Prospective Tracking of Multidrug-Resistant Organism Colonization in U.S. Military Emergency Providers During a Short-Term Deployment to Honduras

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INTRODUCTION

- Multidrug-resistant organisms (MDROs) are a growing global health threat, particularly in low- and middle-income countries with estimated over 3.57 million deaths worldwide in 2019 alone. While the exact predominance of MDRO across Honduras has not been quantified several studies have shown severe rates of MDRO infections, especially highlighting Carbapenem resistance. A trend seen across the developing world in a multifactorial global issue.
- Historically, U.S. military service members have been active across the developing world, and studies have shown they are at risk of becoming colonized with local endemic bacterial species, however these studies primarily focus on wounded soldiers or those remaining in country for extended periods of time. U.S. military medical personnel frequently deploy to resource-limited settings and may be exposed to endemic resistant organisms before returning to U.S. practice.
- We evaluated whether short-term clinical deployment to Honduras was associated with changes in microbiome diversity or acquisition of clinically relevant antimicrobial resistance (AMR) genes. Major AMRs of concern were considered Methicillin-resistant Staphylococcus aureus (MRSA), Extended-spectrum beta-lactamases (ESBL), Carbapenem Resistant Acinetobacter (CRAB).

METHODS

- We conducted a prospective observational pilot study of 25 active-duty U.S. military emergency medicine physicians and physician assistants participating in 2- to 4-week clinical rotations in Tegucigalpa, Honduras.
- Participants were selected by petitioning individuals already completing the Military Emergency Skills in Honduras (MESH) or the Military Unique Curriculum in Honduras (MUCH) programs.
- MESH and MUCH are 2-to-4-week rotations performing clinical care along side partner nation medical teams at Hospital Escuela in Tegucigalpa, Honduras.
- Participants collected paired pre-deployment and post-deployment swabs from the nares, oral cavity, hands, and groin. Microbiome composition was assessed with 16S rRNA sequencing, and AMR genes were assessed using a targeted sequencing panel. Analyses focused on within-subject differences between pre- and post-deployment samples.

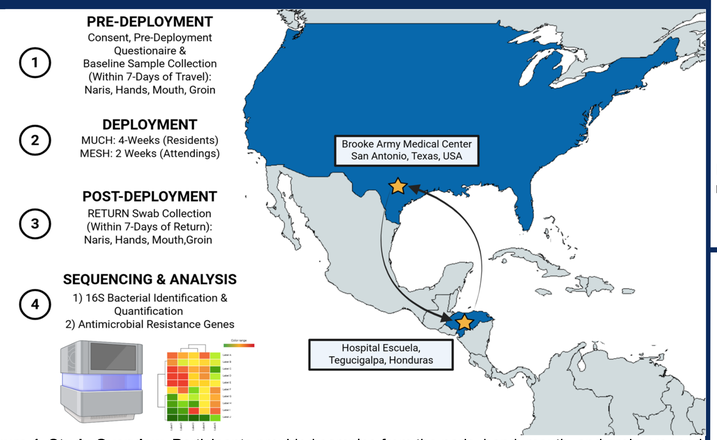

Figure 1. Study Overview. Participants provided samples from the naris, hand, mouth, and groin pre- and post-deployment to Hospital Escuela in Tegucigalpa, Honduras. Map adapted from https://www.mapchart.net/. Figure created in https://BioRender.com.

RESULTS

Demographics & Timing		Pre-deployment Questionnaire Responses		Post-deployment Questionnaire Responses	
Age, years (mean ± SD)	31.1 ± 3.4	Antibiotic use within 30 d, n (%)	0 (0)	Antibiotic use during deployment, n (%)	3 (12%)
Male, n (%)	17 (68%)	Infectious symptoms within 14 d, n (%)	0 (0)	Antibiotics used	Ciprofloxacin/dexamethasone (n = 1); weekly doxycycline prophylaxis (n = 2)
Female, n (%)	8 (32%)	Travel outside the U.S. within 90 d, n (%)	3 (12%)	Development of acute infectious symptoms, n (%)	7 (28%)
Attending physicians, n (%)	7 (28%)	Destinations	Bahamas, Guam, Palau	Symptoms reported	External ear infection (n = 1); upper respiratory tract infection (n = 6)
Resident physicians, n (%)	18 (72%)	History of MRSA, n (%)	0 (0%)	Needle stick injury, n (%)	1 (4%)
Deployment Characteristics				Estimated trauma evaluations (mean ± SD)	16.5 ± 15.4
Duration in Honduras, d (mean ± SD)	17.0 ± 5.1	History of Immunocompromised state, n (%)	0 (0%)	Estimated intubations (mean ± SD)	3.4 ± 2.8
Time from return to sample collection, hours (mean ± SD)	41.0 ± 21.6			Estimated other procedures (mean ± SD)	12.0 ± 8.9

Table 1. Participant Characteristics and Questionnaire Responses.

Disclaimer: The views expressed in this presentation are those of the authors and do not necessarily reflect the official policy or position of the Defense Health Agency, Department of War, nor the U.S. Government. The study protocol was approved by the San Antonio Military Institutional Review Board in compliance with all applicable Federal regulations governing the protection of human subjects. Research data were derived from an approved Institutional Review Board protocol number C.2024.079d. This work is supported by funding from the Defense Health Agency.

RESULTS (Continued)

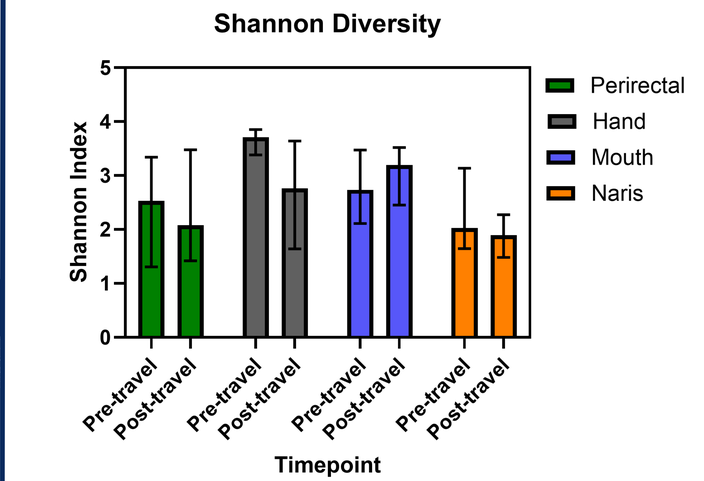

Figure 2. Shannon diversity for peri-rectal (green), hand (grey), mouth (blue), and naris (orange) regions sampled pre- and post-deployment. Shannon index values are expressed as median ± IQR. Statistical significance was set at p<0.05. Mann-Whitney analyses demonstrated no significant difference between pre- and post-deployment diversity.

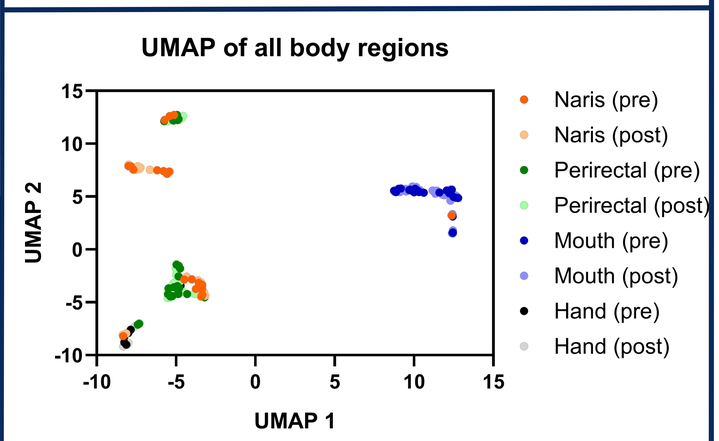

Figure 3. UMAP of pre- (darker-colored) and post-deployment (lighter-colored) microbiome data for the naris (orange), groin (green), mouth (blue), and hand (black) regions.

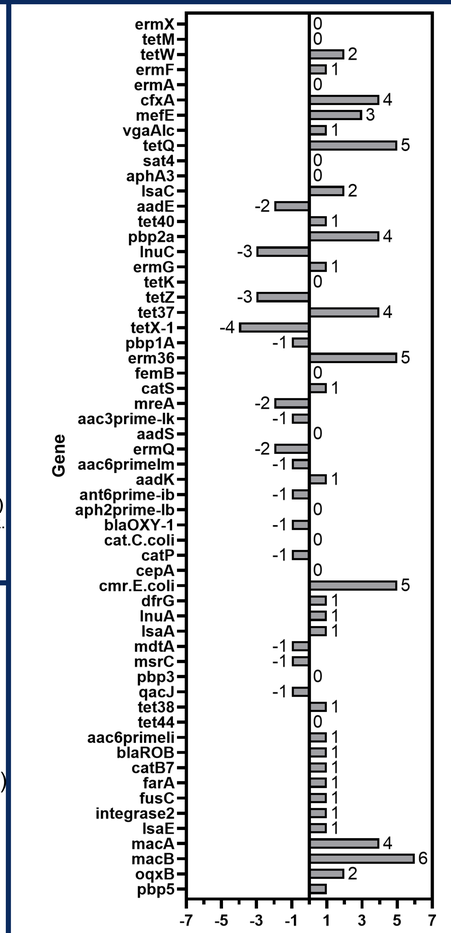

Figure 4. Change in number of subjects expressing antimicrobial resistance (AMR) genes from all sampling sites (groin, hand, mouth, and nose) from pre- to post-deployment (absolute difference calculated as post minus pre # of subjects). Genes are ranked by commonality amongst all 24 subjects from top (most common) to bottom (least common).

CONCLUSIONS

- In this prospective, observational pilot study, short-duration clinical rotations in Honduras were not associated with significant changes in provider microbiome diversity, site-specific microbial community structure, or an increase in AMR genes at the sample sites.
- These results are limited by the small sample size, single cohort of participants and one travel destination, no testing of patients in Honduras to confirm participant exposure to MDROs, variable clinical experiences while on the MESH/MUCH rotations, and inability to link specific AMR genes with specific bacteria.
- Our results provide preliminary reassurance for similar short-duration military medical rotations and show feasibility of paired molecular surveillance in deployed medical providers.