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Analysis of Gut Microbiota Characteristics in Zhuang Ethnic Group Patients with Post-Stroke Cognitive Impairment in Baise City, Guangxi

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Abstract: Objective: To analyze the intestinal microbiota characteristics in patients with post-stroke cognitive impairment (PSCI) in the Zhuang population of Baise, Guangxi, and to provide a theoretical foundation for understanding the pathogenesis of PSCI and the potential application of fecal microbiota transplantation as a therapeutic strategy. Methods: Clinical baseline data were collected from 30 stroke patients admitted to the Affiliated Hospital of Youjiang Medical University for Nationalities from January 2024 to December 2024, who were designated as the stroke group. Additionally, 30 healthy individuals undergoing routine physical examination were selected as the control group, and 30 patients diagnosed with PSCI were included in the PSCI group. Stool samples were collected from all participants. Genomic DNA was extracted using a specialized fecal DNA extraction kit, followed by amplification and sequencing of the 16S rRNA V3-V4 region. Bioinformatics analysis was performed to assess the microbiota composition. Pearson correlation analysis was used to explore the relationship between microbiota indices and PSCI. Results: The Mini-Mental State Examination (MMSE) scores in the stroke (16.33±4.29) and PSCI (20.53±2.24) groups were significantly lower than that of the control group (23.36±2.44) ($P < 0.05$). Similarly, Montreal Cognitive Assessment (MoCA) scores in the stroke (23.58±1.55) and PSCI (26.59±1.48) groups were lower than in the control group (28.33±1.45) ($P < 0.05$). Regarding intestinal microbiota α-diversity, indices such as Chao1 estimator, abundance-based coverage estimator (Ace), Shannon-Wiener diversity index, and Simpson index were significantly lower in the PSCI group compared to the stroke and control groups ($P < 0.05$), whereas no significant difference was observed between the stroke and control groups ($P > 0.05$). At the phylum level, Firmicutes, Bacteroidetes, Actinobacteria, and Proteobacteria were identified as the predominant phyla in all three groups, although their relative abundances differed significantly ($P < 0.05$). The relative abundance of Firmicutes and Actinobacteria was significantly lower in the PSCI group compared to the stroke and control groups, whereas the relative abundance of Bacteroidetes and Proteobacteria was higher in the PSCI group than in the control and stroke groups. At the genus level, the relative abundance of Bifidobacterium and Lactobacillus was lower in the PSCI group compared to the stroke and control groups, while the relative abundance of Bacteroides and Clostridium was higher in the PSCI group ($P < 0.05$). Pearson correlation analysis revealed a positive correlation between PSCI and Bacteroidetes, Proteobacteria, Bacteroides, and Clostridium ($r = 0.327, 0.493, 0.425$, respectively), while a negative correlation was found with Firmicutes, Actinobacteria, Lactobacillus, and Bifidobacterium ($r = -0.261, -0.503, -0.623, -0.456$, respectively) ($P < 0.05$). Conclusion: Significant alterations in the gut microbiota composition were observed in PSCI patients from the Zhuang population in Baise, Guangxi. These changes may be closely associated with the onset and progression of PSCI, providing a basis for future studies on the role of the gut microbiota in PSCI and potential therapeutic strategies such as fecal microbiota transplantation.

Keywords: Post-stroke Cognitive Dysfunction; Guangxi Baise City Zhuang Ethnic Group; Intestinal Flora Characteristics; Correlation.

1. Introduction

Stroke, as one of the leading causes of death and disability worldwide, has attracted significant attention in terms of prevention and treatment. With the continuous advancement of medical technologies, the survival rate of stroke patients has significantly improved. However, the issue of managing post-stroke sequelae, particularly Post-Stroke Cognitive Impairment (PSCI), has become a common long-term complication among stroke patients [1]. PSCI not only severely impacts the quality of life of patients but also places a heavy burden on families and society. Therefore, in-depth research into the pathogenesis of PSCI and potential intervention strategies is of critical value for clinical practice. The gut microbiota, a large microbial community residing in the human gastrointestinal tract, plays a crucial role in digestion, metabolism, immune regulation, and neurological functions [2]. In recent years, the connection between gut microbiota and brain health has become a hot research topic. Numerous studies have indicated that dysbiosis of the gut microbiota is associated with various neurological disorders, such as Alzheimer's disease, Parkinson's disease, and PSCI [3]. Baise City, located in the Guangxi Zhuang Autonomous Region, is a region with a high population of Zhuang ethnic people, characterized by unique geographical and cultural factors. The dietary habits, lifestyle, and genetic background of the Zhuang people may influence the composition and function of their gut microbiota [4]. Therefore, studying the gut microbiota characteristics of PSCI patients in the Zhuang population of Baise City cannot only provide scientific evidence for personalized treatment of stroke patients in the region but also help reveal the potential link between gut

microbiota and post-stroke cognitive impairment [5]. This study aims to explore the gut microbiota characteristics of PSCI patients in the Zhuang population of Baise City, Guangxi, and analyze the intrinsic relationship between these characteristics and PSCI. By collecting fecal samples from patients and conducting high-throughput sequencing to analyze the gut microbiota, along with cognitive function assessments, the study will examine the diversity and compositional changes of the gut microbiota. Furthermore, the study will investigate the interactions between the gut microbiota and host metabolic products, immune status, and inflammatory responses, in order to reveal the potential role of the gut microbiota in PSCI.

2. Objects and Methods

2.1. Research Objects

This study will be conducted at the Affiliated Hospital of Youjiang Medical University for Nationalities, with 30 stroke patients admitted between January 2024 and December 2024 included in the case group, 30 healthy individuals in the control group, and 30 patients diagnosed with Post-Stroke Cognitive Impairment (PSCI) in the PSCI group. Informed consent will be obtained from the patients or their family members. The inclusion criteria for the case group are: 1) patients meeting the diagnostic criteria for stroke[6]; 2) age ≥18 years; 3) first-time stroke event; and 4) no cognitive impairment symptoms, with a Hamilton Depression Rating Scale (HAMD) score ≥10. The inclusion criteria for the healthy group are: 1) no clinical manifestations of stroke; 2) normal blood pressure; and 3) no evidence of infarction lesions on cranial CT or MRI. The inclusion criteria for the PSCI group are: 1) meeting the diagnostic criteria for PSCI[7]; 2) age ≥18 years; 3) clear infarction lesions identified by imaging; and 4) HAMD score <10. All participants in the three groups are from Baise City, Guangxi, and are of the Zhuang ethnic group. The exclusion criteria include: 1) coexisting conditions such as ulcerative colitis or Crohn's disease; 2) malignant gastrointestinal tumors; 3) history of gastrointestinal surgery; 4) history of traumatic brain injury; 5) use of probiotics or antibiotics within the past 3 months; and 6) coexisting organ dysfunction, including liver, kidney, or heart failure. The general demographic characteristics of the three groups were compared ($P > 0.05$), as shown in Table 1.

Table 1. Comparison of clinical baseline data among the three groups [$\bar{x}\pm s$, n=30]

Groups	Age (years)	Gender (Male/female)	Educational level (high school or secondary school and below/College or bachelor's degree and above)	Body Mass index (kg/m^2)
Stroke Group	56.50±8.33	16/14	19/11	21.41±1.33
Healthy group	56.92±7.38	15/15	18/12	21.53±1.61
PSCI group	56.63±8.44	18/12	17/13	21.38±1.44
X^2/t	0.021	0.627	0.278	0.088
P	0.979	0.731	0.870	0.916

2.2. Methods

2.2.1. Data Collection and Cognitive Function Assessment

Basic information such as gender, age, and medical history will be collected from patients. Cognitive function will be assessed by trained professionals using the Mini-Mental State Examination (MMSE) [8] and the Montreal Cognitive Assessment (MoCA) [9]. MMSE scores are classified based on the severity of dementia: mild ≥21 points, moderate 10-20 points, and severe ≤9 points. A MoCA score of ≥26 points are considered normal.

2.2.2. Fecal Sample Collection

Fecal samples will be collected by personnel trained in strict sterile techniques, using fresh stool from the middle to posterior segment of the stool. Each sample will be approximately 4-6g, placed into a sterile cryotube, and immediately stored at -80°C to avoid repeated freeze-thaw cycles. Samples will be transported to the testing site on dry ice at low temperatures.

2.2.3. Fecal DNA Extraction and Detection

Fecal DNA will be extracted using a powerful fecal DNA extraction kit. The procedure is as follows: Approximately 0.15g of the fecal sample will be taken from the -80°C freezer and placed into a Dry Bead Tube. It will be dissolved in a 60°C water bath, followed by heating at 65°C for 10 minutes. After centrifuging at 13,000g for 1 minute, 250μL each of solutions C2, C3, C4, C5, and C6 will be sequentially added, and subsequent steps will follow the instructions in the kit manual. The extracted DNA will be measured for concentration and purity using a NanoDrop 2000 spectrophotometer. Qualified DNA samples will be stored at -20°C for later use.

2.2.4. 16S rRNA V3-V4 Region Amplification and Sequencing

The bacterial universal primers 338F (5'-ACTCCTA CGGGAGGCAGCAG-3') and 806R (5'-GGACTACHVG GGTWTCTAAT-3') will be used to amplify the 16S rRNA V3-V4 region via PCR. The PCR reaction mixture (25μL) consists of: 5×FastPfu Buffer (5μL), 2.5mmol/L dNTPs (2μL), Forward Primer (5μmol/L) (1μL), Reverse Primer (5μmol/L) (1μL), FastPfu Polymerase (0.5μL), DNA template (1μL), and ddH_2O to make up 25μL. The PCR conditions are as follows: 95°C for 3 minutes (pre-denaturation), 95°C for 30s (denaturation), 55°C for 30s (annealing), 72°C for 45s (extension), for 30 cycles, followed by a final extension at 72°C for 10 minutes. The PCR products will be checked by 2% agarose gel electrophoresis, gel-purified, and sent to a sequencing company for Illumina MiSeq sequencing.

2.2.5. Bioinformatics Analysis

Data Quality Control: The paired-end sequencing data obtained from MiSeq will be merged into a single sequence using the FLASH software, based on the overlap between the

PE reads. The quality of the reads and the merging effect will be assessed and filtered using Trimmomatic software. Effective sequences will be obtained by distinguishing the samples based on the barcode and primer sequences at both ends of the sequence, followed by correction of sequence direction to obtain optimized data.

Species Annotation and Evaluation: The optimized sequences will be clustered at a 97% similarity level to group them into Operational Taxonomic Units (OTUs). Taxonomic analysis of the representative OTU sequences will be performed using the Bayesian RDP classifier algorithm to determine the species classification information.

Alpha Diversity Analysis: The Ace index will be used to reflect community richness, and the Shannon index will be used to reflect community diversity. Differences in alpha diversity indices between groups will be tested using analysis of variance (ANOVA).

Species Venn Diagram Analysis: Venn diagrams will be used to analyze the shared and unique OTU numbers across multiple groups of samples, providing a visual representation of the similarity and overlap in species composition among the samples (OTUs at a 97% similarity level).

Community Composition Analysis: Based on the taxonomic analysis results, the community structure composition at the phylum and genus levels will be compared between different groups.

2.3. Statistical Methods

Data analysis will be performed using SPSS 24.0 statistical software. Categorical data will be presented as frequencies (percentages), and comparisons between groups will be made using the chi-square test or Fisher's exact test. The Kolmogorov-Smirnov test will be used to evaluate whether the continuous data follow a normal distribution. For normally distributed continuous data, results will be presented as mean ± standard deviation ($\bar{x}\pm s$), and comparisons between groups will be performed using the two-sample t-test or one-way ANOVA as appropriate.

3. Results

3.1. Cognitive Function Level

The MMSE score and MoCA score of the stroke group and PSCI group were lower than those of the control group ($P < 0.05$), as shown in Table 2.

Table 2. Comparison of cognitive function levels among the three groups [$\bar{x}\pm s$, n=30]

Groups	MMSE	MoCA
Stroke Group	16.33±4.29	23.58±1.55
Healthy Group	23.36±2.44	28.33±1.45
PSCI Group	20.53±2.24	26.59±1.48
t value	38.333	77.628
p value	<0.01	<0.01

3.2. Alpha Diversity Index

Chao1 estimator (Chao1) and Abundance-based Coverage Estimator of patients in PSCI group, Ace, Shannon-Wiener diversity index (Shannon), Simpson's diversity index (Simpson's Diversity Index) The diversity of intestinal flora Alpha such as Simpson index was lower than that of stroke group and healthy group ($P < 0.05$). The stroke group was compared with the healthy group ($P>0.05$), as shown in Table 3.

Table 3. Comparison of Alpha diversity index among the three groups [$\bar{x}\pm s$, n=30]

Groups	Chao1	Ace	Shannon	Simpson
Stroke Group	103.53±4.39	102.60±3.61	4.55±1.29	0.89±0.09
Healthy Group	103.46±2.64	102.43±3.55	4.55±1.33	0.88±0.08
PSCI Group	92.66±4.54	93.57±5.38	3.38±1.22	0.75±0.12
t value	75.103	43.995	8.345	18.997
p value	<0.01	<0.01	<0.01	<0.01

3.3. Comparison of Intestinal Flora Composition and Abundance

Table 4. Comparison of analysis results of intestinal flora composition among the three groups [$\bar{x}\pm s$, n=30]

Groups	Phylum Level				Genus Level			
	Firmicutes	Bacteroidetes	Actinobacteria	Proteobacteria	Lactobacillus	Bifidobacterium	Bacteroides	Clostridium
Stroke Group	40.60±5.44	48.61±4.51	5.42±1.39	8.39±2.19	3.55±1.41	5.66±1.34	25.51±4.38	16.59±4.38
Healthy Group	40.57±5.34	48.49±4.65	5.35±1.64	8.48±2.18	3.65±1.28	5.68±1.27	25.46±4.55	16.55±4.52
PSCI Group	33.56±5.60	53.61±6.48	3.28±1.42	12.55±2.32	2.44±1.58	3.45±1.66	30.65±4.22	21.39±3.52
t value	16.548	9.153	20.042	34.035	6.442	24.196	13.872	13.403
p value	<0.01	<0.01	<0.01	<0.01	0.002	<0.01	<0.01	<0.01

At the phylum level, Firmicutes, Bacteroidetes, actinobacteria and Proteobacteria were the dominant bacteria in the three groups, but their relative abundance was different ($P<0.05$). The relative abundance of firmicutes and actinomycetes in PSCI group was lower than that in healthy group and apoplexy group, and the relative abundance of

Bacteroidetes and Proteobacteria was higher than that in control group and apoplexy group. At the genus level, the relative abundance of Bifidobacterium and Lactobacillus in PSCI group was lower than that in control group and stroke group, while the relative abundance of Bacteroides and Clostridium in PSCI group was higher than that in control group and stroke group (P<0.05), as shown in Table 4.

3.4. Correlation between Intestinal Flora and PSCI

Pearson correlation analysis showed that PSCI patients were positively correlated with Bacteroidetes, Proteobacteria, Bacteroidetes and Clostridium (r=0.327, 0.493, 0.425). It was negatively correlated with Firmicutes, Actinobacteria, Lactobacillus and Bifidobacteria (r=-0.261, -0.503, -0.623, -0.456) and significantly correlated (P < 0.05), as shown in Table 5.

Table 5. Correlation analysis between intestinal flora and PSCI patients (r)

Variables	PSCI	Firmicutes	Bacteroidetes	Actinobacteria	Proteobacteria	Lactobacillus	Bifidobacterium	Clostridium
PSCI	1	-	-	-	-			
Firmicutes	-0.261*	1	-	-	-			
Bacteroidetes	0.327**	0.025	1	-	-			
Actinobacteria	-0.503**	0.135	0.212*	1	-			
Proteobacteria	0.493**	-0.069	0.091	0.282**	1			
Lactobacillus	-0.623**	-0.458*	0.539	0.365	0.445	1		
Bifidobacterium	-0.456**	0.429	0.428	-0.537**	-0.635**		1	
Bacteroides	0.425**	0.336	0.298	0.225*	0.423	0.235	0.275	1
Clostridium	0.539**	0.663**	0.538	0.236	0.245	0.436	0.452	1

Note: P < 0.01; * P < 0.05, correlation is significant.

4. Discussion

In the Zhuang population of Baise City, Guangxi, an in-depth study revealed a downward trend in the alpha diversity of the gut microbiota in PSCI (Post-Stroke Cognitive Impairment) patients, with significant changes in the microbiota structure. These findings suggest a close link between gut microbiota dysbiosis and the onset and progression of PSCI. The alpha diversity indices, as important indicators of gut microbiota diversity and stability, were reflected in this study. The results showed that, compared to the healthy control group and stroke group, PSCI patients had lower Ace and Shannon indices, indicating a reduction in the richness and diversity of their gut microbiota. Previous studies have pointed out that reduced gut microbiota diversity may weaken its beneficial effects on the host, including impaired nutritional metabolism and immune regulation, which may further affect the central nervous system, thus increasing the risk of PSCI [10]. The analysis suggests that PSCI may lead to systemic circulatory disturbances, which in turn affect the blood supply to the gut, damage the intestinal mucosa, and disrupt the intestinal barrier function and homeostasis. Such conditions alter the gut microbiota's living environment and reduce its diversity. Furthermore, PSCI may trigger an imbalance in the neuroregulation between the central nervous system and the enteric nervous system, impairing the autonomic nervous system's normal regulation of the gut, which affects gut motility and secretion, further altering the composition and diversity of the gut microbiota. Various inflammatory factors, such as interleukin-6 (IL-6) and tumor necrosis factor-alpha (TNF-α), are released in large amounts, affecting neuron function and survival, leading to cognitive impairment, which can spread throughout the body and impact gut health [11-12]. Inflammatory factors damage the intestinal mucosal barrier, increase gut permeability, cause microbial translocation, and alter the gut immune microenvironment, inhibiting the growth of beneficial bacteria, promoting the proliferation of harmful bacteria, and reducing microbiota diversity [13]. After stroke, immune cells such as macrophages and neutrophils accumulate in the gut and release substances that damage the intestinal tissue and impair its normal function. In an inflammatory state, the interaction between immune cells and the gut microbiota becomes disrupted, leading to changes in microbiota composition and diversity, further decreasing diversity.

During the treatment of PSCI, patients often use antibiotics to prevent or treat infections. However, antibiotics disrupt the balance of the gut microbiota, leading to the proliferation of drug-resistant bacteria and a reduction in diversity. During hospitalization, a monotonous diet and a closed environment may reduce microbiota diversity, and special microorganisms in the hospital environment may also interfere with gut microbiota balance [14]. Individual genetic backgrounds and lifestyle factors have long-term effects on the gut microbiota. For instance, genetic factors may influence the intestinal mucosa and immune response, while poor lifestyle habits, such as a high-sugar, high-fat diet, lack of exercise, smoking, and alcohol consumption, can damage the balance of the gut microbiota and decrease its diversity. At the phylum level, the relative abundance of Firmicutes and Actinobacteria decreased in the PSCI group, while the relative abundance of Bacteroidetes and Proteobacteria increased. Many bacteria in Firmicutes are involved in energy metabolism and short-chain fatty acid production. The decrease in their relative abundance may disrupt the gut's energy balance and the nutritional supply to intestinal epithelial cells, thereby affecting gut barrier function and neuroregulation [15]. The relative decrease in beneficial bacteria such as Bifidobacterium in Actinobacteria is also unfavorable for maintaining gut microecological balance and exerting beneficial effects on the host. The increased relative abundance of Bacteroidetes and Proteobacteria may be associated with inflammatory responses. Some bacteria in Bacteroidetes can trigger inflammation by producing endotoxins, while Proteobacteria often show overgrowth in intestinal inflammation and their increase may exacerbate systemic inflammation, affecting the central nervous system via the "gut-brain axis" and promoting the progression of PSCI [16].

At the genus level, the relative abundance of

Bifidobacterium and Lactobacillus was lower in the PSCI group, while the relative abundance of Bacteroides and Clostridium was higher. Bifidobacterium and Lactobacillus have antioxidant, anti-inflammatory, and immune-regulating functions. Their reduction leads to decreased antioxidant capacity in the gut, ineffective inhibition of inflammatory responses, and disruption of immune balance [17]. The increased relative abundance of Bacteroides and Clostridium, especially some potentially pathogenic bacteria in Clostridium, may worsen gut microbiota dysbiosis, producing more harmful metabolites and further impacting the gut and brain health [18]. Pearson correlation analysis further confirmed that PSCI patients had a positive correlation with Bacteroidetes, Proteobacteria, Bacteroides, and Clostridium, and a negative correlation with Firmicutes, Actinobacteria, Lactobacillus, and Bifidobacterium. This further emphasizes the significant role these gut microbiota changes play in the development of PSCI.

In summary, this study preliminarily revealed the characteristics of the gut microbiota in PSCI patients from the Zhuang population in Baise City, Guangxi, and its correlation with PSCI. It provides new perspectives for a deeper understanding of the pathogenesis of PSCI and offers a theoretical basis for the clinical diagnosis, treatment, and prevention of PSCI. Further research is needed to fully explore the potential value of gut microbiota in PSCI, aiming to provide more effective methods to improve the prognosis and quality of life of PSCI patients.

5. Conclusion

Pathogenic microorganisms, and further exacerbating the dysbiosis. These changes in the gut microbiota can create a vicious cycle, where the altered gut environment exacerbates cognitive decline, and cognitive dysfunction in turn leads to further gut disturbances. The downward trend in gut microbiota alpha diversity observed in PSCI patients may also reflect a compromised gut-brain axis, which is crucial in maintaining both cognitive function and gut health. The gut-brain axis, a bidirectional communication system between the central nervous system and the gut, is thought to influence cognitive function, emotional regulation, and overall health. Dysbiosis of the gut microbiota can disrupt this communication, leading to inflammation and neuronal damage, thereby contributing to the onset of cognitive impairments such as PSCI. Furthermore, studies have shown that a reduction in gut microbiota diversity is associated with several chronic diseases, including neurodegenerative disorders like Alzheimer's and Parkinson's disease, reinforcing the idea that gut health plays a pivotal role in cognitive function. In the case of PSCI, the reduction in microbial diversity could further impair metabolic processes, including energy homeostasis and neurotransmitter synthesis, which are vital for maintaining cognitive abilities. Interventions aimed at restoring the balance of gut microbiota, such as the use of probiotics, prebiotics, or dietary adjustments, may hold promise as potential therapeutic strategies for mitigating PSCI progression. These approaches could help restore gut microbiota diversity, strengthen the intestinal barrier, and alleviate systemic inflammation, all of which may contribute to better cognitive outcomes for PSCI patients. The relationship between gut microbiota and cognitive function in PSCI highlights the importance of integrated approaches in understanding and treating post-stroke cognitive decline. Future research should explore the mechanisms linking gut microbiota dysbiosis with cognitive dysfunction, with the aim of developing targeted therapies that address both the neurological and gastrointestinal aspects of PSCI.

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References

[1] Han, D., Dilinuer, T., Huang, Z., et al. Research progress on the improvement of cognitive dysfunction after acute stroke by traditional Chinese medicine through regulating the gut-brain axis. Journal of Integrated Traditional Chinese and Western Medicine on Cardiovascular Diseases, 2023, 21(10): 1811-1815.

[2] Chen, H., Yan, X., Zhou, J., et al. Research progress on the correlation between gut microbiota and its metabolites with cognitive dysfunction after stroke. International Journal of Neurology and Neurosurgery, 2020, 47(5): 545-549.

[3] Huang, F., Jia, W. The relationship between gut microbiota and its metabolites with the outcomes of ischemic stroke. International Journal of Cerebrovascular Diseases, 2024, 32(1): 40-44.

[4] Wu, Y., Li, S., Liang, D., et al. The relationship between MTHFR C677T gene polymorphism in the Baise ethnic minority population and the incidence of ischemic stroke. Shandong Medical Journal, 2023, 63(19): 71-75.

[5] Tian, H., Yang, Y., Li, W., et al. Research progress on the role of gut microbiota and its metabolites in the pathogenesis of cognitive dysfunction after stroke. Shandong Medical Journal, 2022, 62(34): 85-88.

[6] Chinese Society of Emergency Medicine, Expert Consensus Group on Assessment and Intervention of Collateral Circulation in Acute Ischemic Stroke. Expert consensus on assessment and intervention of collateral circulation in acute ischemic stroke. Chinese Journal of Emergency Medicine, 2022, 31(10): 1310-1318.

[7] Expert Group of the Stroke Society of China on Research Consensus for Prevention and Treatment of Cognitive Dysfunction after Stroke. Expert consensus on the prevention and treatment of cognitive dysfunction after stroke in China. Chinese Stroke Journal, 2020, 15(2): 158-166.

[8] Ji, H., Hu, C., Zhang, G., et al. Preliminary application of the Mini-Mental State Examination in evaluating cognitive function in patients with glioma. Tumor Research and Clinical, 2012, 24(5): 311-312, 315.

[9] Zhang, L., Liu, X. Study on the reliability and validity of the Chinese version of the Montreal Cognitive Assessment Scale. Nursing Research, 2007, 21(31): 2906-2907. DOI:10.3969/j.issn.1009-6493.2007.31.044.

[10] El Husseini N, Katzan IL, Rost NS, et al; American Heart Association Stroke Council; Council on Cardiovascular and Stroke Nursing; Council on Cardiovascular Radiology and Intervention; Council on Hypertension; and Council on Lifestyle and Cardiometabolic Health. Cognitive Impairment After Ischemic and Hemorrhagic Stroke: A Scientific Statement From the American Heart Association/American Stroke Association. Stroke. 2023,54(6):272-291.

[11] Feng, R., Yu, Q., Li, Y., et al. Study on the characteristics of gut microbiota dysbiosis in patients with cognitive dysfunction after stroke. Journal of Sichuan University (Medical Edition), 2021, 52(6): 966-974.

[12] Wu, B., Zheng, D., Zhang, Z., et al. Effects of low-frequency repetitive transcranial magnetic stimulation combined with probiotics on cognition, motor function, and gut microbiota in stroke patients with depression. Chinese Journal of Microecology, 2020, 32(10): 1182-1185, 1189.

[13] Li, Y., Yu, Q., Huang, L., et al. Correlation between gut microbiota changes and cognitive function in patients with early cognitive decline after stroke. Journal of Sichuan University (Medical Edition), 2022, 53(5): 857-865.

[14] Weterings, R.P., Kessels, R.P., de Leeuw, F.E., et al. Cognitive impairment after a stroke in young adults: A systematic review and meta-analysis. International Journal of Stroke, 2023, 18(8): 888-897.

[15] Lv, Z., Wang, Y., Liu, R., et al. Research progress on the correlation between the gut microbiota-gut-brain axis and cognitive dysfunction after stroke. Journal of Medical Research, 2024, 49(9): 1073-1079.

[16] Tay, J., Morris, R.G., Markus, H.S. Apathy after stroke: Diagnosis, mechanisms, consequences, and treatment. International Journal of Stroke, 2021, 16(5): 510-518.

[17] Liang, J., Dong, J., Yang, Y. Differences in gut microbiota among middle-aged and elderly populations with different stroke risk levels. Journal of Clinical Medicine, [journal issue not provided].

[18] Einstad MS, Saltvedt I, Lydersen S,et al. Associations between post-stroke motor and cognitive function: a cross-sectional study. BMC Geriatr. 2021,21(1):103.