

Supplementary Table Abstract

**Gut microbiota of patients with post-stroke depression in
Chinese population:a systematic review and meta-analysis**

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Supplementary table 1. Search strategies of PubMed databases.

Number	Search Strategies
#1	((((((((((((((((((((((((stroke) OR (strokes)) OR (Cerebrovascular Accident)) OR (Cerebrovascular Accidents)) OR (CVA (Cerebrovascular Accident))) OR (CVAs (Cerebrovascular Accident))) OR (Cerebrovascular Apoplexy)) OR (Apoplexy, Cerebrovascular)) OR (Vascular Accident, Brain)) OR (Brain Vascular Accident)) OR (Brain Vascular Accidents)) OR (Vascular Accidents, Brain)) OR (Cerebrovascular Stroke)) OR (Cerebrovascular Strokes)) OR (Stroke, Cerebrovascular)) OR (Strokes, Cerebrovascular)) OR (Apoplexy)) OR (Cerebral Stroke)) OR (Cerebral Strokes)) OR (Stroke, Cerebral)) OR (Strokes, Cerebral)) OR (Stroke, Acute)) OR (Acute Stroke)) OR (Acute Strokes)) OR (Strokes, Acute)) OR (Cerebrovascular Accident, Acute)) OR (Acute Cerebrovascular Accident)) OR (Acute Cerebrovascular Accidents)) OR (Cerebrovascular Accidents, Acute)
#2	(((((Depression) OR (Depressive Symptoms)) OR (Depressive Symptom)) OR (Symptom, Depressive)) OR (Emotional Depression)) OR (Depression, Emotional)
#3	((((((((((((((((((((((((((Gastrointestinal Microbiome) OR (Gastrointestinal Microbiomes)) OR (Microbiome, Gastrointestinal)) OR (Gut Microbiome)) OR (Gut Microbiomes)) OR (Microbiome, Gut)) OR (Gut Microflora)) OR (Microflora, Gut)) OR (Gut Microbiota)) OR (Gut Microbiotas)) OR (Microbiota, Gut)) OR (Gastrointestinal Flora)) OR (Flora, Gastrointestinal)) OR (Gut Flora)) OR (Flora, Gut)) OR (Gastrointestinal Microbiota)) OR (Gastrointestinal Microbiotas)) OR (Microbiota, Gastrointestinal)) OR (Gastrointestinal Microbial Community)) OR (Gastrointestinal Microbial Communities)) OR (Microbial Community, Gastrointestinal)) OR (Gastrointestinal Microflora)) OR (Microflora, Gastrointestinal)) OR (Gastric Microbiome)) OR (Gastric Microbiomes)) OR (Microbiome, Gastric)) OR (Intestinal Microbiome)) OR (Intestinal Microbiomes) OR (Microbiome, Intestinal)) OR (Intestinal Microbiotas)) OR (Microbiota, Intestinal)) OR (Intestinal Microflora)) OR (Microflora, Intestinal)) OR (Intestinal Flora)) OR (Flora, Intestinal)) OR (Enteric Bacteria)) OR (Bacteria, Enteric)) OR

	(Intestinal Microbiota)
#4	#1 AND #2 AND #3

Supplementary table 2-1. Quality of Cohort studies included in the meta-analysis (NOS)

First Author	Year	Selection	Comparability	Outcome	Total
Shanshan Yao	2023	★★★★	★★	★★★	9
Yingjia Wang	2023	★★★★	★★	★★★	9

Supplementary table 2-2. Quality of Cross-sectional studies included in the meta-analysis (AHRQ)

Study	items											Quality score
	①	②	③	④	⑤	⑥	⑦	⑧	⑨	⑩	⑪	
Xuebin Li ²⁰²²	Y	Y	Y	Y	Y	Y	Y	Y	UC	Y	UC	9
Cuiping Huang ²⁰²²	Y	Y	Y	Y	Y	Y	Y	UC	UC	UC	UC	7
Xudong Guo ²⁰²²	Y	Y	Y	Y	Y	Y	Y	Y	UC	UC	UC	8
Lihua Qin ²⁰²²	Y	Y	Y	Y	Y	Y	Y	Y	UC	Y	UC	9
Yi Kang ²⁰²¹	Y	Y	Y	Y	Y	UC	Y	UC	UC	UC	UC	6
Yinting Huang ²⁰²¹	Y	UC	UC	N	Y	UC	Y	Y	UC	Y	UC	5
Guangshun Han ²⁰²¹	Y	Y	Y	Y	Y	Y	Y	Y	N	UC	UC	8
Yanhong Li ²⁰²¹	Y	Y	Y	Y	Y	UC	Y	Y	UC	UC	UC	7
Yi Ling ²⁰²⁰	Y	Y	Y	Y	Y	UC	Y	Y	N	N	UC	7
Xinyue Sun ²⁰¹⁹	Y	Y	N	N	Y	Y	Y	Y	UC	UC	UC	6
Xuecan Zuo ²⁰¹⁹	Y	Y	Y	Y	Y	Y	Y	Y	UC	UC	UC	8
Wentao Fan ²⁰¹⁶	Y	Y	N	N	Y	UC	UC	UC	UC	Y	UC	4

①Define the source of information (survey, record review)②List inclusion and exclusion criteria for exposed and unexposed subjects (cases and controls) or refer to previous publications ③ Indicate time period used for identifying patients④ Indicate whether or not subjects were consecutive if not population-based ⑤ Indicate if evaluators of subjective components of the study were masked to other aspects of the status of the participants ⑥ Describe any assessments undertaken for quality assurance purposes (e.g., test/retest of primary outcome measurements)⑦Explain any patient exclusions from analysis ⑧Describe how confounding was assessed and/or controlled ⑨If applicable, explain how missing data were handled in the analysis⑩ Summarize patient response rates and completeness of data collection⑪Clarify what follow-up if any, was expected and the percentage of patients for which incomplete data or follow-up was obtained. Y: Yes; N: No; UC: unclear

Supplementary table 3. Bias of the 14 studies included in this meta-analysis based on RoBANS.

Study	Comparability of the target group	Target group selection	Confounders	Measurement of intervention/exposure	Blinding of assessors	Outcome assessment	Incomplete outcome data	Selective outcome reporting
Shanshan Yao ²⁰²³	Low risk	Low risk	Moderate risk	Low risk	Low risk	Low risk	Low risk	Low risk
Yingjia Wang ²⁰²³	Low risk	Low risk	Low risk	Low risk	Low risk	Low risk	Low risk	Low risk
Xuebin Li ²⁰²²	Low risk	Low risk	Moderate risk	Low risk	Low risk	Low risk	Low risk	Low risk
Cuiping Huang ²⁰²²	Low risk	Low risk	Moderate risk	Low risk	Low risk	Low risk	Low risk	Low risk
Xudong Guo ²⁰²²	Low risk	Low risk	Moderate risk	Low risk	Low risk	Low risk	Low risk	Low risk
Lihua Qin ²⁰²²	Low risk	Low risk	Moderate risk	Low risk	Low risk	Low risk	Low risk	Low risk
Yi Kang ²⁰²¹	Low risk	Low risk	Moderate risk	Low risk	Low risk	Low risk	Low risk	Low risk
Yinting Huang ²⁰²¹	Low risk	Low risk	Moderate risk	Low risk	Low risk	Low risk	Low risk	Low risk

Guangshun Han ²⁰²¹	Low risk	Low risk	Moderate risk	Low risk	Low risk	Low risk	Low risk	Low risk
Yanhong Li ²⁰²¹	Low risk	Low risk	Moderate risk	Low risk	Low risk	Low risk	Low risk	Low risk
Yi Ling ²⁰²⁰	Low risk	Low risk	Moderate risk	Low risk	Low risk	Low risk	Low risk	Low risk
Xinyue Sun ²⁰¹⁹	Low risk	Low risk	Moderate risk	Low risk	Low risk	Low risk	Low risk	Low risk
Xuecan Zuo ²⁰¹⁹	Low risk	Low risk	Moderate risk	Low risk	Low risk	Low risk	Low risk	Low risk
Wentao Fan ²⁰¹⁶	Low risk	Low risk	Moderate risk	Low risk	Low risk	Low risk	Low risk	Low risk

Supplementary table 4. Publication bias assessments.

	Begg and Mazumdar rank correlation		Egger's regression intercept test		Duval and Tweedie's trim and fill	
	Tau	P value	Intercept	P value	Observed Hedges' g	Adjusted Hedges' g
<i>P-Pseudomonadota</i>	-0.500	0.220	-3.632	0.064		
<i>P-Bacteroidota</i>	0.500	0.308	2.419	0.212		
<i>P-Bacillota</i>	-0.100	0.806	-0.274	0.947		
<i>P-Fusobacteriota</i>	0	1.000	5.217	0.688		
<i>F-Rikenellaceae</i>	0	1.000	15.815	0.089		
<i>F-Acidaminococcaceae</i>	0	1.000	15.760	0.067	9.362[6.168, 12.557]	3.253[-0.751, 7.257]
<i>F-Fusobacteriaceae</i>	0	1.000	17.570	0.359	3.470[1.988, 4.952]	2.703[1.034, 4.373]
<i>F-Brassicaceae</i>	0.666	0.296	21.277	0.094	4.302[2.156, 6.449]	2.400[0.119, 4.682]
<i>F-Enterobacteriaceae</i>	0.500	0.308	29.179	0.050	5.180[1.843, 8.517]	2.536[-0.702, 5.774]
<i>F-Porphyromonadaceae</i>	0	1.000	12.003	0.301		
<i>F-Erysipelotrichaceae</i>	-0.166	0.734	-20.179	0.111		
<i>F-Bacteroidaceae</i>	0.166	0.734	22.386	0.395		
<i>F-Prevotellaceae</i>	0.833	0.089	1.459	0.013		
<i>F-Ruminococcaceae</i>	0.166	0.734	7.248	0.278		

<i>F-Lachnospiraceae</i>	0.166	0.734	0.096	0.920		
<i>G-Bacillus anthracis</i>	0	1.000	18.355	0.240		
<i>G-Escherichia/Shigella</i>	0.166	0.734	-14.462	0.794		
<i>G-Roseburia</i>	0	1.000	-12.826	0.486		
<i>G-Blautia</i>	0.500	0.308	36.430	0.110	3.639[1.227, 6.051]	1.732[-0.801, 4.265]
<i>G-Lachnospira</i>	0	1.000	-10.475	0.459		
<i>G-Megamonas</i>	0.500	0.308	10.597	0.196	1.509[0.759, 2.259]	1.103[0.282, 1.925]
<i>G-Prevotella</i>	0.166	0.734	6.777	0.691	-1.691[-2.330, -1.053]	-1.956[-2.647, -1.265]
<i>G-Ruminococcus</i>	-0.500	0.308	-12.476	0.194		
<i>G-F. prausnitzii</i>	0.166	0.734	4.523	0.900	2.224[-0.201, 4.650]	1.444[-0.892, 3.782]
<i>G-Curtobacterium</i>	-0.833	0.089	-13.602	0.151		

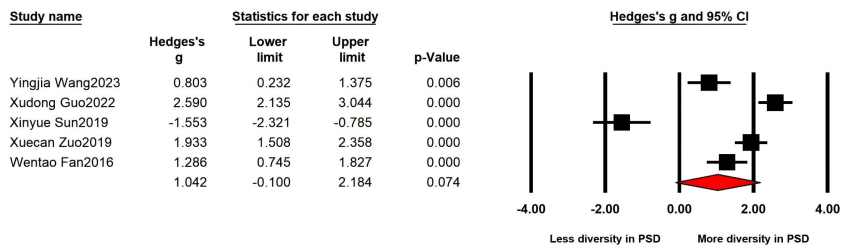
Note: P: phylum; F: family; G: genus; the observed and adjusted effects sizes were reported only when missing studies were found and corrected by Duval and Tweedie's trim and fill. The Hedges' g was presented as overall effect size [lower limit, upper limit].

Supplementary table 5. Heterogeneity analysis and main effect analysis statistical results of α diversity after remove a excluding a study.

α diversity	k	Heterogeneity			Random effects model				Hedges'sg
					95%CI		Test of null (2-Tail)		
		Q	P-value	I ²	Lower limit	Upper limit	Z-value	P-value	
PSD VS HC									
Chao1	4	27.100	0.000	88.930	0.928	2.410	4.417	0.000	1.669
ACE	5	32.937	0.000	87.856	0.203	1.386	2.633	0.008	0.795
Shannon	5	126.013	0.000	96.826	-0.218	2.220	1.609	0.108	1.001
Simpson	4	27.770	0.000	89.197	-0.157	1.157	1.493	0.136	0.500
Fixed effects model									
PSD VS stroke									
Chao1	2	0.403	0.525	0.000	-0.091	0.383	1.209	0.227	0.146
ACE	2	0.718	0.397	0.000	-0.507	0.223	-0.761	0.447	-0.142
Shannon	4	1.313	0.725	0.000	-0.239	0.153	-0.430	0.667	-0.043
Simpson	2	0.663	0.416	0.000	-0.816	-0.087	-2.429	0.015	-0.451

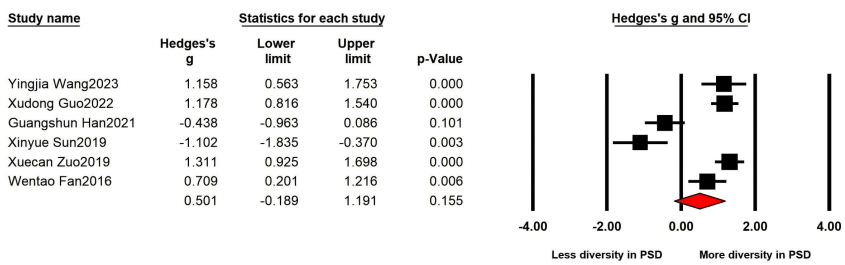
(A)

Chao1: PSD VS HC



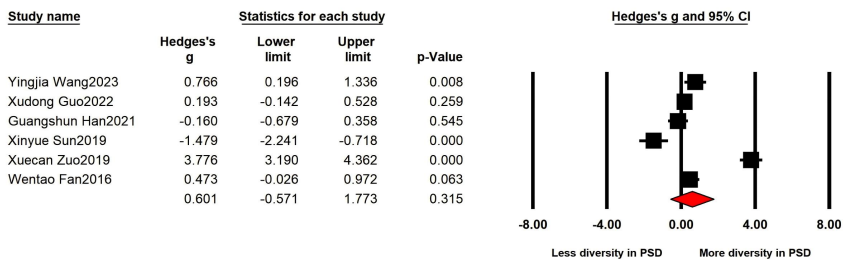
(B)

ACE: PSD VS HC



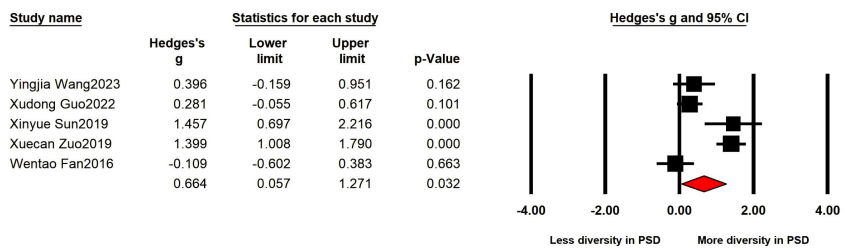
(C)

Shannon: PSD VS HC



(D)

Simpson: PSD VS HC



Supplementary Figure 1. Forest plots of Chao1 index (A); ACE indexes (B); Shannon index (C) and Simpson index (D) in the comparisons between post-stroke depression (PSD) and healthy controls (HC) spectrum.