ANTIMICROBIAL SUSCEPTIBILITY AMONG OROPHARYNGEAL *NEISSERIA* ISOLATES FROM MEN IN A HIV PrEP PROGRAM IN HANOI, VIETNAM

Authors:
Dong HV[1], Adamson PC[2], Pham DH[3], Pham QH[3], Le HHL[3,4], Pham QL[4], Bui HTM[4], Le MG[4], Klausner JD[4]

[1]Division of Pediatric Infectious Diseases, David Geffen School of Medicine at University of California, Los Angeles (UCLA), California, USA, [2]Division of Infectious Diseases, David Geffen School of Medicine at University of California, Los Angeles (UCLA), California, USA, [3]National Hospital for Dermatology and Venereology, Hanoi, Vietnam, [4]Center for Training and Research on Substance Abuse-HIV, Hanoi Medical University, Hanoi, Vietnam, [5]Population and Public Health Sciences, Keck School of Medicine at USC, Los Angeles, California, USA

Background:
Antimicrobial resistance (AMR) among *Neisseria gonorrhoeae* (NG) is an urgent global health concern. Commensal *Neisseria* species in the oropharynx are hypothesized to be a reservoir of AMR genes that are transferred to NG yet few data about AMR among commensal *Neisseria* in populations at risk for AMR exist.

Methods:
From 5/2022 – 12/2023, men-who-have-sex-with-men in an HIV Pre-exposure prophylaxis program in Hanoi, Vietnam, were recruited to study AMR of *Neisseria* in the oral cavity. Participants self-collected oral rinses using 10mL of phosphate buffer solution, which was diluted 1:100 and 1 mL was plated directly onto LB agar containing Vancomycin (3ug/mL) and Trimethoprim (3ug/mL). Gram-negative diplococci isolates were identified using RapID NH system (Remel). Minimum inhibitory concentrations (MIC) to Azithromycin, Ceftriaxone, Cefixime, and Doxycycline were determined using Etests (Biomerieux). CLSI breakpoints for *Neisseria gonorrhoeae* were used for interpretation; doxycycline was interpreted using tetracycline breakpoints.

Results:
There were 42 male participants, the median age was 26 years (IQR 21-28), and 29% (n=12) reported using antibiotics in the past 6 months. In total, 48 *Neisseria* isolates were recovered; *N. sicca/subflava* was the most common species (50%; n=24), followed by *N. mucosa* (38%; n=18). For azithromycin, 85% (n=41) of isolates were non-susceptible, including 25% (n=12) with high level resistance (MIC ≥ 256) of which 67% (8/12) were *N. mucosa*. Non-susceptibility among non-gonococcal *Neisseria* isolates was 3% (n=4) to Ceftriaxone, 3% (n=4) to Cefixime, and 42% (n=20) to doxycycline; most non-susceptible isolates were *N. mucosa.*

Conclusion:
A high prevalence of azithromycin non-susceptibility and low prevalence of cephalosporin non-susceptibility was found in oropharyngeal *Neisseria* from MSM in Hanoi, Vietnam. *N. mucosa* was over-represented among non-susceptible isolates. Further research into the prevalence and genomic determinants of AMR in commensal *Neisseria* from diverse populations is needed to improve our understanding of the relationship to AMR in NG.

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