2021 TEXAS HEALTHCARE ASSOCIATED INFECTIONS (HAI) OUTBREAK REPORT

TEXAS
Health and Human Services

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Abstract

The Texas Department of State Health Services (DSHS) Healthcare Safety (HCS) Investigations Group identifies, responds to, and tracks healthcare associated infection (HAI) outbreaks. Descriptive analyses were conducted on the 2021 HAI outbreak responses and the results were compared with the responses from 2017. A total of 1,331 HAI outbreaks were reported in 2021, with 92% of these outbreaks occurring in long-term care facilities and caused by COVID-19. The other most common organisms involved in 2021 HAI outbreaks were *Acinetobacter, Candida* and *Enterobacterales* species. In 2021, there was a twelvefold increase of HAI outbreaks compared to 2017, primarily due to the COVID-19 pandemic. There were 261 cases of *Candida auris* reported in 2021; 226 of the cases were part of a regional outbreak investigation.
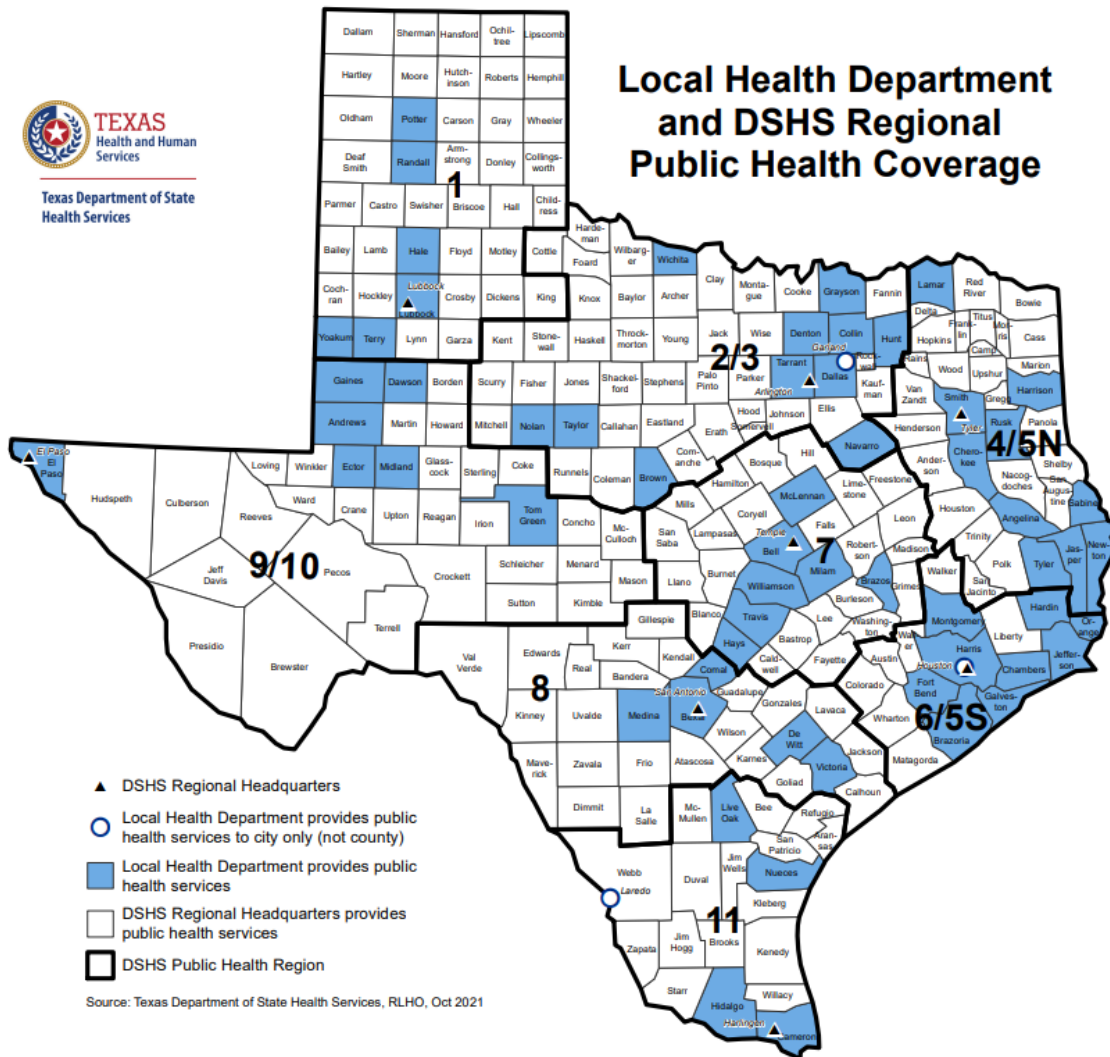
Introduction

The Healthcare Safety Unit (HCSU) within the Texas Department of State Health Services (DSHS) promotes safe and quality healthcare through awareness, education, transparency, monitoring, and response. The HCSU consists of the HCS Investigations Group, the HCS Data Reporting and Training Group, and the Antibiotic Resistance (AR)/Antibiotic Stewardship (AS) Group.

Healthcare Associated Infections (HAI) Epidemiologists, from the HCS Investigations Group, serve as healthcare infection prevention and control experts for public health departments, healthcare facilities, and other stakeholders. The HAI Epidemiologists are assigned to the different DSHS Public Health Regions (PHRs) (Figure 1) to serve as "boots on the ground" to help prevent and contain HAI outbreaks in Texas healthcare facilities. They are the primary investigators for outbreaks that occur in healthcare facilities in counties that do not have a local health department (LHD), and assist LHDs with their outbreak investigations as requested. HAI outbreak investigations include responses to novel and unusual AR organisms, cases of healthcare-associated COVID-19, medical product or device contamination, transplant- or transfusion-related infections, bloodborne pathogen exposure, and any other infections caused by organisms known to be associated with the healthcare facility environment (such as *Legionella pneumophilia*).

Figure 1. Map of Texas DSHS Public Health Regions

In Texas, there are approximately 5,048 healthcare facilities including hospitals, ambulatory surgery centers, free standing emergency medical centers, nursing homes, and assisted living facilities. As per the Texas Health and Safety Code Chapter 81 and the Texas Administrative Code (TAC) Title 25, Chapter 97, facilities are required to report to public health departments any outbreak, exotic disease, or unusual group expression of disease that may be of public health concern.

Methods

HAI outbreaks may be identified and reported by healthcare facilities, laboratories, regulatory agencies, or other public health entities. Subsequently, HAI Epidemiologists conduct investigations to prevent and contain the transmission within the affected healthcare facilities. HAI outbreak responses can include conducting infection control assessments, sharing resources, providing infection prevention and control recommendations, coordinating laboratory testing, and providing trainings. Responses conducted by the HAI Epidemiologists are tracked in a spreadsheet to allow for standardized data collection across the state.

Descriptive data analyses were conducted on HAI outbreak responses that occurred between January 1, 2021 and December 31, 2021 using Microsoft Excel. A comparison between the 2021 and 2017 HAI outbreak responses was performed; 2017 data was the most recent analyzed data available.
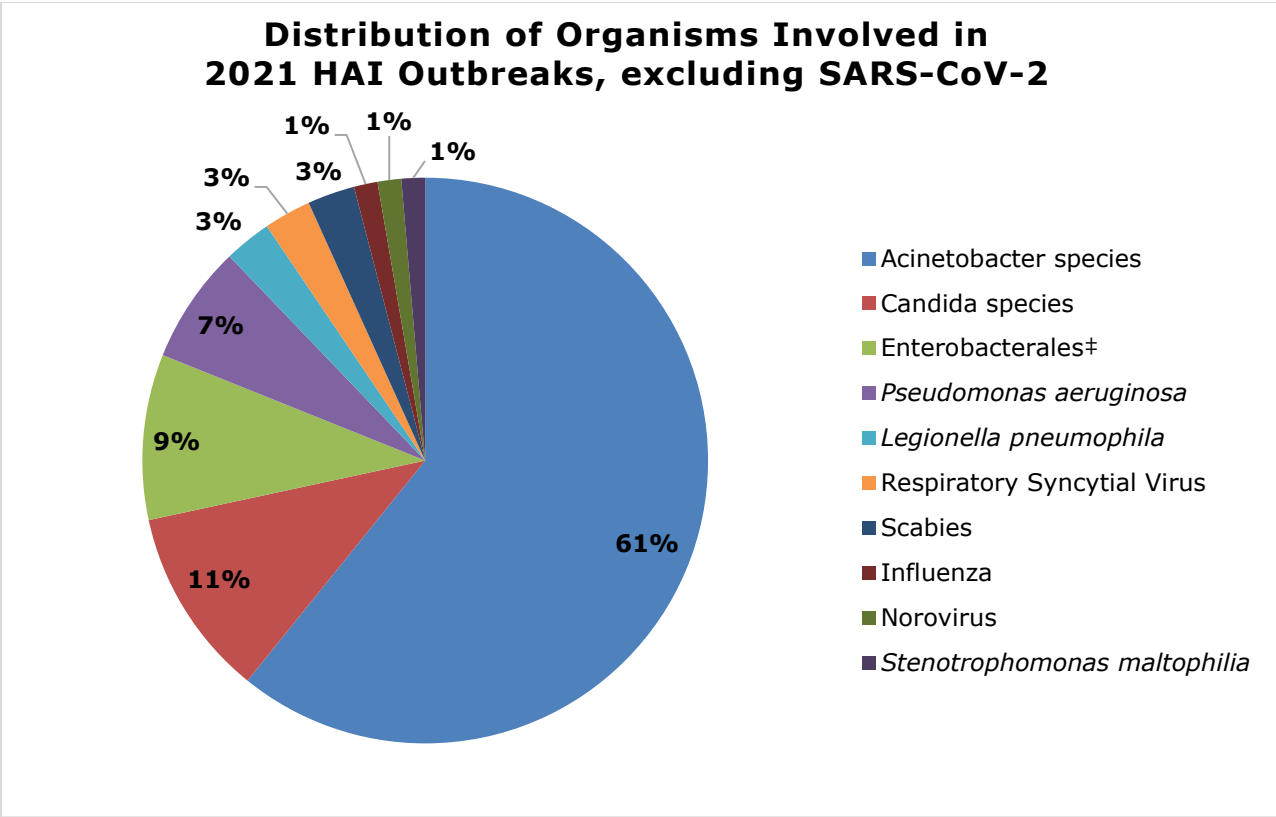
Results

The HCS Investigations Group investigated a total of 1,331 HAI outbreaks between January 1, 2021 and December 31, 2021. The DSHS PHR with the most HAI outbreaks investigated was PHR 2/3, followed by PHR 8 and PHR 11 (Figure 2).
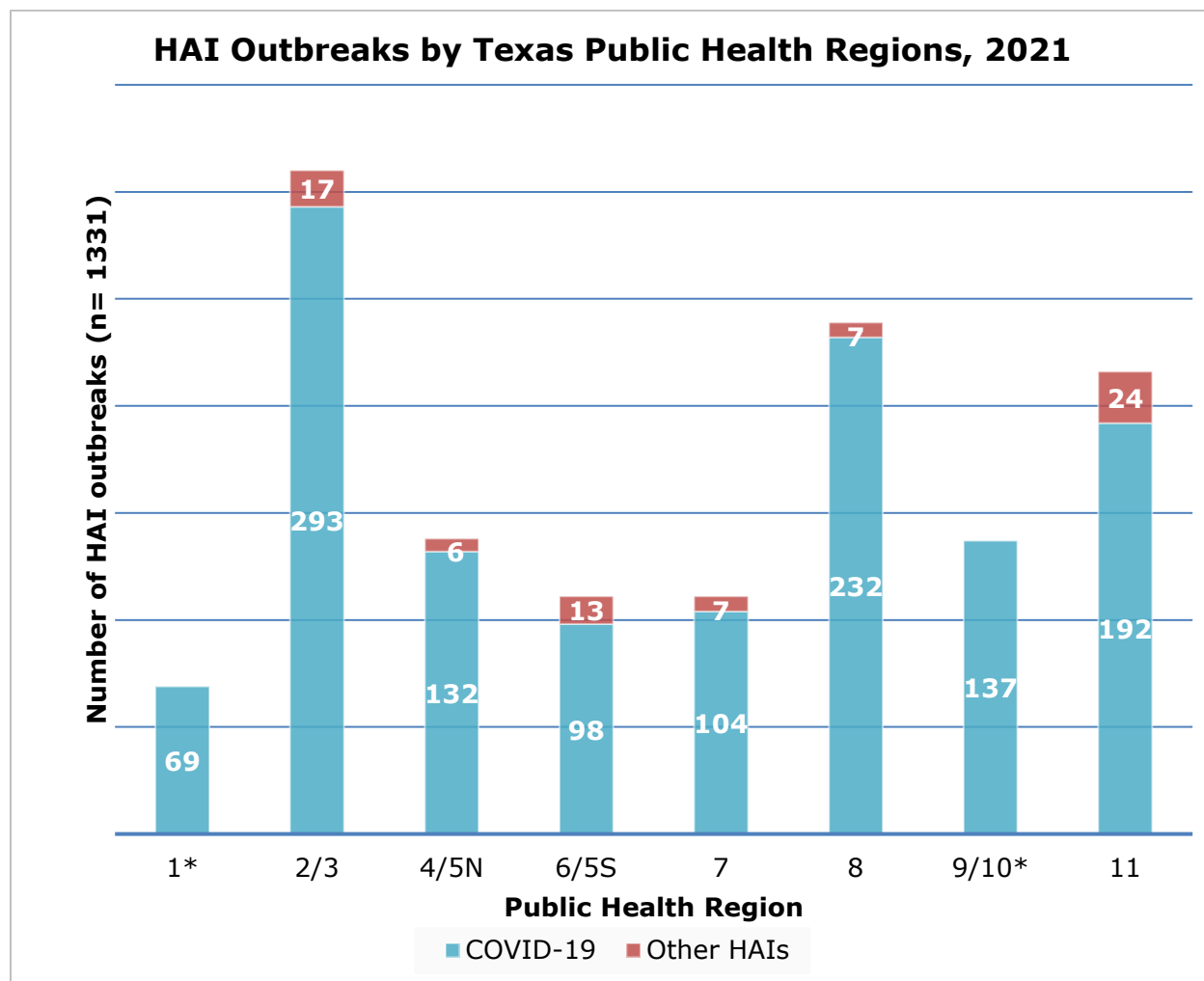
Figure 2. 2021 HAI outbreaks by Public Health Region (PHR) in Texas.

*****Zero non-COVID-19 HAI outbreaks were reported in PHR 1 and PHR 9/10

Of the total outbreaks, 1,257 (94.44%) were caused by SARS-CoV-2, the novel coronavirus responsible for COVID-19. The remaining 74 (5.56%) HAI outbreaks were caused by other organisms including 45 caused by Acinetobacter species (61%), 8 by Candida species (11%) and 7 by Enterobacterales (9%) (Figure 3).

Distribution of Organisms Involved in 2021 HAI Outbreaks, excluding SARS-CoV-2

- Acinetobacter species — 61%
- Candida species — 11%
- Enterobacterales‡ — 9%
- *Pseudomonas aeruginosa* — 7%
- *Legionella pneumophila* — 3%
- Respiratory Syncytial Virus — 3%
- Scabies — 3%
- Influenza — 1%
- Norovirus — 1%
- *Stenotrophomonas maltophilia* — 1%

Figure 3. Organisms involved in 2021 non-COVID-19 HAI outbreaks

‡ Includes *Citrobacter freundii*, *Escherichia coli*, *Klebsiella* species

Of the 1,331 total HAI outbreaks reported in 2021, 1,252 (94.06%) occurred in long-term care facilities (LTCF), which include nursing homes, assisted living facilities, intermediate care facilities, and other congregate settings such as group homes. Notably, the number of outbreaks in LTCFs during the month of December was significantly higher than other months, primarily due to the COVID-19 surge caused by the Omicron variant (Figure 4). Hospitals, including acute care hospitals, long-term acute care hospitals and inpatient rehabilitation facilities accounted for 60 (4.51%) outbreaks, while other settings accounted for 19 (1.43%). Of the 60 outbreaks reported in acute care facilities, 13 (21.67%) involved SARS-CoV-2 and 47 (78.33%) outbreaks reported other organisms.
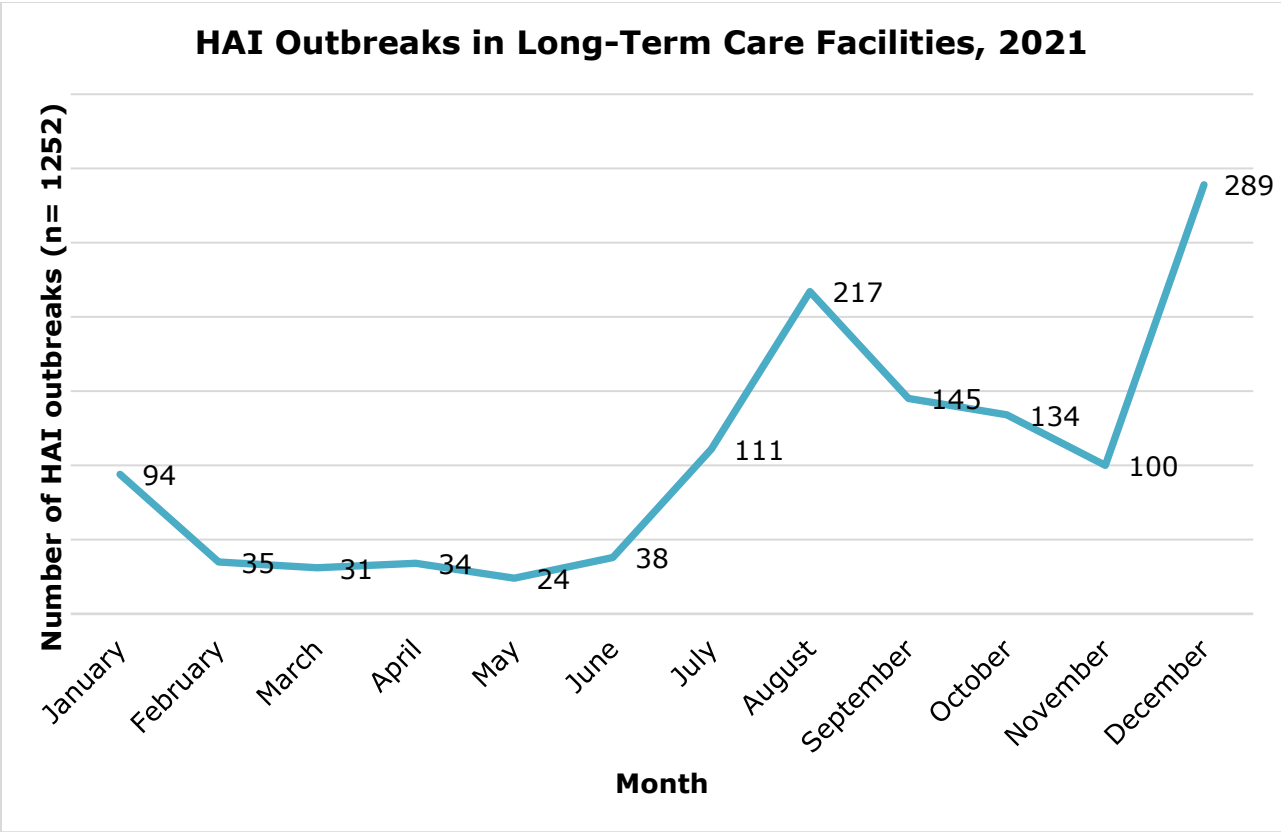
**Figure 4. HAI outbreaks in long-term care facilities by month of response date in 2021.**

Comparison of 2021 and 2017 HAI Outbreak Data

The HCS Investigations Group responded to 1,331 HAI outbreaks in 2021 and 110 outbreaks in 2017. This is a twelvefold increase in outbreaks, primarily due to the COVID-19 pandemic. When removing the COVID-19 outbreaks from the 2021 data, there is not a notable difference between the number of outbreaks. (Table 1, Figure 5).

Table 1. HAI outbreaks across all facilities by month for 2017 and 2021.

	2021	2021, without COVID-19	2017
January	100	3	11
February	36	2	16
March	38	11	14
April	40	10	12
May	34	9	5
June	43	7	3
July	116	3	4
August	231	6	9
September	152	5	3
October	141	9	6
November	105	5	4
December	295	4	23
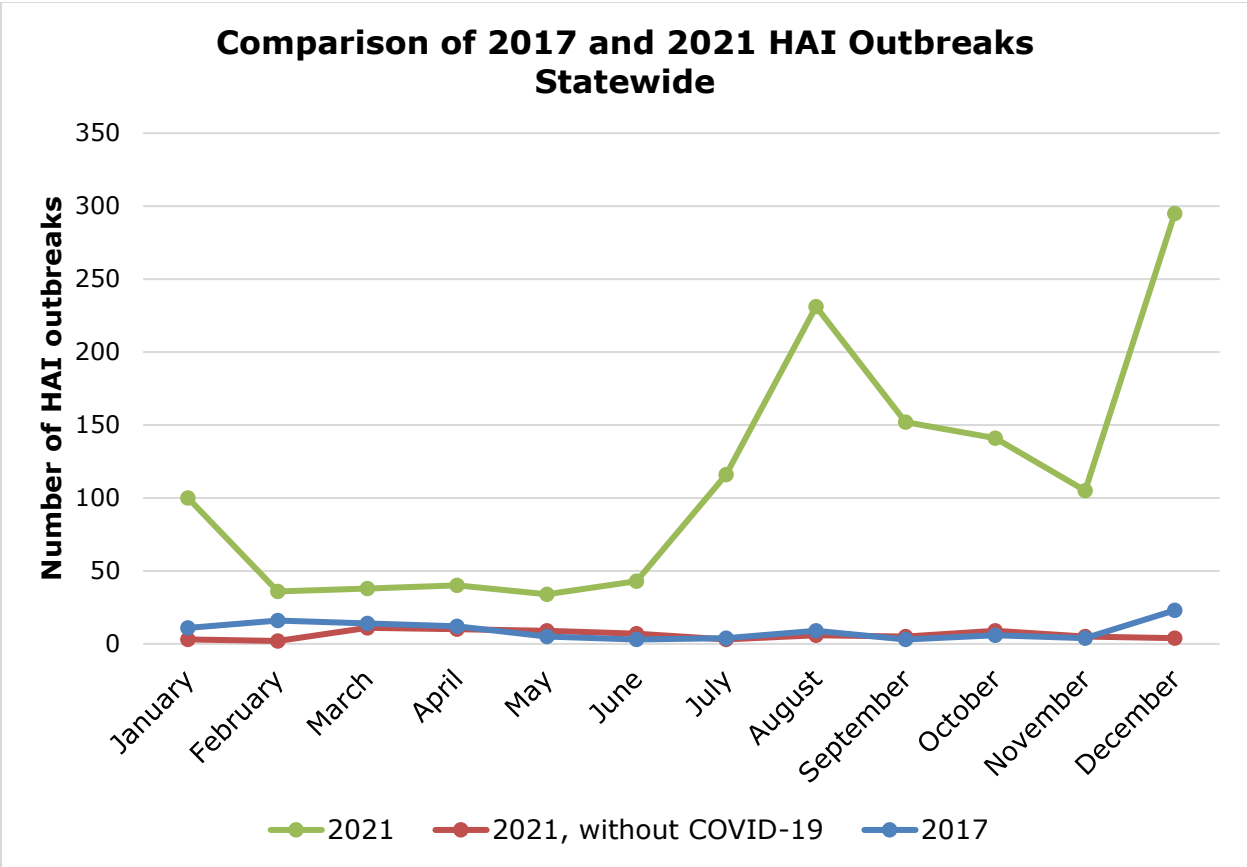
Figure 5. HAI outbreaks across all facilities by month for 2017 and 2021.

Highlighting *Candida auris*

Candida auris is an emerging fungus that has been identified by the Centers for Disease Control and Prevention (CDC) as a serious global health threat. *C. auris* has the capacity to be resistant to antifungals, and some strains are resistant to all three available classes of antifungals. This fungus can be misidentified as other organisms when using standard laboratory methods, which can lead to a delay in the implementation of proper infection prevention and control measures and treatment. Once *C. auris* is established in a healthcare facility it can spread undetected, causing HAI outbreaks.

C. auris was added to the Texas Notifiable Conditions lists in 2021, thus data for previous years is unknown. In 2021, 261 cases of *C. auris* were reported in Texas. Out of those, 226 (86.6%) were identified in PHR 2/3 due to multiple outbreaks in healthcare facilities (Figure 6). Outbreak response investigations were conducted by the HAI Epidemiologists and LHDs following the steps outlined in the Texas Antibiotic Resistance Laboratory Network Response Plan. Responses included conducting infection control assessments in healthcare facilities, providing education, and conducting colonization screenings. Out of the 226 cases from PHR 2/3, 31 (17.7%) were patients with clinical infections and 196 (82.3%) were colonized patients identified through the colonization screenings.
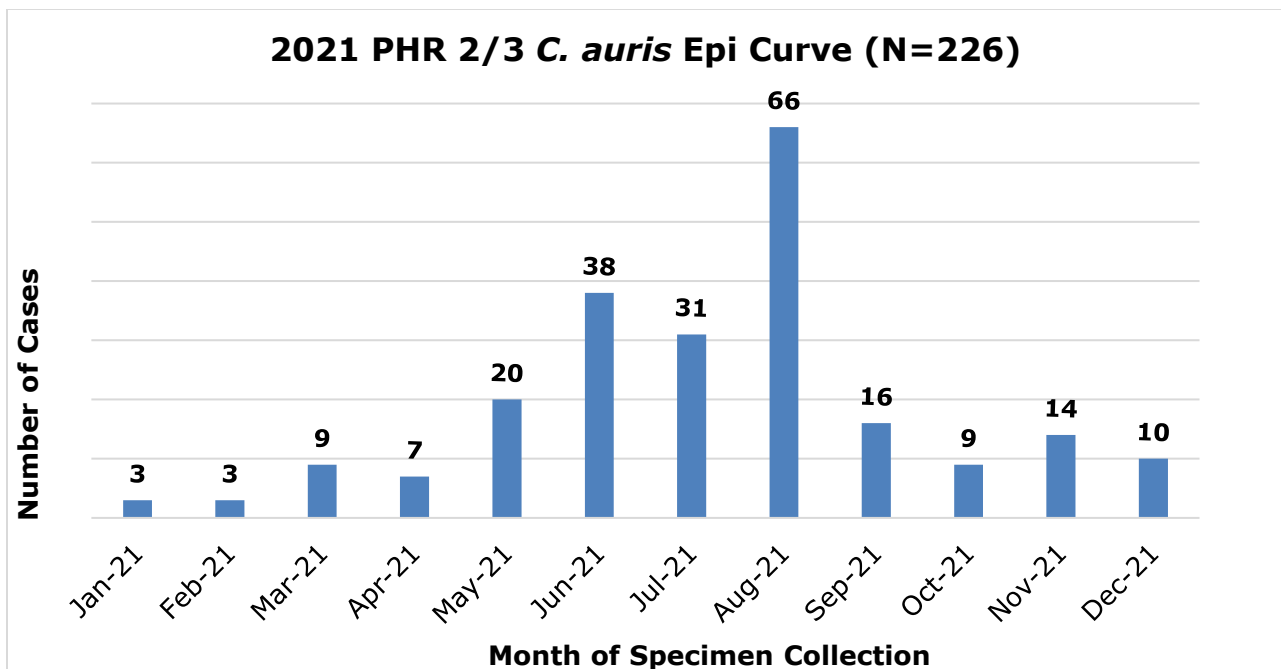

Figure 6. Epi Curve for *Candida auris* in PHR 2/3 for 2021.

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To understand relatedness of the isolates, whole genome sequencing (WGS) was performed on 44 of the cases (Figure 7). Sequencing revealed two clusters of cases that were distantly related to each other. It also showed clusters within and between healthcare facilities, including a cluster of resistant cases that were epi-linked to each other.
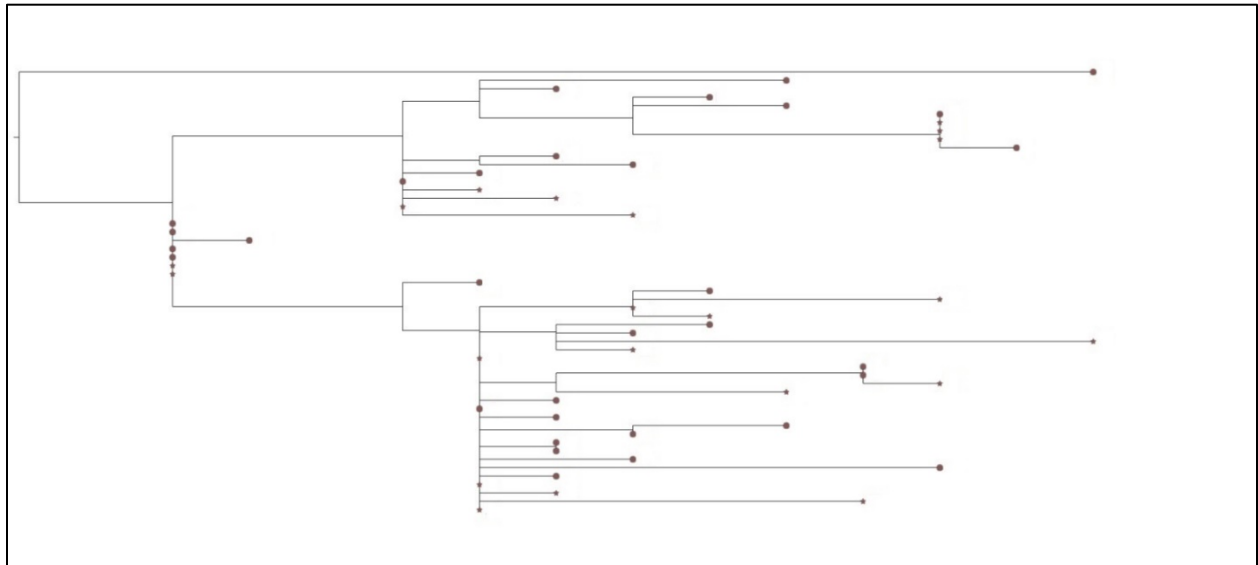
Figure 7. **Whole Genome Sequencing results for the *C. auris* sampled cases.**

Conclusion

Understanding the relatedness of isolates and possible routes of transmission helps guide public health actions and recommendations to prevent and contain outbreaks in healthcare facilities. A coordinated approach between public health and healthcare facilities can reduce HAI outbreaks by ensuring the proper infection prevention measures are in place and information is shared throughout the continuum of care.