isolates. AMR gene predictions for patient one and patient two's *E. coli* and *K. pneumoniae* isolates included an OXA-48-like gene, OXA-181, and an NDM-5 gene. For patient three, the resistance gene identified was an NDM-7, further suggesting a distinct *K. pneumoniae* strain.

Conclusions: WGS results supported the suspicion of facility transmission between patient one and two and ruled out patient three, thus assisting epidemiologists with identification of the most likely outbreak-associated cases. DCLS is developing additional testing capacity to strengthen HAI/AR services including: 1) colonization screening, 2) Oxacillinase gene PCR testing for enhanced Carbapenem-resistant *Acinetobacter baumannii* surveillance, 3) *Candida auris* sequencing for surveillance and outbreak response, and 4) long-read sequencing to further characterize pathogen genomes and potentially enable multi-species outbreak analysis.

2022-2023 Statewide Outbreak of a Rare *Neisseria meningitidis* Serogroup Y Sequence Type

Presenter: Meredith Robinson, MSc, Vaccine Preventable Disease Program Coordinator, Division of Surveillance and Investigation, Office of Epidemiology, Virginia Department of Health

Background: Meningococcal disease, caused by the bacterium *Neisseria meningitidis* (Nm), is a serious illness that presents primarily as meningitis or septicemia. On August 12, 2022, the Virginia Department of Health (VDH) learned of two meningococcal disease patients hospitalized in eastern Virginia whose isolates were identified as Nm serogroup Y (NmY). These cases raised suspicions of a potential NmY outbreak because two additional NmY cases were reported in eastern Virginia in June and July 2022.

Methods: Standard public health case interviews were conducted to collect risk factor information. VDH also conducted active case finding by monitoring syndromic surveillance systems and reviewing medical records of suspected meningitis and meningococcemia patients. All available NmY isolates were forwarded to CDC for whole genome sequencing (WGS) to determine their relatedness.

Results: From June 12, 2022, through July 18, 2023, twenty-seven patients with meningococcal disease met the confirmed case definition for this outbreak. All isolates available for sequencing (22 out of 27) were found to be the same strain, sequence type 1466 within clonal complex 174, and highly genetically related. Outbreak-associated cases were detected in eastern, central, and southwest Virginia. Confirmed patients were 81% Black or African American, 52% female, and had a median age of 43 years (range of 16-80). The majority of patients developed septicemia (67%). Twenty-six patients had no evidence of previous NmY vaccination; five died from complications of meningococcal disease. This outbreak had a higher case fatality rate (CFR) (19%) than the national average NmY CFR between 2017–2020 (6.5-14.6%, depending on the year). Four patients were HIV positive. Medical record evidence of immunosuppression was documented for one patient taking organ transplant anti-rejection medication. The majority of patients (63%) reported tobacco smoking; 22% reported marijuana use, and 7% reported intravenous drug use.

No common risk factor was identified among the outbreak cases, and VDH was unable to define a target population for vaccination. Meningococcal conjugate vaccine (MenACWY) was offered to close contacts as they were believed to be part of the population at increased risk based on the outbreak epidemiology. Local health districts that reported an outbreak case offered vaccine to persons at increased risk due to certain medical conditions (e.g., HIV, sickle cell disease) and to adult residents of localized areas experiencing increased transmission.

Conclusions: The 2022-2023 statewide outbreak of a rare *Neisseria meningitidis* Serogroup Y Sequence Type (ST1466) in Virginia demonstrated the importance of vaccination among individuals at increased risk for meningococcal disease. The relatively high CFR in this outbreak may simply be stochastic based on small numbers, or reflect a hypervirulent strain, or difficulties or delays accessing medical care. During meningococcal disease outbreaks in which a common risk factor is not identified, public health officials should increase communication with healthcare providers about routine vaccine recommendations and consider vaccination of close contacts and persons at increased risk due to certain medical conditions.

Group A Streptococcus Outbreak Investigation in a Long-Term Care Facility, Virginia, 2023

Presenter: Clarissa Bonnefond, MPH, District Epidemiologist, Lord Fairfax Health District

Background: Group A Streptococcus (GAS) primarily infects the respiratory tract, skin, and soft tissue. Invasive GAS (iGAS), in which the bacteria infect a normally sterile body site, is severe and can be life threatening, especially in older adults. The Virginia Department of Health investigated a prolonged GAS outbreak in a skilled nursing facility from March 2022 - July 2023. Cases continued despite multipronged outbreak response.

Methods: A case was defined as invasive (GAS isolated by culture from a normally sterile site), serious noninvasive (GAS isolated by culture from wound/cellulitis, urine, or respiratory secretions) and noninvasive (GAS isolated by culture or detected by rapid antigen test from the throat) with onset in March 2022 or later. Cases were identified through active surveillance, retrospective chart review, colonization screening by skin/throat swab, and culture. Multiple onsite visits were conducted to assess infection control practices at the facility. Genotyping (*emm* type*)* analysis was performed on resident and staff isolates.

Results: From March 2022 to July 2023, 33 (66%) GAS cases were identified among facility residents, and 17 (34%) cases among staff. Eleven resident cases have died. Out of 53 positive specimens, GAS was isolated from throat (28), wounds (17), urine (2), foley (1), and blood (5); 4 residents tested positive from more than one site. There were 5 (10%) invasive cases, 17 (34%) serious noninvasive cases, and 28 (56%) noninvasive cases. Twenty-two (44%) cases were identified through colonization screening; the carriage rate among residents was 6.1%% (16 positive out of 261) and 3% among staff (6 positives out of 200). Sequencing was conducted on 36 isolates, 34 (94.4%) were *emm* type 89 and were within <10 single nucleotide polymorphisms (SNP) apart. Infection prevention assessments identified gaps in hand hygiene, wound care, and environmental cleaning and disinfection.

Conclusions: Genotyping results suggested common source exposure. GAS might have been transmitted several times between colonized or infected residents and staff, causing the extended outbreak. Multiple challenges at the facility contributed to a prolonged outbreak despite aggressive interventions. Challenges included high staff turnover; use of agency staff since the beginning of the COVID-19 pandemic; change in facility ownership; suboptimal infection prevention practices including wound care and environmental cleaning and disinfection; and lack of appropriate active surveillance for GAS infections. Review of epidemiological data, frequent onsite infection prevention assessments, numerous educational sessions, and active follow-up were all crucial strategies for outbreak mitigation.

Scabies Exposure in Response to Delayed Diagnosis in an Acute Care Hospital

Presenter: Karen McGoldrick, MT(ASCP), CIC, CHOP, Infection Preventionist, Sentara Leigh Hospital

Background: Crusted scabies can be difficult to diagnose and is often misdiagnosed because presentation is similar to other skin conditions such as eczema, urticaria, atopic dermatitis, allergic contact dermatitis, and arthropod bites etc. Millions of people worldwide are affected by scabies. A patient from an assisted living facility with multiple diagnoses and rash was admitted to the hospital. The patient had seen a dermatologist at the originating facility and was given steroid creams as treatment for dermatitis. On hospital day four, a second dermatologist was consulted who confirmed crusted scabies. The patient was placed on contact precautions. Exposed healthcare workers were assessed, and prophylaxis treatments were given as per protocol. One month later, an employee and family member were diagnosed with scabies. This employee did not have electronic medical record (EMR) documentation of contact with the index patient, but after a later interview was found to have assisted with the patient in an auxiliary department. Four months after the initial exposure, another employee in the same auxiliary department was diagnosed with scabies.

Methods: A summary of the epidemiology and lifecycle of scabies and discussion of the ensuing scabies investigation timeline will be provided. Also included will be a discussion of employee communication and prophylaxis and the proactive alert of patients possibly exposed to the two employees who contracted scabies. A review of how the Infection Preventionist reported and discussed the cases with the Health Department will also be covered.

Results: All employees identified as exposed to the index patient were given prophylactic treatment and only one of these employees was diagnosed with scabies. Later patients who had possible interactions with the two employees diagnosed with scabies from the auxiliary unit were proactively alerted of the possible exposure.

Conclusions: Discussing infrequently seen diseases is important as they can be challenging to diagnose. The delay in identifying the index scabies case had consequences for both employees, the hospital, and potentially for patients. This discussion can provide further awareness to Infection Preventionists, epidemiologists, and all healthcare professionals in preventing future exposure events.

Evaluation of An Outbreak Investigation of *Candida auris* at Southside Medical Center

Presenters: E. Katrina Saphrey, MPH, CIC, Epidemiologist Sr., Crater Health District, Ashley Cundiff, RN-BC, CIC, and Leann Carter, BSN, RN, Infection Preventionists, Bon Secours-Southside Medical Center and Southern Virginia Medical Center

Background: In January 2023, Southside Medical Center (SMC) identified its first hospital acquired case of *Candida auris* and reported the finding to the Crater Health District. *Candida auris* is a fungal infection that is often multi-drug resistant. An additional case was identified in February 2023 that was epi-linked to the index case, prompting an outbreak investigation that utilized novel approaches to identify potential additional colonized cases and included multiple jurisdictions within the state of Virginia.

Methods: The following steps were taken to contain the outbreak: a bed traceback to determine impacts of transmission within the facility, enhanced surveillance and screening on impacted units, cohorting of known colonized or clinical cases to one designated unit, and flagging medical records of cases and those being screened. Other mitigation strategies included: Situation-Background-Assessment-Recommendation (SBAR) communication to all staff via email and safety huddles, daily Infection Prevention (IP) rounds with Personal Protective Equipment (PPE) audits and just-in-time corrective education, hospital-wide terminal clean using an Environmental Protection Agency (EPA) List P antimicrobial registered product, and room cultures and bioburden testing as a validation method for cleaning and disinfection. The Crater Health District and Central Region staff conducted colonization screenings on individuals whose discharge disposition was to an acute care or congregate facility. Multiple districts collaborated to alert others of exposures and screening needs. Teams across the Virginia Department of Health (VDH) and Centers for Disease Control and Prevention (CDC) were consulted regarding best practices to mitigate the spread of *C. auris* in acute care settings. Virginia also collaborated with the Maryland Public Health Laboratory to ensure additional laboratory capacity.

Results: On March 1, 2023, 42 patients were screened on the two impacted units at SMC, and on March 15, 2023, 33 patients were screened. No new positives were detected. On March 22, 2023, 38 patients were screened, and one patient was positive who was later found to be associated with another facility's outbreak of *C. auris.* Over a span of two-weeks, specimens were collected on 21 patients across 10 facilities and three colonized cases were detected (attack rate of 14%). Two additional colonized cases were detected from other districts. In total, seven clinical cases (two converted from colonization) and three colonized cases were associated with the outbreak from January 2023 to April 2023.

Conclusions: Environmental cleaning, strict PPE and hand hygiene practices, re-education of staff and collaborating with VDH curbed transmission within SMC. Although burdensome, following exposed discharged patients forward proved to detect an additional colonized case, thereby reducing the risk of additional outbreaks in downstream facilities.

Nonfatal and Fatal Firearm Injury Surveillance in Virginia

Presenter: Erin Austin, MPH, Epidemiology Program Supervisor, Division of Population Health Data, Office of Family Health Services, Virginia Department of Health

Background: Nonfatal and fatal firearm injuries are a public health problem affecting communities throughout Virginia, however, prior to 2020, public health surveillance of firearm injuries was limited. With support of federal funding from the Centers for Disease Control and Prevention, the Virginia Department of Health (VDH) Offices of Epidemiology and Family Health Services collaborated to improve surveillance and analysis of firearm injuries with the goals of 1) describing firearm injury trends, 2) identifying populations disproportionately impacted, and 3) publishing firearm injury data products.

Methods: VDH analyzed firearm injury data from 2016 through 2021 using three data sources: 1) emergency department (ED) visits reported by hospital-based and free-standing EDs in Virginia; 2) inpatient hospitalization data from licensed hospitals in Virginia; and 3) death certificate data certified by the National Center for Health Statistics. With input from a multidisciplinary advisory board, VDH developed a data dissemination plan prioritizing the following data products: interactive data dashboards of ED visits and firearm-related deaths, a detailed data brief, and infographics highlighting key findings.

Results: Surveillance findings identified increases in firearm injury ED visits (41% increase), nonfatal hospitalizations (8%), and deaths (21%) from 2016 to 2021 in Virginia. The majority of deaths by firearm among Virginians in that same period were by suicide (62%), followed by homicide (35%). Males contributed approximately 85% of firearm ED visits, hospitalizations, and deaths compared to females. Youth and young adults aged 15 to 24 had the highest count and percent of firearm injury ED visits (4,809, 38%), hospitalizations (1,676, 39%), and deaths (1,338, 21%). VDH published three data products using surveillance findings: firearm injury ED visits dashboard (June 2022), firearm-related deaths dashboard (May 2023), and *Firearm Injuries in Virginia, 2016-2021* data brief (May 2023).

Conclusions: Firearm injuries are a growing public health problem in Virginia, as demonstrated by increases in nonfatal and fatal firearm injuries between 2016 and 2021. Surveillance findings, now available in publicly accessible data products, show that males and persons between the ages of 15 and 24 carry a disproportionate burden of firearm injury ED visits, hospitalizations, and deaths in Virginia. Additionally, most firearm-related deaths from 2016 to 2021 were suicide, followed by homicide. Increased surveillance efforts highlight the need for more firearm injury prevention activities focused on males, young adults, and suicide.

Associations Between Historical Redlining and Birth Outcomes In Virginia. A 2016-2020 Study.

Presenter: Ksenia Primich, MPH, a-IPC, NHSN External Data Validation Specialist, Division of Clinical Epidemiology, Office of Epidemiology, Virginia Department of Health

Background: Despite being one of the wealthiest nations, disparities in adverse birth outcomes persist across racial and ethnic lines in the United States. A growing body of research suggests that historic redlining is related to current neighborhood characteristics, including increased minority presence, higher prevalence of poverty, and greater social vulnerability. Redlining was the practice of grading a neighborhood's mortgage creditworthiness, implemented by the federally sponsored Homeowners' Loan Corporation (HOLC) via color-coded maps of major cities in the US. This practice effectively isolated Black people in areas that would experience lower levels of investment than their White counterparts. Today, those same neighborhoods suffer from lower life expectancy, higher incidence of chronic diseases, and poorer health outcomes in general. Therefore, this study sought to explore the association between residing in historically redlined neighborhoods and adverse birth outcomes.

Methods: This was a cross-sectional study using data on live births from Virginia Vital Records from 2016-2020 in the following five areas for which redlining data are available: Richmond, Newport News-Norfolk-Virginia Beach, Lynchburg, and Roanoke. The outcomes of interest were preterm birth (PTB), low birthweight (LBW), and small-for-gestational age (SGA). Logistic regression was used to model the association between historical redlining and the birth outcomes, accounting for potential confounders (race, age, education level, health insurance type, income, and smoking status). SAS version 9.4 was used to perform statistical analyses.

Results: In total, there were N=112,130 births occurring between 2016–2020 in the five areas of interest that were screened for inclusion eligibility, 34,534 (30.8%) of which fell inside HOLC-graded regions and were included in the final analysis. The proportion of preterm births ranged from 4.02% in grade A ("best") to 51.50% in grade D ("hazardous"). The odds ratio of having a preterm birth for HOLC grade D versus A was 1.36 (95% CI = [1.12-1.66]) after adjustment for income, education, insurance, and WIC status, as well as health behaviors (smoking, hypertension, and diabetes).

Conclusions: The primary finding of this study was that even 80 years after the HOLC grades were delineated by the US government, they remained associated with contemporary risk of adverse birth outcomes, with worsening HOLC grades being associated with adverse birth outcomes.

Disease Progression of a Chronic Mpox Case in the Crater Health District

Presenter: Courtney Ayers, BS, District Epidemiologist, Henrico County Health District

Introduction: On May 20, 2022, CDC issued an alert to notify clinicians of mpox infections in the United States and other previously non-endemic countries. Mpox cases usually recover within two to four weeks, however, illness can be more severe in immunocompromised individuals. Crater Health District (CHD) investigated a case whose illness has lasted eight months and is still ongoing.

Case Description: On Saturday, November 12, 2022, a positive orthopoxvirus detected via polymerase chain reaction (PCR) was reported to the CHD. The sample was collected at an urgent care for a patient who reported a body rash. The individual was interviewed by the Deputy Epidemiologist the same day that the results were received. He reported having sex with an unknown partner in October and had no way of contacting the sexual partner. The patient was asked about his HIV status and stated he was negative. Tecovirimat (TPOXX) was considered for treatment, but it was determined to not be warranted due to the lesions already being crusted over. The urgent care reached out Tuesday to CHD to report his positive HIV result and that they had made multiple failed attempts to reach the patient to inform him of his status. The Deputy Epidemiologist worked with the Disease Investigation Specialist to investigate if the patient had been informed of his HIV status, and it was documented that his status was disclosed nine months prior. CHD made multiple attempts to reach the individual to readdress his HIV status and ensure linkage to treatment, but attempts were unsuccessful. After the initial interview with the patient, he developed more lesions of worsening severity on his face, arms, legs, torso, and genitals. From November to April, the patient was hospitalized six times for varying length of stay: from three days to nineteen days, with an average of eight days. Hospitalizations were needed to manage fevers associated with infections, severity of sores, and pain. During his first hospitalization on November 26, the patient met the criteria for AIDS. However, he was not started on antiretroviral therapy until December 21. He received his first course of TPOXX on November 28 and was treated with multiple rounds over the next few months with no improvement in his sores. Since his final hospital discharge at the end of May 2023, he has had multiple outpatient visits to check the status of his lesions. While lesions are mainly crusted over and healing well, specimens collected in July 2023 still yielded PCR positive results for orthopoxvirus.

Discussion: In March 2023, CHD received notification that wastewater encompassing our jurisdiction and part of another had detectable levels of mpox for four weeks. This led CHD to enhance education and outreach regarding mpox in our locality and reconvene mpox testing at our health department clinic. Despite this outreach and increased testing, new cases were not detected. We hypothesized that the identified chronic case may be the reason for positive wastewater. We shared this suspicion with CDC for further investigation. One lesson learned from this patient is to strengthen communication between local health departments, hospital partners, state health departments, and the CDC. In addition, we have also considered that earlier initiation of TPOXX may have made a difference in his length of illness. More research is still needed to discuss factors attributed to chronic mpox, infectious period in these cases, and threshold needed to trigger positive wastewater samples. However, one conclusion that is clear is that mpox, especially chronic cases, is debilitating. Prevention through safe sex and vaccination is key.

Local Investigation of Hepatitis C Labs: An Important and Worthwhile Effort

Presenter: Shawn Harper, BSN, RN, CIC, Public Health Nurse III, Fairfax County Health Department

Background: Hepatitis C is a liver infection caused by the hepatitis C virus (HCV) that is spread by direct contact with infected blood. Hepatitis C is one of over 80 reportable conditions to public health in Virginia, but unlike most other conditions positive hepatitis C labs are generally not investigated by local public health investigators. Known gaps in electronic lab reporting (ELR) of negative hepatitis C labs inhibits identification of acute hepatitis C cases (i.e., seroconversion) and results in non-cases being misclassified as probable, chronic hepatitis C cases (i.e., positive antibody with unreported negative PCR). This report aims to capture the process and outcomes of the Fairfax County Health Department's (FCHD) effort to accurately identify the local hepatitis C disease burden.

Methods: A public health nurse (PHN) reviewed all new positive hepatitis C labs reported from January to July 2023. A medical record review was conducted, if needed, to establish the case status with the goal to find unreported labs and have no cases classified as probable, and to update case demographic information, identify exposures, and determine pregnancy and treatment status. In addition, in consistent clinical settings, we conducted case finding among pregnant people to identify unreported cases of perinatal hepatitis C and neonatal abstinence syndrome (NAS). Case interviews are only attempted for acute and perinatal hepatitis C cases.

Results: From January through July 2023, 279 Fairfax Health District residents were reported with positive hepatitis C labs. Of these, 145 (52%) were able to be classified as not a case solely from information received through ELRs. To determine case status or gather additional case information, 134 (48%) medical record reviews were conducted. Overall, 169 (61%) individuals were classified as not a case, including 24 (14%) that were reclassified after investigation identified a previously non-reported negative PCR lab. Three recent seroconversions were identified based on unreported previously non-reactive HCV antibody results. Following interviews, these three acute cases were identified to have been exposed while receiving medical care in Pakistan; two of the individuals had undergone dialysis and one had a surgical procedure. CDC data identify Pakistan as the country with the highest number of hepatitis C infections and having an infection rate >3%. Of 107 (38%) chronic cases, 78 (73%) were classified as confirmed and 29 (27%) as probable. 12 (41%) of the probable cases did not have a PCR result following a positive serology because a major commercial laboratory allows providers to order an antibody test without a reflex to PCR. Among 81 acute and chronic confirmed cases, 26 (32%) confirmed chronic cases had started treatment at the time the investigation was closed. Among cases that have not started treatment, 21 (36%) were uninsured or had Medicare/Medicaid insurance. Among 18 cases where the reason they had not started treatment could be determined from medical record review, 11 (61%) indicated it was not a current health priority of the patient, 3 (17%) were pregnant or breastfeeding, 2 (11%) end of life decision, and 2 (11%) were incarcerated without access. Case finding efforts identified four perinatal, hepatitis C and one NAS case, which were all previously unreported to public health.

Conclusions: Our efforts to locally investigate hepatitis C labs has allowed us to more accurately quantify the burden of disease in our community to use in disease control efforts. Importantly, we found incomplete lab ordering practices and gaps in linkage to treatment among vulnerable populations that we are working to address.

Impacts of Data Modernization on Rabies Exposure Reporting and Public Health Response, Fairfax County, 2023

Presenter: Kirsten Kohl Hampshire, MPH, Environmental Health Specialist, Fairfax County Health Department

Background: As the most populous Health District in Virginia, Fairfax County generally sees a high burden of rabid animals and potential rabies exposures. The Fairfax County Health Department (FCHD) works alongside Fairfax County Animal Protection Police (APP) to address this complex response and mitigate disease risk to county residents. A critical factor in the prevention and control of rabies is routine veterinary care and vaccination of domesticated pets. While potential rabies exposures are common in veterinary facilities, most exposure reports are received from medical providers in the Fairfax Health District (FHD). FCHD modernized and improved their electronic rabies exposure reporting systems and directed outreach to veterinary facilities to increase reporting and improve timeliness for public health response.

Methods: In 2019, FCHD launched an online animal bite and rabid animal reporting system via REDCap (Research Electronic Data Capture), which allowed for real-time reporting of animal bites and suspect rabies exposures with direct connection to FCHD and APP. In 2022, the reporting system was enhanced to meet a need for improved access for veterinary facilities to report bites and scratches to veterinary staff or facility guests, and exposures to domestic pets by high-risk vectors. A large outreach effort was made to provide county veterinary facilities with educational materials for staff and clients, and to reiterate the importance of reporting.

Results: In September 2022, FCHD sent educational packets to 116 veterinary facilities in the county with the goal of improving knowledge of rabies exposure reporting and procedures among veterinary staff and the public. From September 2022 to September 2023, an 116% reporting increase was seen compared to the previous year (253 to 117 reports). Of the 253 reports received, 159 were for staff members bitten by a veterinary patient and 62 were for pet owners or other guests bitten by a pet. In addition, veterinary facilities reported 32 domestic animal exposures to high-risk vectors virtually, something that previously could only be reported by call and response of an APP officer.

Conclusions: Considering the severity of rabies virus infections, public health has an essential responsibility to investigate possible exposures and make recommendations as quickly as possible. FCHD's data modernization project allows for real-time reporting of animal bite events and tailored responses based on priority and risk level. The relationship between veterinarians and public health improved because the reporting system was tailored specifically to meet the needs of veterinary facilities, which ultimately increases positive health impacts on the community. These essential data modernization concepts can be applied to many different disease investigations and increases the overall ability to provide timely and thorough public health recommendations.

Cryptosporidiosis Outbreak Associated with Baby Calves at a State Prison Farm

Presenter: Emilie Schweikert, MPH, CHES, District Epidemiologist, Chesterfield Health District

Background: Cryptosporidiosis is a disease that causes watery diarrhea in humans and animals caused by the microscopic parasite *Cryptosporidium.* In late March 2023, the Chesterfield Health District (CHD) identified a cluster of cases of cryptosporidiosis among offenders at a state prison who worked at the prison dairy and beef farms with baby calves.

Methods: In late March 2023, CHD received two reports of offenders at a state prison testing positive for *Cryptosporidium* species on EIA antigen tests. The District Epidemiologist interviewed a nurse at the clinic who reported both inmates work at the prison dairy farm. The clinic had not received any other recent reports of gastrointestinal illness among offenders. Virginia Department of Health (VDH) coordinated with Virginia Department of Corrections (DOC) to conduct a site visit on April 6th. VDH and DOC staff assessed offender living conditions, working conditions on the farm, and interviewed probable cases.

Results: Between January 13 and April 5, 2023, four laboratory positive cases of cryptosporidiosis were identified among offenders who worked on the farm located within the prison work center with the dairy and/or beef calves. Although intermittent cases of "scours disease" were reported among the calves, the herd seemed healthy overall and proper animal husbandry practices appeared to be in place. The site visit revealed the only available sinks on the farm for both hand washing and meal preparation were in the break house which was far from calf maternity pens. Water bottles had no designated storage area and were frequently left on the ground. Case interviews revealed that farm workers received limited training on safety protocols for interacting with cattle despite being in extended close contact with them. Cases did report showering immediately upon return to their living spaces, however they were not consistently provided the opportunity to change clothes before leaving the farm. Finally, offenders at this prison who report illness are often transferred to another state correctional facility, disincentivizing them to notify staff when they are ill.

Conclusions: Prison workers who interact with farm animals may be at an increased risk for zoonotic disease exposure and transmission. Thorough education and training of infectious diseases that could be acquired from farm animals and best practices for worker safety are needed to protect this population. A site visit and close coordination with farm and prison staff were critical steps in developing recommendations to prevent further spread of illness.

Highly Pathogenic Avian Influenza Response in Two Commercial Flocks in Rockingham County, Virginia, 2023

Presenter: Travis Oishi, MPH, District Epidemiologist, Central Shenandoah Health District

Background: Highly pathogenic avian influenza (HPAI) A(H5N1) is a virus primarily seen in birds, with rare instances of human infections. HPAI is highly contagious and often fatal in birds, and poultry with symptoms resembling HPAI are depopulated within 24 hours or less. HPAI has been an ongoing issue nationwide. In a May 2022 interim report by the Animal and Plant Health Inspection Service (APHIS), HPAI was detected in 174 backyard flocks and 220 commercial flocks, resulting in the loss of 38 million birds and an export loss of $800 million. In January 2023, Virginia encountered its first detection of HPAI in two commercial poultry flocks in Rockingham County, resulting in the loss of approximately 36,400 birds. This report describes the Central Shenandoah Health District's (CSHD) response to these events.

Methods: The CSHD worked with the Virginia Department of Agriculture and Consumer Services (VDACS) to receive notifications of persons potentially exposed to infective material during an HPAI response. Persons with potential exposure consisted of members of VDACS, the United States Department of Agriculture (USDA) staff, farm owners/workers, and bird disposal contractors. CSHD epidemiologists and public health nurses completed individual exposure assessments via phone on persons returning from the HPAI sites. After each exposure assessment, the person was instructed to self-monitor for flu-like symptoms for ten days from last exposure and to notify the local health department if they developed any symptoms. CSHD notified local healthcare providers of this HPAI response and developed processes for sending specimens to the Virginia state laboratory for influenza testing. CSHD developed a REDCap survey tool to record the individual exposure assessments, document contact attempts, and to maintain an accurate count of individuals currently under symptom monitoring.

Results: The HPAI response at the two sites in Rockingham County resulted in the active monitoring of 32 people. Of the 32, 16 were residents of CSHD, 15 were residents of other health districts, and one was an out of state resident. Of the 16 CSHD residents, eight were deployed to the two sites more than once due to their involvement with both depopulation and composting processes. Exposure assessments were completed with each deployment, resulting in 25 exposure assessments. All 16 individuals completed symptom monitoring for 10 days from last exposure. Two individuals developed influenza-like illness; specimens were collected and sent to the Virginia state laboratory for testing and both tested negative for influenza, including the influenza strain H5N1.

Conclusions: In January 2023, the CSHD responded to HPAI events at two poultry farms in Rockingham County. These two events resulted in the loss of approximately 36,300 birds and potential exposure to 32 workers. The CSHD completed exposure assessments and monitoring of their 16 residents. While two developed influenza-like illness, no one developed HPAI, or influenza H5N1. Using a centralized record keeping system in REDCap led to a more streamlined exposure assessment and symptom monitoring process. The CSHD REDCap tool has been adapted for statewide use.

Bite Me: Improving the Required Reporting of Rabies Post-Exposure Prophylaxis at a Local Emergency Department

Meagan Helmick, PhD, MPH, CHES, District Director, Mount Rogers Health District (Note: this abstract was selected for presentation but was unable to be presented at the VES)

Background: The Code of Virginia and the Board of Health Regulations for Disease Reporting and Control, requires all rabies treatment, post-exposure be reported to the local health department within three days of initiation of the treatment. However, this is often delayed or unreported in many health districts. In Roanoke City and Alleghany Health Districts these reports are typically faxed to the local health department (LHD) and are often incomplete and sometimes illegible. To help improve the required reporting and follow-up, the LHD created a REDCap reporting project.

Methods: Using REDCap, a project was developed that allowed local providers to report electronically to the LHD when they initiated post-exposure rabies treatment. The southwest regional deputy epidemiologist worked closely with the local nurse epidemiologist and environmental health staff to allow the project to streamline reporting and follow-up. The project consists of two data collection instruments: a public survey for the provider to use and a follow-up survey for the local health department to record information. This was piloted at a regional emergency department (ED), where the LHD was previously receiving very limited reports of rabies post exposure treatment. A job aid was provided for the reporters at the regional health system's main emergency room.

Results: In the two months prior to the initiation of this project no reports of post-exposure were reported to the local health department from the piloted ED. In the first two months of this project (June-July 2023) 33 reports were submitted to the local health department. Of those 33 reports, 3 were non-exposures (e.g., snake bites), 14 were bites for which PEP was initiated, and 16 were bites for which PEP was not initiated either because it was not indicated or because it was referred to the LHD for further investigation (e.g., bite by a known animal).

Conclusions: Having an electronic option for reporting post-exposure rabies treatment takes a substantial burden off the provider and the LHD. The provider can report by using their laptop or phone and the LHD can follow-up promptly in the same manner. Because LHD staff is emailed immediately when a new report is submitted, they can quickly follow-up with the necessary individuals. While the reporting is not perfect, it has greatly improved in the first two months of the project. Looking at new ways to reduce barriers for local providers to comply with reportable disease regulations, while also improving the data received when they report, has been an enormous benefit of this project that could be implemented in any local health department.

Notes

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Special thanks to Donald Moore for coordinating the 2023 Virginia Epidemiology Seminar.

Awards

The People's Choice Award

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. 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.