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Brief Report

Group A *Streptococcus* outbreak among residents and employees of two skilled nursing facilities: North Carolina, 2017

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In this report, we summarize the results of surveillance, on-site assessments, and molecular analysis conducted as part of a group A *Streptococcus* outbreak investigation in 2 skilled nursing facilities.

We identified cases in 24 individuals (6 deaths) and infection prevention deficiencies. Isolates from 14 individuals represented the globally emergent clade 3 *emm89* strain.

Molecular analysis suggests that the 2 outbreaks were related. Wound care practices and 1 symptomatic shared employee may have facilitated transmission. Strict adherence to infection prevention practices is needed to prevent group A *Streptococcus* transmission.

The Centers for Disease Control and Prevention's (CDC) Emerging Infections Program network Active Bacterial Core surveillance tracks cases of invasive group A *Streptococcus* (GAS) in 10 designated sites across the United States, representing approximately 10% of the population. Using 1998-2003 surveillance data, Thigpen et al[1] calculated the incidence of invasive GAS infection among long-term care facility (LTCF) residents ≥65 years of age to be almost 6 times as high as community-based elderly residents (41.0 vs 6.9 cases per 100,000 population) in 2000. Additionally, LTCF case patients ≥65 years of age were 1.5 times as likely to die from infection as similarly aged community-based case patients (33% vs 21%).[1]

Invasive GAS is reportable to the North Carolina Division of Public Health and investigated by local health departments. Because residents of LTCFs (eg, skilled nursing facilities [SNFs]) are at a higher risk of GAS-associated mortality compared to similarly aged persons in the community, we conduct active surveillance when a case of invasive GAS in an LTCF is reported to detect additional cases and colonized individuals and to prevent outbreaks.[1,2] Eighteen GAS outbreaks were reported to North Carolina Division of Public Health in 2017; all were from LTCFs.

In January 2017, we investigated 2 GAS outbreaks in SNFs owned by the same company in the same county to identify risk factors for inter- and intra-facility transmission.

METHODS

Case definition and additional case finding

We defined cases as either a symptomatic invasive or noninvasive GAS infection or an asymptomatic GAS colonization in a resident or employee of either SNF (SNF A or SNF B). GAS was identified by culture or rapid diagnostic test from a specimen collected between November 24, 2016 and July 22, 2017 in SNF A or between December 10, 2016 and October 4, 2017 in SNF B. An individual could have more than 1 GAS case. GAS cases identified in 1 individual from the same specimen type (eg, wound) on the same date were counted as 1 GAS case.

We conducted retrospective surveillance going back 1 month from the specimen collection date of the first invasive GAS case and active surveillance going forward 4 months from the specimen collection date for the most recent GAS case in each SNF. Identification of an additional invasive or noninvasive case in a facility was considered an outbreak. After initial identification of an outbreak, the following sites were cultured from all residents: pharynx, skin lesions, and indwelling catheter sites (excluding Foley catheters). Employees were

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surveyed for symptoms of GAS infection; if an employee was symptomatic, they were referred for a rapid diagnostic test or culture of the pharynx and any skin lesions. Infected and colonized individuals were treated as clinically indicated. This screening process was repeated if an additional case of infection was identified.

Site visits

We issued control measures and conducted site visits at both SNFs to review infection prevention (IP) policies and observe direct resident care, environmental cleaning and disinfection, hand hygiene (HH), and other IP practices.[3]

Laboratory analysis

We submitted isolates from 14 residents and 1 employee (63% of individuals with cases) to the CDC for whole genome sequencing (WGS) and analysis as described by Chochua et al.[4] The CDC performed library construction and sequencing as described by Metcalf et al.[5]

RESULTS

Description of cases

At least 1 GAS case was identified in 8 of 90 (9%) residents and 2 of 140 (1%) employees at SNF A, and in 12 of 130 (9%) residents and 2 of 87 (2%) employees at SNF B (Fig 1). Median age was 74 years for residents and 44 years for employees. Eleven (55%) residents and 2 (50%) employees were women. All employees were identified by throat culture or rapid diagnostic test. Among 20 residents with cases, 11 (55%) were identified from wound cultures, 4 (20%) from blood cultures, 3 (15%) from throat cultures, 1 (5%) from a nasopharyngeal culture, and 1 (5%) from throat and wound cultures. Five of 19 residents (26%) for whom hospitalization information was available were hospitalized for their illness at 3 different hospitals; of these, 4 had invasive cases identified from blood and 1 was identified from a wound. All 4 residents with invasive cases had cellulitis or wounds at the time of admission to the hospital. Six of 20 (30%) residents died.

Site visit findings

We identified IP deficiencies related to HH, environmental cleaning and disinfection, and general IP at both SNFs. Employees missed opportunities for HH and HH supplies were not readily available. Neither SNF conducted routine audits with feedback on adherence to HH, appropriate use of personal protective equipment, or cleaning and disinfection procedures. Wound care equipment (eg, scissors) was used on multiple residents without appropriate disinfection between residents. Symptoms of GAS were not included on employee sick logs. Control measures were issued to address these deficiencies.

Laboratory results

Isolates from 13 residents and 1 employee shared the same T agglutination complex, T13. One resident isolate was T agglutination complex T12. WGS analysis revealed that all T13 isolates were *emm* subtype *emm89.0* and represented the globally emergent clade 3 *emm89* strain. A phylogenetic tree of sequences was assembled for available *emm89.0* isolates from 12 residents and 1 employee (Fig 2). A maximum pairwise difference of 3 single nucleotide polymorphisms across the GAS core genome (approximately 1.8 Mbp) indicated close temporal relatedness.[4,6]

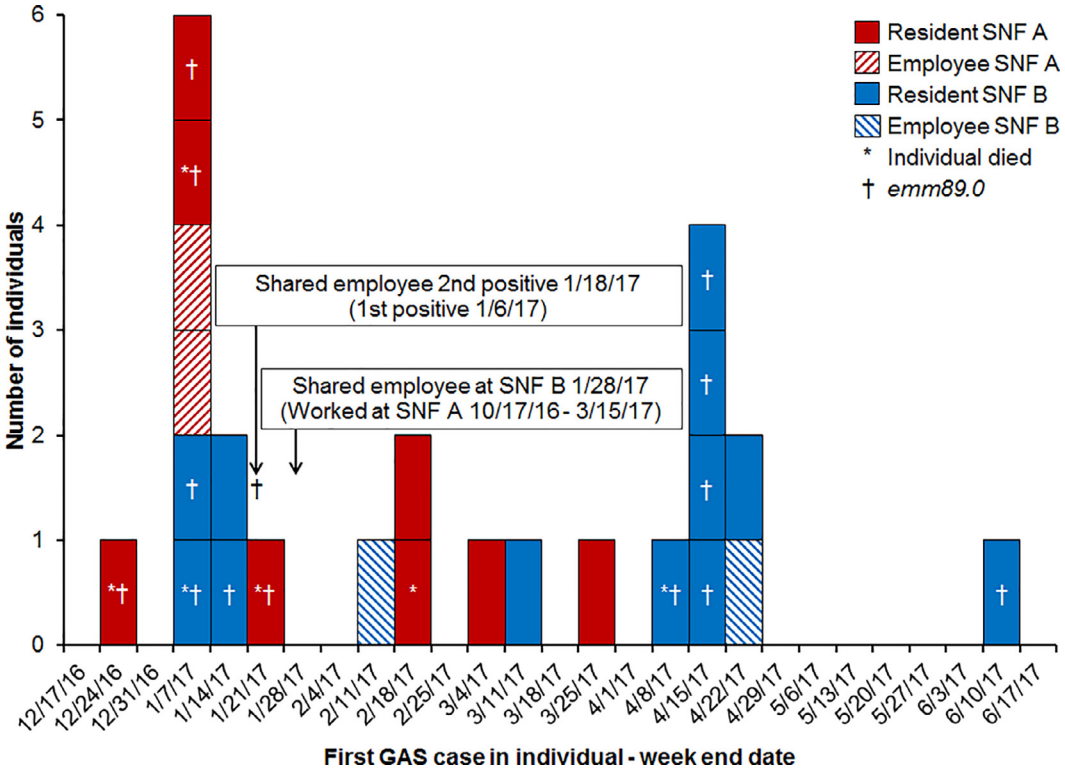

Fig 1. Residents and employees with group A *Streptococcus* (GAS) case(s) (N = 24) in 2 skilled nursing facilities (SNF A and SNF B) by week end date, in which a case was first identified by positive culture or rapid diagnostic test in North Carolina from December 2016 to June 2017. Individual survival and whether or not isolate *emm* subtype matched the outbreak *emm89.0* strain are also indicated. *Indicates the individual died. †Indicates *emm89.0* strain was isolated.

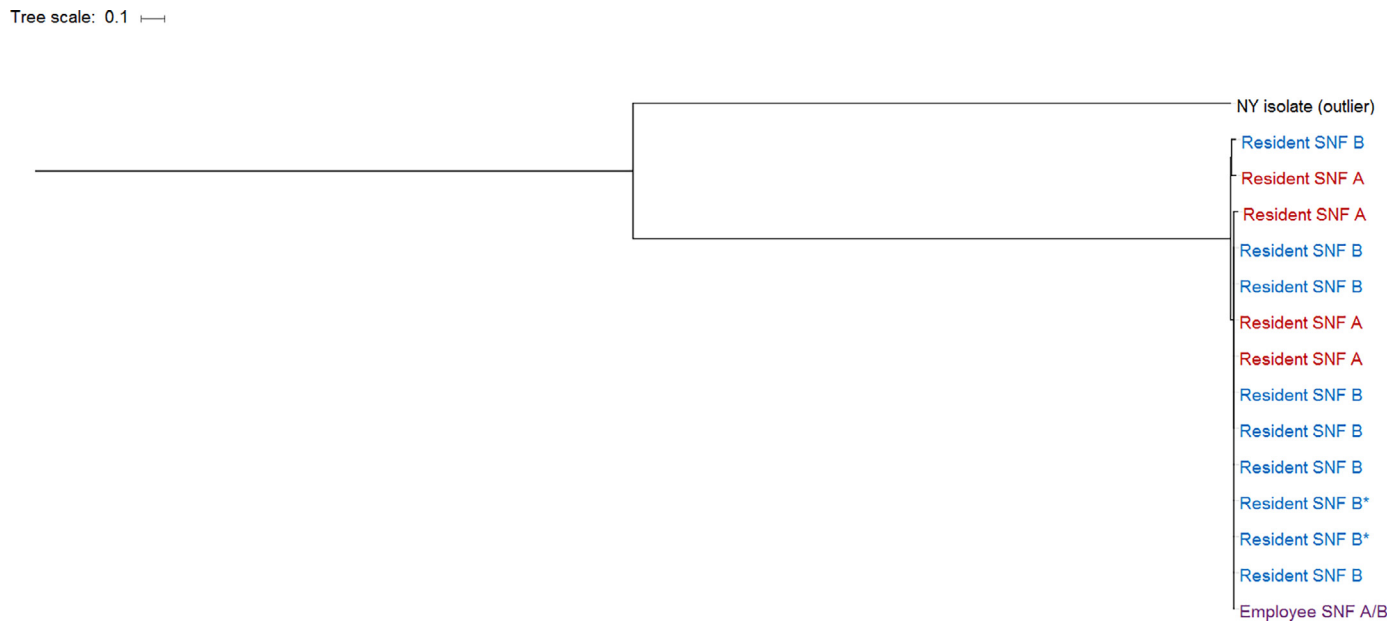

Fig 2. Phylogenetic analysis of isolates from 12 residents and 1 employee with group A *Streptococcus* identified during outbreaks in 2 skilled nursing facilities (SNFs; SNF A: red text; SNF B: blue text; SNF A and SNF B: purple text). All isolates shared the same T agglutination complex, T13, were *emm* subtype *emm89.0*, and represented the globally emergent clade 3 *emm89* strain. A maximum pairwise difference of 3 single nucleotide polymorphisms across the group A *Streptococcus* core genome (approximately 1.8 Mbp) indicated close temporal relatedness of these isolates. NY isolate represents an outlier *emm89.0* group A *Streptococcus* isolate from New York. *Indicates 2 isolates from the same resident.

Identification of a GAS carrier

Two employees worked at both SNFs during the surveillance period and performed wound care. One employee had pharyngitis, tested positive for GAS, and was treated twice in January 2017. This employee's isolate matched the outbreak *emm89.0* strain. The employee remained positive for GAS 12 days after initial treatment and resolution of pharyngitis, suggesting that this employee was a GAS carrier. We provided individual control measures, which included the following: wearing a face mask when performing wound care until a negative throat culture was obtained, strictly adhering to HH, wearing situation-appropriate personal protective equipment, and practicing appropriate aseptic technique. The asymptomatic employee performed weekly wound care at both SNFs. Pharyngeal swabs collected on the asymptomatic employee in January and late April and a rectal swab collected in late April were negative for GAS.

DISCUSSION

Case fatality among residents (30%) in this investigation was higher than that published for community cases ≥65 years of age (21%) but comparable to LTCF residents ≥65 years of age.[1,2] IP deficiencies were identified at both SNFs, demonstrating the need for strict adherence to IP practices to prevent GAS transmission.

WGS results suggest that the 2 outbreaks were related. Isolates collected from the symptomatic shared employee and residents at both SNFs had a maximum pairwise difference of 3 single nucleotide polymorphisms across the GAS core genome, suggesting a common source. Residents were reportedly not transferred between SNFs and no GAS outbreaks were reported by acute care hospitals during this timeframe. Once a case of GAS was identified in an SNF, ongoing transmission was likely facilitated by IP deficiencies, especially in wound care practices. One symptomatic shared employee was unlikely to be the source of either outbreak because of the timing of their illness and the inability to determine a precise colonization date. However, this employee may have facilitated ongoing GAS transmission, as the employee performed wound care and 55% of individuals with GAS were identified from wound cultures. The globally emergent clade 3 *emm89* strain has been among the 5 most frequently occurring GAS types in the United States each year since 2012, and has increasing frequency in Finland, Iceland, and the United Kingdom.[4,7,8] Studies suggest this strain may be capable of causing carriage and invasive disease owing to mutations that cause capsule loss and increased production of virulence factors.[6-8] A definitive outbreak source was not identified.

CONCLUSIONS

Health care facilities should adhere to standard and transmission-based precautions per published guidelines.[3] During outbreaks, it is important for public health officials to inquire if facilities share employees and consider implementing individual control measures for employees who may be GAS carriers and perform direct patient care.

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