122 were analyzed. Of the study patients, 24 (51%) were female, 13 (27%) had active infections, and 15 (32%) were on contact precautions. Because fomites were split in half, patients in the left and right study arms were identical. Overall, the median total colony-forming-units (CFU) of study fomites was 1,348 (IQR, 398–2,365): 468 (IQR, 161–1,230) for the left side study arm and 540 (IQR, 102–1,221) for the right study arm ($P = .45$). At the sample level, 52 (43%), 15 (12%), and 37 (30%) of 122 samples harbored any CIPs, AMR CIPs, or non-AMR CIPs, respectively. At the fomite level, 27 (44%), 5 (8%), 15(25%), and 7 (11%) of 61 fomites harbored any CIPs, only AMR-CIPs, only non-AMR CIPs, or both AMR and non-AMR CIPs, respectively. Generally, therapy balls were the most contaminated study fomites (n = 2,237; IQR, 1,425–2,658), and walking aids were most frequently contaminated with any CIPs (n = 26, 72%), AMR CIPs (n = 8, 22%), and non-AMR CIPs (n = 15, 47%). **Discussion:** Following routine disinfection, frequently used PT equipment remained heavily contaminated and harbored AMR and non-AMR CIPs, supporting the notion that PT equipment is difficult to disinfect via standard disinfection. Additionally, left-, and right-side fomite divisions had similar pathogens, suggesting that this sampling model of intrapatient comparisons may be helpful for resolving case-mix issues in future studies. Future work should focus on PT-specific enhanced disinfection strategies to improve the disinfection of PT equipment.

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Disclosures: None

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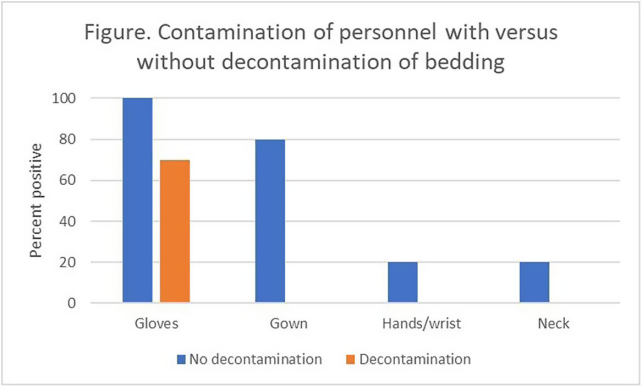
Presentation Type:
Poster Presentation - Poster Presentation
Subject Category: Disinfection/Sterilization
Decontamination of bedding reduces the risk for contamination of personnel changing bedding: A simulation study
Jennifer Cadnum; Andrew Osborne; Samir Memic; Curtis Donskey and Maria Torres-Teran

Background: The recent worldwide outbreak of Mpox virus infections has raised concern about the potential for nosocomial acquisition during handling of contaminated bedding or clothing. We conducted simulations to test the hypothesis that decontamination of bedding prior to handling could reduce the risk for contamination of personnel. **Methods:** We conducted a crossover trial to test the effectiveness of spraying contaminated bedding with a hydrogen peroxide disinfectant in reducing contamination of personnel during handling of the contaminated bedding. Bedding was contaminated on top and bottom surfaces with aerosolized bacteriophage MS2. Personnel (N = 10) wearing a cover gown and gloves removed the bedding from a patient bed and placed it into a hamper both with and without prior hydrogen peroxide spray decontamination. After handling the bedding, samples were collected to assess viral contamination of gloves, cover gown, neck or chest, and hands or wrists. **Results:** Contamination of the gloves and cover gown of personnel occurred frequently during handling of bedding and 20% of participants had contamination of their hands or wrists and neck after the simulation (Fig.). Decontamination of the bedding reduced contamination of the gloves and eliminated contamination of the cover gown, hands or wrists, or neck. **Conclusion:** Decontamination of bedding prior to handling could be an effective strategy to reduce the risk for nosocomial acquisition of Mpox by healthcare personnel.



Disclosures: None

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Presentation Type:
Poster Presentation - Poster Presentation
Subject Category: Emerging Pathogens
Healthcare personnel with laboratory-confirmed mpox in California
Allison Bailey; Jane Siegel; Shua Chai; David Bui; Robert Snyder; Linda Lewis; Kayla Saadeh; J.B. Bertumen and Erin Epson

Objectives: Few reports have been published about the transmission of mpox in healthcare settings. During the 2022 multinational outbreak, the California Department of Public Health (CDPH) conducted a systematic review of healthcare personnel (HCP) with mpox, including their community and occupational exposures, to understand the transmission risk in healthcare settings. We also sought to inform return-to-work protocols by describing the frequency of HCP working while symptomatic for mpox and identifying occurrences of secondary transmission from infected HCP to patients. **Methods:** We analyzed surveillance data for laboratory-confirmed mpox cases in California with symptom onset from May 17 to September 30, 2022, collected by investigators at local health departments and reported to the CDPH. The reported data were supplemented by review of free-text variables, interview notes, and other files uploaded to state and county disease surveillance data registries. We identified HCP as all persons working in healthcare settings with potential for direct or indirect exposure to patients or infectious materials, including clinical and nonclinical staff but excluding remote workers. **Results:** The CDPH received reports of 3,176 mpox cases during the study period: 109 were HCP. Of the 109 HCP identified from 19 counties, 78 (72%) were aged 30–49 years, 102 (94%) were male, and 43 (39%) were Hispanic or Latino. Also, 29 HCP (27%) had received at least 1 dose of the JYNNEOS vaccine. Occupations requiring frequent physical interactions with patients were reported for 66 individuals (61%). During interviews with local health department investigators, nearly all HCP (n = 98, 90%) reported potential or confirmed sources of community exposure; 1 had confirmed occupational exposure with symptom onset 9 days after a sharps injury acquired during collection of an mpox specimen for testing. Of the 60 HCP who provided information about the days they worked, 35 (58%) worked while symptomatic, for a mean of 3.14 days (median, 2; IQR, 3). Also, 2 HCP worked for 12 days after symptom onset. No secondary cases of mpox were associated with HCP reported to the CDPH. **Conclusions:** This analysis suggests that HCP are more likely to be exposed to mpox in community settings than healthcare settings. The findings support recommendations against sharps use for mpox specimen collection. Although transmission between symptomatic HCP and patients was not reported, HCP can decrease opportunities for mpox transmission by closely monitoring themselves for symptoms after potential exposures and staying home from work if symptoms develop.

Disclosures: None

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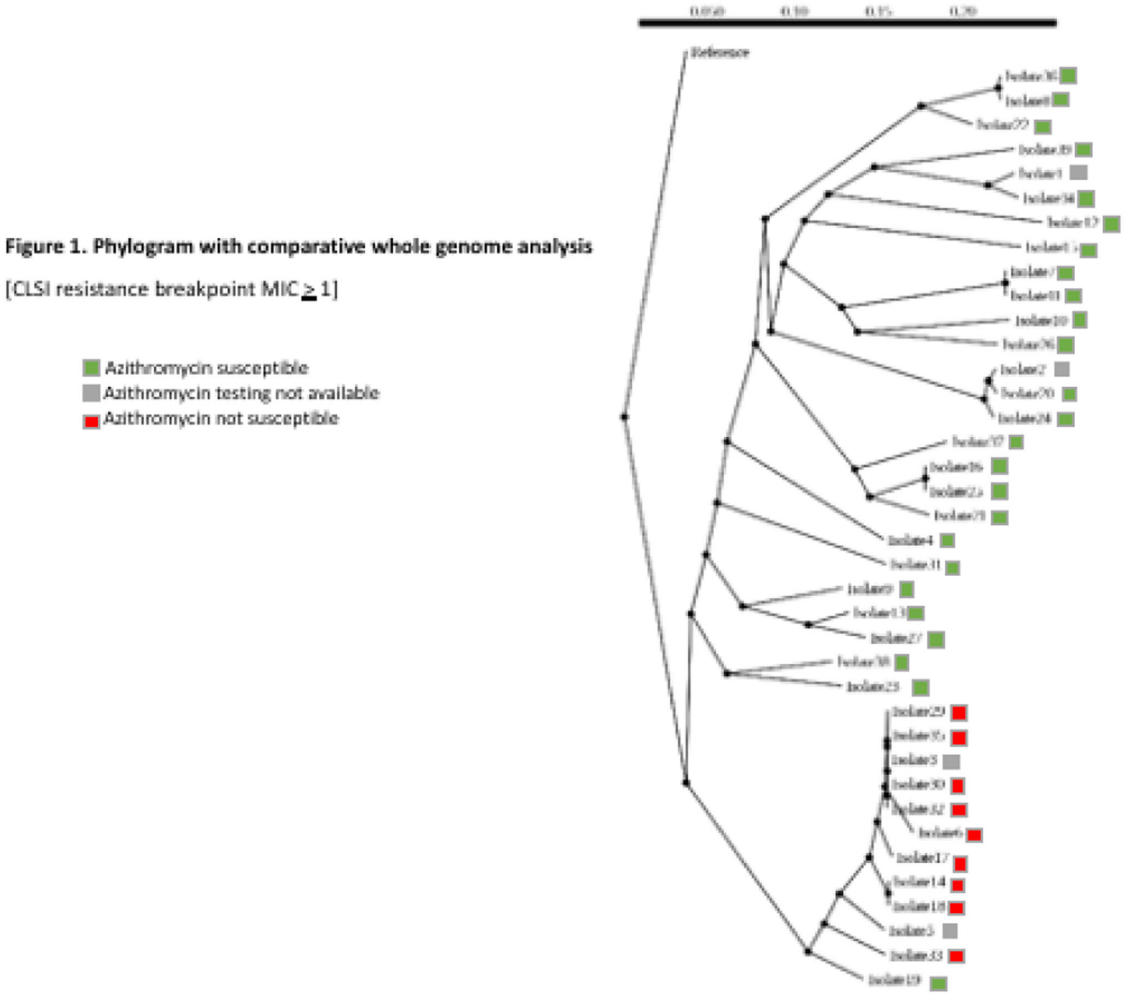

Figure 1. Phylogram with comparative whole genome analysis

[CLSI resistance breakpoint MIC ≥ 1]

Presentation Type:
Poster Presentation - Poster Presentation
Subject Category: Emerging Pathogens

Genetic relatedness among *Neisseria gonorrhoeae* isolates in southeastern Michigan

Anita Shallal; Robert Tibbets; Katherine Gurdziel; Dora Vager; Marcus Zervos and Geehan Suleyman

Background: Antimicrobial resistance (AMR) in *Neisseria gonorrhoeae* (NG) is an emerging public health crisis. Whole-genome sequencing (WGS) is an efficient way of predicting AMR determinants and their spread in the population. In a previous study, genotype–phenotype correlation analyses among NG isolates to determine antimicrobial resistance revealed discordance for azithromycin (AZM) and ceftriaxone (CRO) compared to other antibiotics. We investigated the evolutionary relatedness of NG isolated from patients with sexually transmitted infection (STI) using WGS in southeastern Michigan. **Methods:** Isolates, corresponding demographic data, and minimum inhibitory concentrations (MIC) via E-test (CRO) and broth microdilution (AZM) were obtained from the Michigan Department of Health and Human Services. Whole-genome libraries were prepared using the QIAseq FX kit followed by sequencing on a NovaSeq6000 (>200X Coverage); samples were aligned to NG reference strain TUM19854 (NZ_AP023069.1) using Snippy before phylogenetic tree generation using Neighbor-joining clustering on the core.aln files. Phylogenetic trees were visualized using ATGC:PRESTO. **Results:** In total, 38 isolates were analyzed. Demographic data and susceptibility testing results are noted in Table 1. Most isolates were from males (63%), Blacks (44.7%), individuals living in Detroit City proper (47.3%), and those with unknown HIV status (55.2%). More than one-third had prior STI, including NG. All isolates were susceptible to CRO (CLSI susceptible breakpoint MIC, 1). Within the phylogenetic tree, 8 main branches were identified (Fig. 1). Moreover, 1 branch contained a cluster with 12 closely related isolates, which included the 9 isolates with nonsusceptible AZM. Nearly all isolates in that cluster had been collected from Detroit City proper and Wayne County, suggesting epidemiological overlap and potential spread of resistant strains in those counties.

Conclusions: Comparative whole-genome and phylogenetic analyses among a subset of NG isolates revealed clustering of AZM resistance strains, suggesting a genomic component to AMR. Further studies are needed to determine the utility of WGS in diagnosis, outbreak investigations, and management of NG infections.

Disclosures: None

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