CLINICAL RESEARCH

e-ISSN 1643-3750
© Med Sci Monit, 2026; 32: e953589
DOI: 10.12659/MSM.953589

Received: 2026.03.28
Accepted: 2026.06.16
Available online: 2026.06.26
Published: 2026.XX.XX

Probiotics Accelerate Microbiota and Metabolic Pathway Recovery Following Colonoscopy Bowel Preparation in Ulcerative Colitis

Authors' Contribution:
Study Design A
Data Collection B
Statistical Analysis C
Data Interpretation D
Manuscript Preparation E
Literature Search F
Funds Collection G

ABCE 1,2 Xiaohan Ma*
ABC 1,2 Jing Guan*
ACD 1,2 Guangpeng Liu*
CD 1,2 Beibei Tian
DE 1,2 Chengcheng Tong
AEFG 1,2 Xi Chen

1 Department of Gastroenterology, First Affiliated Hospital of Anhui Medical University, Hefei, Anhui, PR China
2 Anhui Provincial Key Laboratory of Digestive Disease, First Affiliated Hospital of Anhui Medical University, Hefei, Anhui, PR China

* Xiaohan Ma, Jing Guan, and Guangpeng Liu contributed to this study equally

Corresponding Author: Xi Chen, Department of Gastroenterology, The First Affiliated Hospital of Anhui Medical University, No. 218, Jixi Road, Hefei, 230022, Anhui, China, e-mail: chenxi@ahmu.edu.cn

Financial support: This work was supported by the National Natural Science Foundation of China (82073947) and the Natural Science Research Project of the Anhui Educational Committee (2023AH053284)

Conflict of interest: None declared

Background: Polyethylene glycol (PEG)-based bowel preparation before colonoscopy can disrupt gut microbiota, particularly in patients with ulcerative colitis (UC), who already exhibit baseline dysbiosis and impaired microbial resilience. This study evaluated microbiota recovery after bowel preparation and the effects of probiotic supplementation.

Material/Methods: In this single-center, open-label trial (ChiCTR2200064456), 79 participants (40 healthy controls and 39 patients with UC) undergoing colonoscopy were randomized to receive probiotics or no probiotics for 28 days after colonoscopy. Fecal samples collected at baseline and on days 2, 14, and 28 were analyzed using 16S rRNA gene sequencing to assess microbial diversity, composition, and predicted functional pathways.

Results: Bowel preparation significantly reduced α diversity and altered β diversity in healthy controls, with gradual recovery by day 28. patients with UC exhibited lower baseline diversity and delayed microbiota recovery. Probiotic supplementation modestly improved microbial recovery in healthy individuals and more substantially improved Shannon diversity and evenness in patients with UC. Probiotics were associated with enrichment of beneficial short-chain fatty acid–producing taxa, including *Faecalibacterium, Blautia,* and Lachnospiraceae, together with reductions in *Proteobacteria* and *Fusobacteria*. Predicted functional pathways related to energy metabolism and nucleotide biosynthesis were transiently suppressed after bowel preparation and showed partial recovery over time.

Conclusions: PEG-based bowel preparation induces reversible gut microbiota disruption, with slower recovery in patients with UC. Probiotic supplementation after colonoscopy was associated with improved microbial diversity and enrichment of beneficial taxa, particularly in patients with UC.
Clinical trial: ChiCTR2200064456.

Keywords: Digestive System Diseases • Probiotics

Abbreviations: **BMI**, body mass index; **H&E**, hematoxylin and eosin; **IBD**, inflammatory bowel disease; **NA**, healthy probiotics group; **ND**, healthy control group; **PEG**, polyethylene glycol; **UA**, ulcerative colitis probiotics group; **UC**: ulcerative colitis; **UD**, ulcerative colitis group

Full-text PDF: https://www.medscimonit.com/abstract/index/idArt/953589

5504 2 11 41

Indexed in: [Current Contents/Clinical Medicine] [SCI Expanded] [ISI Alerting System] [ISI Journals Master List] [Index Medicus/MEDLINE] [EMBASE/Excerpta Medica] [Chemical Abstracts/CAS]

Introduction

Colonoscopy remains the gold standard for colorectal cancer screening and is essential for the detection, diagnosis, and surveillance of various intestinal diseases [1]. The success of colonoscopy critically depends on effective bowel preparation, which ensures adequate mucosal visualization for accurate diagnosis and safe therapeutic intervention [2]. Among available agents, polyethylene glycol (PEG) electrolyte solutions are widely regarded as the preferred choice due to their proven efficacy, safety profile, and ease of administration [3,4]. However, emerging evidence suggests that bowel preparation may adversely impact the gut microbiota, a factor increasingly recognized for its role in intestinal and systemic health [5].

Several studies have demonstrated significant shifts in the composition and diversity of fecal microbiota following large-volume bowel cleansing [6-8]. These alterations often include a reduction in microbial diversity and compositional imbalance. Yet, contradictory findings from smaller studies indicate minimal changes in diversity, despite reductions in total bacterial load [6-9]. Thus, the extent and consistency of bowel preparation-induced microbiota disruption remain poorly understood.

Ulcerative colitis (UC), a subtype of inflammatory bowel disease (IBD), is characterized by chronic inflammation and a well-documented dysbiosis of the gut microbiome [10]. While bowel preparation can transiently alter the microbiota in healthy individuals, these effects may be more pronounced and prolonged in patients with UC. Prior research has reported that gut microbiota alterations can persist for up to 4 weeks after colonoscopy, with patients with UC showing greater instability than non-IBD controls [6-8,11]. Moreover, bowel preparation in patients with UC may heighten the risk of complications such as toxic megacolon, gastrointestinal bleeding, and perforation [12]. Clinical observations suggest that symptom exacerbation after colonoscopy often coincides with delayed restoration of the gut microbiota, emphasizing the need to better understand this recovery process [7].

Probiotics have emerged as a promising strategy to restore gut microbial balance, particularly in the context of IBD and post-procedural recovery [10,12,13]. Nevertheless, few studies have rigorously evaluated their effects on gastrointestinal symptoms and microbiome reconstitution following bowel preparation in both healthy and diseased populations [12,13]. Preliminary findings suggest that probiotic supplementation can facilitate the recovery of microbial diversity and composition, while also improving clinical outcomes [14]. Probiotics may facilitate gut microbiota recovery through several complementary mechanisms, including reinforcement of intestinal epithelial barrier integrity, production of beneficial metabolites such as short-chain fatty acids, competitive inhibition of pathogenic bacteria, and modulation of mucosal immune responses by reducing pro-inflammatory cytokine signaling and promoting immune homeostasis [15].

This study aims to address key gaps in our understanding by investigating whether standardized bowel preparation induces distinct microbial changes in healthy individuals compared with patients with UC. By evaluating gut microbiota profiles before and 1 month after colonoscopy, we aim to elucidate the trajectory of microbial restoration in both populations. Additionally, the study examines the potential of probiotic supplementation to accelerate microbiota recovery and restore microbial metabolic functions following bowel preparation. These findings could inform optimized bowel preparation protocols and support the development of targeted interventions to minimize gut microbiota disruption, ultimately improving patient safety and therapeutic outcomes in UC management.

Material and Methods

Ethics Approval

This study was approved by the Ethics Committee of the First Affiliated Hospital of Anhui Medical University and was registered with the Chinese Clinical Trial Registry (registration number: ChiCTR2200064456). All procedures performed in the study involving human participants were in accordance with the Declaration of Helsinki. Prior to enrollment, all participants provided written informed consent after being thoroughly informed about the study's purpose and procedures.

Study Design and Participants

This single-center, open-label clinical trial was conducted at the First Affiliated Hospital of Anhui Medical University between October 2022 and February 2024. The study enrolled healthy individuals and patients with mild to moderate UC who were scheduled for colonoscopy, either as part of routine preventive screening or follow-up care.

Participants were eligible if they were between 20 and 70 years old, able and willing to provide informed consent, and were instructed to maintain their usual dietary habits and to avoid major dietary changes throughout the study period. Healthy controls were required to have no prior history of intestinal diseases, while patients with UC needed to meet the diagnostic criteria outlined in the "Consensus Opinion on the Diagnosis and Treatment of Inflammatory Bowel Disease," with confirmed mild to moderate disease activity. Participants were excluded if they were pregnant or lactating, had severe systemic or organic diseases, were diagnosed with severe UC, or had polyps larger than 0.5 cm or complications such as bleeding or perforation

Indexed in: [Current Contents/Clinical Medicine] [SCI Expanded] [ISI Alerting System] [ISI Journals Master List] [Index Medicus/MEDLINE] [EMBASE/Excerpta Medica] [Chemical Abstracts/CAS]

detected during colonoscopy. The use of antibiotics, antacids, or probiotics within 1 month prior to sampling, as well as recent infections within the past 3 months, were also exclusionary.

Demographic and clinical data were collected at baseline, including age, sex, body mass index (BMI), lifestyle factors such as smoking and alcohol consumption, existing comorbidities, colonoscopy indications, and dietary habits.

Randomization and Probiotic Intervention

Participants were randomly assigned into either a probiotic treatment group or a non-probiotic control group using a random number table method. The 2 groups were balanced in terms of baseline demographic and clinical characteristics, with no statistically significant differences observed.

Participants in the probiotic group received oral capsules containing a combination of *Bifidobacterium*, *Lactobacillus*, and *Enterococcus*, formulated by Shanghai Xinyi Pharmaceutical Co, Ltd. Each 210 mg capsule contained at least 1.0×10^7 colony-forming units of viable bacteria, including *Lactobacillus plantarum*, *Lactobacillus acidophilus*, and *Enterococcus faecalis*. Capsules were administered at a dose of 630 mg twice daily for 28 consecutive days, starting the day after colonoscopy. Probiotic supplementation was initiated after colonoscopy rather than before bowel preparation because the objective of this study was to evaluate microbiota recovery following PEG-induced perturbation, not to improve bowel cleansing efficacy. Patients with severe UC or colonoscopy-related complications, including bleeding or perforation, were excluded. Therefore, probiotics were administered only after completion of colonoscopy in clinically stable participants. Previous studies have reported the use of probiotics after colonoscopy and in patients with UC, supporting the safety and biological rationale of this approach [16-18].

Bowel Preparation and Colonoscopy Procedure

A standardized 4-L PEG regimen was used for all participants to ensure consistency across study groups. Only patients with mild to moderate ulcerative colitis were enrolled, and individuals with severe disease or major comorbidities were excluded. Bowel preparation quality was assessed using the Boston Bowel Preparation Scale, and no serious bowel preparation-related adverse events were observed. Although lower-volume PEG regimens have demonstrated good efficacy and tolerability in patients with inflammatory bowel disease, the 4-L PEG regimen remains a commonly used and well-established preparation protocol. Participants were provided with an instructional manual outlining the bowel preparation process. The preparation protocol began with a low-fiber diet for 3 days, followed by a soft diet on the evening before the procedure. Bowel cleansing was achieved using a total of 4 L of a PEG electrolyte solution. The first 2 L were ingested between 7: 00 and 9: 00 PM the night before colonoscopy, and the remaining 2 L were consumed at least 4 hours before the procedure.

Colonoscopy procedures were performed under intravenous general anesthesia administered by anesthesiologists using a combination of propofol, etomidate, and remifentanil. Room air was used for insufflation. All procedures were conducted by experienced endoscopists, and cecal intubation was successfully achieved in all cases. Polyps smaller than 0.5 cm were removed using biopsy forceps. The quality of bowel preparation was evaluated using the Boston Bowel Preparation Scale.

Sample Collection and Processing

Participants were stratified into 4 subgroups: healthy individuals without probiotics (ND group), healthy individuals with probiotics (NA group), UC patients without probiotics (UD group), and UC patients with probiotics (UA group). The ND group included 14 men and 6 women, the NA group included 10 men and 10 women, the UD group included 9 men and 11 women, and the UA group included of 9 men and 10 women.

Stool samples were collected at 4 key time points: 3 days before colonoscopy (day 0), 1 day after colonoscopy (day 2), and on day 14 and day 28 after colonoscopy. All participants adhered to a standardized collection protocol using sterile fecal DNA stabilization kits provided by Avison Gene Technology Co, Ltd. The collected samples were immediately transported to the hospital's digestive endoscopy center, stored at -80 °C, and subsequently shipped on dry ice to Novogene Sequencing Center (Tianjin, China) for downstream analysis.

Sample Size Estimation

Sample size calculation was based on the Shannon diversity index, a key indicator of gut microbiota diversity. The 4 study groups—ND, NA, UD, and UA—were assumed to be of equal size. Mean and standard deviation estimates for each group were drawn from preliminary data (NC: 4.783 ± 0.626; NA: 5.573 ± 0.252; UD: 4.402 ± 0.370; UA: 4.707 ± 0.431). Using a type I error rate of 0.05 and a type II error rate of 0.1, the minimum sample size required for each group was calculated to be 9. A total of 79 participants were ultimately enrolled: 20 in each of the ND, NA, and UD groups, and 19 in the UA group.

16S rRNA Gene Sequencing and Bioinformatics Analysis

Genomic DNA was extracted from stool samples using the QIAamp Fast DNA Stool Mini Kit (Qiagen, Germany). The V3-V4 hypervariable region of the 16S rRNA gene was amplified using the primer pair 341F (CCTAYGGGRBGCASCAG) and 806R

Indexed in: [Current Contents/Clinical Medicine] [SCI Expanded] [ISI Alerting System] [ISI Journals Master List] [Index Medicus/MEDLINE] [EMBASE/Excerpta Medica] [Chemical Abstracts/CAS]

Table 1. Baseline characteristics of healthy control cohort: healthy probiotics (NA group) and healthy control (ND group).

	ND group (n = 20)	NA group (n = 20)	*P* value
Male, n(%)	14 (70)	10 (50)	0.197
Age, y (mean ± SD)	42.05 ± 12.47	46.30 ± 11.68	0.273
BMI, kg/m^2 (mean ± SD)	23.13 ± 3.21	23.18 ± 3.38	0.959
Comorbidities			0.597
Hypertension	2 (10)	4 (20)	
Dyslipidemia	2 (10)	1 (5)	
Alcohol history	7 (35)	11 (55)	0.204
Current smoker	7 (35)	5 (25)	0.49
Indication of colonoscopy			0.376
Screening	18 (90)	16 (80)	
Post-polypectomy surveillance	2 (10)	4 (20)	
Bowel preparation			1
Good	13 (65)	13 (65)	
Poor	7 (35)	7 (35)	
Findings of colonoscopy			1
Normal	12 (60)	12 (60)	
Polyp	8 (40)	8 (40)	
Post-colonoscopy complications			
Abdominal pain	3 (15)	1 (5)	0.292
Bloating	4 (20)	3 (15)	0.677
Diarrhea	4 (20)	3 (15)	0.677

(GGACTACNNGGGTATCTAAT). Sequencing libraries were constructed using the TruSeq DNA PCR-Free Sample Preparation Kit and sequenced on an Illumina NovaSeq platform with paired-end 2 × 250 bp reads.

Bioinformatic processing included merging paired-end reads with FLASH (v1.2.11), primer trimming using Cutadapt (v1.18), and quality filtering with fastp (v0.23.1). Chimera sequences were identified and removed using VSEARCH (v2.16.0). Amplicon sequence variants (ASVs) were denoised and identified using the DADA2 pipeline in QIIME2 (v2022.02), resulting in 7207 unique ASVs across 316 samples, with a minimum read count of 31 455 per sample. Taxonomic classification was performed against the SILVA 138 database, and ASVs contributing less than 0.001% of total sequences were excluded from analysis.

Alpha diversity metrics, including Shannon, Chao1, and Evenness indices, were calculated from rarefied ASV tables. Beta diversity was assessed using UniFrac distances and visualized through principal coordinate analysis. Taxonomic compositions at the phylum and genus levels were analyzed using the R package Vegan (v2.6-6.1). Differences in microbial community structure were assessed using PERMANOVA, and group comparisons of alpha diversity were conducted using the Wilcoxon test. Differentially abundant taxa were identified with linear discriminant analysis effect size (LEfSe), as implemented in the R package microbiomeMarker, using an LDA threshold of 2.0 and a significance level of $P < 0.05$. Functional profiling of microbial communities was predicted using PICRUSt2 (v2.5.2) with MetaCyc pathway annotation. Functional differences were determined using ANOVA ($P < 0.01$, prevalence > 10%) and visualized as heatmaps comparing day 2 to days 0, 14, and 28 within each group. These analyses provide predictions of microbial functional potential based on 16S rRNA gene data and do not represent direct measurements of gene expression or metabolite abundance.

Histological Evaluation

Distal colonic tissue biopsies were collected during colonoscopy and immediately rinsed 3 times with phosphate-buffered

Indexed in: [Current Contents/Clinical Medicine] [SCI Expanded] [ISI Alerting System] [ISI Journals Master List] [Index Medicus/MEDLINE] [EMBASE/Excerpta Medica] [Chemical Abstracts/CAS]

Table 2. Baseline characteristics of ulcerative colitis cohort: ulcerative colitis (UD group) and ulcerative colitis probiotics (UA group).

	UD (n = 20)	UA (n = 19)	*P* value
Male, n(%)	9 (45)	9 (47.37)	0.882
Age, y (mean ± SD)	43.65 ± 13.57	47.84 ± 11.81	0.311
BMI, kg/m^2 (mean ± SD)	22.22 ± 2.48	21.76 ± 2.56	0.575
Time since diagnosis (y)	4 (6.5)	8 (12)	0.174
Hypertension	0 (0)	2 (10.53)	0.136
Maximal disease extent			0.733
Ulcerative protitis (E1)	9 (45)	7 (36.84)	
Left-sided (E2)	6 (30)	8 (42.11)	
Pancolitis (E3)	5 (25)	4 (21.05)	
Disease activity			0.238
Mayo < 3 (remission)	6 (30)	2 (10.53)	
3 ≤ Mayo < 6 (mild)	8 (40)	12 (63.16)	
6 ≤ Mayo ≤ 10 (moderate)	6 (30)	5 (26.32)	
Medications			0.97
Oral 5-ASA	19 (95)	18 (94.74)	
TNF inhibitors	1 (5)	1 (5.26)	
Bowel preparation			0.517
Good	19 (95)	17 (89.47)	
Poor	1 (5)	2 (10.53)	

Abbreviations: BMI, body mass index; ASA, aminosalicylic acid; TNF, tumor necrosis factor.

saline. The tissues were fixed overnight in 4% paraformaldehyde, embedded in paraffin, and sectioned at a thickness of 4 μm. Sections were processed through an ethanol gradient, stained with hematoxylin and eosin (H&E), and evaluated under a light microscope (Leica, Germany) at 200× magnification to assess mucosal structure and inflammation. Histological assessment was performed for descriptive purposes only, and no standardized scoring system, such as the Nancy Index, was applied.

Statistical Analysis

All statistical analyses were performed using R software (v4.3.2). Comparisons between 2 groups were conducted using the Wilcoxon rank-sum test. For comparisons among more than 2 groups, the Kruskal–Wallis test was used when data did not meet assumptions of normality, followed by Dunn's post hoc test with Benjamini-Hochberg false discovery rate correction for multiple comparisons. Analysis of variance (ANOVA) was applied only when data were approximately normally distributed and exhibited homogeneity of variance. Microbial community differences were assessed using PERMANOVA based on distance matrices. Statistical significance was defined as $P < 0.05$ unless otherwise specified.

Results

Participant Enrollment and Baseline Characteristics

Between October 2022 and February 2024, a total of 97 participants were screened for enrollment. Following the exclusion of 7 individuals who declined participation and 11 who did not meet eligibility criteria, 79 participants were included in the final analysis. These included 40 healthy volunteers and 39 patients diagnosed with UC. Each group was randomly assigned to receive either standard care (non-probiotic) or probiotic supplementation.

Indexed in: [Current Contents/Clinical Medicine] [SCI Expanded] [ISI Alerting System] [ISI Journals Master List] [Index Medicus/MEDLINE] [EMBASE/Excerpta Medica] [Chemical Abstracts/CAS]

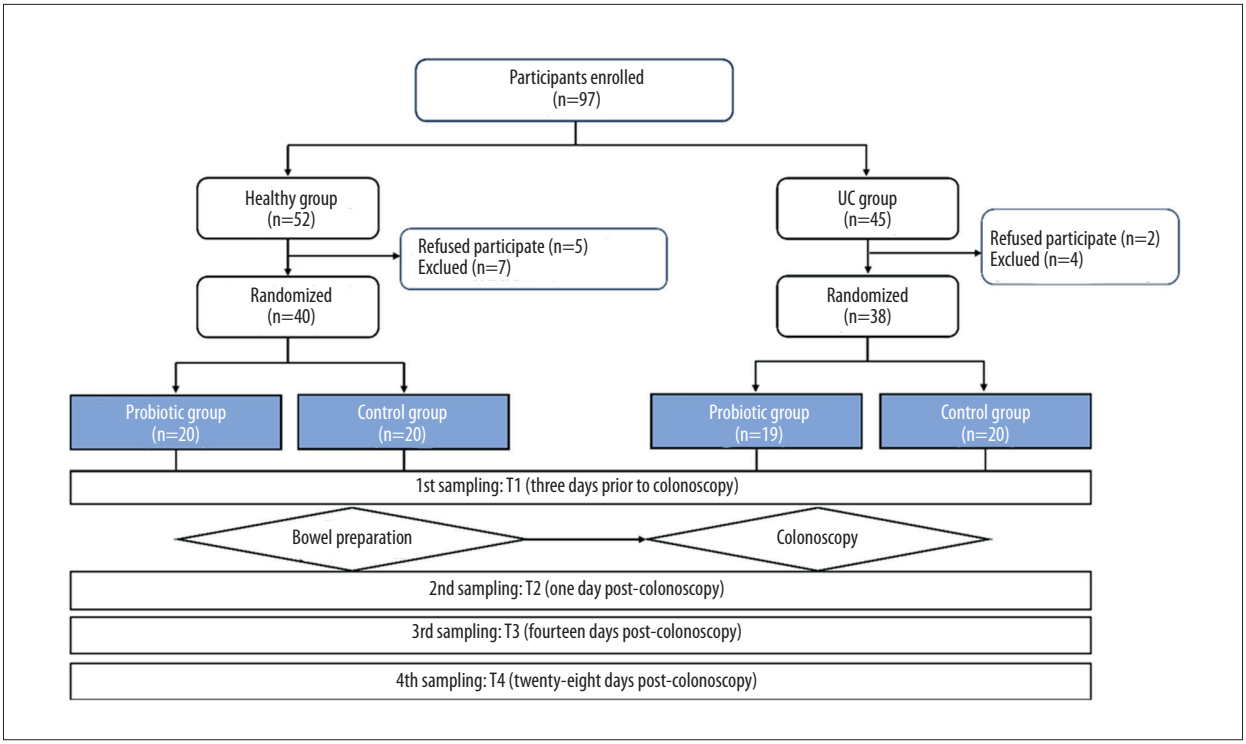


Figure 1. Flowchart illustrating the study design, participant enrollment, group allocation, intervention, and follow-up time points.

In the healthy cohort, the non-probiotic group (ND) consisted of 14 men and 6 women, with a mean age of 42.05 ± 12.47 years. The probiotic group (NA) included 10 men and 10 women, with a mean age of 46.30 ± 11.68 years. No statistically significant differences were observed between these 2 groups in baseline characteristics such as BMI, smoking and alcohol history, comorbidities, indications for colonoscopy, bowel preparation method, colonoscopic findings, or procedure-related complications (**Table 1**).

Among patients with UC, the non-probiotic group (UD) included 9 men and 11 women, with a mean age of 43.65 ± 13.57 years and a median disease duration of 4 (6.5) years. The probiotic group (UA) consisted of 9 men and 10 women, with a mean age of 47.84 ± 11.81 years and a median disease duration of 8 (12) years. Baseline variables, including BMI, smoking/alcohol history, disease extent and severity, bowel preparation regimen, and medical therapy, were comparable between the UC subgroups. Notably, the baseline modified Mayo scores showed no statistically significant difference between the 2 UC patient groups ($P > 0.05$), indicating balanced group allocation (**Table 2**).

A visual summary of the study design and participant flow is provided in **Figure 1**. Representative colonoscopy images and descriptive histological sections using H&E staining illustrate the mucosal damage, inflammatory infiltrate, and crypt architectural distortion typical of UC, contrasting with the intact mucosa in healthy controls (**Figure 2A, 2B**).

Bowel Preparation Alters Gut Microbiota Diversity in Healthy Individuals but Less So in UC Patients

Gut microbiota diversity was assessed using alpha (α) and beta (β) diversity metrics at 4 time points: day 0 (3 days before colonoscopy), day 2 (1 day after colonoscopy), day 14 (14 days after colonoscopy), and day 28 (28 days after colonoscopy).

In healthy individuals without probiotic supplementation (ND group), bowel preparation led to a significant reduction in α diversity on day 2, as reflected in decreased Chao1, Shannon, and evenness indices (**Figure 2C-2E**). These metrics gradually recovered by day 14 and returned near baseline by day 28. Beta diversity analysis using unweighted UniFrac distances revealed a clear disruption in microbial community structure on day 2, which largely normalized by day 14 and day 28 (**Figure 2F**).

In contrast, the UC non-probiotic group (UD group) showed no significant changes in α-diversity indices over the same period (**Figure 2G-2I**). Although microbial composition shifted slightly on day 2, as shown by unweighted UniFrac analysis, the changes were not statistically significant and appeared to resolve by day 28 (**Figure 2J**).

Indexed in: [Current Contents/Clinical Medicine] [SCI Expanded] [ISI Alerting System] [ISI Journals Master List] [Index Medicus/MEDLINE] [EMBASE/Excerpta Medica] [Chemical Abstracts/CAS]

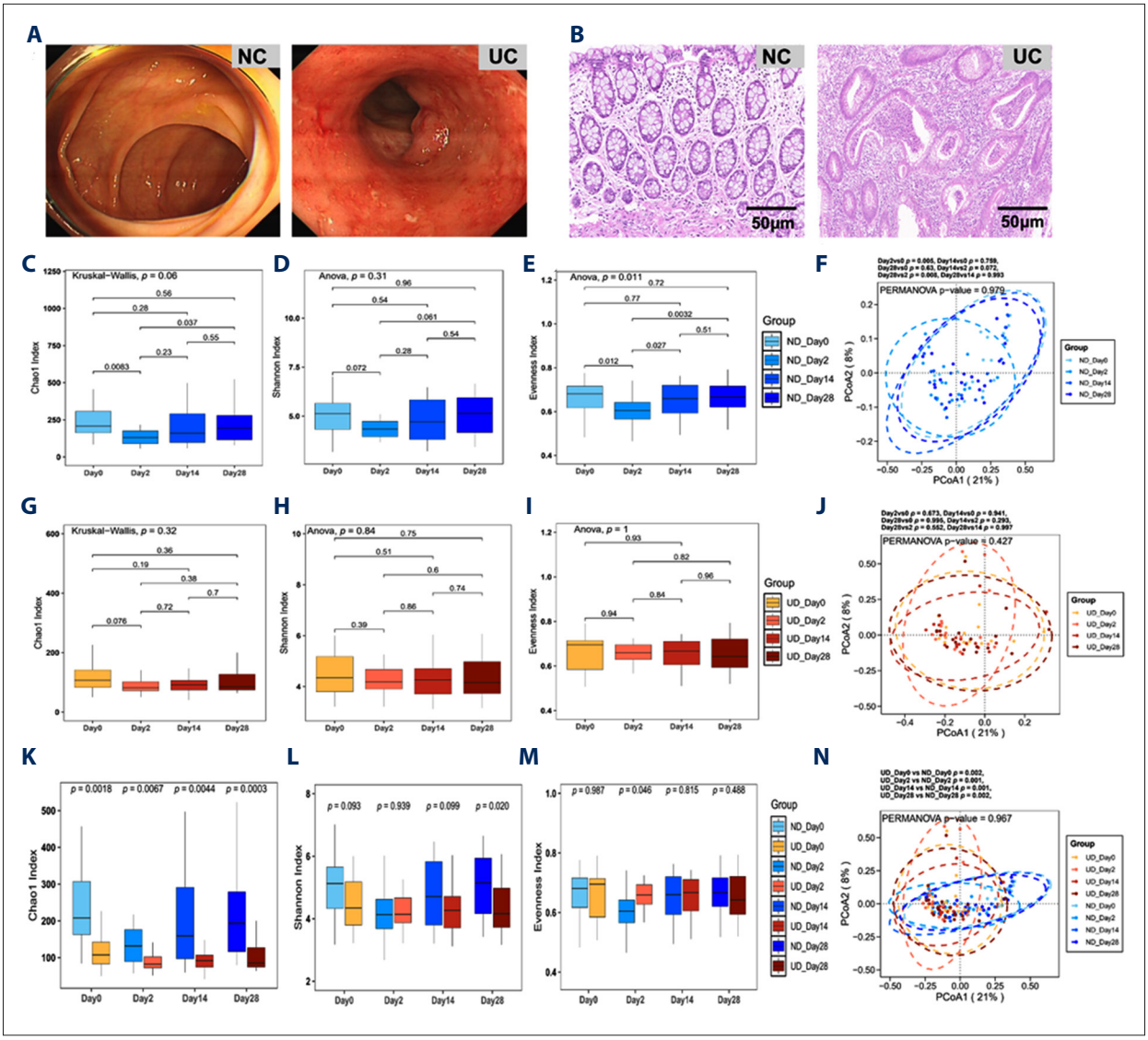


Figure 2. Comparisons of gut microbiota diversity in healthy control (ND) and ulcerative colitis (UD) groups. (**A**) Representative colonoscopy images of healthy volunteers and patients with UC. (**B**) Histopathological evaluation of colonic mucosa using hematoxylin and eosin (H&E) staining; scale bar = 50 μm. (**C-E**) Chao1, Shannon, and evenness indices for ND group at 4 time points. (**F**) Unweighted UniFrac distances for ND group over time. (**G-I**) Chao1, Shannon, and evenness indices for UD group at 4 time points. (**J**) Unweighted UniFrac distances for UD group over time. (**K-M**) Comparisons of Chao1, Shannon, and evenness indices between ND and UD groups. (**N**) Unweighted UniFrac distances between ND and UD groups at each time point. Abbreviations: ND, healthy control group; UD, ulcerative colitis group.

At baseline, patients with UC had significantly reduced microbial richness and diversity compared with healthy controls, evidenced by lower Chao1 and Shannon indices (**Figure 2K-2M**). This baseline dysbiosis persisted throughout the study period. Beta diversity remained consistently distinct between UC and healthy participants, suggesting a stable but altered microbial ecosystem in UC (**Figure 2N**).

Probiotic Supplementation Enhances Microbial Recovery Following Bowel Preparation

To assess the impact of probiotics on microbiota recovery, diversity indices in the probiotic-treated groups (NA and UA) were compared with their respective controls (ND and UD) on days 14 and 28.

Indexed in: [Current Contents/Clinical Medicine] [SCI Expanded] [ISI Alerting System] [ISI Journals Master List] [Index Medicus/MEDLINE] [EMBASE/Excerpta Medica] [Chemical Abstracts/CAS]

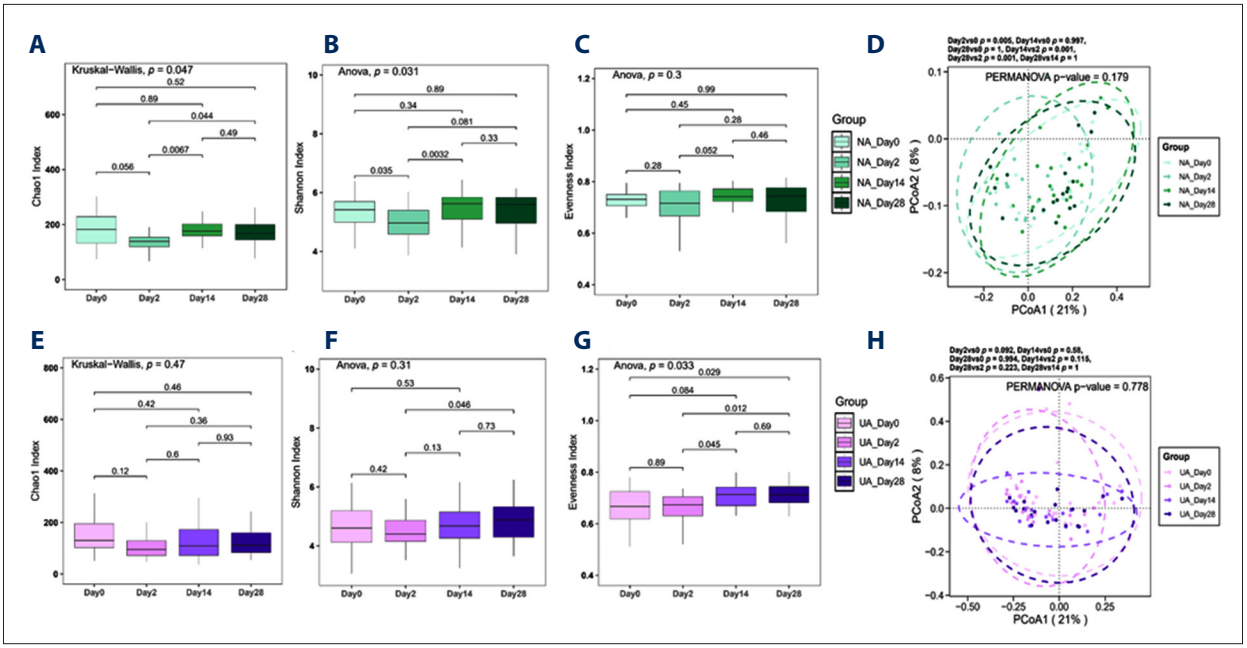
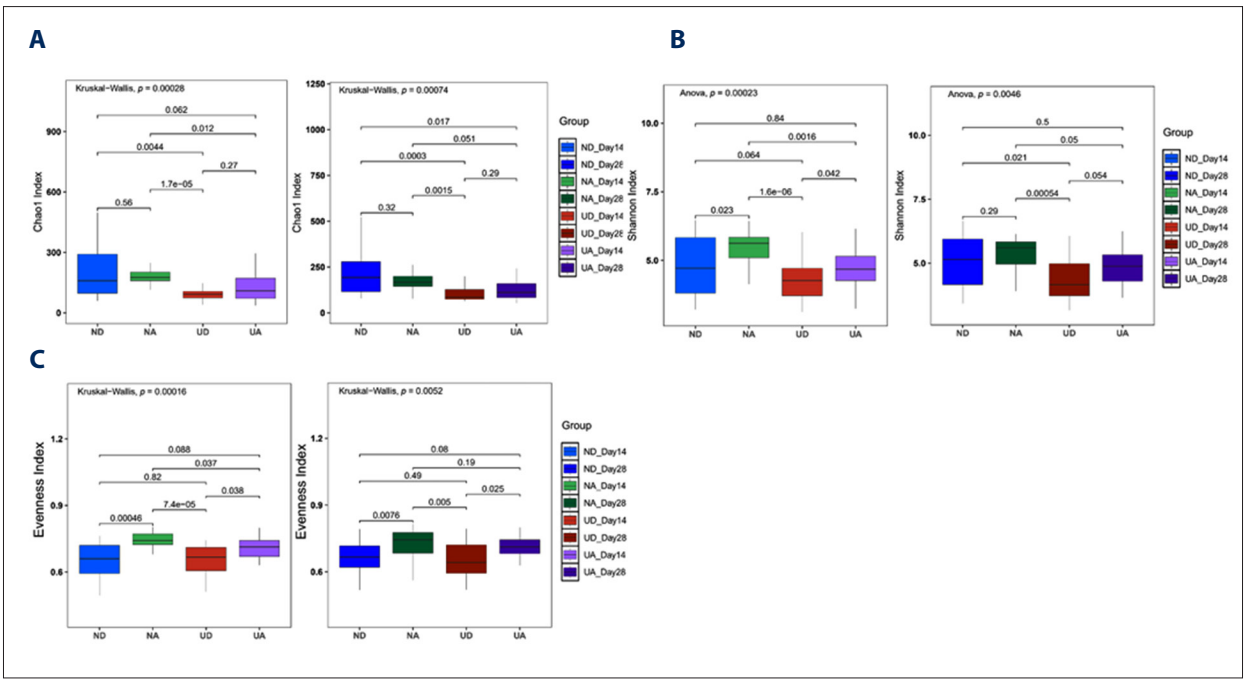


Figure 3. Changes in gut microbiota diversity in healthy probiotics (NA) and ulcerative colitis probiotics (UA) groups. (**A-C**) Chao1, Shannon, and evenness indices for NA group at 4 time points. (**D**) Unweighted UniFrac distances for NA group over time. (**E-G**) Chao1, Shannon, and evenness indices for UA group at 4 time points. (**H**) Unweighted UniFrac distances for UA group over time. Abbreviations: NA, healthy probiotics group; UA, ulcerative colitis probiotics group.

In healthy individuals, probiotic supplementation did not significantly alter the trajectory of α-diversity recovery compared with the ND group (**Figure 3A-3C**). Both groups experienced similar diversity reductions following bowel cleansing and recovered over time. Beta diversity analysis mirrored these findings, with significant disruption at day 2 and gradual normalization by day 28 (**Figure 3D**).

In contrast, probiotic supplementation in patients with UC (UA group) significantly improved microbial evenness by days 14



Indexed in: [Current Contents/Clinical Medicine] [SCI Expanded] [ISI Alerting System] [ISI Journals Master List] [Index Medicus/MEDLINE] [EMBASE/Excerpta Medica] [Chemical Abstracts/CAS]

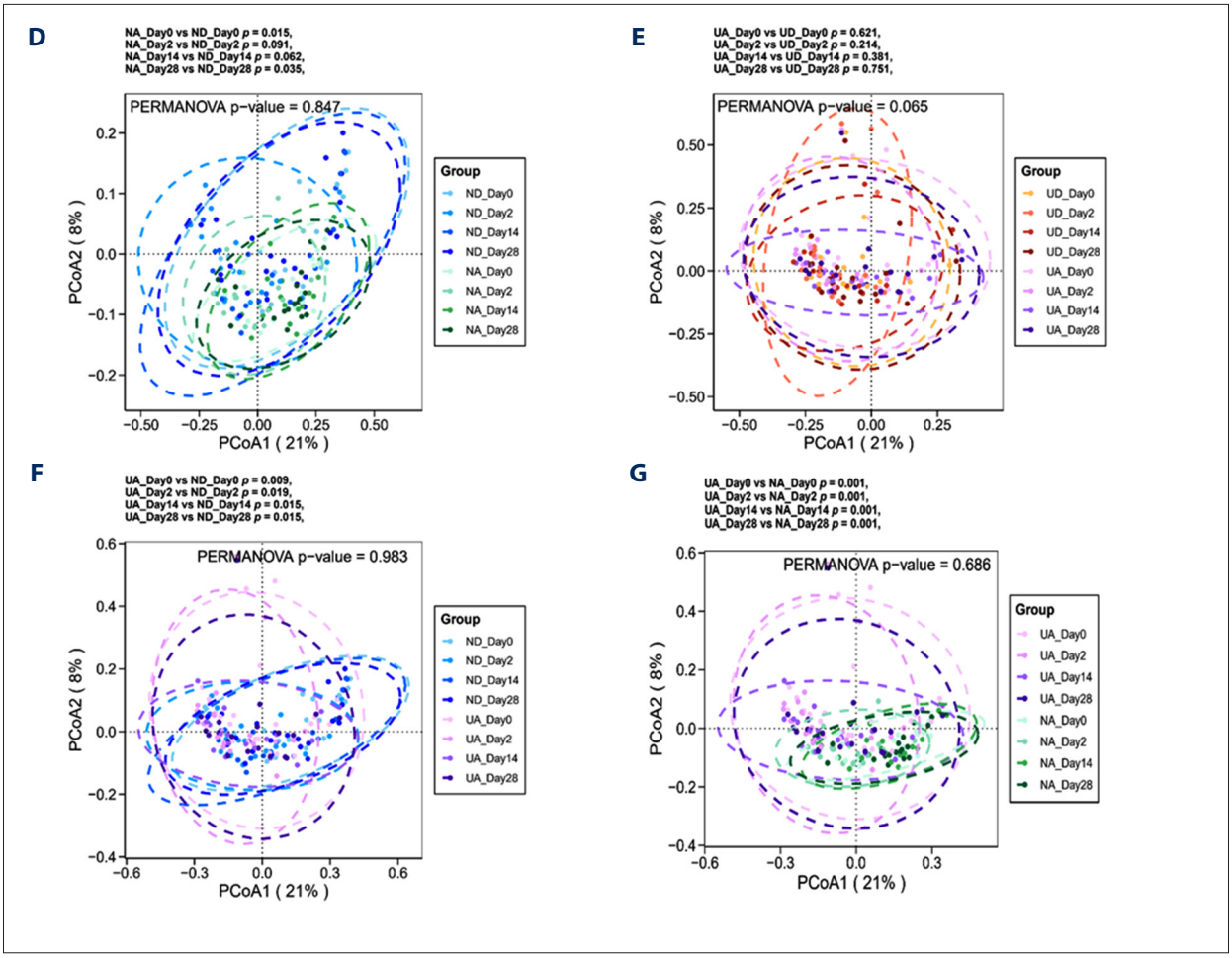


Figure 4. Effects of probiotic supplementation on gut microbiota diversity. (**A-C**) Chao1, Shannon, and evenness indices at days 14 and 28 in ND, NA, UD, and UA groups. (**D-G**) Unweighted UniFrac distance comparisons: (**D**) ND vs NA, (**E**) UD vs UA, (**F**) ND vs UA, (**G**) NA vs UA over time. Abbreviations: ND, healthy control group; UD, ulcerative colitis group; NA, healthy probiotics group; UA, ulcerative colitis probiotics group; PCoA, principal coordinates analysis.

and 28 compared with day 2 (**Figure 3E-3G**). Although beta diversity differences over time within the UA group were not statistically significant, trends suggested a more stable recovery pattern (**Figure 3H**).

Comparative analysis between the NA and ND groups on day 14 revealed significantly higher evenness in the probiotic group, and by day 28, both the Shannon and evenness indices were significantly improved in the NA group (**Figure 4A-4C**). These shifts were accompanied by notable differences in microbial community structure (**Figure 4D**).

In patients with UC, probiotic supplementation significantly increased Shannon and evenness indices at days 14 and 28 compared with UD (**Figure 4A-4C**). By day 14, microbial diversity in the UA group approached that of healthy ND controls, although it remained distinct from the NA group. By day 28, UA diversity levels were comparable to ND and approaching NA levels. However, beta diversity analysis indicated that microbial community structure in UA remained distinct from both the ND and NA groups (**Figure 4E-4G**).

Taxonomic Shifts Induced by Bowel Preparation and Modulated by Probiotics

Taxonomic composition was analyzed at both the phylum and genus levels across all groups and time points. At the phylum level, Firmicutes decreased after bowel preparation, whereas *Proteobacteria* transiently increased. In the UD group, bowel preparation was associated with a more pronounced transient increase in Proteobacteria on day 2 compared with the other groups (**Figure 5A**). At the genus level, *Escherichia-Shigella* also transiently increased in the UD group after bowel preparation, whereas this pattern was not evident in healthy participants. These findings suggest greater susceptibility of the UC microbiota to expansion of facultative anaerobic and

Indexed in: [Current Contents/Clinical Medicine] [SCI Expanded] [ISI Alerting System] [ISI Journals Master List] [Index Medicus/MEDLINE] [EMBASE/Excerpta Medica] [Chemical Abstracts/CAS]

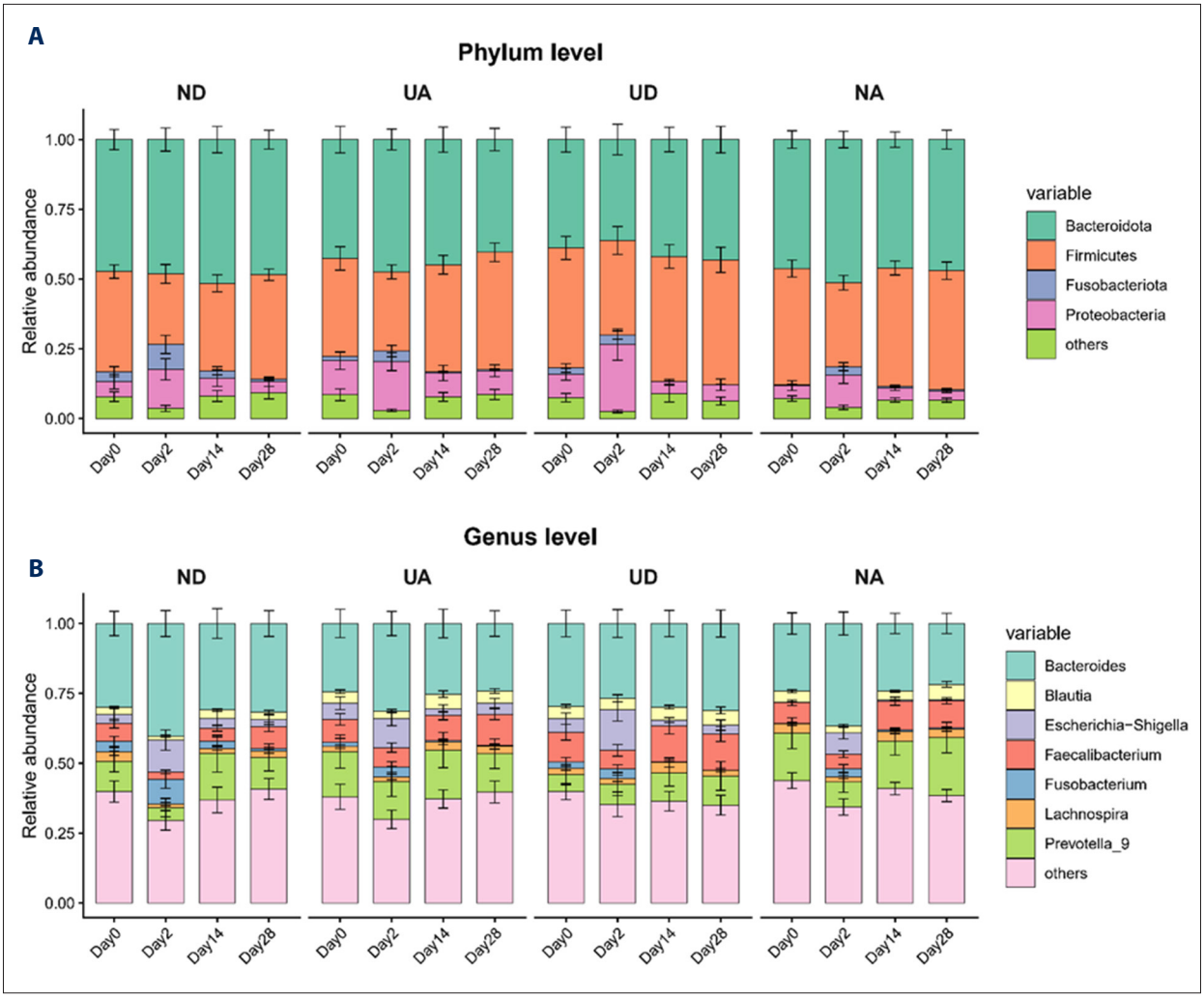


Figure 5. Taxonomic composition of gut microbiota. (**A**) Relative abundance at the phylum level in ND, NA, UD, and UA groups. (**B**) Relative abundance at the genus level in ND, NA, UD, and UA groups. Abbreviations: ND, healthy control group; UD, ulcerative colitis group; NA, healthy probiotics group; UA, ulcerative colitis probiotics group.

potentially pro-inflammatory taxa following ecological disturbance (**Figure 5B**).

In the ND group, bowel preparation triggered a temporary increase in *Proteobacteria* and *Fusobacteria*, alongside a reduction in Firmicutes by day 2. These changes normalized by day 14 (**Figure 6A**). Genera such as *Escherichia-Shigella* and *Fusobacterium* rose sharply, while beneficial taxa including *Blautia*, Lachnospira, and *Faecalibacterium* declined before recovering (**Figure 7A**).

The NA group showed similar overall patterns; however, probiotic supplementation was associated with an increase in Firmicutes at the phylum level and enhanced recovery of beneficial taxa, including *Faecalibacterium* and members of the Lachnospiraceae family, by day 14 (**Figures 6B, 7B**).

In the UC group, bowel preparation caused increases in *Proteobacteria* and *Fusobacteria* and decreases in Firmicutes and *Actinobacteria*, although these shifts were not statistically significant. By day 28, *Actinobacteria* abundance had increased, whereas Firmicutes showed a trend toward recovery that did not reach statistical significance (**Figure 6C**). At the genus level, key beneficial bacteria such as *Blautia* and *Faecalibacterium* declined initially and showed a non-significant trend toward increased abundance by day 14 (**Figure 7C**).

In the UA group, probiotic treatment significantly increased Firmicutes abundance on days 14 and 28 compared with UD (**Figure 6D**). In the UA group, probiotic supplementation was associated with significant increases in the abundances of *Blautia* and *Faecalibacterium* at day 28 compared with day 2, suggesting recovery of beneficial short-chain fatty acid–producing taxa (**Figure 7D**).

Indexed in: [Current Contents/Clinical Medicine] [SCI Expanded] [ISI Alerting System] [ISI Journals Master List] [Index Medicus/MEDLINE] [EMBASE/Excerpta Medica] [Chemical Abstracts/CAS]

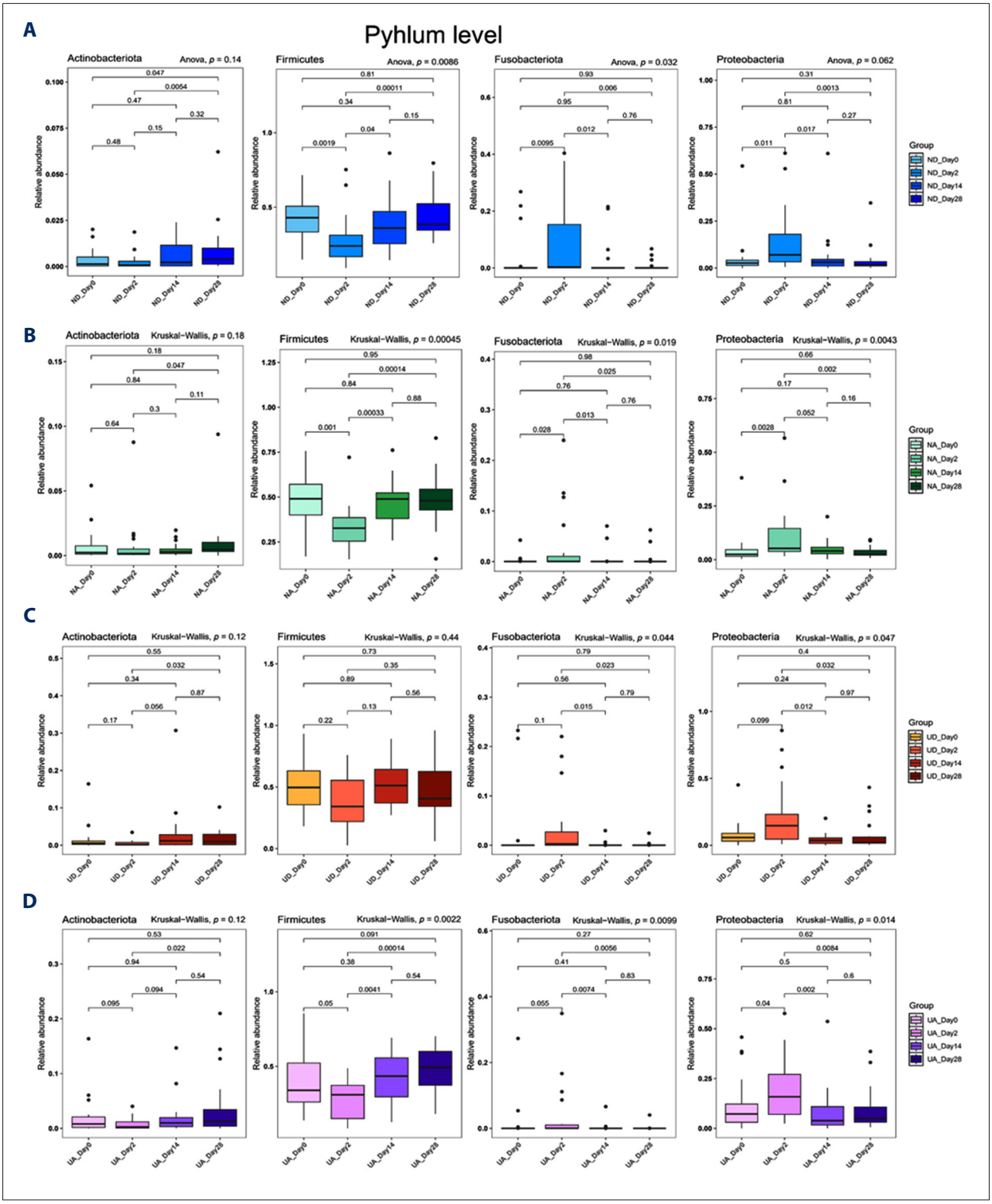


Figure 6. Temporal changes in phylum-level taxonomy. (**A-D**) Relative abundance of major phyla at 4 time points in (**A**) ND, (**B**) NA, (**C**) UD, and (**D**) UA groups. Abbreviations: ND, healthy control group; UD, ulcerative colitis group; NA, healthy probiotics group; UA, ulcerative colitis probiotics group.

Indexed in: [Current Contents/Clinical Medicine] [SCI Expanded] [ISI Alerting System] [ISI Journals Master List] [Index Medicus/MEDLINE] [EMBASE/Excerpta Medica] [Chemical Abstracts/CAS]

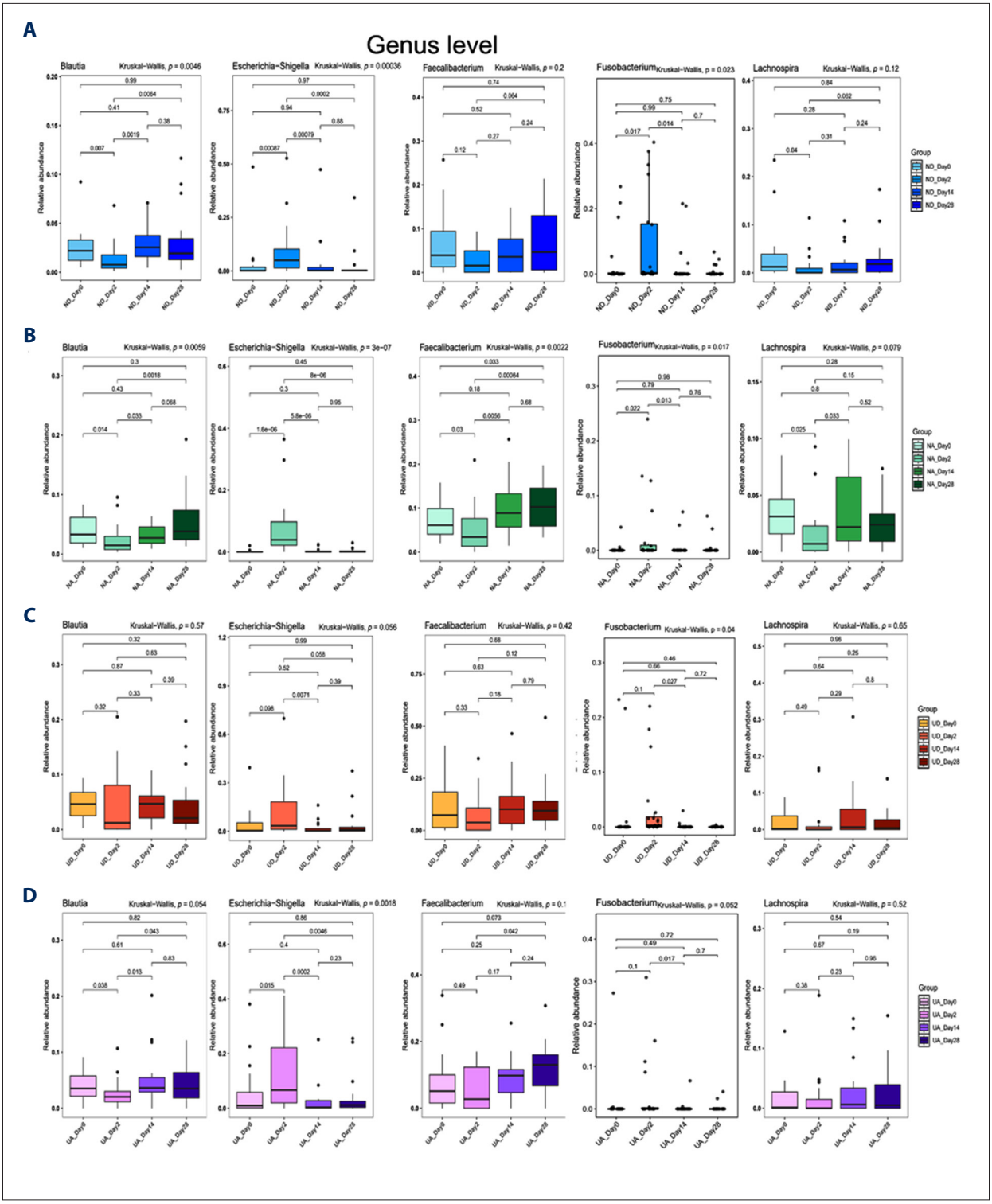


Figure 7. Temporal changes in genus-level taxonomy. (**A-D**) Relative abundance of key genera at 4 time points in (**A**) ND, (**B**) NA, (**C**) UD, and (**D**) UA groups. Abbreviations: ND, healthy control group; UD, ulcerative colitis group; NA, healthy probiotics group; UA, ulcerative colitis probiotics group.

Indexed in: [Current Contents/Clinical Medicine] [SCI Expanded] [ISI Alerting System] [ISI Journals Master List] [Index Medicus/MEDLINE] [EMBASE/Excerpta Medica] [Chemical Abstracts/CAS]

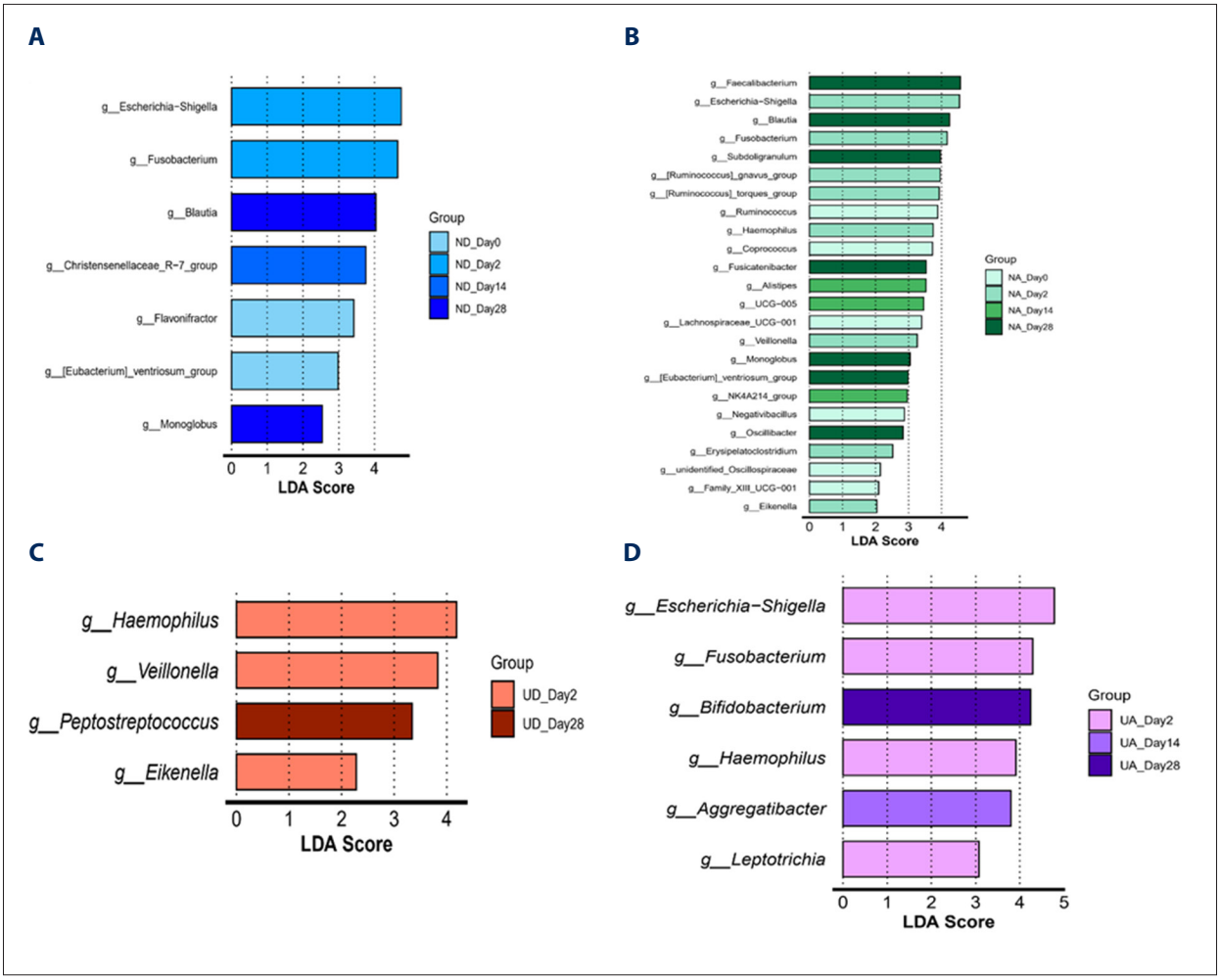


Figure 8. Comparisons of differential taxonomic features based on results of LEfSe analysis among different time points. (**A**) Comparisons of differential taxonomic features based on results of LEfSe analysis among different time points of healthy control group (ND). (**B**) Comparisons of differential taxonomic features based on results of LEfSe analysis among different time points of healthy probiotics group (NA). (**C**) Comparisons of differential taxonomic features based on results of LEfSe analysis among different time points of ulcerative colitis group (UD). (**D**) Comparisons of differential taxonomic features based on results of LEfSe analysis among different time points of ulcerative colitis probiotics group (UA). Abbreviations: ND, healthy control group; UD, ulcerative colitis group; NA, healthy probiotics group; UA, ulcerative colitis probiotics group.

Identification of Key Bacterial Genera and Their Correlation with Microbial Diversity

To better understand probiotic-driven shifts in gut microbiota, LEfSe analysis was performed. In the UA group, probiotic supplementation enriched several taxa that are commonly regarded as beneficial in ulcerative colitis, including *Blautia*, *Faecalibacterium*, *Lactobacillus*, and members of the Lachnospiraceae family (**Figure 8**), as well as *Butyricicoccus*, *Oscillibacter*, *Coprococcus*, and *Eubacterium ventriosum* (**Figure 9**). Many of these taxa are short-chain fatty acid–producing commensals associated with maintenance of epithelial barrier integrity, immune regulation, and reduced intestinal inflammation.

Comparisons between the ND and NA groups revealed that probiotic supplementation was associated with enrichment of key butyrate-producing taxa, including *Roseburia*, *Eubacterium hallii*, and *Lachnospira*, together with a reduction in opportunistic taxa such as *Fusobacterium* (**Figure 10A**). In patients with UC, probiotic supplementation was associated with a trend toward enrichment of beneficial commensal taxa. *Sutterella* demonstrated a non-significant enrichment trend at day 14 (**Figure 10A**), whereas unidentified_Ruminococcaceae, a representative operational taxonomic unit within the Ruminococcaceae family, met our predefined LEfSe significance criteria at day 28 (**Figure 10C**).

Indexed in: [Current Contents/Clinical Medicine] [SCI Expanded] [ISI Alerting System] [ISI Journals Master List] [Index Medicus/MEDLINE] [EMBASE/Excerpta Medica] [Chemical Abstracts/CAS]

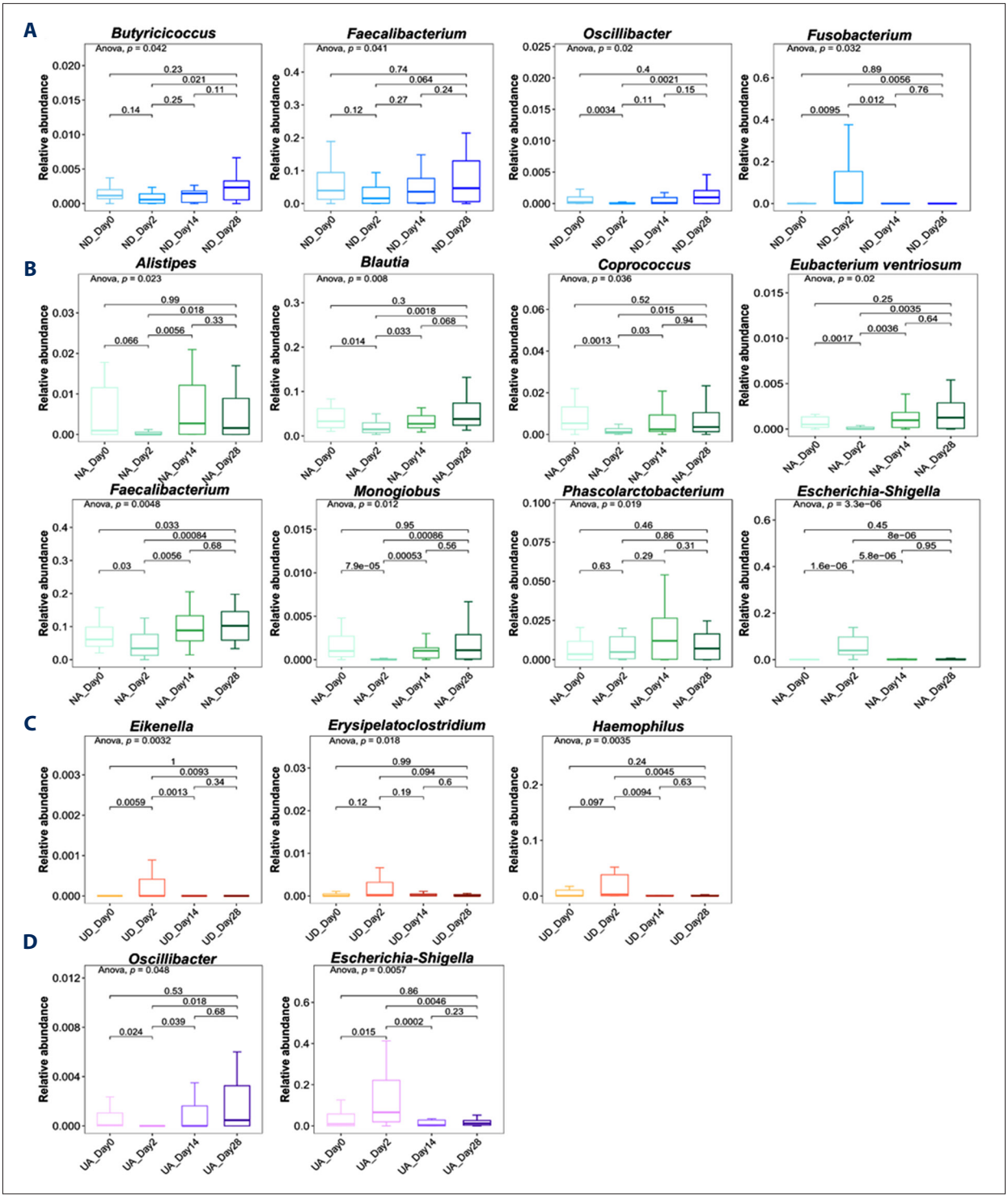


Figure 9. Relative abundances of differential taxonomic features based on results of LEfSe analysis. (**A**) Relative abundances of differential taxonomic features based on results of LEfSe analysis of healthy control group (ND). (**B**) Relative abundances of differential taxonomic features based on results of LEfSe analysis of healthy probiotics group (NA). (**C**) Relative abundances of differential taxonomic features based on results of LEfSe analysis of ulcerative colitis group (UD). (**D**) Relative abundances of differential taxonomic features based on results of LEfSe analysis of ulcerative colitis probiotics group (UA) at different time points. Abbreviations: ND, healthy control group; UD, ulcerative colitis group; NA, healthy probiotics group; UA, ulcerative colitis probiotics group.

Indexed in: [Current Contents/Clinical Medicine] [SCI Expanded] [ISI Alerting System] [ISI Journals Master List] [Index Medicus/MEDLINE] [EMBASE/Excerpta Medica] [Chemical Abstracts/CAS]

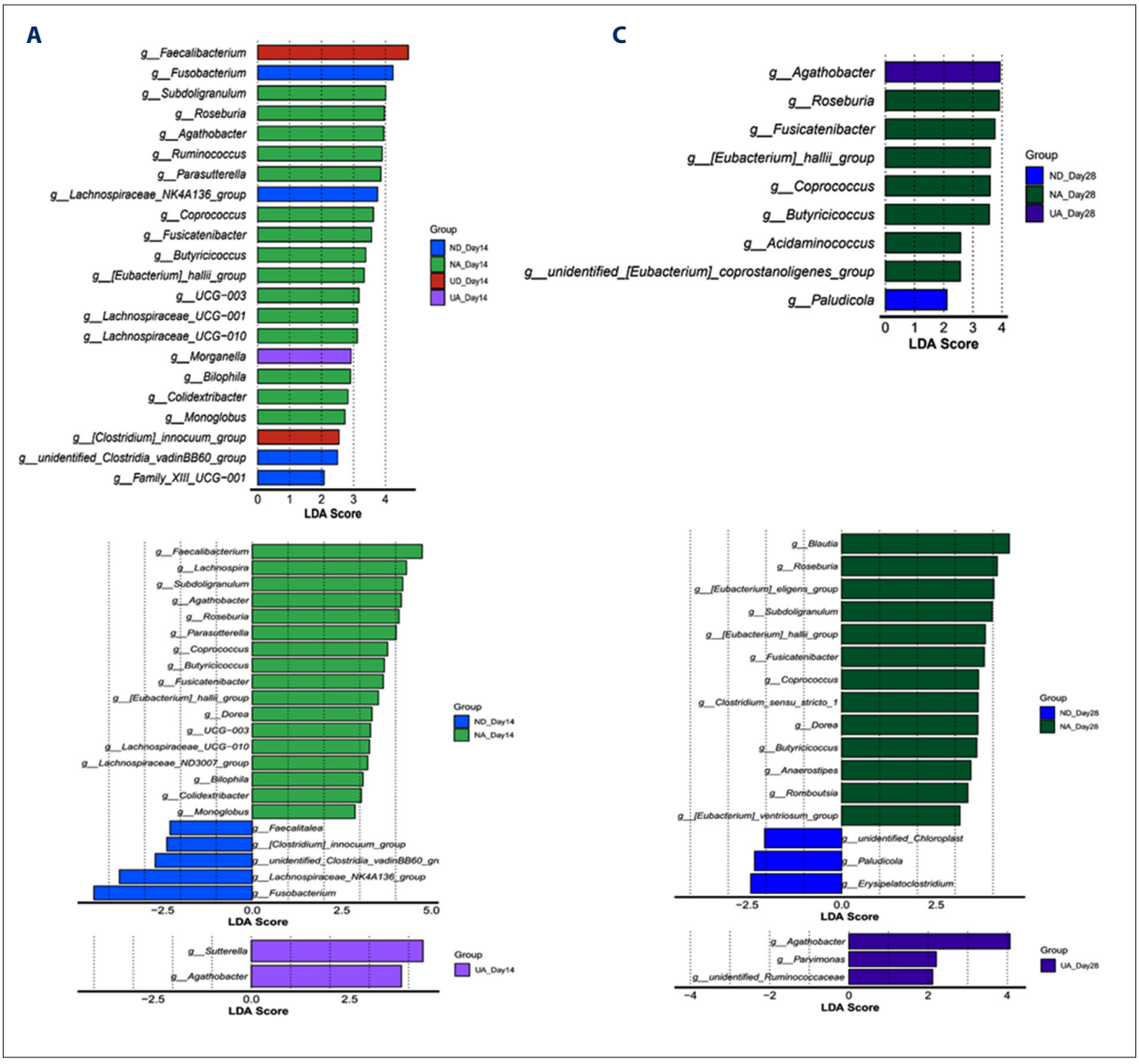
Correlation analysis identified weak positive associations between α diversity and several beneficial taxa, including *Faecalibacterium*, *Roseburia*, *Blautia*, and members of the Lachnospiraceae family. These findings suggest an association with overall microbial diversity but do not imply a direct or causal effect. Inversely, *Fusobacterium* and *Erysipelatoclostridium*, negatively associated with diversity, were reduced in the NA and UA groups (**Figure 10B, 10D**).

Predicted Functional Recovery of Microbial Metabolic Pathways

Prediction of microbial functional pathways using PICRUSt2 suggested that bowel preparation was associated with a transient reduction in several metabolic pathways, including the non-oxidative branch of the pentose phosphate pathway and purine biosynthesis pathways such as 5-aminoimidazole ribonucleotide biosynthesis (**Figure 11A-11D**). These predicted functional impairments became less pronounced by day 14 and day 28, but many pathways remained below baseline levels, indicating only partial and incomplete restoration of microbial functional potential after bowel preparation.

Discussion

This study offers a comprehensive evaluation of how bowel preparation influences gut microbiota dynamics and investigates the potential of probiotic supplementation to accelerate microbial recovery in healthy individuals and patients with UC. Our findings indicate that bowel cleansing induces transient but significant disruptions in microbiota diversity,



Indexed in: [Current Contents/Clinical Medicine] [SCI Expanded] [ISI Alerting System] [ISI Journals Master List] [Index Medicus/MEDLINE] [EMBASE/Excerpta Medica] [Chemical Abstracts/CAS]

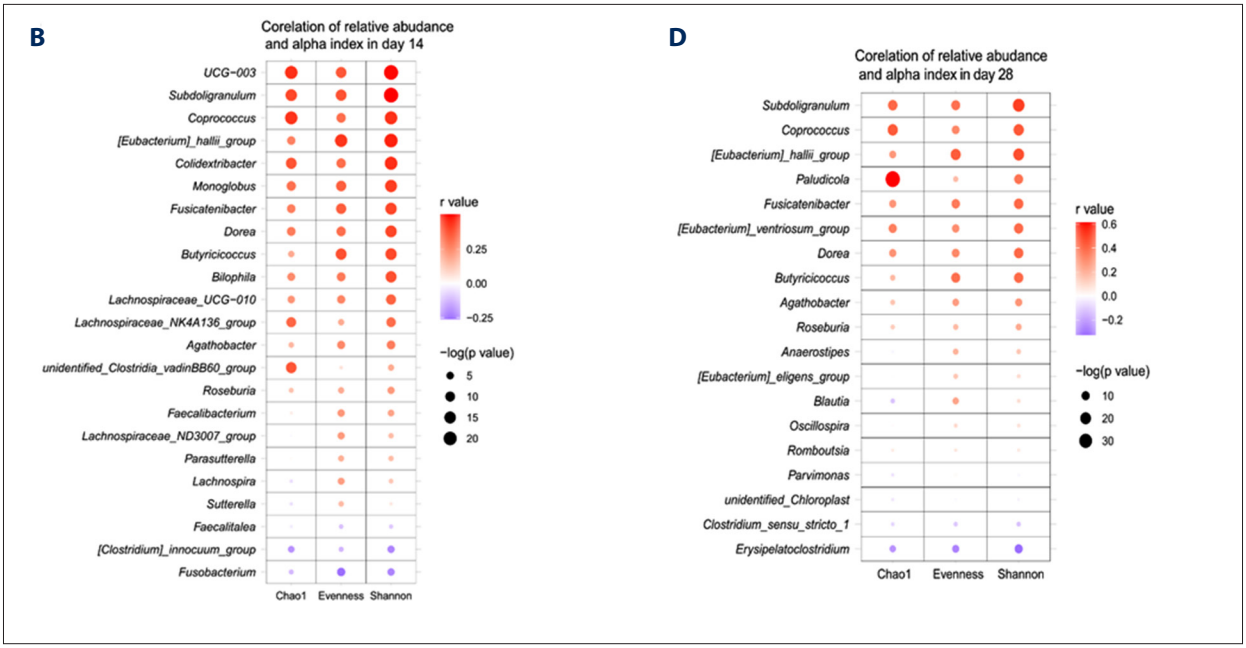


Figure 10. Differential taxa and their association with microbial diversity. (**A**) LEfSe analysis of differential taxa: intergroup comparisons of ND, NA, UD, UA, paired comparisons of ND vs NA and UD vs UA at day 14. (**B**) Correlation between α-diversity indices and relative abundance of differential genera at day 14. (**C**) LEfSe analysis of differential taxa: intergroup comparisons of ND, NA, UD, UA, paired comparisons of ND vs NA and UD vs UA at day 28. (**D**) Correlation between α-diversity indices and relative abundance. Abbreviations: ND, healthy control group; UD, ulcerative colitis group; NA, healthy probiotics group; UA, ulcerative colitis probiotics group.

composition, and metabolic function, with recovery trajectories differing markedly between healthy participants and those with UC. Notably, probiotic supplementation enhanced microbiota restoration, particularly in the UC cohort.

In healthy participants, bowel preparation led to a marked reduction in α-diversity indices, including Chao1, Shannon, and evenness, accompanied by significant alterations in β diversity and microbial community composition. These effects were most pronounced on day 2 after the procedure, with partial recovery evident by day 14, and near-baseline levels restored by day 28. These observations align with prior studies highlighting the resilience of the gut microbiota following transient perturbations, such as colonoscopy preparation [9,11,19]. Unlike studies evaluating probiotics before colonoscopy to improve bowel preparation, our study focused on post-colonoscopy microbial restoration. Although PEG-based bowel preparation may cause transient mucosal irritation, probiotics were started only after colonoscopy in patients without severe UC or procedure-related complications. This design was intended to minimize safety concerns while targeting the early recovery phase of the intestinal microbiota [16].

In contrast, patients with UC exhibited an already dysbiotic microbial baseline, which was further destabilized by bowel preparation. While β-diversity changes were not statistically significant, likely due to high interindividual variability and baseline dysbiosis, taxonomic analyses revealed reductions in beneficial phyla such as Firmicutes and increases in potentially pathogenic groups including *Proteobacteria* and *Fusobacteria*. At the genus level, patients with UC showed decreased abundances of key commensals—*Blautia*, *Faecalibacterium*, and *Lachnospira*—and an increase in *Escherichia-Shigella*, a genus associated with intestinal inflammation. These disruptions resolved more slowly than in healthy individuals, suggesting impaired microbial resilience in the context of chronic inflammation.

The delayed recovery of the gut microbiota observed in patients with UC likely reflects impaired ecological resilience resulting from complex host-microbe interactions. The transient enrichment of *Proteobacteria* and *Escherichia-Shigella* observed predominantly in the UD group may reflect the impaired ecological resilience characteristic of ulcerative colitis. Facultative anaerobic and inflammation-associated taxa are better adapted to the oxidative and inflammatory intestinal environment associated with UC and may rapidly expand following bowel preparation–induced perturbation. In contrast, the microbiota of healthy individuals appeared more resistant to this transient dysbiotic shift, suggesting greater microbial stability and recovery capacity. First, chronic intestinal inflammation creates a self-reinforcing cycle in which

Indexed in: [Current Contents/Clinical Medicine] [SCI Expanded] [ISI Alerting System] [ISI Journals Master List] [Index Medicus/MEDLINE] [EMBASE/Excerpta Medica] [Chemical Abstracts/CAS]

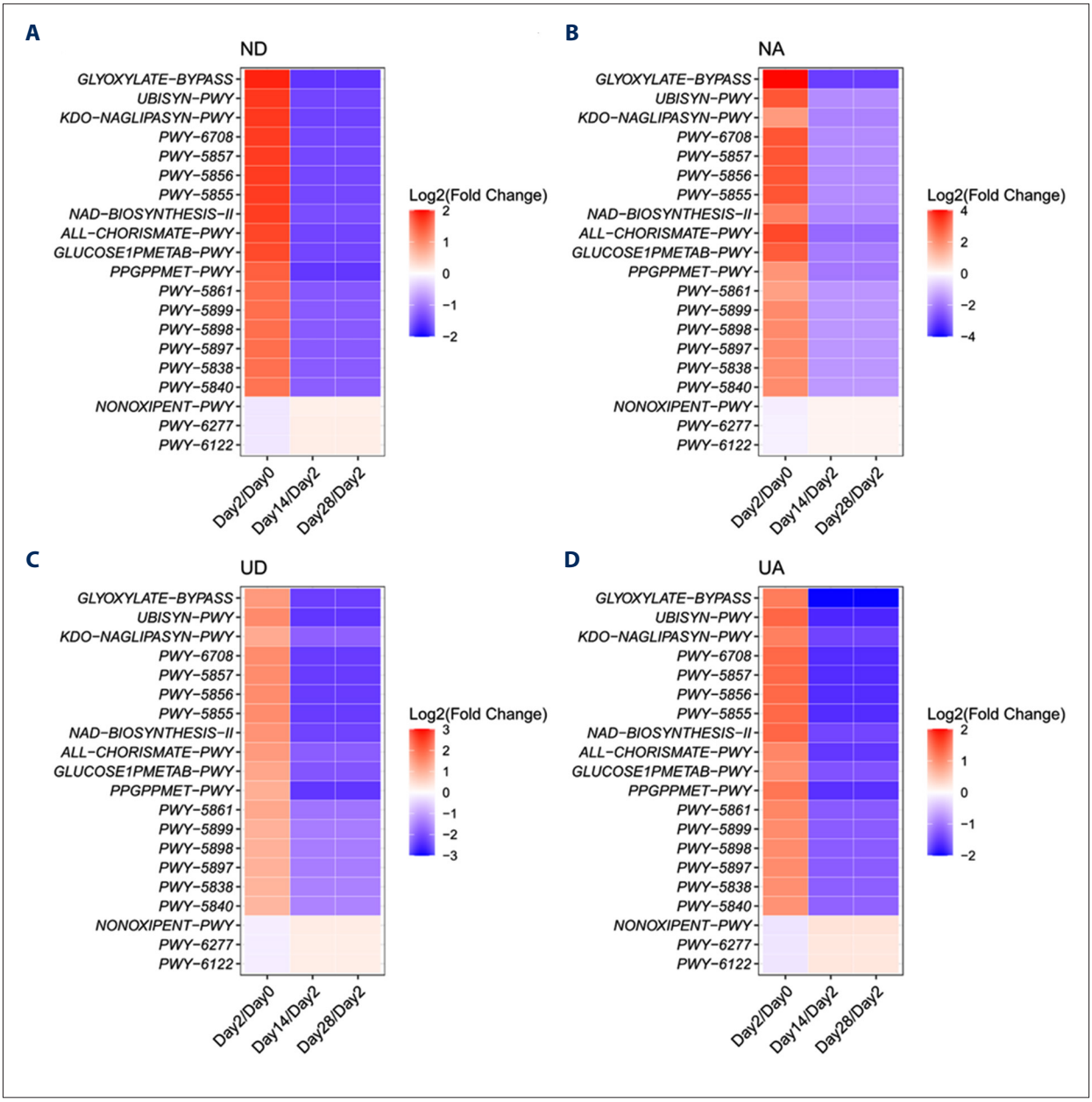


Figure 11. Predicted microbial metabolic pathways affected by bowel preparation and probiotics. (**A-D**) Significantly altered MetaCyc pathways at different time points in (**A**) ND, (**B**) NA, (**C**) UD, and (**D**) UA groups. Abbreviations: ND, healthy control group; UD, ulcerative colitis group; NA, healthy probiotics group; UA, ulcerative colitis probiotics group.

elevated reactive oxygen species and antimicrobial peptides selectively suppress obligate anaerobic commensals, such as *Faecalibacterium prausnitzii*, while favoring facultative anaerobes, including *Escherichia-Shigella*, that are more tolerant to oxidative stress. This inflammatory environment promotes persistent dysbiosis and limits the capacity of the microbiota to return to its pre-perturbation state. Second, disruption of the intestinal mucus barrier may contribute to delayed recovery. PEG bowel preparation can mechanically disturb the mucus layer, and this effect may be amplified in UC, in which MUC2 production and mucin glycosylation are frequently altered. Loss of this protective interface may hinder recolonization by beneficial mucosa-associated microorganisms. Third, the UC microbiota is characterized by reduced diversity and weaker interspecies interactions, resulting in lower ecological complexity and diminished functional redundancy. According to ecological stability theory, such simplified microbial networks are more vulnerable to perturbations and less able to recover efficiently after disturbances such as bowel preparation. Together, these mechanisms may explain the slower and

Indexed in: [Current Contents/Clinical Medicine] [SCI Expanded] [ISI Alerting System] [ISI Journals Master List] [Index Medicus/MEDLINE] [EMBASE/Excerpta Medica] [Chemical Abstracts/CAS]

less complete restoration of the gut microbiota in patients with UC compared with healthy individuals. One of the key strengths of this study is the investigation of probiotic supplementation as a strategy to facilitate microbial recovery after bowel preparation. In healthy individuals, while probiotics did not substantially alter the overall community structure at the phylum level, they were associated with increased abundance of beneficial, short-chain fatty acid–producing genera such as *Faecalibacterium*, *Roseburia*, and *Eubacterium*. These taxa are known to contribute to mucosal integrity, immunomodulation, and anti-inflammatory effects [20-22].

In patients with UC, probiotic supplementation exerted a more pronounced effect. It not only enhanced α diversity but also shifted the microbial composition toward a healthier profile, characterized by increased Firmicutes and reduced *Proteobacteria* and *Fusobacteria*. Many of the taxa enriched after probiotic supplementation have been linked to favorable outcomes in ulcerative colitis. *Faecalibacterium*, *Blautia*, *Butyricicoccus*, *Coprococcus*, and *Eubacterium ventriosum* are important producers of short-chain fatty acids, particularly butyrate, which supports epithelial barrier function and suppresses mucosal inflammation [23]. Members of the Lachnospiraceae family and *Oscillibacter* are also associated with microbial homeostasis and anti-inflammatory activity [24,25]. *Lactobacillus* is a well-established probiotic genus with documented effects on mucosal immune regulation and barrier integrity [26]. Reduced abundance of these taxa has frequently been reported in active UC, suggesting that their restoration may reflect a shift toward a healthier microbial ecosystem [27]. At the genus level, there was a notable enrichment of *Sutterella* and *Blautia*, and members of the Ruminococcaceae family, all of which have been linked to reduced inflammation and improved disease outcomes in IBD [28-31]. By day 28, the microbial diversity of patients with UC receiving probiotics approached that of healthy controls, underscoring the potential role of targeted microbial therapies in promoting gut homeostasis. Although our study demonstrates associations between probiotic supplementation and accelerated microbiota recovery, the underlying mechanisms are likely multifactorial and cannot be directly established from the current data. Probiotics may exert direct and indirect effects on the intestinal ecosystem. Direct mechanisms include competitive exclusion of pathobionts, reduction of luminal pH, and production of antimicrobial compounds such as bacteriocins, which can suppress opportunistic bacteria. Indirectly, probiotics may enhance epithelial barrier integrity by upregulating tight junction proteins and modulate mucosal immune responses, including the promotion of regulatory T-cell differentiation and attenuation of pro-inflammatory cytokine signaling [32]. In addition, probiotic strains such as *Bifidobacterium* and *Lactobacillus* may function as metabolic initiators by fermenting complex carbohydrates into acetate and lactate. These metabolites can serve as substrates for secondary fermenters, including butyrate-producing commensals such as *Faecalibacterium*, *Roseburia*, and *Blautia*, thereby promoting metabolic cross-feeding and restoring a more stable and health-associated microbial network. These mechanisms provide a plausible explanation for the enrichment of short-chain fatty acid–producing taxa observed after probiotic supplementation, particularly in patients with UC [33]. Because this study was observational at the microbiome level, these mechanistic interpretations remain hypothetical and require validation through targeted experimental and metabolomic studies.

Beyond taxonomic alterations, predicted functional analysis suggested that bowel preparation was associated with suppression of several microbial pathways related to energy metabolism and nucleotide biosynthesis, including the non-oxidative pentose phosphate pathway and purine nucleotide biosynthesis. Because similar temporal patterns were observed across multiple groups, these alterations likely reflect generalized microbial stress responses following bowel preparation rather than pathways specifically linked to UC progression. Such predicted functional suppression may nevertheless contribute to impaired microbial resilience and delayed restoration of intestinal homeostasis [34-38]. Encouragingly, these pathways showed gradual recovery over the study period, with probiotic supplementation likely playing a supportive role in restoring functional microbial capacity.

The longitudinal design of this study, incorporating serial sampling and 16S rRNA sequencing of 316 fecal samples, provides robust temporal insights into the microbiota's response to bowel preparation and probiotic intervention. Furthermore, by comparing healthy individuals and patients with UC, this study offers novel evidence of differential microbiota resilience and recovery in health and disease.

However, several limitations should be considered when interpreting the findings of this study. First, the open-label design may have introduced performance bias, as participants' awareness of receiving probiotic supplementation could have influenced behaviors such as diet and medication adherence. However, the primary outcomes were based on objective 16S rRNA sequencing data, which are less susceptible to expectation-related bias. Future studies should adopt double-blind, placebo-controlled designs to minimize this potential source of bias. Second, predicted functional pathway analysis was performed using PICRUSt2, which infers microbial functional potential from 16S rRNA gene profiles and reference genomes rather than directly measuring metagenomic, transcriptomic, or metabolomic activity. Accordingly, these results should be interpreted as hypothesis-generating and require validation using shotgun metagenomics and targeted metabolomic approaches, including short-chain fatty acid measurements.

Indexed in: [Current Contents/Clinical Medicine] [SCI Expanded] [ISI Alerting System] [ISI Journals Master List] [Index Medicus/MEDLINE] [EMBASE/Excerpta Medica] [Chemical Abstracts/CAS]

Third, diet is a major determinant of gut microbiota composition. Although participants were instructed to maintain their habitual dietary patterns and avoid substantial dietary changes during the study, detailed dietary records and formal dietary monitoring were not performed. Consequently, residual dietary confounding cannot be excluded. Future trials should incorporate standardized dietary assessment, such as food diaries, validated dietary questionnaires, or controlled meal protocols. Fourth, although the sample size was calculated a priori based on the Shannon diversity index and exceeded the minimum required number of participants per group, the overall cohort size remains moderate for a microbiome study. Statistical power may therefore be limited for subgroup analyses and for detecting subtle changes in low-abundance taxa and predicted pathways. Larger multicenter studies are needed to validate and extend these findings. Additionally, this study did not systematically collect and report quantitative patient symptom scores, UC disease activity indices, or standardized adverse event data during the 28-day follow-up. While bedside assessments using the modified Truelove and Witts classification and routine clinical inquiry revealed no serious adverse events or clinically significant UC flares, future studies should incorporate validated clinical outcome measures to comprehensively assess the clinical benefits and safety of probiotic supplementation. Therefore, the conclusions of the present study are restricted to microbiome and predicted functional outcomes rather than direct clinical efficacy.

Interestingly, the glyoxylate bypass pathway remained relatively suppressed in the probiotic-treated groups at day 14 and day 28. The glyoxylate bypass enables microorganisms to utilize 2-carbon substrates such as acetate and may reflect ongoing metabolic adaptation during microbial recovery. One possible explanation is that probiotic supplementation promotes metabolic cross-feeding interactions within the intestinal ecosystem. Probiotic-associated taxa, including *Bifidobacterium* and *Lactobacillus*, can generate acetate and lactate through carbohydrate fermentation, which may subsequently serve as substrates for secondary fermenters and butyrate-producing bacteria such as *Faecalibacterium*, *Eubacterium*, and *Anaerostipes* [39,40]. This trophic interaction may facilitate restoration of short-chain fatty acid production and improve the intestinal microenvironment after PEG-induced dysbiosis. Similar synergistic cross-feeding mechanisms have been described in studies involving lactate-utilizing butyrate producers and probiotic co-administration in UC models [40,41].

From a translational perspective, our findings suggest that probiotic supplementation may be most relevant for patients with UC, particularly those in clinical remission who exhibit persistent baseline dysbiosis and reduced microbial resilience. In contrast, the benefits in healthy individuals undergoing routine screening appear to be more modest, reflecting the greater intrinsic resilience of the normal gut microbiota. The timing of intervention may also be important. Because bowel preparation induces an acute disruption of the intestinal ecosystem, initiation of probiotic supplementation immediately after colonoscopy may take advantage of a transient "window of opportunity" during which microbial communities are more susceptible to ecological restructuring. In the present study, probiotics were administered for 28 days beginning the day after colonoscopy, and this regimen was associated with progressive restoration of microbial diversity and predicted functional potential. However, the optimal treatment duration and strain composition remain to be determined. Future dose-finding and comparative trials should evaluate different treatment durations, including 4- to 8-week regimens, and assess probiotic strains with well-characterized immunomodulatory and barrier-supportive properties, such as *Bifidobacterium longum* and *Lactobacillus rhamnosus* GG. These findings provide a rationale for testing early post-colonoscopy probiotic supplementation as a targeted strategy to promote microbiota recovery in patients with UC.

Conclusions

In conclusion, bowel preparation induces significant but reversible disruptions in gut microbiota composition and function, with recovery occurring more slowly in patients with UC than in healthy individuals. Probiotic supplementation after colonoscopy promotes the restoration of microbial diversity, enriches beneficial taxa, and is associated with the predicted recovery of key microbial metabolic pathways—particularly in patients with UC. These findings suggest that incorporating probiotic interventions into clinical practice may help mitigate bowel preparation–induced dysbiosis, ultimately improving safety and outcomes in vulnerable populations. Further large-scale, multi-center studies are warranted to validate these results and refine probiotic strategies for gut microbiota restoration.

Data Availability

The datasets generated during the current study are available in the NCBI repository [https://www.ncbi.nlm.nih.gov/bioproject/PRJNA1280500].

Declaration of Figures' Authenticity

All figures submitted have been created by the authors who confirm that the images are original with no duplication and have not been previously published in whole or in part.

Indexed in: [Current Contents/Clinical Medicine] [SCI Expanded] [ISI Alerting System] [ISI Journals Master List] [Index Medicus/MEDLINE] [EMBASE/Excerpta Medica] [Chemical Abstracts/CAS]

References:

1. Rex DK, Anderson JC, Butterly LF, et al. Quality indicators for colonoscopy. Gastrointest Endosc. 2024;100(3):352-81
2. Shahini E, Sinagra E, Vitello A, et al. Factors affecting the quality of bowel preparation for colonoscopy in hard-to-prepare patients: Evidence from the literature. World J Gastroenterol. 2023;29(11):1685-707
3. Zawaly K, Rumbolt C, Abou-Setta AM, et al. The efficacy of split-dose bowel preparations for polyp detection: A systematic review and meta-analysis. Am J Gastroenterol. 2019;114(6):884-92
4. Zheng ZL, Zheng QF, Wang LQ, Liu Y. Bowel preparation before colonoscopy: Consequences, mechanisms, and treatment of intestinal dysbiosis. World J Gastroenterol. 2025;31(2):100589
5. Nalluri-Butz H, Bobel MC, Nugent J, et al. A pilot study demonstrating the impact of surgical bowel preparation on intestinal microbiota composition following colon and rectal surgery. Sci Rep. 2022;12(1):10559
6. Gorkiewicz G, Thallinger GG, Trajanoski S, et al. Alterations in the colonic microbiota in response to osmotic diarrhea. PLoS One. 2013;8(2):e55817
7. Shobar RM, Velineni S, Keshavarzian A, et al. The effects of bowel preparation on microbiota-related metrics differ in health and in inflammatory bowel disease and for the mucosal and luminal microbiota compartments. Clin Transl Gastroenterol. 2016;7(2):e143
8. Drago L, Toscano M, De Grandi R, Casini V, Pace F. Persisting changes of intestinal microbiota after bowel lavage and colonoscopy. Eur J Gastroenterol Hepatol. 2016; 28(5):532-37
9. O'Brien CL, Allison GE, Grimpen F, Pavli P. Impact of colonoscopy bowel preparation on intestinal microbiota. PLoS One. 2013;8(5):e62815
10. Guo P, Wang W, Xiang Q, et al. Engineered probiotic ameliorates ulcerative colitis by restoring gut microbiota and redox homeostasis. Cell Host Microbe. 2024;32(9):1502-18.e9
11. Jalanka J, Salonen A, Salojarvi J, et al. Effects of bowel cleansing on the intestinal microbiota. Gut. 2015; 64(10):1562-68
12. D'Souza B, Slack T, Wong SW, et al. Randomized controlled trial of probiotics after colonoscopy. ANZ J Surg. 2017;87(9):E65-E69
13. Deng X, Tian H, Yang R, et al. Oral probiotics alleviate intestinal dysbacteriosis for people receiving bowel preparation. Front Med (Lausanne). 2020;7:73
14. Mullaney TG, Lam D, Kluger R, D'Souza B. Randomized controlled trial of probiotic use for post-colonoscopy symptoms. ANZ J Surg. 2019;89(3):234-38
15. Hu Y, Chen Z, Xu C, et al. Disturbances of the gut microbiota and microbiota-derived metabolites in inflammatory bowel disease. Nutrients. 2022;14(23):5140
16. Piciucchi M, Rossi A, Satriano A, Manta R. Is it advisable to use probiotics routinely after a colonoscopy? A rapid comprehensive review of the evidence. Med Sci (Basel). 2025;13(2):76
17. Muzellina VN, Alvianto S, Widjanarko ND. Utilization of probiotics in relieving post-colonoscopy gastrointestinal symptoms: A systematic review and meta-analysis. Rom J Intern Med. 2024; 62(4):387-403
18. Wei H, Wang J, Xiao X, et al. Effect of probiotics on the gut microbiota after colonoscopy: A multicenter, randomized, placebo-controlled clinical study. J Gastroenterol Hepatol. 2026; 41(1):128-39
19. Harrell L, Wang Y, Antonopoulos D, et al. Standard colonic lavage alters the natural state of mucosal-associated microbiota in the human colon. PLoS One. 2012;7(2):e32545
20. Mohebali N, Weigel M, Hain T, et al. *Faecalibacterium prausnitzii*, *Bacteroides faecis* and *Roseburia intestinalis* attenuate clinical symptoms of experimental colitis by regulating Treg/Th17 cell balance and intestinal barrier integrity. Biomed Pharmacother. 2023;167:115568
21. Faden H. The Role of *Faecalibacterium*, *Roseburia*, and *Butyrate* in inflammatory bowel disease. Dig Dis. 2022;40(6):793-95
22. Parada Venegas D, De la Fuente MK, Landskron G, et al. Short chain fatty acids (SCFAs)-mediated gut epithelial and immune regulation and its relevance for inflammatory bowel diseases. Front Immunol. 2019;10:277
23. Li G, Lin J, Zhang C, et al. Microbiota metabolite butyrate constrains neutrophil functions and ameliorates mucosal inflammation in inflammatory bowel disease. Gut Microbes. 2021;13(1):1968257
24. Zhou J, Li M, Chen Q, et al. Programmable probiotics modulate inflammation and gut microbiota for inflammatory bowel disease treatment after effective oral delivery. Nat Commun. 2022;13(1):3432
25. Huang S, Chen J, Cui Z, et al. Lachnospiraceae-derived butyrate mediates protection of high fermentable fiber against placental inflammation in gestational diabetes mellitus. Sci Adv. 2023;9(44):eadi7337
26. Hou Q, Ye L, Liu H, et al. Lactobacillus accelerates ISCs regeneration to protect the integrity of intestinal mucosa through activation of STAT3 signaling pathway induced by LPLs secretion of IL-22. Cell Death Differ. 2018; 25(9):1657-70
27. Schirmer M, Strazar M, Avila-Pacheco J, et al. Linking microbial genes to plasma and stool metabolites uncovers host-microbial interactions underlying ulcerative colitis disease course. Cell Host Microbe. 2024; 32(2):209-26.e7
28. Aggarwal N, Kitano S, Puah GRY, et al. Microbiome and human health: Current understanding, engineering, and enabling technologies. Chem Rev. 2023;123(1):31-72
29. Morgan XC, Kabakchiev B, Waldron L, et al. Associations between host gene expression, the mucosal microbiome, and clinical outcome in the pelvic pouch of patients with inflammatory bowel disease. Genome Biol. 2015;16(1):67
30. Fite A, Macfarlane S, Furrie E, et al. Longitudinal analyses of gut mucosal microbiotas in ulcerative colitis in relation to patient age and disease severity and duration. J Clin Microbiol. 2013;51(3):849-56
31. Butera A, Di Paola M, Vitali F, et al. IL-13 mRNA tissue content identifies two subsets of adult ulcerative colitis patients with different clinical and mucosa-associated microbiota profiles. J Crohns Colitis. 2020;14(3):369-80
32. Cristofori F, Dargenio VN, Dargenio C, et al. Anti-inflammatory and immunomodulatory effects of probiotics in gut inflammation: A door to the body. Front Immunol. 2021;12:578386
33. Roy S, Dhaneshwar S. Role of prebiotics, probiotics, and synbiotics in management of inflammatory bowel disease: Current perspectives. World J Gastroenterol. 2023;29(14):2078-100
34. Cao C, Wang L, Ai C, et al. Impact of *Lycium barbarum* arabinogalactan on the fecal metabolome in a DSS-induced chronic colitis mouse model. Food Funct. 2022;13(16):8703-16
35. TeSlaa T, Ralser M, Fan J, Rabinowitz JD. The pentose phosphate pathway in health and disease. Nat Metab. 2023;5(8):1275-89
36. Bai A, Ma AG, Yong M, et al. AMPK agonist downregulates innate and adaptive immune responses in TNBS-induced murine acute and relapsing colitis. Biochem Pharmacol. 2010;80(11):1708-17
37. Zhang T, Zhong H, Lin L, et al. Core microbiome-associated proteins associated with ulcerative colitis interact with cytokines for synergistic or antagonistic effects on gut bacteria. ISME J. 2024;18(1):wrae146
38. Li Y, Yan M, Zhang M, et al. Scutellarin alleviated ulcerative colitis through gut microbiota-mediated cAMP/PKA/NF-kappaB pathway. Biochem Biophys Res Commun. 2024;735:150837
39. Belenguer A, Duncan SH, Calder AG, et al. Two routes of metabolic cross-feeding between *Bifidobacterium adolescentis* and butyrate-producing anaerobes from the human gut. Appl Environ Microbiol. 2006; 72(5):3593-99
40. Inokuma K, Sasaki D, Shintani T, et al. Combination of probiotics enhancing butyrogenesis in colonic microbiota model of patients with ulcerative colitis. Appl Microbiol Biotechnol. 2025;109(1):117
41. Zhao H, Zhou Y, Xu J, et al. Short-chain fatty acid-producing bacterial strains attenuate experimental ulcerative colitis by promoting M2 macrophage polarization via JAK/STAT3/FOXO3 axis inactivation. J Transl Med. 2024;22(1):369

Indexed in: [Current Contents/Clinical Medicine] [SCI Expanded] [ISI Alerting System] [ISI Journals Master List] [Index Medicus/MEDLINE] [EMBASE/Excerpta Medica] [Chemical Abstracts/CAS]