

Fig. 2.

machine in the ward, a sink in the shared washroom, and a sink in the patient room) belonged to the same clone (Fig. 2). **Conclusions:** The hospital water environment was contaminated with *R. mucosa*, and the same clone caused bacteremia in 2 separate patients, suggesting nosocomial transmission of *R. mucosa* possibly linked to contaminated water, environment, and/or patient care.

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Poster Presentation

A Novel On-Site Volunteer Community Infection Prevention Team Prevented Outbreaks at a Hurricane Harvey Mega-Shelter Carolee Estelle, UT Southwestern Medical Center; Julie Trivedi, UT Southwestern Medical Center; Patricia Jackson, Children's Medical Center Dallas; Doramarie Arocha, UTSW Dallas; Wendy Chung, Dallas County Department of Health Services; Jennifer Ochieng, Parkland Hospital; Dena Taherzadeh, Parkland Health and Hospital System; Pranavi Sreeramoju, University of Texas Southwestern Medical Center; Michael Sebert, UT Southwestern; Trish Perl, UT Southwestern Medical Center

Background: In the setting of global warming, natural disasters are increasing in pace and scope. Although natural disasters themselves do not cause outbreaks, the breakdowns in sanitary infrastructure and the displacement of populations, often to crowded shelters, have caused outbreaks. On August 26, 2017, category 4 hurricane Harvey made landfall near Corpus Christi, Texas, causing catastrophic flooding and displacing >30,000 residents from the Southern Gulf Coast region. Dallas accepted >3,800 evacuees at the Kay Bailey Hutchison Convention Center mega-shelter for 23 days, where a medical clinic was erected in the convention center parking garage. The medical clinic uniquely included a dedicated infection prevention team composed of local volunteer infection preventionists, healthcare epidemiologists, infectious diseases providers, and health department personnel. Methods: Evacuees were housed at the Dallas mega-shelter from August 29 through September 20. The infection prevention team maintained a presence of 3-4 members during clinical operations in shifts. The team conducted an initial needs assessment upon opening of the shelter medical clinic, facilitated acquisition of adequate numbers of hand sanitizer stations, sinks with running water, portable hand-washing stations, portable toilets and showers, and cleaning products. The infection prevention team coordinated and oversaw environmental cleaning services (EVS) carried out by local hospital EVS staff. Protocols for cleaning, disinfection, communicable disease testing, isolation, and treatment were created. In addition, education and training materials for the

implementation of these protocols were distributed to volunteer staff. The infection preventionists created and provided oversight of the designated isolation units for respiratory, gastrointestinal and dermatologic infections of outbreak potential. Infection prevention rounding tools were developed and executed daily in the clinic, at the on-site daycare center, dining area, and the general shelter dormitory. Vaccination for influenza was formalized under a protocol and administered at the clinic and via mobile vaccination teams in the chronic illness section of the dormitory. Results: In tota3,829 residents were housed at the mega-shelter for 23 days. Moreover, 1,560 patients were seen in 2,654 clinic visits at the shelter medical clinic. In total, 48 (19%) clinic visits were for respiratory symptoms, 228 (9%) were for dermatologic problems, and 215 (8%) were for gastrointestinal symptoms. Also, 32 patients were referred to the isolation unit within the clinic. Overall, 98 influenza vaccines were administered. There was 1 confirmed case of influenza and 1 confirmed case of norovirus. Conclusions: No known transmission of communicable diseases occurred in this long-term, natural disaster-related mega-shelter, likely attributed to having a comprehensive infection prevention team of on-site volunteers available throughout the shelter operation. This model should be considered in future large-scale shelter settings to prevent disease transmission.

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A Pilot Study of Valley Fever Tweets

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Background: Twitter is used by officials to distribute public health messages and by the public to post information about ongoing afflictions. Because tweets originate from geographically and socially diverse sources, scholars have used this social media data to analyze the spread of diseases like flu [Alessio Signorini 2011], asthma [Philip Harber 2019] and mental health disorders [Chandler McClellan, 2017]. To our knowledge, no Twitter analysis has been performed for Valley fever. Valley fever is a fungal infection caused by the *Coccidioides* organism, mostly found in Arizona and California. Objective: We analyzed tweets concerning Valley fever to evaluate content, location, and timing. Methods: We collected tweets using the Twitter search application programming interface using the terms "Valley fever," "cocci"

