



Short-term probiotic supplementation affects the diversity, genetics, growth, and interactions of the native gut microbiome

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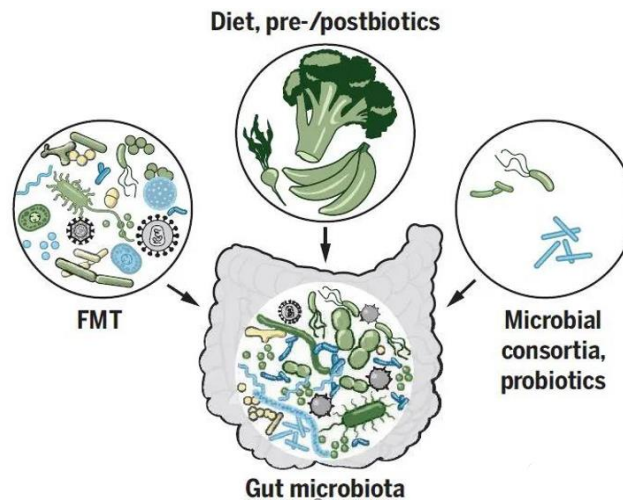
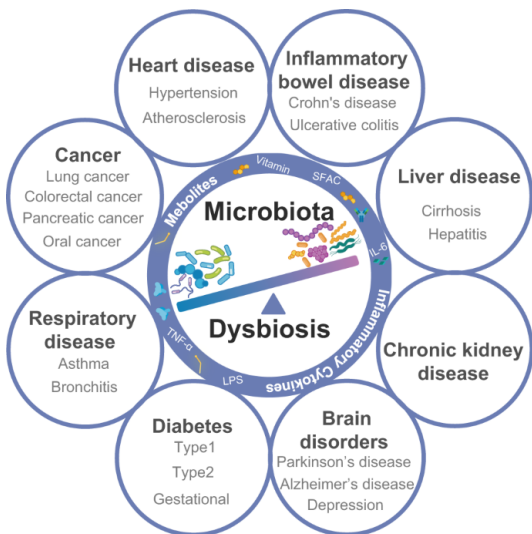


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Introduction

- ❑ The human gut harbors a highly diverse and dynamic microbiome that plays a crucial role in maintaining overall health and physiological homeostasis.
- ❑ Probiotics are a promising strategy for supporting gut health. Both preclinical and clinical studies have demonstrated the potential of probiotic supplementation in managing various health conditions. However, the effects of probiotic can vary significantly among individuals.
- ❑ The precise mechanisms through which probiotics interact with and reshape the native gut microbiota, especially at the species and genetic levels, remain underexplored.



Microbiota Supplementation with **Bifidobacterium and Lactobacillus** Modifies the Preterm Infant Gut Microbiota and Metabolome: An Observational Study

Cristina Alcon-Giner, Matthew J Dalby, Shabnonam Caim, Jennifer Ketskemety, Alex Shaw, Kathleen Sim,

Melissa AE La

Fahmina Fardt,

Lindsay J Hall

subsp. BB-12 Protects against Antibiotic-Induced Functional and Compositional Changes in Human Fecal Microbiome

Daniel Merenstein, Claire M Fraser, Robert F Roberts, Tian Liu, Silvia Grant-Beurmann, Tina P Tan,

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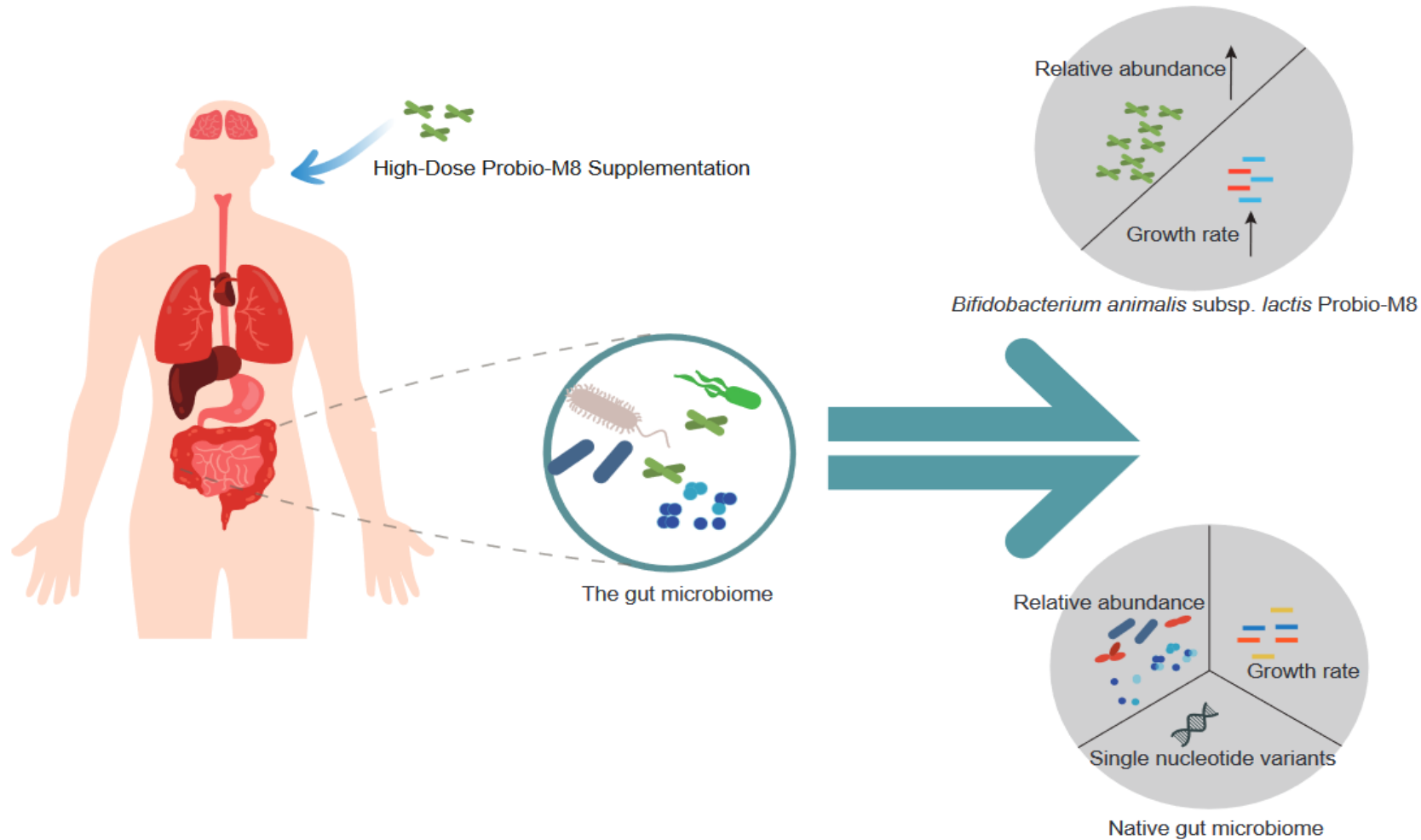
Probiotic consumption relieved human stress and anxiety symptoms possibly via modulating the neuroactive potential of the gut microbiota

Probiotic supplementation improves cognitive function and mood with changes in gut microbiota in community-dwelling elderly: A randomized, double-blind, placebo-controlled, multicenter trial

Chong-Su Kim, Lina Cha, Minju Sim, Sungwoong Jung, Woo Young Chun, Hyun Wook Baik, Dong-Mi Shin



Highlights

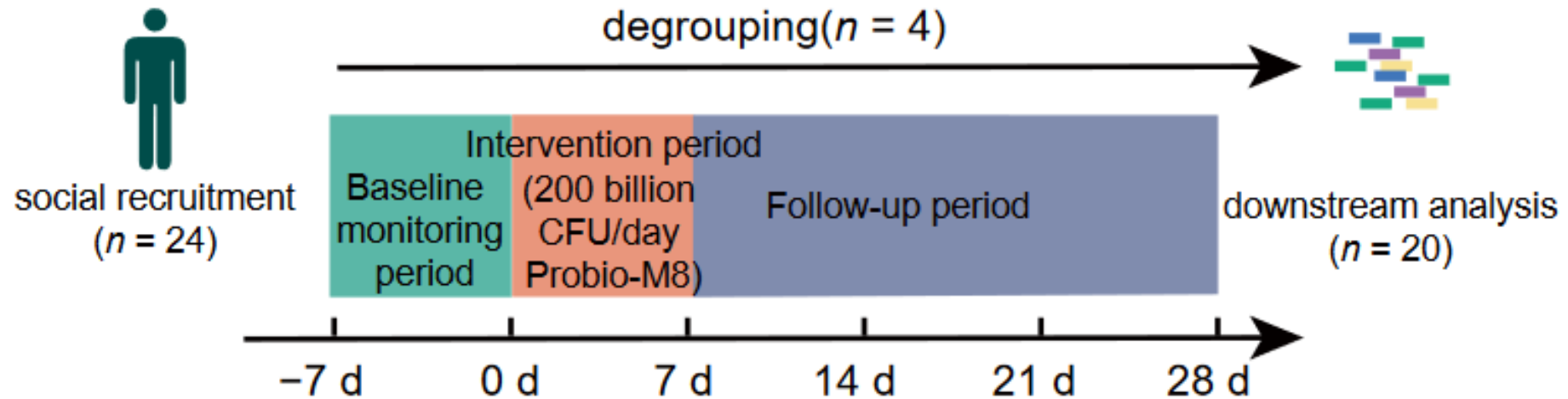


- ❑ This study intervened with high-dose probiotic Probio-M8 in healthy individuals and conducted deep metagenomic sequencing on multiple fecal samples to investigate the impact of the probiotic on gut microbiota from both macro and micro diversity perspectives.



Trial design

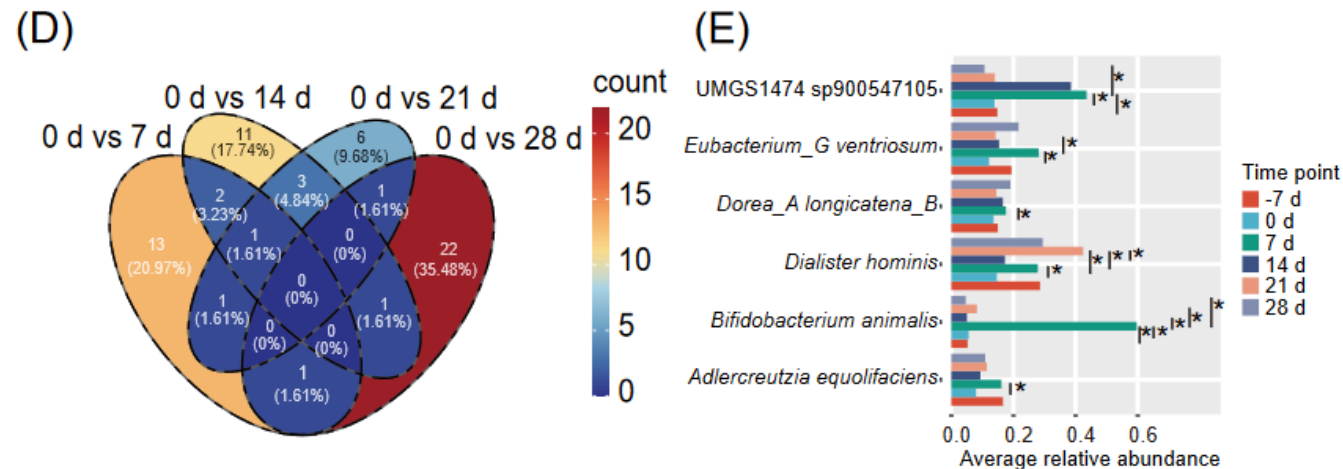
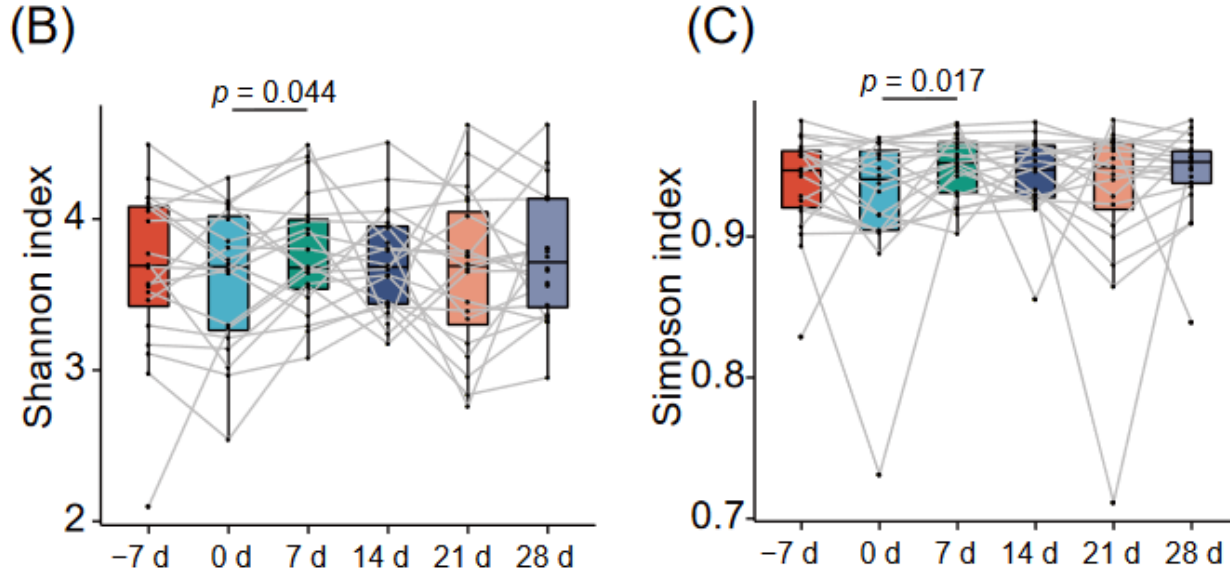
(A)



- ❑ This study conducted a one-week high-dose probiotic Probio-M8 intervention (200 billion CFU/day) with healthy individuals. Fecal samples were collected at six time points: before the probiotic intervention, after the intervention, and at three follow-up weeks. The fecal samples were subsequently analyzed using deep metagenomic sequencing.



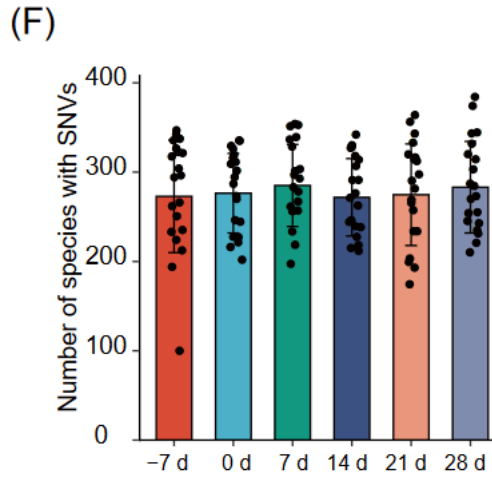
Results



- Following the administration of Probio-M8, both diversity indices showed a significant increase ($p < 0.05$), demonstrating that the intervention effectively enhanced the gut microbiota diversity.
- Notably, *Bifidobacterium animalis* demonstrated a significant increase in abundance at day 7 compared to baseline period. Analysis using average nucleotide identity (ANI) confirmed that the increased abundance was primarily due to the administered Probio-M8 strain.



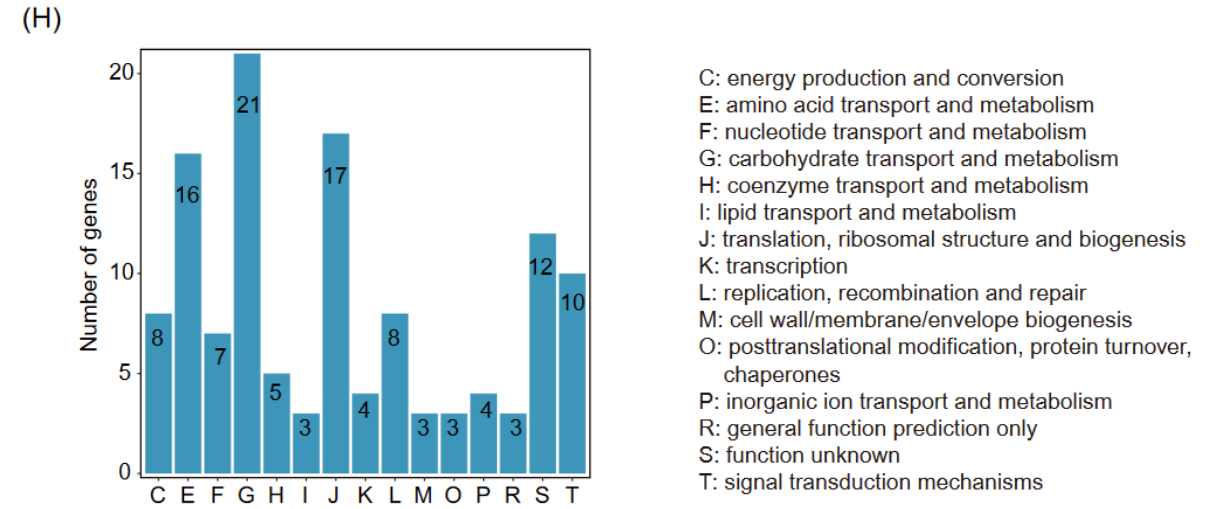
Results



(G)

Position	mutation type
12	N
11	N
11	S
10	S
10	N
10	S
10	N
10	I
10	S
10	S
10	S
10	S

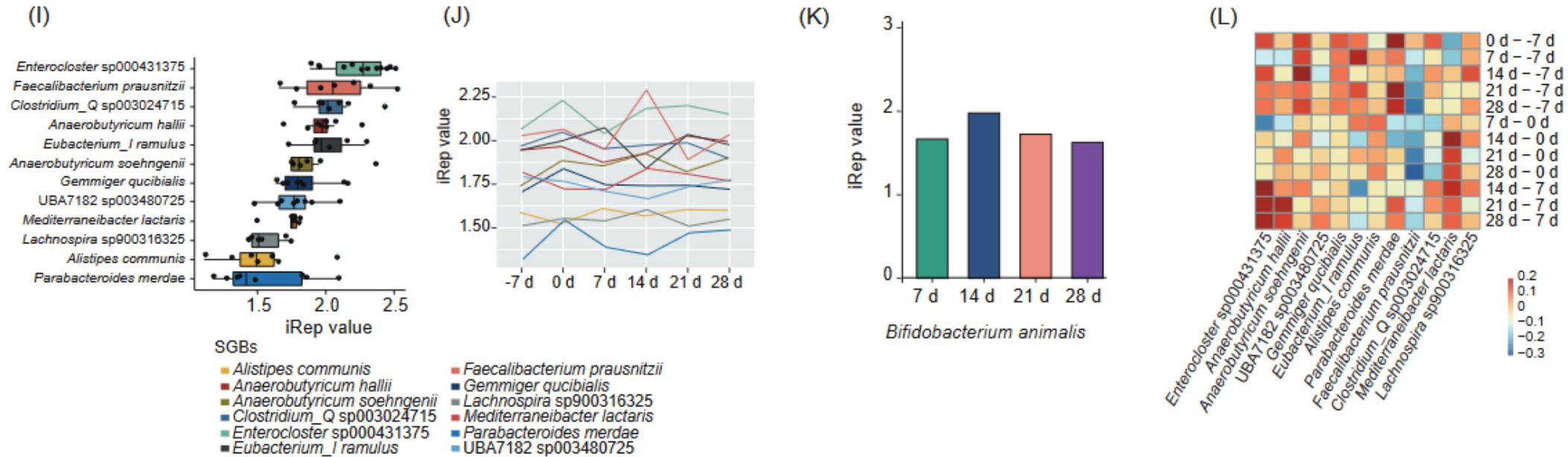
Number of individuals at the 0 day and 7 day mutant site



- ❑ Our findings revealed a non-significant increase in the number of species harboring SNVs following Probio-M8 administration at day 7 compared to the baseline period.
- ❑ SNV loci were classified as shared or non-shared, based on whether more than 50% of the loci differed between pre- and post-intervention. Among them, 2,442 non-shared loci were distributed across 120 genes, 21 of which were associated with carbohydrate transport and metabolism.



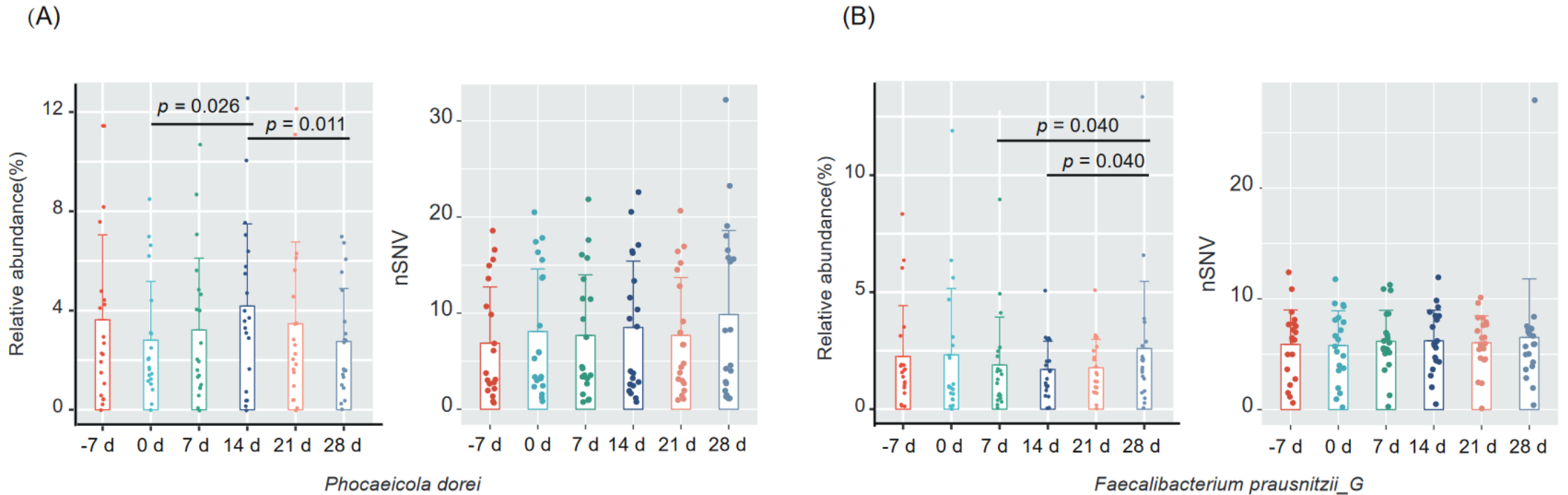
Results



- The replication rate of different strains was different after probiotic consumption.
- We observed an increased replication rate following Probio-M8 consumption, with the iRep value almost reaching 2 at 14 d.
- Probiotics can influence the growth dynamics of the indigenous gut microbiota.



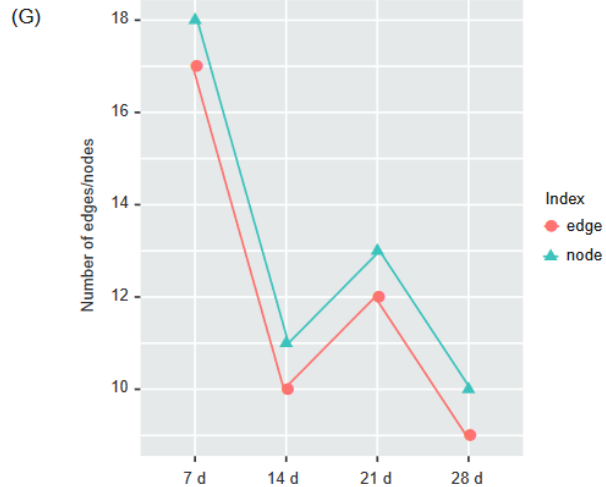
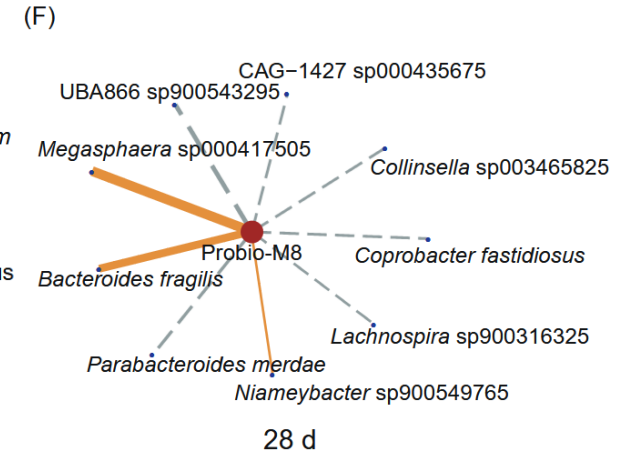
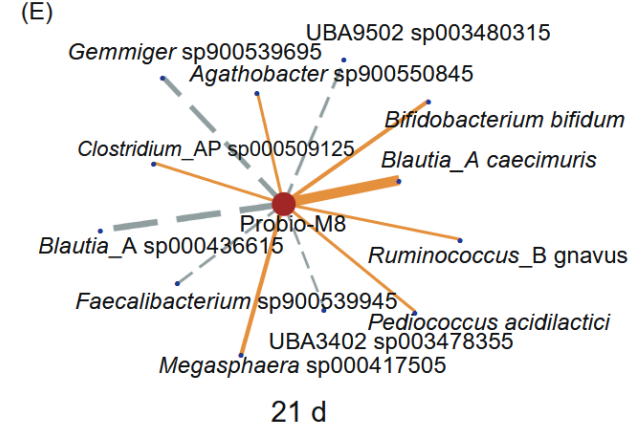
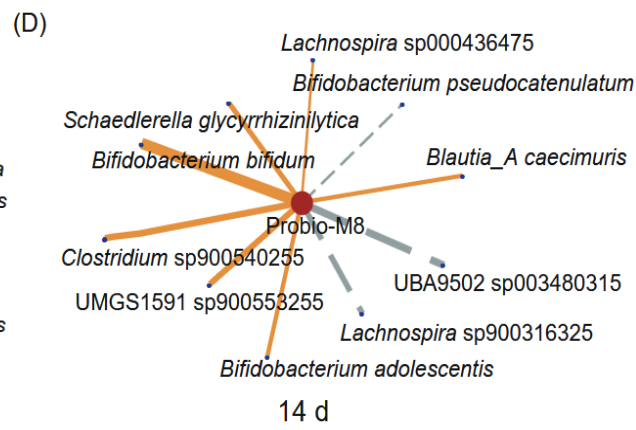
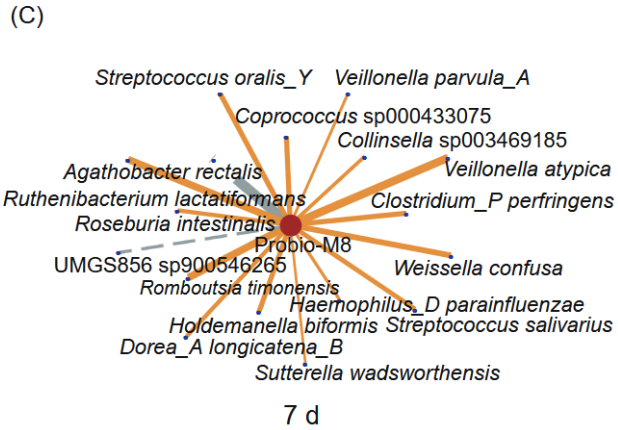
Results



- Despite significant post-interventional shifts in the relative abundance of certain dominant species, no significant differences were observed in the nSNV across these species at any time points. Therefore, while the Probio-M8 intervention led to notable ecological shifts within the gut microbial community, these changes were not accompanied by significant genetic adaptations within the dominant species over the study period.



Results



□ Probio-M8 exhibited the highest number of associations with other resident gut microbes at day 7, indicating an expansion of its interaction network following the intervention. Quantification of the nodes and edges in the network centered around Probio-M8 showed that both metrics peaked at day 7 but declined subsequently during follow-up, suggesting that the enhanced connectivity was transient.



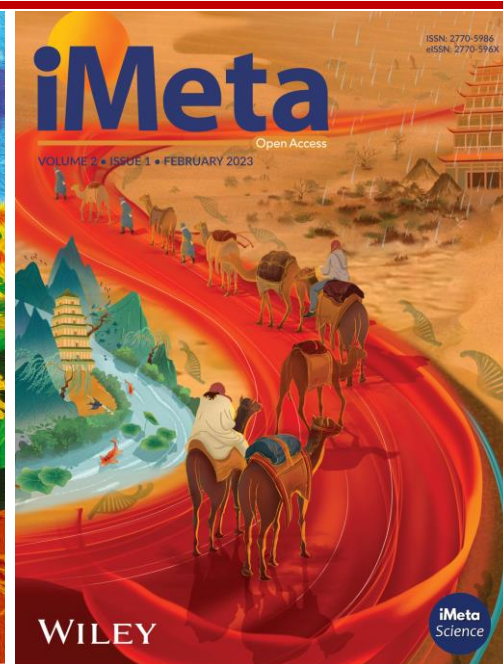
Summary

- ❑ Short-term administration of Probio-M8 enhanced gut microbial diversity and influenced key microbial properties, including nucleotide variation, growth dynamics, and inter-bacterial interactions.
- ❑ The microbial community appears to undergo rapid and multifaceted ecological adjustments, potentially preceding longer-term evolutionary changes.

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