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GUT MICROBIOME BIOMARKERS AND PERSONALIZED PROBIOTIC CORRECTION IN MILITARY PTSD

Background/Aim. Post-traumatic stress disorder (PTSD) is a significant challenge in military medicine, increasingly linked to the systemic and gut-microbiome dysregulation. This study aimed to characterize the gut microbiome of Ukrainian military personnel with PTSD, identify a reproducible core microbiome, and inform a microbiome-based risk-stratification model and personalized probiotic strain selection. **Methods.** Gut microbiota profiling was performed in $n = 41$ male Ukrainian military personnel with PTSD (DSM-5-TR), comprising two platform-based cohorts: Cohort 1 ($n = 18$, Illumina MiSeq, 16S rRNA V3–V4) and Cohort 2 ($n = 23$, Oxford Nanopore MinION, full-length 16S rRNA; HAC v4.3.0, $Q \geq 10$). No non-PTSD comparator group was included in this analysis; findings are a descriptive characterization within a larger ongoing project ($n = 300$) that also includes combat-exposed non-PTSD, IDP and healthy-control arms, to be reported separately. Core taxa were defined as present in $\geq 75\%$ of samples at $>0.1\%$ relative abundance; co-occurrence networks used SparCC (1,000 bootstraps, $|r| \geq 0.3$, pseudo- $P < 0.05$, BH-FDR < 0.05). Candidate probiotic strains were selected using the literature-established criteria (antagonism to pathobionts, acid resistance, organic acid production), corroborated by preliminary in vitro screening. **Results.** Across both cohorts, a reproducible core microbiome dominated by *Bacillota* (*Faecalibacterium prausnitzii*, *F. duncaniae*) and *Bacteroidota* (*Segatella copri*) was identified despite pronounced inter-individual heterogeneity (a single taxon often exceeded 40–60% relative abundance per patient). PCA showed clear separation by sequencing platform (PC1), indicating a technical batch effect; alpha-diversity comparisons were therefore exploratory (Wilcoxon test), and beta-diversity centroids differed by platform (PERMANOVA, 999 permutations). Network analysis identified *Faecalibacterium duncaniae* as a central hub, positively linked to *Marseillibacter massiliensis* and *Walteria intestinalis* and negatively to *Blautia fibrosolvens*. Based on antagonism, acid resistance and organic-acid production, candidate strains (*Lactiplantibacillus plantarum* A, *L. plantarum* IBM B-7413, *L. bulgaricus* A22, *Lacticaeibacillus rhamnosus* S25) were selected for a personalized probiotic prototype, DefendX. A preliminary Microbiome-Based Risk Score integrating these features was formulated; its predictive performance (sensitivity, specificity, AUC) is currently being validated in the extended cohort. **Conclusions.** In the absence of a matched comparator, these findings characterize a reproducible, platform-independent core gut microbiome in PTSD rather than confirm PTSD-specific dysbiosis. The Microbiome-Based Risk Score and the DefendX probiotic remain an in vitro/in silico-stage laboratory prototype; their diagnostic and therapeutic potential for military medicine requires validation in larger, controlled studies before clinical application can be considered. **Grants.** Ministry of Education and Science of Ukraine, project No. 0124U004303 (2024–2026).

Keywords: PTSD; gut microbiome; biomarkers; risk score; personalized probiotics; DefendX; military medicine

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