Surveillance of Antimicrobial Resistance in *Neisseria gonorrhoeae* and *Mycoplasma genitalium* in DOW Beneficiaries within INDOPACOM

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Background

Sexually transmitted infections (STIs) are a significant concern for military operational readiness and healthcare costs, with an observable rise in cases since 2009[a]. The threat is compounded by increasing antimicrobial resistance (AMR), especially in *Neisseria gonorrhoeae* (GC) and the emerging pathogen *Mycoplasma genitalium* (MG). *N. gonorrhoeae* has developed resistance to nearly every antibiotic used against it, while *M. genitalium* shows high-level resistance to both macrolides and fluoroquinolones.

This surveillance project characterizes AMR prevalence in these pathogens and assesses co-infection rates at Madigan Army Medical Center (MAMC) in Washington and Tripler Army Medical Center (TAMC) in Hawaii, two key INDOPACOM sites. The transient nature of military personnel, coupled with tourism from Asia and the Pacific, may amplify the transmission of resistant strains, making such surveillance critical.

[a]Office of the Deputy Assistant Secretary of Defense (Military Community and Family Policy) Demographics Profile of the Military Community. 2012.

Methods

- Positive clinical specimens from MAMC and TAMC were used for this surveillance.
- GC-positive - 61 samples from MAMC (84% Male) and 86 samples from TAMC (91% Male).
- MG-positive - 15 samples from MAMC (93% Male) and 15 samples from TAMC (80% Male).
- Samples consisted of urine and swabs (throat, rectal, endocervical, vaginal, and urethral) and analyzed using NAAT on the Hologic Panther.
- DNA was extracted using the QIAGEN EZ One DSP Virus Kit.
- The NextSeq1000 and the Illumina Urinary Pathogen Identification Panel (UPIP) were used to sequence and identify AMR markers.
- The UPIP analysis pipeline on BaseSpace (Illumina) was used for species identification and AMR detection.

Results

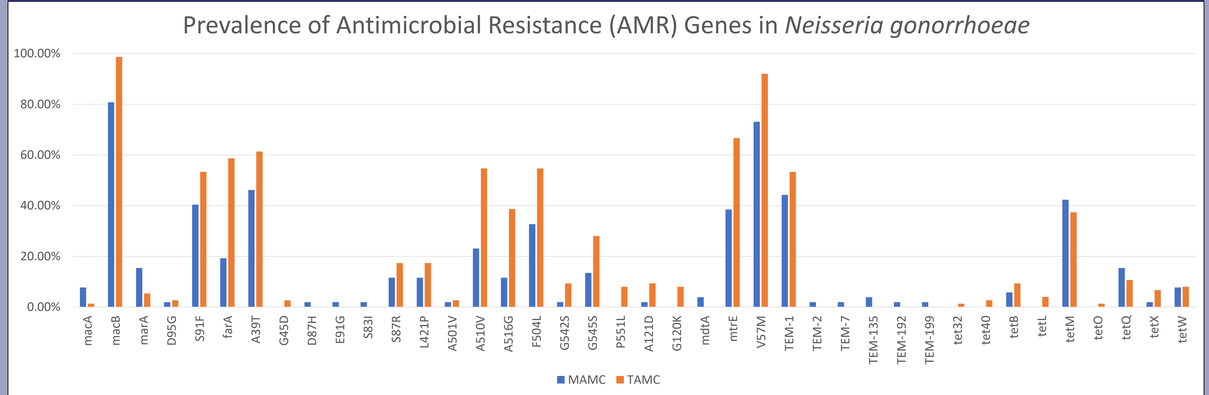

Figure 1: This figure illustrates the prevalence of antimicrobial resistance (AMR)-associated genes in *Neisseria gonorrhoeae* isolates from MAMC (Blue) and TAMC (Orange) cohorts. While genes like macB, V57M, and A39T are highly prevalent at both sites, most resistance determinants—such as the key marker *mtrE* (detected in nearly 67% of TAMC isolates)—show a consistently higher prevalence in the TAMC cohort. These site-specific genetic variations provide critical insights for localized molecular surveillance and resistance tracking.

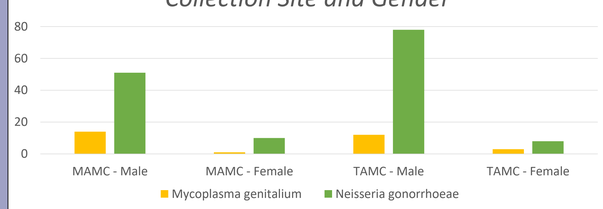

Figure 2: This figure provides a comparative analysis of the prevalence of *Mycoplasma genitalium* (Yellow) and *Neisseria gonorrhoeae* (Green) stratified by both collection site and gender. The most prominent finding is the overwhelmingly high prevalence of *N. gonorrhoeae* in male patients, whereas the prevalence of *M. genitalium* remains comparatively low across all categories. Male cohorts at both MAMC and TAMC shows significantly higher numbers of infections compared to their female counterparts. Furthermore, there is a notable geographic disparity in the disease burden, as the TAMC male population exhibits a substantially higher prevalence of gonococcal infections than the MAMC male population.

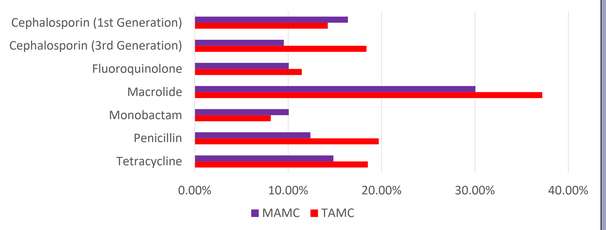

Figure 3: This figure presents a comparative analysis of antimicrobial resistance in *Neisseria gonorrhoeae* isolates from two distinct populations, MAMC (Purple) and TAMC (Red), displaying the percentage of resistant isolates across seven key antibiotic classes. Both cohorts exhibit critically high resistance to Macrolides (reaching 37% at TAMC and 30% at MAMC) alongside notable resistance to first-line, standard-of-care 3rd Generation Cephalosporins (which is higher in the TAMC cohort at ~18%). Site-specific differences are highly evident across the remaining classes, with Tetracycline resistance being more pronounced in the MAMC cohort and Penicillin resistance appearing significantly more prominent in the TAMC cohort.

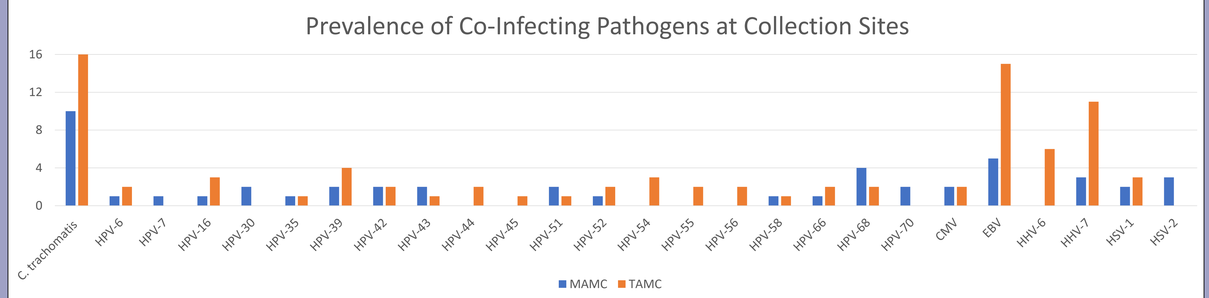

Figure 4: This figure provides an analysis of co-infecting pathogens found in patients at MAMC and TAMC, displaying case counts of concurrent bacterial and viral infections. The TAMC cohort exhibits a significantly higher and more diverse burden of co-infections compared to the MAMC cohort, driven primarily by concurrent *Chlamydia trachomatis* (16 cases), *Epstein-Barr Virus* (15 cases), and *Human Herpesvirus 7* (11 cases). Conversely, MAMC faces a more localized challenge dominated overwhelmingly by *C. trachomatis* (10 cases) but notably exhibits a higher prevalence of HPV-68, a high-risk oncogenic viral strain linked to future malignancies. TAMC exhibits a much wider variety of high-risk Human Papillomavirus (HPV) strains compared to MAMC. Ultimately, these distinct epidemiological signatures underscore a critical need for site-specific, comprehensive diagnostic strategies to effectively manage patient care at each military treatment facility.

Learning Objectives

1. Explain the strategic importance of monitoring antimicrobial resistance (AMR) in pathogens like *Neisseria gonorrhoeae* and *Mycoplasma genitalium*.
2. Describe a significant threat of *GC* and *MG* to individual health, operational readiness, and the military healthcare system.
3. Analyze and compare the regional differences in AMR patterns and co-infection rates.

Conclusion

- *Neisseria gonorrhoeae* is significantly more prevalent than *Mycoplasma genitalium* and overwhelmingly concentrated in male patients, with the highest overall infection burden observed in the TAMC male cohort.
- The TAMC cohort exhibits a significantly higher prevalence of critical antimicrobial resistance genes (such as mtrE at ~67%) compared to MAMC though both cohorts share high levels of macB, V57M, and A39T resistance determinants.
- Both sites exhibit critical resistance to Macrolides (37% at TAMC) and first-line 3rd Generation Cephalosporins (18% at TAMC), with MAMC showing higher Tetracycline resistance and TAMC showing higher Penicillin resistance.

Discussion

High prevalence of antimicrobial resistance markers and site-specific variation in mutations/co-infections highlight the critical need for regional multi-site surveillance to track transmission and guide targeted military health interventions.

Acknowledgements

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This was done as a public health surveillance project and did not require IRB approval.