ORIGINAL ARTICLE

CONTENTS

Interaction between gut microbiota and antibiotic resistance in patients with PTSD: Data from a cohort study

Oleksandra Pallah[1], Ivan Lypei[1,2], Svitlana Burmei[1,2], Lesya Yusko[1], Nadiya Boyko[1,2]
[1]UZHHOROD NATIONAL UNIVERSITY, UZHHOROD, UKRAINE
[2]EDIENS, LLC, VELYKI LAZY, UKRAINE

ABSTRACT

Aim: To analyze the composition of gut microbiota, antibiotic resistance profiles of isolated strains, and biochemical blood parameters in individuals with and without PTSD.

Materials and Methods: A cohort study was conducted involving 82 participants: 40 patients diagnosed with PTSD and 42 without PTSD (control group). All subjects completed the PCL-5 questionnaire and underwent clinical examination, biochemical blood testing, and microbiological analysis of fecal samples. Bacterial identification and antibiotic susceptibility testing were performed using standardized culturomic and EUCAST methods.

Results: PTSD patients showed a significantly higher prevalence of opportunistic microorganisms, including Klebsiella pneumoniae and Enterobacter cloacae, and a reduction in beneficial strains such as Lactobacillus casei. Increased resistance to carbapenems and macrolides was noted in the PTSD group. Biochemical analysis revealed hyperglycemia, elevated liver enzymes, decreased total protein, and increased markers of inflammation. These findings demonstrated significant correlations between gut dysbiosis, antibiotic resistance, and systemic metabolic alterations.

Conclusions: The study confirms a link between gut microbiota composition, antimicrobial resistance, and metabolic dysregulation in PTSD patients. These results may inform the development of integrated diagnostic approaches and targeted interventions in PTSD management.

KEY WORDS: PTSD, gut microbiota, antibiotic resistance, dysbiosis, biochemical markers

Wiad Lek. 2025;78(11):2343-2351. doi: 10.36740/WLek/211723 DOI

INTRODUCTION

Post-traumatic stress disorder (PTSD) is a complex neuroimmune condition that does not always develop even after severe trauma exposure. It emerges as a result of traumatic experiences and excessive stress, affecting patients' cognitive functions, emotional state, and physical health. Studies, particularly in the context of the war in Ukraine, confirm that PTSD significantly reduces quality of life, disrupts social adaptation, and increases the risk of comorbid disorders, including depression and generalized anxiety disorder [1, 2]

Recent studies (2019–2025) demonstrates increased interest in the impact of microbiota on mental health, particularly regarding disorders such as post-traumatic stress disorder (PTSD) [3, 4]. It has been proven that the microbiota plays a key role in the regulation of the "gut-brain" and "gut-immunity" axes, interacting with the central nervous and immune systems through metabolites (e.g., short-chain fatty acids – butyrate, propionate, acetate), neurotransmitters (serotonin, γ-aminobutyric acid), and inflammatory cascade mechanisms [5].

Changes in the composition of microbiota cause systemic inflammation and can influence the levels of both systemic and neuroinflammation. These inflammatory processes, in turn, affect the development of depressive and anxiety disorders and can alter the body's response to stress [6].

Moreover, experimental models demonstrate that microbiota transplantation from individuals with PTSD to germ-free rats can induce behavioral changes characteristic of increased anxiety and hyperarousal [7].

Alongside microbiota, biochemical blood markers play an important role in the diagnosis and understanding of PTSD pathophysiology, reflecting metabolic state, inflammatory activity, and the functioning of internal organs. Changes in levels of glucose, liver enzymes (ALT, AST), creatinine, protein, leukocytes, and platelets may result from chronic stress as well as indicate systemic effects of an altered gut microbial composition. This is supported by the findings by Zhou et al. (2020), who demonstrated that systemic inflammation associated with PTSD is accompanied by biochemical changes in

the blood, including hyperglycemia, liver and kidney dysfunction [8].

Similar changes have also been described in the paper of Foster et al. (2022), who emphasize the connection between metabolic processes, microbial profile, and the psycho-emotional state of an individual [9].

Thus, combining microbiological analysis with screening of biochemical markers enables a more comprehensive understanding of the physiological state of patients with PTSD and identifies potential targets for therapeutic intervention.

As was mentioned, the gut microbiota is not only a defined component of immune defense but also a key regulator of the "gut-brain" axis. Disruptions in the composition and functions of the gut microbiota, particularly dysbiosis, can lead to enhanced inflammatory processes, impaired intestinal barrier function, and altered production of neurotransmitters [10-12].

Consequently, it may contribute to the worsening of psycho-emotional disorders, including PTSD.

At the same time, it has been proven that dysbiosis can increase the risk of intestinal colonization by opportunistic microorganisms, among which multidrug-resistant bacterial strains are often found [13]. In patients with PTSD, who often undergo treatment in hospital settings, the risk of colonization by resistant opportunistic microorganisms increases significantly. This is associated both with the widespread use of antibiotics and with microbiota changes induced by chronic stress [14]. Moreover, broad-spectrum antibiotics reduce microbiota diversity, leading to an imbalance between beneficial and opportunistic microorganisms.

Thus, disruption of the gut microbiota not only intensifies inflammatory processes and affects mental health but also creates preconditions for the development of antibiotic resistance, complicating the course of the underlying disease and requiring a comprehensive treatment approach.

The use of probiotics may help restore microbiota balance and reduce the risk of antibiotic resistance. Studies have shown that certain probiotic strains are capable of inhibiting survivance of multidrug-resistant bacteria and disrupting their biofilms, thereby reducing antibiotic resistance [15-18].

The data obtained indicates the potential of gut microbiota as a therapeutic target in the correction of mental disorders, which justifies usage of probiotics, prebiotics, and dietary recommendations in a comprehensive approach to psychiatric therapy.

AIM

To analyze the composition of gut microbiota, antibiotic resistance profiles of isolated strains, and biochemical blood parameters in individuals with and without PTSD.

MATERIALS AND METHODS

The study included 82 individuals, divided into two main groups: a group of patients diagnosed with PTSD (n=40) and a group without signs of PTSD (n=42), which served as the control. Patients were hospitalized at Uzhhorod City Multidisciplinary Hospital and the regional psychiatric facility in Berehove (September–December 2024). All individuals provided written informed consent prior to enrollment. Each participant underwent a comprehensive assessment that included the administration of the PTSD Checklist for DSM-5 (PCL-5), a clinical medical examination, and laboratory testing. Laboratory evaluations consisted of general and biochemical blood tests to support the clinical findings and explore potential physiological correlations of PTSD.

Gut microbiota was examined by culturomic technique by using of plating of fecal samples, serial dilution on selective and chromogenic nutrient media [19]. After cultivation at 37 °C for 24–48 hours, colony-forming units (CFUs) of bacteria were counted. Fecal samples were collected in sterile containers and transported to the laboratory. Bacterial identification was carried out based on morphological, biochemical, and serological characteristics.

The study of antibiotic resistance of microorganisms was conducted using the disk diffusion method in accordance with EUCAST standards (2023) [20, 21]. A standard set of disks with 12 key antibiotics was used, covering representatives of carbapenems, beta-lactams, macrolides, fluoroquinolones, and aminoglycosides.

Statistical analysis was performed using SPSS v.26. The χ^2 test was used for frequency comparisons, the Mann–Whitney U test for quantitative variables, and Pearson's correlation analysis (r) was applied.

ETHICS

The research was conducted in accordance with ethical standards. All patients gave informed consent.

RESULTS

The results of the microbiological analysis of fecal samples indicate alterations in the gut microbiota of patients with PTSD. Compared to the control group, differences were noted both in the spectrum of isolated microorganisms and in their antibiotic resistance.

Microbiological examination of fecal samples revealed significant changes in the gut microbiota composition of patients with PTSD (n=40) compared to the control group (n=42). These differences included the spectrum of isolated microorganisms, their concentration profiles, and antibiotic resistance.

In the control group, the dominance of representatives of the normal microbiota with minimal presence

Table 1. Species composition and concentration of generous microorganisms in feces of control group participants

Microorganism species	Detection frequency (%)	Number of isolates (n)	Concentration (CFU/mL; M ± SD)
Escherichia coli	45%	19	$(2.1 \pm 0.3) \times 10^6$
Bacteroides thetaiotaomicron	27%	11	$(7.8 \pm 1.2) \times 10^7$
Lactobacillus casei	18%	8	$(1.3 \pm 0.2) \times 10^6$
Enterobacter cloacae	5%	2	$(9.5 \pm 1.0) \times 10^3$
Staphylococcus aureus	7%	3	$(1.2 \pm 0.3) \times 10^4$

Source: compiled by the authors of this study

Table 2. Microorganisms identified by advanced analysis (n=40)

Isolates	Number of patients (n=40)
Klebsiella pneumoniae	7
Enterobacter cloacae	5
Proteus mirabilis	4
Staphylococcus aureus	8
Corynebacterium spp.	3
Lactobacillus casei (decreased number)	13

Source: compiled by the authors of this study

Table 3. Susceptibility of *Klebsiella pneumoniae* (n=7)

№	Antibiotic	EUCAST Breakpoints (mm)		Inhibition Zone (mm ± SD)
		S ≥	R <	
1	Meropenem	≥ 22	< 22	11.0 ± 1.6
2	Imipenem/Cilastatin	≥ 22	< 19	13.5 ± 2.1
3	Ceftriaxone	≥ 25	< 22	12.3 ± 2.0
4	Azithromycin	≥ 17	< 13	11.8 ± 2.4
5	Levofloxacin	≥ 23	< 19	10.9 ± 1.5

Source: compiled by the authors of this study

of opportunistic forms was observed (Table 1). Specifically, *Escherichia coli* was detected in 45% of samples (19 isolates) at an average concentration of $(2.1 \pm 0.3) \times 10^6$ CFU/mL. A significant portion of the microbial composition also consisted of *Bacteroides thetaiotaomicron* (27%; 11 isolates) at amount of $(7.8 \pm 1.2) \times 10^7$ CFU/mL. *Lactobacillus casei*, as key beneficial microbes, were isolated in 18% of samples (8 isolates) at a level of $(1.3 \pm 0.2) \times 10^6$ CFU/mL.

Among the opportunistic microorganisms in the control group, *Enterobacter cloacae* (5%; 2 isolates) and *Staphylococcus aureus* (7%; 3 isolates) were found sporadically, with concentrations of $(9.5 \pm 1.0) \times 10^3$ CFU/mL and $(1.2 \pm 0.3) \times 10^4$ CFU/mL, respectively. These values only slightly exceeded reference levels and were not clinically significant, indicating the preservation of eubiotic balance in participants without signs of PTSD.

Further analysis of the microbiological profile of patients with PTSD (n=40) included the quantitative determination of key representatives of commensal and opportunistic microbiota. The study covered four main bacterial groups: physiologically important commensals (*E. coli* lac+, *Enterococcus faecalis*, *Lactobacillus casei*) and opportunistic pathogens (*Enterobacter cloacae*, *Klebsiella pneumoniae*, *Staphylococcus aureus* MRSA). Additionally, for a subset of patients (n=13), an extended evaluation was conducted, including detailed antibiogram and microbiological characterization of the isolates.

E. coli lac+ was detected in all samples, with concentrations ranging from 10^7 to 10^8 CFU/mL, which corresponds to physiological norms for a major facultative anaerobe. This indicator suggests the preservation of a baseline level of obligate intestinal microbiota even in the presence of dysbiosis. At the same time, the quantity of *Lactobacillus casei* in most patients was below the reference range (10^6–10^8 CFU/mL). This indicates a reduction in the mucosal barrier function of the intestine and suggests weakened colonization resistance.

Enterococcus faecalis concentrations varied widely – from 10^3 to 10^8 CFU/mL. This discrepancy may reflect individual characteristics of microbial status as well as responses to

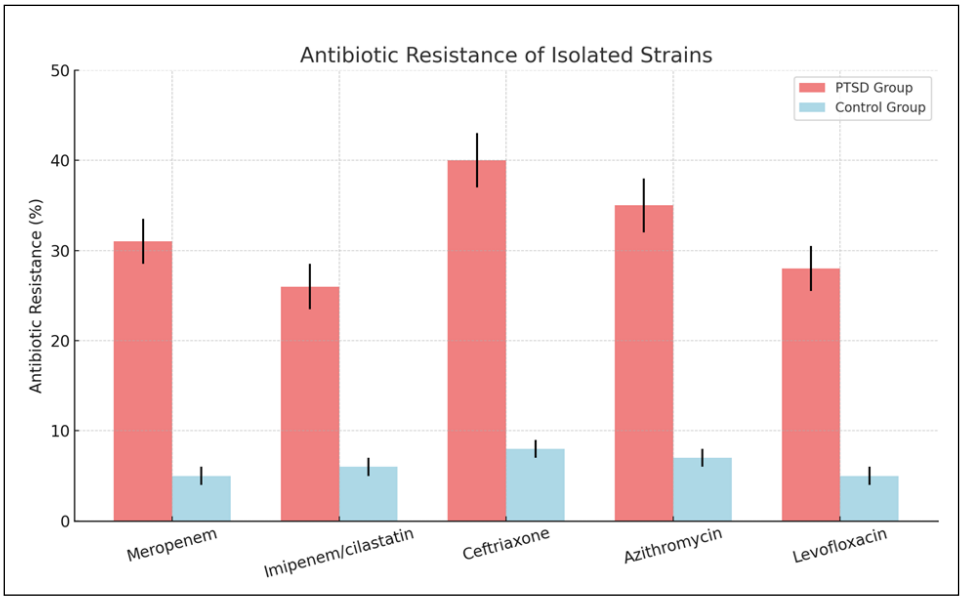

Fig. 1. Antibiotic resistance of isolated strains
Picture taken by the authors

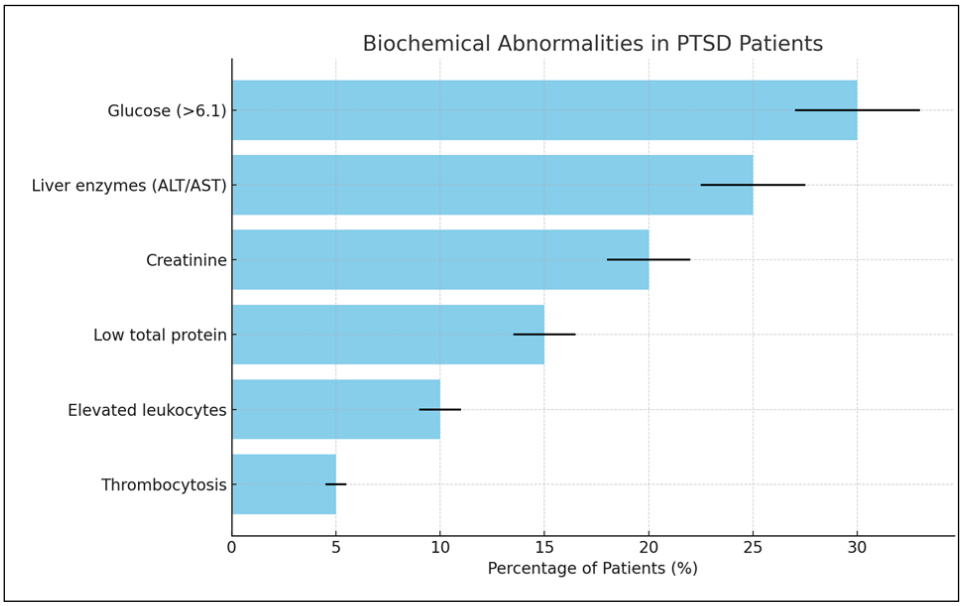

Fig. 2. Biochemical abnormalities in PTSD patients
Picture taken by the authors

external factors, including antibiotic therapy, stress, and dietary changes. The most significant microbiological burden was associated with opportunistic members of the *Enterobacteriaceae* family, particularly *Klebsiella pneumoniae* and *Enterobacter cloacae* These accounted for more than 65% of all isolated strains, with concentrations mostly exceeding 10^6 CFU/mL. Such values significantly surpass the clinically acceptable level (<10^4 CFU/mL) and may indicate active colonization of the intestinal mucosa and a translocation potential of these strains.

In 13 patients, *Staphylococcus aureus* was identified, including methicillin-resistant strains (MRSA). Concentrations of this pathogen exceeded 10^6 CFU/mL, which may point to endogenous colonization of the skin or mucous membranes. Considering many patients' medical histories, including prolonged hospitalizations and repeated antibiotic use, the probability of nosocomial origin for these strains is high.

In an in-depth study of participants (n=40), which included antibiotic resistance profiling and refined bacteriological identification, these same trends were confirmed. Specifically, among all isolated strains, the proportion of *Klebsiella pneumoniae*, *Enterobacter cloacae*, and *Proteus mirabilis* together accounted for more than 65% of the total. These species are associated with opportunistic infections, often multidrug-resistant, and are capable of forming stable biofilms, which complicates their elimination.

Further analysis of the microbiological profile of patients with PTSD (n=40) included quantitative determination of the main representatives of commensal and opportunistic microbiota. Specifically, among all isolated strains, the proportion of *Klebsiella pneumoniae*, *Enterobacter cloacae*, and *Proteus mirabilis* together accounted for over 65% of the total. These species are associated with opportunistic infections, are often

Table 4. Susceptibility profile of *Enterobacter cloacae* (n=5)

№	Antibiotic	EUCAST Breakpoints (mm)		Inhibition Zone (mm ± SD)
		S ≥	R <	
1	Meropenem	≥ 22	< 22	12.3 ± 1.8
2	Imipenem/Cilastatin	≥ 22	< 19	14.2 ± 2.1
3	Cefepime	≥ 27	< 24	13.5 ± 1.9
4	Cefotaxime	≥ 20	< 17	12.9 ± 2.4
5	Ciprofloxacin	≥ 25	< 22	13.8 ± 2.0
6	Amikacin	≥ 18	< 18	16.0 ± 2.3

Source: compiled by the authors of this study

Table 5. Susceptibility profile of *Staphylococcus aureus* (n=8)

№	Antibiotic	EUCAST Breakpoints (mm)		Inhibition Zone (mm ± SD)
		S ≥	R <	
1	Azithromycin	≥ 13	< 13	11.9 ± 2.1
2	Ciprofloxacin	≥ 50	< 17	13.2 ± 2.4
3	Levofloxacin	≥ 50	< 22	14.4 ± 1.7
4	Linezolid	≥ 21	< 21	22.3 ± 1.1
5	Fusidic acid	≥ 24	< 24	25.1 ± 1.5

Source: compiled by the authors of this study

multidrug-resistant, and form stable biofilms, which complicate their elimination (Table 2).

Bifidobacterium spp. were not detected in the fecal samples. Antibiotic susceptibility testing showed a high level of resistance in the PTSD group (n=40) to the following drugs:

- Meropenem: 31% resistant strains;
- Imipenem/cilastatin: 26%;
- Ceftriaxone: 40%;
- Azithromycin: 35%;
- Levofloxacin: 28%.

In contrast, in the control group, only a few isolates showed resistance to the mentioned drugs (not exceeding 5–8%) (Fig.1).

According to the results of this analysis, the proportion of isolates resistant to meropenem was 69.2% (28 out of 40 patients), more than double the overall rate. Similar values were observed for levofloxacin – also 69.2% (28 out of 40), ceftriaxone – 38.5% (15 out of 40), azithromycin – 38.5%, and imipenem/cilastatin – 38.5%.

Such a level of resistance observed in PTSD patients not only aligns with overall trends in the study but also highlights the severe microbiological profiles within the subgroup exhibiting pronounced colonization. In particular, all *Klebsiella pneumoniae* strains (n=7) were resistant to at least four classes of antibiotics–carbapenems, fluoroquinolones, macrolides, and beta-lactams (Table 3).

A similar resistance profile was observed in *Enterobacter cloacae* (n=5)–none of the isolates were susceptible to ceftriaxone, levofloxacin, or imipenem (Table 4).

In 80% of *Staphylococcus spp.* isolations (6 out of 8), an MRSA-like phenotype was identified with multiple resistance to fluoroquinolones, macrolides, and ampicillin, while partial susceptibility to linezolid and fusidic acid was retained (Table 5).

These results suggest that, under PTSD-modified immune status and hospital environmental conditions, a stable bacterial colonization burden is formed, dominated by multidrug-resistant Enterobacteriaceae and Gram-positive cocci. Of particular concern is the detection of *Corynebacterium spp.*, which was found to be completely resistant to all tested drugs, including linezolid, vancomycin, and rifampicin. Although this was a single case, it illustrates the risk of emerging super-resistant isolates in patients with a history of repeated hospitalizations.

In the control group (n=42), such pathogens were detected much less frequently, and resistance to key antibiotics did not exceed 5–8% in any case. Compared to the PTSD group, these differences were statistically significant ($p<0.05$; χ^2), allowing PTSD-associated microbial colonization to be considered an independent risk factor in the formation of multidrug-resistant status.

Thus, antibiotic resistance rates in the PTSD group were found to be significantly higher than in the control group, with particularly high resistance to carbapenems and macrolides. This pattern suggests colonization by microorganisms that potentially pose an epidemiological threat in hospital environments.

Additionally, a biochemical blood analysis was performed, the results of which confirmed systemic chang-

es characteristic of PTSD patients (Fig. 2). In 40% of individuals, blood glucose levels exceeded the normal range (6.23 ± 0.88 mmol/L), indicating hyperglycemia likely associated with activation of the stress response. Liver enzymes (ALT, AST) were elevated in 33% of participants, suggesting liver dysfunction. Creatinine levels were above normal in 25% of individuals, and total protein was decreased in a significant number of patients, which may indicate catabolic processes or insufficient protein intake. An increase in leukocytes was observed in 20% of individuals, and thrombocytosis in 15%, pointing to activation of inflammatory processes.

Thus, biochemical blood analysis reflects systemic changes that suggest a physiological response to stress and a possible influence of microbial imbalance. In particular, elevated glucose may result from activation of gluconeogenesis via the HPA (hypothalamic–pituitary–adrenal) axis, while elevated ALT and AST levels indicate hepatocyte cytolysis, likely linked to the effects of bacterial endotoxins. Decreased protein levels may point of to disrupted protein metabolism or malabsorption syndrome, which often accompanies inflammatory bowel disorders.

In patients diagnosed with PTSD, changes in renal function (elevated creatinine) and reduced total protein were also recorded, indicating possible catabolic processes. Additionally, thrombocytosis and elevated leukocyte counts were observed in some patients, consistent with a probable chronic inflammatory state. Therefore, the results of microbiological analysis are directly related to biochemical markers that indicate a systemic impact of PTSD on the body.

PRINCIPAL COMPONENT ANALYSIS AND CORRELATION ANALYSIS

For integrative assessment of the relationships between gut microbiota, antibiotic resistance, and blood biochemical parameters in patients with PTSD, a principal component analysis (PCA) was conducted. This approach allowed the identification of the main factors driving the variability of the parameters studied and the establishment of key axes linking microbiota composition and systemic metabolic markers.

The analysis revealed that the first principal component (PC1) accounted for 42% of the data variance and was most strongly associated with elevated levels of opportunistic Enterobacteriaceae (particularly *Klebsiella pneumoniae*, *Enterobacter cloacae*), as well as high antibiotic resistance (notably to carbapenems and macrolides). At the same time, it showed a negative correlation with the abundance of probiotic forms (*Lactobacillus casei*, *Bifidobacterium spp.*). The second component (PC2), which explained 25% of the variance, was predominantly driven by blood biochemical parameters, including elevated glucose, ALT, AST, and creatinine levels.

Pearson correlation analysis demonstrated statistically significant associations between increased abundance of opportunistic bacteria (*Klebsiella pneumoniae*, *Proteus mirabilis*, *Enterobacter cloacae*) and the following biochemical indicators:

- Glucose level ($r = 0.58$; $p < 0.01$)
- ALT level ($r = 0.49$; $p < 0.05$)
- Creatinine ($r = 0.52$; $p < 0.05$)
- Elevated leukocytes ($r = 0.45$; $p < 0.05$)

Conversely, the abundance of *Lactobacillus casei* had an inverse correlation with glucose level ($r = –0.47$; $p < 0.05$) and liver enzymes ($r = –0.42$; $p < 0.05$), suggesting a potential protective role of probiotic bacteria against the development of metabolic disturbances.

Additionally, a high level of antibiotic resistance in strains (*Klebsiella pneumoniae*, *Enterobacter cloacae*) to meropenem and ceftriaxone was directly correlated with increased intestinal colonization by these microorganisms ($r = 0.61$; $p < 0.01$) and the frequency of hospitalizations ($r = 0.54$; $p < 0.05$).

Thus, the results of the analysis support the hypothesis of a unified pathophysiological complex that links microbiome alterations, the development of antibiotic resistance, and systemic metabolic disorders in patients with PTSD. The findings underscore the need for a comprehensive treatment approach for such patients, which includes simultaneous assessment of microbiota status, antibiotic resistance levels, and key blood biochemical parameters.

DISCUSSION

The results of our study are consistent with the findings of Cryan & Dinan (2019), who demonstrated that microbiota directly affects central nervous system functioning through the regulation of key neurotransmitters [22]. Specifically, the authors describe that metabolic products of certain gut bacteria, including *Lactobacillus* and *Bifidobacterium*, can stimulate the synthesis of gamma-aminobutyric acid (GABA) – the main inhibitory neurotransmitter involved in reducing anxiety. They also report effects on tryptophan metabolism and serotonin synthesis neurotransmitter that plays a crucial role in mood regulation. Through the "gut-brain axis," cortisol secretion – the primary stress hormone is also modulated, and its concentration can be influenced by the microbiota. Therefore, changes in gut microbial composition may directly affect emotional state, anxiety, and the ability to adapt to stress.

Foster et al. (2022) likewise emphasize that the state of microbiota is closely linked to immune system modulation, particularly through effects on regulatory T-cells and the production of anti-inflammatory cytokines [23]. The authors highlight that shifts in microbial composition may promote either activation or suppression of the immune response, which, in turn, affects the hypothalamic–pituitary–adrenal (HPA) axis and cortisol secretion regulation – the key stress hormone. Under normal conditions, symbiotic microbiota maintains a balance between pro-inflammatory and anti-inflammatory signals, whereas dysbiosis disrupts this balance, potentially contributing to the development of anxiety and depressive disorders, including PTSD. Moreover, their research shows that some bacterial metabolites, especially short-chain fatty acids (SCFAs), play an important role in reducing systemic inflammation and improving stress adaptation through effects on the nervous and endocrine systems.

In the study by Kelly et al. (2016), a reduction in *Faecalibacterium prausnitzii* – one of the key anti-inflammatory members of the microbiota–was observed in PTSD patients, correlating with increased levels of inflammatory cytokines [24]. Our results confirm these findings, as we observed an increase in gram-negative pathogens capable of triggering inflammatory pathways via LPS (lipopolysaccharides).

Furthermore, according to WHO and CDC guidelines [25, 26], the detected resistance to carbapenems is an indicator of critically important health threats. Our findings underscore the need to adapt treatment protocols based on epidemiological context and local resistance profiles.

Another important observation concerns the role of hospitalization and living conditions, as noted by Zhou et al. (2020), who emphasized that psychiatric patients are at increased risk of colonization with multidrug-resistant microbiota due to frequent hospitalizations, prolonged inpatient stays, and repeated antibiotic treatments [27].

Thus, the results of this study add new evidence supporting the hypothesis of a link between mental health, microbiota, and antibiotic resistance. They underscore the importance of an integrative approach to PTSD treatment that includes microbiological and nutritional monitoring.

CONCLUSIONS

1. PTSD patients showed significant gut dysbiosis, with increased levels of opportunistic bacteria (*Klebsiella pneumoniae*, *Enterobacter cloacae*, *Proteus mirabilis*, *Staphylococcus aureus*) and reduced commensals (*Lactobacillus casei*, *Bifidobacterium spp.*), potentially contributing to psycho-emotional disturbances via gut–brain axis disruption.
2. In a PTSD subgroup, 77% had clinically significant colonization by multidrug-resistant Gram-negative pathogens. Some patients exhibited co-colonization with multiple strains, including *Corynebacterium spp.* resistant to all tested antibiotics.
3. High antibiotic resistance was observed in the PTSD subgroup: meropenem and levofloxacin resistance reached 69.2%; azithromycin, ceftriaxone, and imipenem/cilastatin resistance was 38.5%. *K. pneumoniae* isolates showed resistance to ≥4 antibiotic classes.
4. Biochemical analyses indicated stress-related metabolic shifts–hyperglycemia, elevated ALT/AST, dysproteinemia, creatininemia, and inflammation–correlating with Enterobacteriaceae levels and antibiotic resistance.
5. PCA revealed that microbial resistance and opportunistic colonization were primary factors driving patient variability; higher probiotic abundance inversely correlated with pathological biochemical markers.
6. Strong correlations were identified between Enterobacteriaceae levels and glucose ($r = 0.58$), ALT ($r = 0.49$), and creatinine ($r = 0.52$), implicating dysbiosis and endotoxemia in PTSD pathogenesis.
7. The findings support a multidisciplinary PTSD treatment approach involving microbiota screening, resistance profiling, biochemical monitoring, and personalized probiotic/nutritional interventions.
8. Multidrug-resistant colonization may serve as a predictive marker for PTSD severity and prognosis, highlighting the role of gut microbiota in systemic and neuropsychiatric dysfunction.

REFERENCES

1. Yehuda R, Hoge CW, McFarlane AC et al. Post-traumatic stress disorder. Nat Rev Dis Primers. 2020;6:11. doi:10.1038/s41572-020-0167-5. DOI
2. Priebe S, Giacco D, El-Nagib R. Public mental health, trauma, and post-traumatic stress disorder after war and displacement: Evidence from Ukraine. Lancet Psychiatry. 2023;10(3):200–210. doi:10.1016/S2215-0366(23)00021-4. DOI
3. Xiong RG, Li J, Cheng J et al. The role of gut microbiota in anxiety, depression, and other mental disorders as well as the protective effects of dietary components. Nutrients. 2023;15(14):3258. doi:10.3390/nu15143258. DOI

4. Foster JA, Rinaman L, Cryan JF. Stress and the gut-brain axis: Regulation by the microbiome. Neurobiol Stress. 2022;14:100321. doi:10.1016/j.ynstr.2021.100321. DOI
5. Liu L, Wang H, Chen X et al. Gut microbiota and its metabolites in depression: from pathogenesis to treatment. Biomed. 2023;90:104527. doi:10.1016/j.ebiom.2023.104527. DOI
6. Nikel K, Stojko M, Smolarczyk J, Piegza M. The impact of gut microbiota on the development of anxiety symptoms–a narrative review. Nutrients. 2025;17(6):933. doi:10.3390/nu17060933. DOI
7. Zhao F, Guan S, Fu Y et al. Lycium barbarum polysaccharide attenuates emotional injury of offspring elicited by prenatal chronic stress in rats via regulation of gut microbiota. Biomed Pharmacother. 2021;143:112087. doi:10.1016/j.biopha.2021.112087. DOI
8. Zhou Y, Cui Y, Wang J. Colonization with multidrug-resistant organisms in psychiatric hospitals: Prevalence and risk factors. Int J Infect Dis. 2020;93:146–152. doi:10.1016/j.ijid.2020.01.030. DOI
9. Cryan JF, O'Riordan KJ, Sandhu K et al. The gut microbiome in neurological disorders. Lancet Neurol. 2020;19(2):179–194. doi:10.1016/S1474-4422(19)30356-4. DOI
10. Dinan TG, Cryan JF. The microbiome-gut-brain axis in health and disease. Gastroenterol Clin North Am. 2017;46(1):77–89. doi:10.1016/j.gtc.2016.09.007. DOI
11. Morais LH, Schreiber HL, Mazmanian SK. The gut microbiota-brain axis in behaviour and brain disorders. Nat Rev Microbiol. 2021;19(4):241–255. doi:10.1038/s41579-020-00460-0. DOI
12. Bonten MJM et al. Emerging multidrug-resistant Gram-negative bacteria in the gut microbiota of hospitalized patients. Clin Microbiol Rev. 2020;33(2):e00104-19. doi:10.1128/CMR.00104-19. DOI
13. Pamer EG. Resurrecting the intestinal microbiota to combat antibiotic-resistant pathogens. Science. 2016;352(6285):535–538. doi:10.1126/science.aad9382. DOI
14. Abdelhamid AG, Esaam A, Hazaa MM. Cell-free preparations of probiotics exerted antibacterial and antibiofilm activities against multidrug resistant E. coli. Saudi Pharm J. 2018;26(5):603–607. doi:10.1016/j.jsps.2018.03.004. DOI
15. Ohland CL, Macnaughton WK. Probiotic bacteria and intestinal epithelial barrier function. Am J Physiol Gastrointest Liver Physiol. 2010;298(6):G807–G819. doi:10.1152/ajpgi.00243.2009. DOI
16. Hemarajata P, Versalovic J. Effects of probiotics on gut microbiota: Mechanisms of intestinal immunomodulation and neuromodulation. Ther Adv Gastroenterol. 2013;6(1):39–51. doi:10.1177/1756283X12459294. DOI
17. Pallah OV, Meleshko TV, Tymoshchuk SA et al. How to escape 'the ESKAPE pathogens' using plant extracts. SciRise Biol Sci. 2019;(5-6):30–37.
18. Yusko LS, Burmei SA, Lemko IS et al. The use of personalized pharmabiotics as one of the approaches to the rehabilitation of post-covid patients. Mikrobiolohichnyi Zhurnal. 2024;86(4):64–75. doi:10.15407/microbiolj86.04.064. DOI
19. European Committee on Antimicrobial Susceptibility Testing (EUCAST). Breakpoint tables for interpretation of MICs and zone diameters. 2023. https://www.eucast.org [Accessed 16 March 2025]
20. World Health Organization. Global action plan on antimicrobial resistance. Geneva: WHO. 2021. https://www.who.int [Accessed 16 March 2025]
21. Centers for Disease Control and Prevention (CDC). Antibiotic resistance threats in the United States. Atlanta: CDC. 2023. https://www.cdc.gov [Accessed 16 March 2025]
22. Kulia A, Petrov VO, Sabo Yu et al. Antibiotic resistance of opportunistic microorganisms isolated in Hungarian and Ukrainian non-infectious hospitals. [Rezystentnist' do antybiotykiv umovno-patohennykh mikroorhanizmiv, vydilenykh v uhors'kykh ta ukrayins'kykh neinfektsiynykh likarnyakh]. Uzhhorodskyy natsional'nyy universytet. 2009. (Ukrainian)
23. Cryan JF, O'Riordan KJ, Cowan CSM et al. The microbiota-gut-brain axis. Physiol Rev. 2019;99(4):1877–2013. doi:10.1152/physrev.00018.2018. DOI
24. Foster AL, Smith BD, Nguyen CT, Lee EJ. Gut microbiota-mediated regulation of regulatory T cells and anti-inflammatory cytokine production. Front Immunol. 2022;13:1477187. doi:10.3389/fmicb.2024.1477187. DOI
25. Kelly JR, Kennedy PJ, Cryan JF et al. Breaking down the barriers: The gut microbiome, intestinal permeability and stress-related psychiatric disorders. Front Cell Neurosci. 2016;9:392. doi:10.3389/fncel.2015.00392. DOI
26. Centers for Disease Control and Prevention (CDC). Antibiotic resistance threats in the United States. Atlanta: CDC. 2023. https://www.cdc.gov [Accessed 16 March 2025]
27. Zhou Y, Cui Y, Wang J. Colonization with multidrug-resistant organisms in psychiatric hospitals: prevalence and risk factors. Int J Infect Dis. 2020;93:146–152. doi:10.1016/j.ijid.2020.01.030. DOI

The authors would like to express sincere gratitude to Uzhhorod City Multidisciplinary Hospital and the regional psychiatric facility in Berehove and Ediens LLC for their valuable support and cooperation during the research. Their assistance in providing access to data and facilitating communication with staff and patients was essential to the success of this study.

CONFLICT OF INTEREST
The Authors declare no conflict of interest

CORRESPONDING AUTHOR
Oleksandra Pallah
Uzhhorod National University
14 Universytetska St, 88000 Uzhhorod, Ukraine
e-mail: oleksandra.pallah@uzhnu.edu.ua

ORCID AND CONTRIBUTIONSHIP
Oleksandra Pallah: 0000-0003-3636-6621 B C D F
Ivan Lypei: 0009-0005-2743-4911 A B F
Svitlana Burmei: 0000-0002-8157-4262 B C F
Lesya Yusko: 0000-0002-7072-0703 D F
Nadiya Boyko: 0000-0002-2467-7513 A E F

A – Work concept and design, B – Data collection and analysis, C – Responsibility for statistical analysis, D – Writing the article, E – Critical review, F – Final approval of the article

RECEIVED: 06.07.2025
ACCEPTED: 25.10.2025