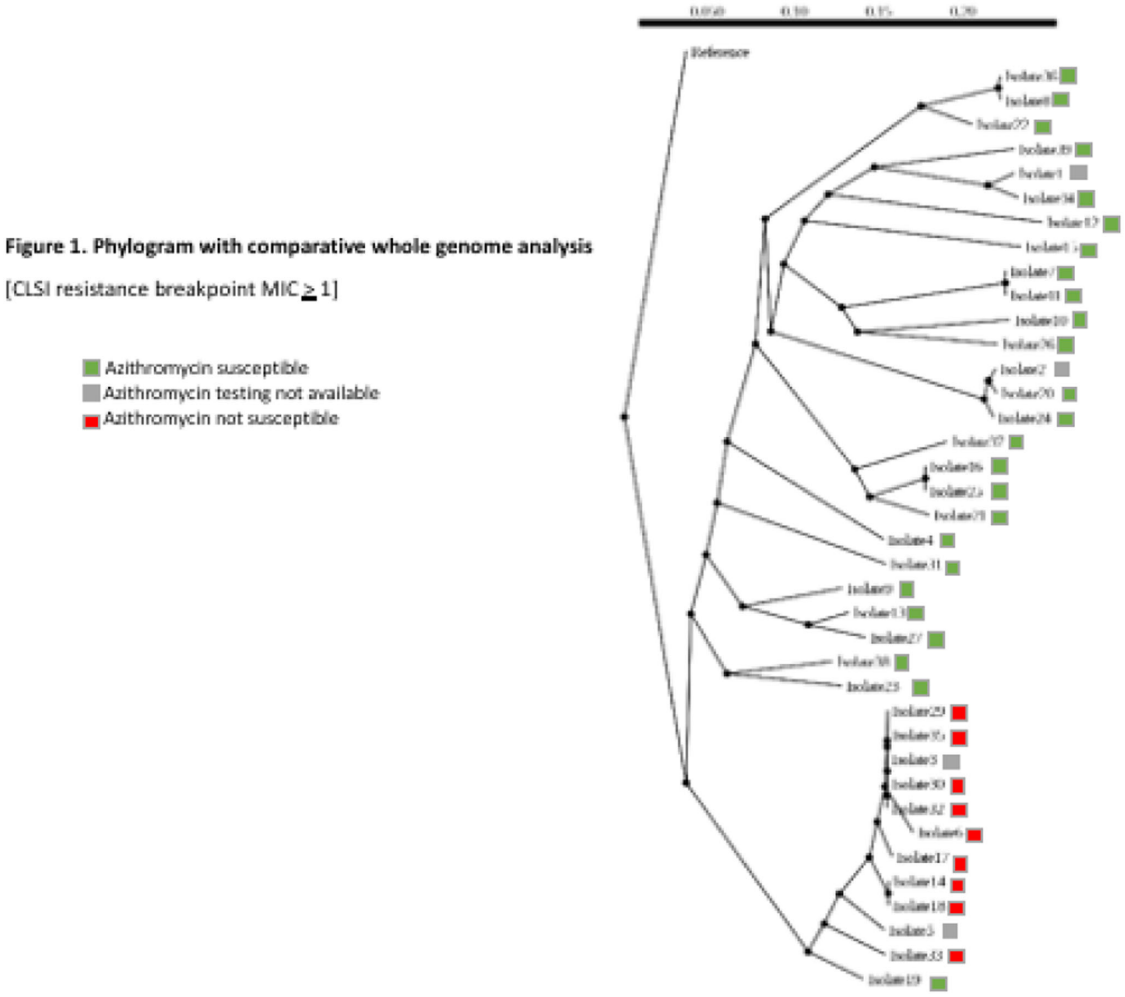

Figure 1. Phylogram with comparative whole genome analysis

[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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Table 1. Demographic characteristics corresponding to isolates

Characteristic	Number (%) (n=38)
Age, median [IQR]	25 [13.5] Range: 13 – 56
Male sex	24 (63%)
Race	
- Caucasian	10 (26.3%)
- Black	17 (44.7%)
- Other	4 (10.5%)
- Unknown	7 (18.4%)
Ethnicity	
- Hispanic	1 (2.6%)
- Not Hispanic	19 (50%)
- Unknown	18 (47.3%)
Southeast Michigan county	
- Detroit City proper	18 (47.3%)
- Wayne County	7 (18.4%)
- Oakland County	6 (15.7%)
- Macomb County	6 (15.7%)
- Statewide	1 (2.6%)
HIV status	
- Positive	6 (15.7%)
- Negative	11 (28.9%)
- Unknown	21 (55.2%)
Sexual orientation	
- Female having sex with males	14 (44.7%)
- Male having sex with females and males	2 (5.2%)
- Male having sex with males	4 (10.5%)
- Unknown	18 (47.3%)
Previous NG infection	
- More than once	5 (13.2%)
- Once	8 (21%)
- No	25 (65.8%)
Previous other sexually transmitted infection	
- More than once	9 (23.7%)
- Once	5 (13.1%)
- No	24 (63.2%)
Specimen source	
- Blood	1 (2.6%)
- Urine	18 (47.3%)
- Cervix, vagina	11 (28.9%)
- Throat	3 (7.9%)
- Perianal, rectal	3 (7.9%)
- Penis	1 (2.6%)

Presentation Type:
Poster Presentation - Poster Presentation
Subject Category: Emerging Pathogens
Mpox exposure on a congregate inpatient psychiatry unit: Description of the investigation and outcomes—New York City, 2022
Waleed Malik; Justin Chan; Simon Dosovitz; Clyde Gilmore and Jeanne Cosico

Background: In May 2022, New York City (NYC) experienced a large outbreak of human mpox (clade IIb). Data on mpox transmission following exposure in healthcare facilities in nonendemic settings are limited. Because mpox was previously not seen in NYC, our healthcare staff may not always recognize a suspected case and therefore may neglect to implement timely infection prevention and control measures, leading to infectious exposures. The risk of transmission from unrecognized mpox may be higher in inpatient psychiatric units where direct physical contact is more common in the setting of common spaces for patients. In July 2022, a patient was admitted to NYC Health + Hospitals–Bellevue (Bellevue) psychiatry with signs and symptoms of mpox that were not recognized for 4 days, at which point the patient was tested for mpox and was isolated. We describe the investigation of staff and patients exposed during the 4 days prior to diagnosis and isolation of the index patient, and we report on the outcome mpox infection among those exposed. **Methods:** This study was a retrospective chart review of adult patients admitted to and staff working on an inpatient psychiatric unit where the patient with mpox was admitted to Bellevue, the largest municipal hospital in NYC. Each individual was classified regarding degree of exposure, based on criteria from the CDC, and was offered postexposure mpox vaccination where indicated. We describe the nature of contact with the patient for those with high-risk exposures. The outcome of interest was development of mpox infection during 21 days after last exposure. **Results:** In total, 29 patients and 84 staff members were identified to have been on the psychiatric unit prior to isolation of the index case of mpox. All exposed individuals were monitored for signs and symptoms of mpox for 21 days after last exposure. The exposed and unexposed patients were kept apart in the psychiatric unit. All patients who had contact were classified as having a low-to-intermediate risk exposure. Among 23 staff members exposed, 8 had high-risk exposures, 4 had intermediate-risk exposures, and 11 had low-risk exposures. Those with high-risk exposures were offered Jynneos as postexposure vaccination, but they declined. None of the exposed staff or patients developed mpox during the follow-up period. **Conclusions:** Mpox transmission was not observed despite several exposures in a congregate psychiatry unit. Given limited data, further studies are needed to better understand transmission risk in congregate healthcare settings.
Disclosures: None

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Subject Category: Environmental Cleaning
Effect of dry hydrogen peroxide on *Candida auris* environmental contamination
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Background: *Candida auris* is an emerging pathogen that exhibits broad antimicrobial resistance and causes highly morbid infections. Prolonged survival on surfaces has been demonstrated, and standard disinfectants may not achieve adequate disinfection. Persistent patient colonization and constant environmental recontamination poses an infection risk that may be mitigated by no touch disinfection systems. We evaluated the efficacy of continuous dry hydrogen peroxide (DHP) exposure on *C. auris* environmental contamination. **Methods:** The study was conducted in a large tertiary-care center where multiple patients were identified as either infected or colonized with *C. auris*. DHP-emitting systems were installed in the ventilation systems dedicated to the adult burn intensive care and children's cardiac intensive care units. Composite surface samples were collected in a sample of patient rooms and shared clinical workspaces among units with current *C. auris* patients, before and after installation of the DHP system, and from areas with and without exposure to DHP. The samples included "high touch" surfaces near the patient, the general area of the patient room, shared medical equipment for the unit, shared staff work areas, and equipment dedicated to individual staff members (Table 1). Presence of *C. auris* was determined by polymerase chain reaction (PCR). Association between DHP exposure and *C. auris* contamination was determined using the Fisher exact test. **Results:** In the presence of *C. auris* patients, 5 baseline samples per unit were taken before DHP was installed, and then 5 samples per unit were taken on days 7, 14, and 28 after installation. Prior to initiation of DHP, 7 (70%) of 10 samples were PCR positive for *C. auris*. After DHP installation, a statistically significant decrease to 5 (16.7%) of 30 samples ($P < .05$) was observed. In total, 20 samples (5 before installation and 15 after installation) were collected from units without DHP on the same days. At baseline, 2 (40%) of 5 samples were PCR positive for *C. auris*. During subsequent periods, 4 (27%) 15 samples were positive ($P = .66$). No adverse effects were reported by

Table 1: Composite sample collection areas

Composite sample description:	Composite swab includes:
High touch surfaces near patient	Bedside Table, Ventilator if present, bed rails, nurse call button
General patient room area	Curtain, window sill, glove box, keyboard, sink or counter surface
Shared medical equipment	Glucometer, Vitals machine
Shared staff areas outside patient room	Nursing desk or counter, nursing keyboard and mouse
Staff only equipment	Stethoscope, mobile phones, workstation on wheels