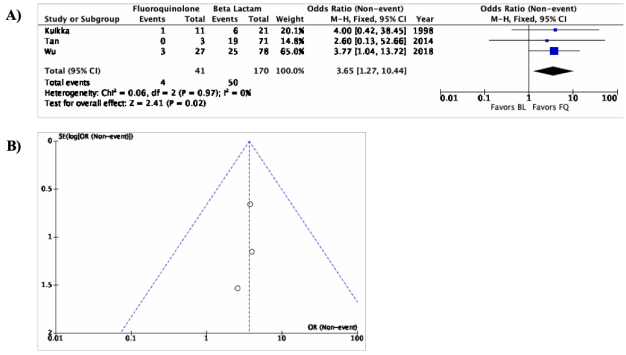

Figure 2. A) Forest plot showing FQ monotherapy is associated with increased survival compared to BL monotherapy using a fixed-effects model. **B)** Funnel plot showing the studies included in the meta-analysis.

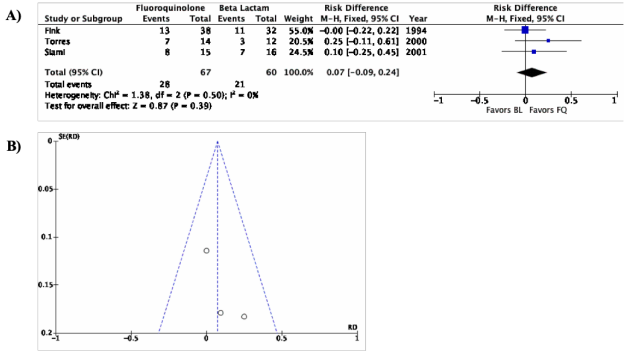

Figure 3. A) Forest plot showing FQ monotherapy is associated with similar bacteriological eradication rates compared to BL monotherapy using a fixed-effects model. **B)** Funnel plot showing the studies included in the meta-analysis.

Conclusion: The data appear to suggest FQ monotherapy is significantly associated with increased survival in PA bacteremia and associated with similar rates of bacteriological eradication in pneumonia and skin and soft tissue infection caused by PA compared to BL monotherapy. However, more research is needed to make meaningful clinical recommendations.

Disclosures: **All Authors**: No reported disclosures

130. increase in Multidrug Resistance (2011–2018) and the Emergence of Extensive Drug Resistance (2020) in shigella Sonnei in the United States

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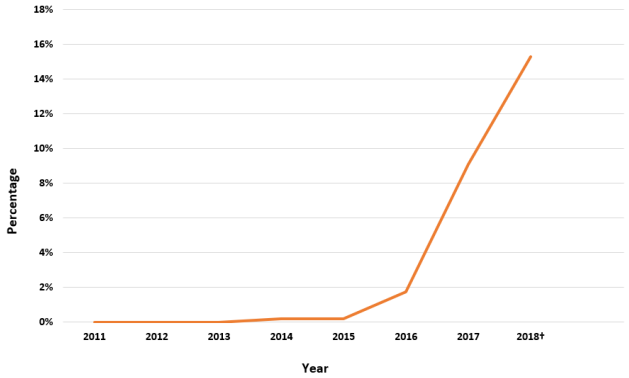
Session: O-25. Hot Topics in Bacteria and Viral Infections

Background: Multidrug-resistant (MDR) *Shigella sonnei* infections are a serious public health threat, and outbreaks are common among men who have sex with men (MSM). In February 2020, Australia's Department of Health notified CDC of extensively drug-resistant (XDR) *S. sonnei* in 2 Australian residents linked to a cruise that departed from Florida. We describe an international outbreak of XDR *S. sonnei and* report on trends in MDR among *S. sonnei* in the United States.

Methods: Health departments (HDs) submit every 20th *Shigella* isolate to CDC's National Antimicrobial Resistance Monitoring System (NARMS) laboratory for susceptibility testing. We defined MDR as decreased susceptibility to azithromycin (MIC ≥32 µg/mL) with resistance to ampicillin, ciprofloxacin, and cotrimoxazole, and XDR as MDR with additional resistance to ceftriaxone. We used PulseNet, the national subtyping network for enteric disease surveillance, to identify US isolates related to the Australian XDR isolates by short-read whole genome sequencing. We screened these isolates for resistance determinants (ResFinder v3.0) and plasmid replicons (PlasmidFinder) and obtained patient histories from HDs. We used long-read sequencing to generate closed plasmid sequences for 2 XDR isolates.

Results: NARMS tested 2,781 *S. sonnei* surveillance isolates during 2011–2018; 80 (2.9%) were MDR, including 1 (0.04%) that was XDR. MDR isolates were from men (87%), women (9%), and children (4%). MDR increased from 0% in 2011 to 15.3% in 2018 (Figure). In 2020, we identified XDR isolates from 3 US residents on the same cruise as the Australians. The US residents were 41–42 year-old men; 2 with available information were MSM. The US and Australian isolates were highly related (0–1 alleles). Short-read sequence data from all 3 US isolates mapped to the $bla_{CTX\text{-}M\text{-}27}$ harboring IncFII plasmids from the 2 Australian isolates with >99% nucleotide identity. $bla_{CTX\text{-}M\text{-}27}$ genes confer ceftriaxone resistance.

Increase in Percentage of Shigella sonnei Isolates with Multidrug Resistance* in the United States, 2011–2018†



* Multidrug resistance defined as decreased susceptibility to azithromycin (MIC ≥32 µg/mL) with resistance to ampicillin, ciprofloxacin, and cotrimoxazole.

† Data from 2018 is preliminary.

Conclusion: MDR *S. sonnei* is increasing and is most often identified among men. XDR *S. sonnei* infections are emerging and are resistant to all recommended antibiotics, making them difficult to treat without IV antibiotics. This outbreak illustrates the alarming capacity for XDR *S. sonnei* to disseminate globally among at-risk populations, such as MSM.

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131. The Protective Role of Mucosal Interferons in Infants with Respiratory Syncytial Virus (RSV) Infection

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Session: O-25. Hot Topics in Bacteria and Viral Infections

Background: Despite the high burden associated with RSV infection in young children the factors that determine disease severity are not well understood. The objective of this study was to assess the association of mucosal cytokine profiles, RSV loads (VL) and RSV disease severity.

Methods: Single-center, prospective study in previously healthy infants with mild (outpatients; OP), moderate (inpatient-IP; ward) or severe (IP-PICU) RSV infection. Mid-turbinate swabs were obtained to measure VL by PCR, and cytokine concentrations (conc.) using a 13-plex panel that included type I (IFN-α2), II (IFN-γ), and III (IFN-λ2/λ3) interferons (IFN), and inflammatory cytokines. Multivariable analyses were performed to identify factors predictive of disease severity.

Results: From 2014 to 2019 we enrolled 219 infants: 78 with mild RSV infection (OP; median [IQR] age, 6 [3.4–10.5] mo.), 101 with moderate disease (3.5 [1.3–8.3] mo.), and 40 with severe disease (2.3 [1.5–5.7] mo.). Duration of symptoms at enrollment was 4 (3–5) days and comparable between OP and IP, yet RSV VL in OP were significantly higher than in IP (8.1 [7.4–8.6] vs 7.4 [6.4–8.1] $\log_{10}$ copies/mL; p< 0.01) with no differences between ward and PICU infants. Median conc. of IFN-α2, IFN-γ, and IFN-λ2/λ3 were significantly higher in OP vs IP irrespective of hospitalization unit (Table 1). IP-10 conc. were also higher in OP and in ward patients vs PICU patients (p< 0.0001) and were independently associated with lower odds of supplemental O_2 needs (OR, 95% CI: 0.4 [0.22–0.69]; p< 0.01) and PICU admission (0.4 [0.23–0.67]; p=0.001). In addition, higher IFN-λ2/λ3 conc. were nearly associated with lower odds of prolonged O_2 use (OR: 0.35 [0.11–1.07]; p=0.07), and prolonged hospitalization (OR: 0.42 [0.16–1.03]; p=0.06).