**Background.** Opioid misuse is epidemic in the United States (US), and persons who inject drugs are at increased risk for serious bacterial and fungal infections, including Candida bloodstream infections. Historically, candidemia has occurred almost exclusively among patients with severe underlying illness and extensive healthcare exposure. We examined whether the opioid crisis may be having an impact on the epidemiology of candidemia in the United States.

**Methods.** Using data from 200 US hospitals reporting to the Premier Healthcare Database (PHD) between 2012–2017, we conducted a retrospective study among hospitalized persons ≥ 18 years. Candidemia was defined by any blood culture yielding Candida species. Drug use-associated (DUA)-candidemia hospitalizations were defined as hospitalizations having both candidemia and at least one ICD-9-CM or ICD-10-CM diagnostic code for recreational drug use; drugs were classified as opioids, cocaine, amphetamines, or other drugs (excluding cannabis, alcohol, and nicotine). We described the characteristics and annual trends of candidemia hospitalizations stratified by drug use.

**Results.** Of 7,590 candidemia hospitalizations during 2012–2017, 679 (9%) were DUA-candidemia. During this time, the rate of DUA-candidemia increased from 3.6 to 9.1 per 100,000 hospitalizations, while the rate of non-DUA-candidemia decreased from 64.7 to 55.6 per 100,000 hospitalizations. Patients with DUA-candidemia were younger (median 40 vs. 64 years), had a longer length of stay (median 14 vs. 13 days), and had lower in-hospital mortality (12% vs. 26%). Among DUA-candidemia hospitalizations, opioids accounted for 73% of attributes identified. Among patients aged 18–44 years, the proportion of candidemia hospitalizations associated with drug use more than tripled from 13% in 2012 to 43% in 2017 (Figure 1).

**Conclusion.** DUA-candidemia hospitalizations increased almost 3-fold during 2012–2017, with drug use identified in nearly half of candidemia patients aged 18–44 years in 2017. These data suggest that the opioid crisis is having an impact on the epidemiology of candidemia in the United States, especially among young adults, underscoring an additional negative consequence of the ongoing crisis.

**Disclosures.** All authors: No reported disclosures.

2464. Partnerships in the Field: Using Real-time Sequencing to Enhance Epidemiologic Investigation and Response to a Norovirus Outbreak

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**Session:** 257. HAi: Outbreaks
Saturday, October 5, 2019: 12:15 PM

**Background.** Norovirus is a common cause of infectious gastroenteritis and frequently leads to hospital-based outbreaks of gastrointestinal (GI) illness. We utilized hospital-wide surveillance to detect outbreaks of GI illness among patients and healthcare workers (HCW). Real-time norovirus sequencing was applied to establish conclusive links between patient cases.

**Methods.** Patient cases of healthcare-associated GI illness were detected through house-wide microbiologic surveillance. HCW cases were defined as acute episodes of vomiting and/or diarrhea that began within 48 hours of the last shift. Outbreak procedures were implemented on a unit when 3 or more cases were identified within 48 hours. Traditional epidemiologic methods were used, including an epidemic curve and line listing, while instituting local control measures. De-identified clinical stool samples positive for norovirus from any hospital unit during the defined outbreak time period were analyzed. Sanger sequencing was performed using primer sets targeting the norovirus VP1 capsid and polymericase regions. Capillary electrophoresis was implemented on a 3500 Genetic Analyzer (Applied Biosystems) and analysis was performed via MEGAGAT.

**Results.** Epidemiologic surveillance identified a norovirus outbreak involving 11 patients on a single unit. Sequencing was performed on 20 norovirus positive stool samples, of which 13 shared 100% identity across both the VP1 and polymerase regions. Of these 13, 10 specimens were from patients epidemiologically linked to the outbreak; 3 specimens were from patients located on 2 geographically separate floors, not epidemiologically linked to the outbreak. Identification of cases outside of the outbreak unit prompted additional hospital-wide infection prevention interventions, including increased education and messaging, changes in hand hygiene practice, and prohibition of shared food for staff.

**Conclusion.** Real-time sequencing confirmed epidemiologically linked cases of norovirus during an outbreak and identified additional transmission events not detected by conventional epidemiologic methods. Partnership between hospital epidemiology and the laboratory identified the need for hospital-wide infection prevention measures to halt ongoing transmission.

**Disclosures.** All authors: No reported disclosures.