DISEASE PREVENTION AND EPIDEMIOLOGY NEWSLETTER

EpiNotes

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IN THIS ISSUE:

Historical Perspective: What's With Bats and Viruses?

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Bats are not "flying rats," but they are the only mammal that flies ("flying" squirrels glide). The physiological adaptations that enable flight may hold the key as to why bats play such a prominent role in emerging infectious diseases.

What do SARS, Nipah, Ebola, Marburg, Hendra, and SARS-CoV-2 viruses have in common? ***Bats.***

Turn back the clock to 1967: Severe and frightening hemorrhagic fever outbreaks occur simultaneously in multiple laboratories in Europe among persons exposed to African green monkeys imported from Uganda for research purposes. Seven people die from a virus that came to be named Marburg. Fast forward to 1980: Two tourists contract Marburg after visiting Kenya's Kitum Cave; one dies. Another tourist visiting the cave dies of Marburg in 1987.

Meanwhile, in 1976, a new virus named Ebola infects more than 300 people in the Congo River Basin, reportedly killing 88% of those infected, followed by periodic and deadly outbreaks in Central and West Africa. Jump to 1994 and another continent: Hendra hemorrhagic virus kills 13 horses and their trainer in Australia. On yet another continent in 1999: Newly identified Nipah virus causes 300 human cases and more than 100 deaths in Malaysia. The severe acute respiratory syndrome (SARS) virus emerges from China in 2003, and infects approximately 8,000 people worldwide, killing nearly 800. Phylogenetic studies go on to implicate bats as reservoir for all of these viruses. Though some controversy remains, most molecular biologists have concluded that the recent SARS-CoV-2 virus, too, originated in bats.

Why do these viruses re-combine in bats?
Bats gather as mixed species living communally in large colonies, travel over long distances, enjoy promiscuous sexual behavior, and are exposed to wild and domesticated animals during foraging trips,

all of which allow opportunity for infection and genetic reassortment. Bats are highly social, grooming one another and even regurgitating food to other adults.

But why don't the bats themselves get sick? Hypotheses abound. Perhaps bats evolved mechanisms to deal with the high oxidative stress induced by flying and then can cope with these stressors from infection. Maybe it is simply that higher body temperatures during flight suppress viral illness. One popular theory is that bats have a more powerful innate immune response to viruses. The revolution in molecular biology has brought new, surprising light to this question.

Genomic sequencing of multiple bat species that harbor these viruses has demonstrated that they have dramatically different natural killer cell receptors, MHC class I genes, and type I interferons from other mammals. Bats have a dampened STING (stimulator of interferon genes) response that prevents the hyperimmune inflammatory response seen with severe COVID-19 (the disease caused by the SARS-CoV-2 virus), so that bats can asymptomatically host viruses that are pathogenic in humans. STING can be overactivated by oxidative DNA damage. This mutation may have evolved to tolerate flight's high metabolic demands, but it secondarily allows immune tolerance.

Photo by Jane Kelly

Is this a public health issue? Yes. The vast majority of bats do not transmit disease to humans. However, as climate change causes animal migration to new habitats, as humans make deeper inroads into previously wild settings, as the bushmeat trade flourishes causing more ecological imbalance, and domesticated animals share bat territory, there is ever more opportunity for viruses to recombine and jump to humans. Understanding the molecular underpinnings of emerging infectious diseases is a first step. Public health action to minimize zoonotic spread, and better grasp of the mechanisms of disease vulnerability and resilience can help us move forward in combatting future pandemics to come.

Remember, bats are our friends. They are a keystone species important to insect control, seed dispersal, and plant fertilization. Sixty-seven plant families rely on bats as their major or exclusive pollinators including cacao -- you wouldn't want to go without chocolate, would you?

References

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https://www.cdc.gov/cdctv/diseaseandconditions/outbreaks/uganda-python-cave.html

Caring for our Afghan Allies

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The resettlement of our Afghan allies and their families in the United States, known as Operation Allies Welcome, has been a historic and unprecedented effort. Since August 2021, tens of thousands of Afghans have moved through eight military bases before finding more permanent homes in communities across the country. South Carolina has been welcoming hundreds of Afghan families as part of this effort. Awareness of immigration health screening processes and strong public health standards on these bases can help prepare healthcare providers in providing care for these patients.

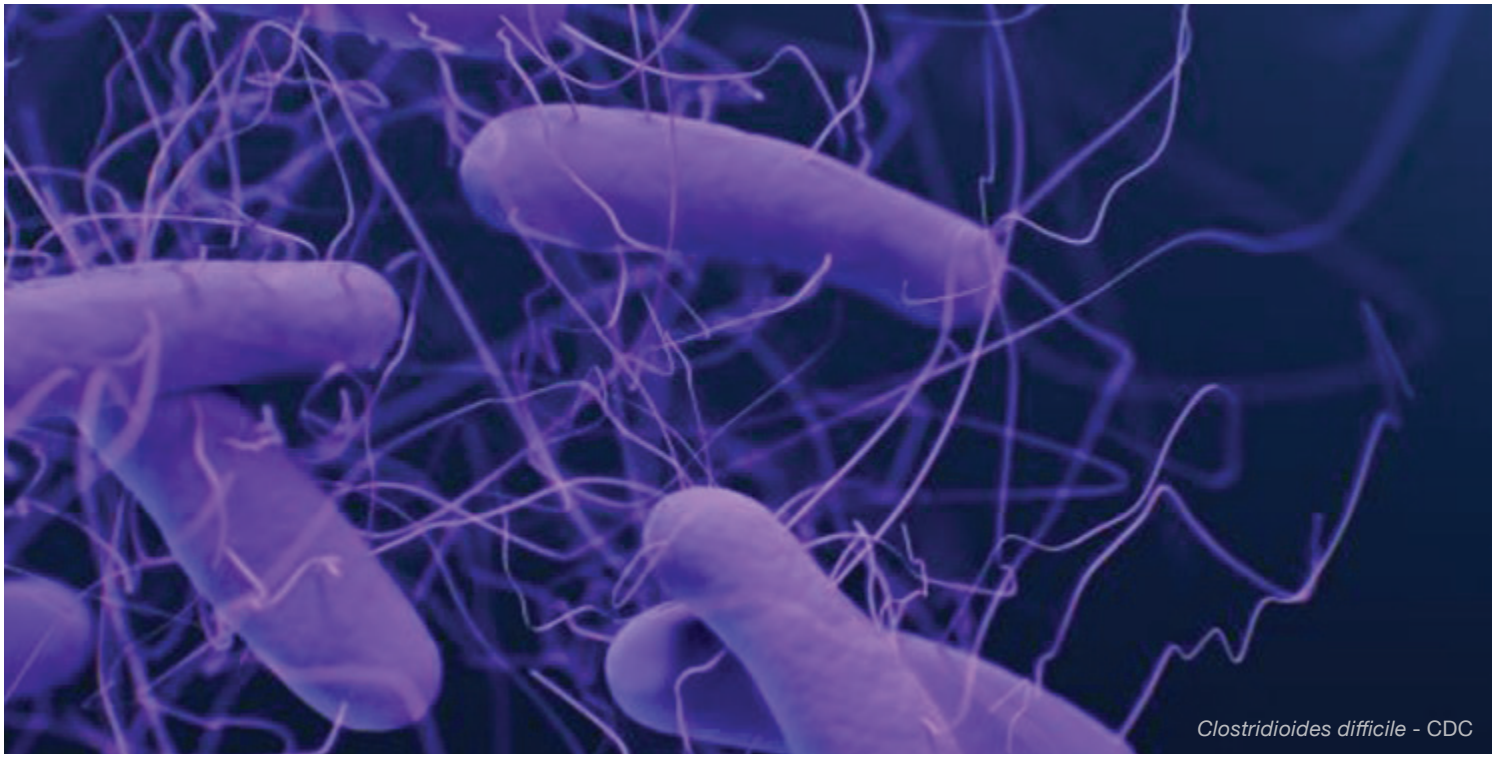
Public health teams comprised of federal staff and contractors have been working to support the mission of Operations Allies Welcome on the eight Safe Haven bases. Many of the basic needs have been taken care of at these locations, including housing, sanitation, medical screening, widespread vaccination, and public health education. Together with state and local health departments, these public health teams work to make life on a Safe Haven base healthier and safer for everyone while resettlement efforts are ongoing.

As part of this work, mass vaccination campaigns have been implemented for adults and children to provide broad coverage against vaccine-preventable diseases. Some cases of measles among Afghans early in the operation period (see CDC HAN) prompted initial concern about spread into the surrounding community. The risk of disease spread was averted with strong vaccine uptake, rigorous quarantine and isolation, and rapid access to health care. As a result, no additional measles cases have been identified on or off the Safe Haven bases since September 2021. These public health victories demonstrate the powerful tools we have available to protect the public health and how quickly outbreaks can end when we implement evidence-based public health interventions.

Another public health success is the tuberculosis (TB) screening and treatment program. All refugees and immigrants, including those coming from Afghanistan, are screened for TB as part of the immigration process. Refugees and immigrants with active TB receive treatment in partnership with state health departments. Together with the CDC, state health departments are working to transfer individual cases between states during the resettlement process so that treatment is not interrupted. Individuals with latent TB have been identified during the medical screening process and notified to start treatment after resettlement. There is ongoing monitoring on the Safe Haven bases of individuals with latent TB in case of reactivation.

As Afghans resettle in our communities, countering stigma is an important issue public health and clinical practitioners can address to continue this public health work. Because of measles, leishmaniasis, TB, and other diseases, there may be perceptions that our Afghan allies will spread disease in local communities. Perceptions of differences in cultural hygiene practices and socioeconomic status exacerbate the stigma. In reality, the Afghans being resettled have excellent uptake of vaccines and likely have less risk of spreading vaccine-preventable diseases than the communities they are entering. For example, as of November 2021, nearly all adult and teenaged Afghans on the Safe Haven bases are fully vaccinated against COVID-19. On some bases, weeks have passed without a single COVID-19 case identified among the thousands of Afghan guests.

The resettlement and integration process for Afghans is complex, and they will face challenges in the process. Having to fight the stigma of carrying diseases should not be one. However, by understanding the vaccination and medical screening processes and by providing appropriate health care as necessary, public health and clinical practitioners can be leaders in the efforts to integrate our Afghan allies into local communities.



Clostridioides difficile - CDC

Rise in Healthcare Associated Infections Experienced During the COVID-19 Pandemic

Healthcare Associated Infections Section*
Division of Acute Disease Epidemiology

In 2016, the U.S. Department of Health and Human Services (HHS) released The National Action Plan to Prevent Health Care-Associated Infection Road Map to Elimination (HAI Action Plan), which specified targets of HAI reduction from 2015 to 2020 for Acute Care Hospitals (ACHs).

These targets, or goals, addressed reductions in central line-associated bloodstream infections (CLABSI) and catheter-associated urinary tracts infections (CAUTI) in intensive care units and ward-located patients, intensive healthcare associated methicillin-resistant *Staphylococcus aureus* (MRSA) infections, hospital-onset (HO) *Clostridioides difficile* infections (CDIs), and surgical site infections (SSIs), including 39 inpatient surgical procedure categories reported to the National Healthcare Safety Network (NHSN). These reductions were broken down by progress per year with 2020 being the final targe t from the 2015 baseline, with a final target of 50% reduction of CLABSIs, 25% reduction of CAUTIs, 50% reduction in Invasive MRSA and HO MRSA, 30% reduction in HO CDIs and Clostridioides difficile-related hospitalizations, and a 30% reduction in SSIs. To track the progress of these HAI reductions, the Centers for Disease Control and Prevention (CDC) publishes the HAI Progress Report using data reported into NHSN. The HAI Progress Report uses infection-specific standardized infection ratios (SIRs) to track the progress of the above-mentioned infections from the 2015 baseline. The SIRs show if a facility had more observed infections than expected (SIR >1) or less observed infections than predicted (SIR<1). The report also includes the standardized utilization ratios (SURs) to measure device usage by comparing the observed device usage versus the predicted device usage.

Prior to the 2020 COVID-19 pandemic, great progress was made to reduce the targeted infections nationwide from the 2015 baseline; however, due to unforeseen challenges, many infection rates increased dramatically during the first year of the pandemic. Disruption of services and changes in care delivery, such as higher than usual hospitalization rates of critical patients, staffing shortages, supply shortages, and other challenges of the COVID-19 pandemic, may have resulted in decreased surveillance activities and NHSN reporting frequency, and increased incidence of HAIs.

To relieve facilities of some burden in reporting requirements, CMS implemented the extraordinary circumstance exception (ECE) Policy, allowing facilities to not report into NHSN for data from 10/1/2019-6/20/2022; however, DHEC required facilities to retroactively enter this data into NHSN due to HIDA Reporting Requirements.

CDC's analysis of data for 2020 compared to 2019 for these targeted infections showed significant increases in CLABSI, CAUTI, VAE and MRSA bacteremia. The overall increases from 2019 Quarter 4 to 2020 Quarter 4 were as follows: 47% in CLABSIs over all locations, 19% in CAUTIs over all locations, 45% increase in VAEs over all locations. *C. difficile* infections were observed to decrease in all quarters of 2020. When comparing 2019 to 2020 data, South Carolina (SC) Acute Care Hospitals (ACHs) had no significant changes in CLABSIs, CAUTIs, MRSA Bacteremia, and SSIs; however, there was a significant increase in VAEs. Long Term Acute Care Hospitals (LTACHs) in SC experienced a significant increase in CLASBIs, MRSA Bacteremia, and VAE during this time. CAUTIs in LTACHs had no significant change. SC Inpatient Rehabilitation Facilities (IRFs) experienced no significant changes in CLABSIs, CAUTIs, or MRSA Bacteremia during this period.

Overall, facilities in the state, like the nation, had significant decreases in CDIs from 2019 to 2020. Due to the challenges posed by the COVID-19 pandemic, SC did not meet the HHS targets in ACHs for CLABSIs, CAUTIs, SSIs (including colon surgery and abdominal hysterectomy) or MRSA Bacteremia; however, ACHs did meet the target for *C. difficile* infections. For specific data and other information, refer to CDC's Antibiotic Resistance & Patient Safety Portal for South Carolina.

***HAI section staff members:**
Alison Jamison-Haggwood, Patricia Kopp, Rebecca Walker, Natasha Sanders, Hannah Ruegner, Terri Hannibal, Max Habicht, Jennifer Donehue, and Jewel Coleman

New Delhi Metallo-beta-lactamase (NDM) Outbreak in a SC Acute Care Hospital

Healthcare Associated Infections Section*
Division of Acute Disease Epidemiology

Beta (β)-lactam antibiotics have been some of the earliest and broadest antibiotics used to treat bacterial infections. However, with the evolution of bacteria producing resistance mechanisms, the effectiveness of these antibiotics has become threatened.

Per the CDC's Antibiotic Resistance Threats in the United States 2019 Report, beta (β)-lactam antibiotic effectiveness is dwindling due to *Enterobacteriaceae* production of extended-spectrum beta-lactamase (ESBL) enzymes, which break down most beta-lactam antibiotics, specifically penicillins and cephalosporins. Carbapenem antibiotics, a beta-lactam, were some of the last remaining treatment options for ESBL-producing bacteria. However, in the late 2000s, the *Enterobacteriaceae* bacteria family, specifically *Klebsiella pneumoniae (K. pneumoniae)* and *Escherichia coli (E. coli),* were found to produce carbapenemase enzymes, henceforth being named carbapenem-resistant *Enterobacterales* (CRE). These CREs can produce many different carbapenemases; the five most common are K. pneumoniae carbapenemase (KPC), Oxacillinase-48 (OXA-48), New Delhi Metallo-beta-lactamase (NDM), Verona integron-encoded metallo-beta-lactamase (VIM), and Imipenemase (IMP).

The CDC classifies CRE as an urgent threat that requires urgent and aggressive action. The evolution of CRE is significant due to the increased resistance to antibiotics and the bacteria's ability to carry mobile genetic elements that can be shared between bacteria. Those at greatest risk of developing a CRE infection include those who require indwelling devices and those who take long course of some antibiotics.

As per the SC List of Reportable Conditions, isolates with identified carbapenem resistance or carbapenemase production are to be submitted to DHEC's public health laboratory (PHL) for confirmatory testing. In September 2021, PHL notified the HAI section of isolates testing positive for *Klebsiella pneumoniae* NDM. The pathogen was isolated from respiratory culture specimens taken from three patients in the same medical intensive care unit at a SC acute care hospital. The HAI Section notified and worked collaboratively with the hospital's infection preventionist (IP) to mitigate and prevent further spread in the unit and the rest of the facility.

Two rounds of colonization screenings were performed on remaining bedded patients on the unit, all resulting as negative for carbapenemase production. In addition to immediate measures implemented by the hospital's IP, the HAI section conducted an onsite assessment of the facility's infection control practices, using a modified infection control assessment and response (ICAR) tool, in collaboration with the IP on the affected unit. The ICAR revealed the following infection prevention and control gaps and weaknesses: staff not changing gloves between patient care, staff not wearing appropriate PPE for contact precautions, lack of disinfection of mobile equipment and point-of-care (POC) testing devices between use, difficulty ensuring staff are properly educated on the use of cleaning and disinfectant products due to unavailability of products leading to frequent product changes. Recommendations to mitigate gaps were provided to the hospital IP. A follow-up onsite visit is scheduled to ensure all gaps have been mitigated.

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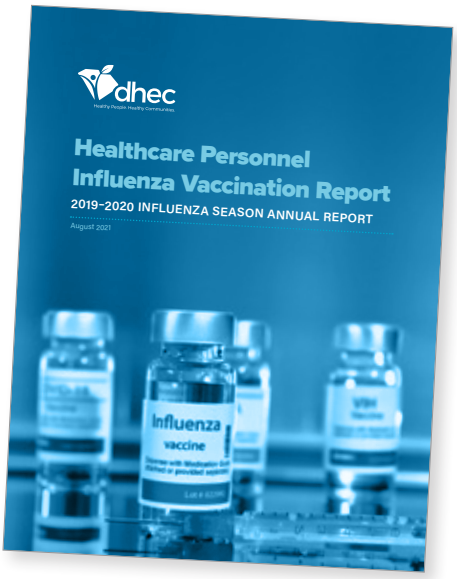
2019-2020 Healthcare Personnel Influenza Vaccination Report Published

Healthcare Associated Infections Section*
Division of Acute Disease Epidemiology

As of August 2021, the HAI Section of DHEC's Division of Acute Disease Epidemiology completed and published its annual review of influenza vaccination among healthcare personnel (HCP) working in SC hospitals during the 2019-2020 influenza season. The 2019-2020 Healthcare Personnel Influenza Vaccination Report was compiled in accordance with the SC Hospital Infections Disclosure Act (HIDA) as per the S.C. Code Section 44-7-2430 and S.C. Code Section 44-7-2440. The report compares influenza vaccination rates by HCP and facility type (i.e., acute care hospital, critical access hospitals, long-term acute care hospitals, and inpatient rehabilitation facilities), SC vaccination rates to national trends, and vaccination rates over the past eight influenza seasons. The report provides some general conclusions as well as data limitations and serves as a valuable tool for healthcare facilities to improve influenza vaccination rates amongst their HCP, thereby promoting a safer environment for all.



Please contact the Healthcare Association Infections Section at hai_section@dhec.sc.gov with any questions.

*HAI section staff members:
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Updates for the 2022 S.C. List of Reportable Conditions (LORC)

Marya Barker
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Division of Acute Disease Epidemiology

Changes in the List of Reportable Conditions Section:

- The Urgently reportable category explanation was changed to read:

  * Urgently reportable within 24 hours by electronic notification (email SCIONHelp@dhec.sc.gov for details. The SCIONHelp email address may not be used for case reporting.) or by phone if electronic notification not possible.

- Carbapenem-resistant *Enterobacteriaceae* (CRE) was changed to Carbapenem-resistant *Enterobacterales* and *Acinetobacter baumanii* was changed to *Acinetobacter* species and the footnotes were updated.
- The additional designation of SARS-CoV-2 was added to Coronavirus Disease 2019 (COVID-19) and the footnote was updated.
- All HIV CD4 count laboratory test results are now reportable (positive and negative).
- All HIV viral load laboratory test results are now reportable (positive and negative).
- HIV 1/2 antibody and antigen results have been further specified as reportable in the following manner:
  - HIV 1/2 AB/AG results (rapid)
  - HIV 1/2 AB/AG results (confirmatory, all positive and negative) (L)
  - HIV 1/2 AB/AG + and/or detectable viral load with each pregnancy
- Rabies Post-exposure prophylaxis administration is no longer reportable. Animal (mammal) bites remain reportable to the Animal Control personnel. Footnote 6 that provided details for rabies post-exposure prophylaxis guidance was removed.
- *Staphylococcus aureus*, vancomycin-resistant or intermediate now requires a VA >8 MIC.
- Syphilis: congenital, primary, or secondary (lesion or rash) or Darkfield positive has footnote 17 added to it.
- Syphilis: early latent, latent, tertiary, or positive serological test has footnote 18 added to it.

Changes in the Footnotes Section:

Please review all footnotes for changes. Due to the removal of footnote 6 (rabies PEP), all subsequent footnotes were renumbered. The following footnotes were edited to provide additional details or to reflect changes in the reportable conditions. Footnotes 17 and 18 are completely new this year.

- Footnote 8: Carbapenem-resistant *Enterobacterales* and *Acinetobacter* species from all specimen types.
- Footnote 10: Submit isolate from patients of any age, ALL CSF isolates, and invasive sterile body sites that are non-susceptible to any relevant antibiotics according to CLSI.
- Footnote 11: Submit isolates to the PHL from ALL non-mucoid *P. aeruginosa* isolates resistant to imipenem, meropenem, or doripenem and non-susceptible to cefepime or ceftazidime.
- Footnote 12: All blood lead results are reportable within 30 days. Any elevated results (3.5 mcg/dL or greater) are reportable within 7 days.
- Footnote 14: Submit all isolates identified as *C. auris* and any yeast isolates that may be misidentified using a yeast identification method that is not able to accurately detect *C. auris* (refer to cdc.gov/fungal/candida-auris/identification.html).
- Footnote 16: COVID-19 cases, deaths, and multisystem inflammatory syndrome in children are urgently reportable within 24 hours. All COVID-19 tests and test results (positives, genetic lineage, negatives, indeterminate) are required to be reported. Detailed information about reporting COVID-19 results: scdhec.gov/sites/default/files/Library/CR-012859.pdf.
- Footnote 17: Report the results of all congenital syphilis follow-up tests (positive or negative).
- Footnote 18: Report all test results (treponemal & nontreponemal) if at least one serological test is positive

Changes in the What to Report Section

Treatment was added to this section to reflect the DHEC 1129 Disease Report Card.

Changes in the How to Report Section

The methods of reporting for **HIV, AIDS, and STDs (excluding Hepatitis)** and **Lead** were edited to reflect the order in which each program prefers that reports be made.

Changes in the How to Report Tuberculosis Section

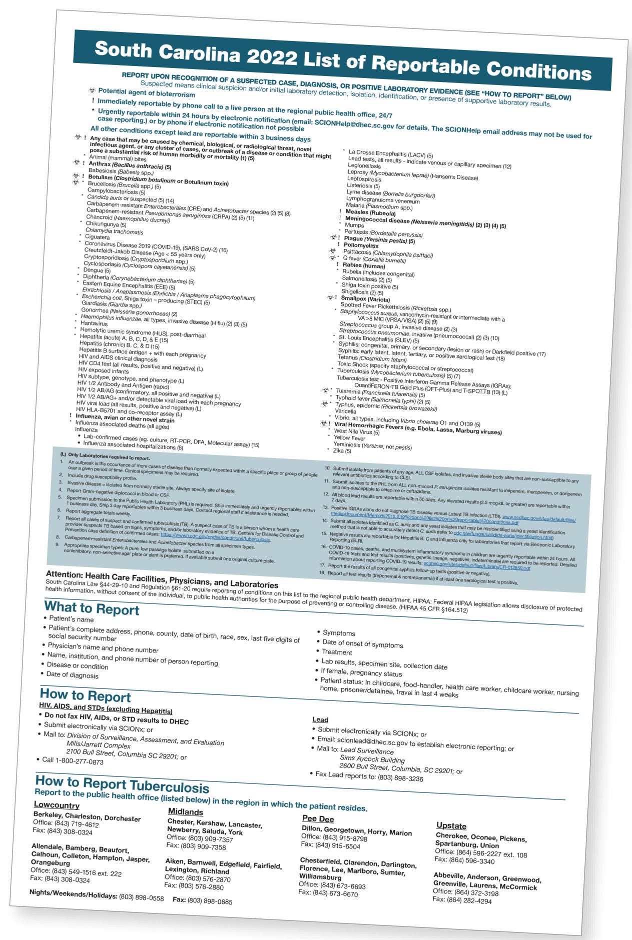
The fax number for Lowcountry's TB program was changed so that both areas use (843) 308-0324.

Saluda county was moved to the first Midlands TB area.

Changes in the How to Report Other Conditions Section

Reporting instructions in this section were expanded to incorporate more details for each reporting timeframe. Instructions now read:

Report Immediate conditions by phone and Urgent conditions within 24 hours by electronic notification* by phone if electronic notification not possible. Report all other conditions electronically* or by mail within 3 days to the appropriate public health office in the region in which the patient resides. *Email SCIONhelp@dhec.sc.gov for details. The SCIONHelp email address may not be used for case reporting.



South Carolina 2022 List of Reportable Conditions

REPORT UPON RECOGNITION OF A SUSPECTED CASE, DIAGNOSIS, OR POSITIVE LABORATORY EVIDENCE (SEE "HOW TO REPORT" BELOW)
Suspected means clinical suspicion and/or initial laboratory detection, isolation, identification, or presence of supportive laboratory results.

☣ **Potential agent of bioterrorism**
! **Immediately reportable by phone call to a live person at the regional public health office, 24/7**
* **Urgently reportable within 24 hours by electronic notification (email: SCIONHelp@dhec.sc.gov for details. The SCIONHelp email address may not be used for case reporting.) or by phone if electronic notification not possible**
All other conditions except lead are reportable within 3 business days

☣ ! **Any case that may be caused by chemical, biological, or radiological threat, novel infectious agent, or any cluster of cases, or outbreak of a disease or condition that might pose a substantial risk of human morbidity or mortality (1) (5)**
* Animal (mammal) bites
☣ ! **Anthrax *(Bacillus anthracis)* (5)**
Babesiosis *(Babesia* spp.)
☣ ! **Botulism (*Clostridium botulinum* or Botulinum toxin)**
☣ * Brucellosis *(Brucella* spp.) (5)
Campylobacteriosis (5)
* *Candida auris* or suspected (5) (14)
Carbapenem-resistant *Enterobacterales* (CRE) and *Acinetobacter* species (2) (5) (8)
Carbapenem-resistant *Pseudomonas aeruginosa* (CRPA) (2) (5) (11)
Chancroid *(Haemophilus ducreyi)*
* Chikungunya (5)
Chlamydia trachomatis
* Ciguatera
* Coronavirus Disease 2019 (COVID-19), (SARS CoV-2) (16)
Creutzfeldt-Jakob Disease (Age < 55 years only)
Cryptosporidiosis *(Cryptosporidium* spp.)
Cyclosporiasis *(Cyclospora cayetanensis)* (5)
* Dengue (5)
* Diphtheria *(Corynebacterium diphtheriae)* (5)
* Eastern Equine Encephalitis (EEE) (5)
Ehrlichiosis / Anaplasmosis (Ehrlichia / Anaplasma phagocytophilum)
* *Escherichia coli*, Shiga toxin – producing (STEC) (5)
Giardiasis *(Giardia* spp.)
Gonorrhea *(Neisseria gonorrhoeae)* (2)
* *Haemophilus influenzae*, all types, invasive disease (H flu) (2) (3) (5)
* Hantavirus
* Hemolytic uremic syndrome (HUS), post-diarrheal
* Hepatitis (acute) A, B, C, D, & E (15)
Hepatitis (chronic) B, C, & D (15)
Hepatitis B surface antigen + with each pregnancy
HIV and AIDS clinical diagnosis
HIV CD4 test (all results, positive and negative) (L)
HIV exposed infants
HIV subtype, genotype, and phenotype (L)
HIV 1/2 Antibody and Antigen (rapid)
HIV 1/2 AB/AG (confirmatory, all positive and negative) (L)
HIV 1/2 AB/AG+ and/or detectable viral load with each pregnancy
HIV viral load (all results, positive and negative) (L)
HIV HLA-B5701 and co-receptor assay (L)
! **Influenza, avian or other novel strain**
* Influenza associated deaths (all ages)
Influenza
- Lab-confirmed cases (eg. culture, RT-PCR, DFA, Molecular assay) (15)
- Influenza associated hospitalizations (6)

* La Crosse Encephalitis (LACV) (5)
Lead tests, all results - indicate venous or capillary specimen (12)
Legionellosis
Leprosy *(Mycobacterium leprae)* (Hansen's Disease)
Leptospirosis
Listeriosis (5)
Lyme disease *(Borrelia burgdorferi)*
Lymphogranuloma venereum
Malaria *(Plasmodium* spp.)
! **Measles (Rubeola)**
! **Meningococcal disease *(Neisseria meningitidis)* (2) (3) (4) (5)**
* Mumps
* Pertussis *(Bordetella pertussis)*
☣ ! **Plague *(Yersinia pestis)* (5)**
! **Poliomyelitis**
☣ Psittacosis *(Chlamydophila psittaci)*
☣ * Q fever *(Coxiella burnetii)*
! **Rabies (human)**
* Rubella (includes congenital)
Salmonellosis (2) (5)
* Shiga toxin positive (5)
Shigellosis (2) (5)
☣ ! **Smallpox (Variola)**
Spotted Fever Rickettsiosis *(Rickettsia* spp.)
* *Staphylococcus aureus*, vancomycin-resistant or intermediate with a VA >8 MIC (VRSA/VISA) (2) (5) (9)
Streptococcus group A, invasive disease (2) (3)
Streptococcus pneumoniae, invasive (pneumococcal) (2) (3) (10)
* St. Louis Encephalitis (SLEV) (5)
* Syphilis: congenital, primary, or secondary (lesion or rash) or Darkfield positive (17)
Syphilis: early latent, latent, tertiary, or positive serological test (18)
Tetanus *(Clostridium tetani)*
Toxic Shock (specify staphylococcal or streptococcal)
* Tuberculosis *(Mycobacterium tuberculosis)* (5) (7)
Tuberculosis test - Positive Interferon Gamma Release Assays (IGRAs): QuantiFERON-TB Gold Plus (QFT-Plus) and T-SPOT.TB (13) (L)
☣ * Tularemia *(Francisella tularensis)* (5)
* Typhoid fever *(Salmonella typhi)* (2) (5)
☣ * Typhus, epidemic *(Rickettsia prowazekii)*
Varicella
* Vibrio, all types, including *Vibrio cholerae* O1 and O139 (5)
☣ ! **Viral Hemorrhagic Fevers (e.g. Ebola, Lassa, Marburg viruses)**
* West Nile Virus (5)
* Yellow Fever
Yersiniosis (*Yersinia*, not *pestis*)
* Zika (5)

(L) Only Laboratories required to report.
1. An outbreak is the occurrence of more cases of disease than normally expected within a specific place or group of people over a given period of time. Clinical specimens may be required.
2. Include drug susceptibility profile.
3. Invasive disease = isolated from normally sterile site. Always specify site of isolate.
4. Report Gram-negative diplococci in blood or CSF.
5. Specimen submission to the Public Health Laboratory (PHL) is required. Ship immediately and urgently reportables within 1 business day. Ship 3 day reportables within 3 business days. Contact regional staff if assistance is needed.
6. Report aggregate totals weekly.
7. Report all cases of suspect and confirmed tuberculosis (TB). A suspect case of TB is a person whom a health care provider suspects TB based on signs, symptoms, and/or laboratory evidence of TB. Centers for Disease Control and Prevention case definition of confirmed cases: https://wwwn.cdc.gov/nndss/conditions/tuberculosis.
8. Carbapenem-resistant *Enterobacterales* and *Acinetobacter* species from all specimen types.
9. Appropriate specimen types: A pure, low passage isolate submitted on a noninhibitory, non-selective agar plate or slant is preferred. If available submit one original culture plate.
10. Submit isolate from patients of any age, ALL CSF isolates, and invasive sterile body sites that are non-susceptible to any relevant antibiotics according to CLSI.
11. Submit isolates to the PHL from ALL non-mucoid *P. aeruginosa* isolates resistant to imipenem, meropenem, or doripenem and non-susceptible to cefepime or ceftazidime.
12. All blood lead results are reportable within 30 days. Any elevated results (3.5 mcg/dL or greater) are reportable within 7 days.
13. Positive IGRAs alone do not diagnose TB disease versus Latent TB Infection (LTBI). www.scdhec.gov/sites/default/files/media/document/Memo%2010.2.19%20on%20list%20of%20reportable%20conditions.pdf
14. Submit all isolates identified as *C. auris* and any yeast isolates that may be misidentified using a yeast identification method that is not able to accurately detect *C. auris* (refer to cdc.gov/fungal/candida-auris/identification.html)
15. Negative results are reportable for Hepatitis B, C and Influenza only for laboratories that report via Electronic Laboratory Reporting (ELR).
16. COVID-19 cases, deaths, and multisystem inflammatory syndrome in children are urgently reportable within 24 hours. All COVID-19 tests and test results (positives, genetic lineage, negatives, indeterminate) are required to be reported. Detailed information about reporting COVID-19 results: scdhec.gov/sites/default/files/Library/CR-012859.pdf
17. Report the results of all congenital syphilis follow-up tests (positive or negative).
18. Report all test results (treponemal & nontreponemal) if at least one serological test is positive.

Attention: Health Care Facilities, Physicians, and Laboratories
South Carolina Law §44-29-10 and Regulation §61-20 require reporting of conditions on this list to the regional public health department. HIPAA: Federal HIPAA legislation allows disclosure of protected health information, without consent of the individual, to public health authorities for the purpose of preventing or controlling disease. (HIPAA 45 CFR §164.512)

What to Report
- Patient's name
- Patient's complete address, phone, county, date of birth, race, sex, last five digits of social security number
- Physician's name and phone number
- Name, institution, and phone number of person reporting
- Disease or condition
- Date of diagnosis
- Symptoms
- Date of onset of symptoms
- Treatment
- Lab results, specimen site, collection date
- If female, pregnancy status
- Patient status: In childcare, food-handler, health care worker, childcare worker, nursing home, prisoner/detainee, travel in last 4 weeks

How to Report
HIV, AIDS, and STDs (excluding Hepatitis)
- **Do not fax HIV, AIDs, or STD results to DHEC**
- Submit electronically via SCIONx; or
- Mail to: *Division of Surveillance, Assessment, and Evaluation*
  Mills/Jarrett Complex
  2100 Bull Street, Columbia SC 29201; or
- Call 1-800-277-0873

Lead
- Submit electronically via SCIONx; or
- Email: scionlead@dhec.sc.gov to establish electronic reporting; or
- Mail to: *Lead Surveillance*
  Sims Aycock Building
  2600 Bull Street, Columbia, SC 29201; or
- Fax Lead reports to: (803) 898-3236

How to Report Tuberculosis
Report to the public health office (listed below) in the region in which the patient resides.

Lowcountry
Berkeley, Charleston, Dorchester
Office: (843) 719-4612
Fax: (843) 308-0324

Allendale, Bamberg, Beaufort, Calhoun, Colleton, Hampton, Jasper, Orangeburg
Office: (843) 549-1516 ext. 222
Fax: (843) 308-0324

Midlands
Chester, Kershaw, Lancaster, Newberry, Saluda, York
Office: (803) 909-7357
Fax: (803) 909-7358

Aiken, Barnwell, Edgefield, Fairfield, Lexington, Richland
Office: (803) 576-2870
Fax: (803) 576-2880

Pee Dee
Dillon, Georgetown, Horry, Marion
Office: (843) 915-8798
Fax: (843) 915-6504

Chesterfield, Clarendon, Darlington, Florence, Lee, Marlboro, Sumter, Williamsburg
Office: (843) 673-6693
Fax: (843) 673-6670

Upstate
Cherokee, Oconee, Pickens, Spartanburg, Union
Office: (864) 596-2227 ext. 108
Fax: (864) 596-3340

Abbeville, Anderson, Greenwood, Greenville, Laurens, McCormick
Office: (864) 372-3198
Fax: (864) 282-4294

Nights/Weekends/Holidays: (803) 898-0558 **Fax:** (803) 898-0685

Elizabethkingia miricola Outbreak in a SC Acute Care Hospital

Healthcare Associated Infections Section*
Division of Acute Disease Epidemiology

Microorganisms in the genus *Elizabethkingia* are common in natural environments, such as water and soil, and also can be found in the tap water of hospitals. However, they rarely cause infections. In the last decade, several new species have been discovered and in 2003, a novel species, Chryseobacterium miricola, was identified from water condensation collected in 1997 on the Russian Mir space station. It was assigned to the genus *Elizabethkingia*, along with *Elizabethkingia meningoseptica*, and was renamed *Elizabethkingia miricola (E. miricola)*.

Elizabethkingia species are considered to be multi-drug resistant, and in recent years, this genus has emerged as a cause of life-threatening infections in humans, particularly in immunocompromised patients. Since its discovery, *E. miricola* has been sporadically reported to cause pneumonia, bacteremia, urinary tract infection, and periodontitis. The first described strain of *E. miricola* was isolated from severely immunocompromised patients and was thought to cause nosocomial pneumonia. Most recently, *E. miricola* has become a significant opportunistic pathogen in patients with cystic fibrosis in the United Kingdom.

In October 2021, the HAI section was notified by an Acute Care Hospital's Infection Preventionist (IP) that *E. miricola* was isolated in the sputum and endotracheal aspirate of two patients in an intensive care unit (ICU). In response, the HAI section and hospital representatives conducted a conference call with the Centers for Disease Control and Prevention (CDC). The facility's mitigation measures were in-line with the CDC's recommendations. The IPs conducted a thorough environmental assessment, which included cultures of the oxygen intake, water from a sink outside of a patient's room, the sink handles/drains in the patient rooms, and an aerator found on a sink faucet outside of a patient's room. The aerator was also removed. Surveillance cultures were collected on the patients that were in the rooms adjacent to the two index cases as well as on any patients admitted while the two index patients remained in the ICU.

Sputum cultures were collected from patients who could produce them, as well as rectal cultures. Environmental cultures conducted by the facility found two non-adjacent sinks that grew Chryseobacterium; while another sink grew a gram-negative rod that was not able to be identified.

An onsite assessment was conducted by the HAI section to assist the facility with identifying potential water sources and auditing infection control practices (ICP). The assessment revealed that IP staff were proactively taking actions to ensure there was no risk of patient-to-patient transmission. A process was in place for cleaning all equipment, including cleaning equipment responsibilities. One ICP gap was noted during the visit, in which two staff members were observed donning gloves without first performing hand hygiene.

The IPs met with leadership, ICU staff, and environmental cleaning staff, resulting in the implementation of additional mitigation measures, including the use of pre-moistened/waterless chlorhexidine, single-use pack wipes for patient bathing, medical grade water for nebulizer rinses, bottled drinking water, and a contracted water system treatment in collaboration with Plant Operations. A follow-up call with the CDC, facility representatives, and the HAI section determined that additional water sampling and whole genome sequencing by the CDC would not be warranted. The facility continues to monitor through its normal surveillance program, finding no additional cases to date.

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Historical Perspective: Plague and COVID-19

Jane Kelly, MD
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Division of Acute Disease Epidemiology

As historian Barbara Tuchman noted in her book A Distant Mirror: The Calamitous 14th Century, the Plague that killed one-third of Europe rent the fabric of society. Serfs were in short supply for harvesting crops that might otherwise rot in the fields. Previously, many were "paid" for their work only by being allowed to glean leftovers after the harvest. Laborers could now demand wages. Peasant uprisings demanded attention to class struggles. Incredibly, something good emerged from something devastating. Pandemics have a way of upsetting the norm.

COVID-19 is no different.

Now, more than two years into COVID, there are workforce shortages. As in post-plague Medieval times, post-COVID modern workers now have the leverage to demand better pay and working conditions. Problems that went long ignored, such as the need for affordable workplace childcare and employer policies allowing sick leave for family care, were suddenly front and center. Teleworking gave employees a taste of increased flexibility. A demand to return to work in person caused some to re-think how much they love their jobs. Early retirement, especially among workers in health care settings, followed the wave of dangerous COVID exposure working conditions.

As employers compete for employees, good things may come. More reasonable pay, better health insurance packages, childcare options, work time/place flexibility, less rigid criteria for hire, acceptance of greater diversity of skill sets, and safer work environments. One scary thing, though: preparing for the impact of long COVID.

The exact criteria for long-COVID, or post-acute syndrome of COVID-19 (PASC), are not yet clearly defined. To the extent that long-COVID limits one's ability to do some activities, the Americans with Disabilities Act (ADA) considers long-COVID a disability. There may be literally millions of workers affected by long-COVID. How will this play out in the workforce? Requests for shorter more flexible hours, workplace accommodations, changes in healthcare coverage? Perhaps increased awareness of structural barriers and a more inclusive atmosphere for people with disabilities?

The Plague changed Medieval societal structures. COVID has changed Modern ones. Let's use this opportunity to examine injustices, revise policies and address inequities. Can we make something good emerge from something devastating?

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