

P40-15-26 Host BMI Influences Gut Microbial Metabolic Pathways in Individuals With Tuberculosis

Rose Kottapalli¹, Catherine H Kagemann¹, Komal Jain², Madolyn Dauphinais³, Senbagavalli Prakash Babu², Nonika Rajkumari², Chelsie Cintron³, Subitha Lakshminarayanan², Sonali Sarkar², Prakash Babu Narasimhan², Pranay Sinha³, Saurabh Mehta¹

¹ Cornell University, United States

² Jawaharlal Institute of Postgraduate Medical Education and Research, India

³ Boston University Chobanian & Avedisian School of Medicine, United States

Objectives: India has the highest burden of tuberculosis (TB), with the greatest prevalence and incidence of new cases. Body mass index (BMI), a commonly used indicator of nutritional status, is strongly associated with TB risk and disease progression and may influence host-microbiome metabolic interactions. The objective of this study is to investigate how BMI influences gut microbial metabolic pathways among individuals with TB disease.

Methods: Data were obtained from the TB LEOPARD (NCT05048485) clinical dataset (N=36). Due to the high prevalence of infection with *Necator americanus*, analyses were restricted to individuals infected with this species (N=10) compared to those not infected with parasites (N=17). Differential abundance of microbial species and KEGG metabolic pathways was assessed using ZicoSeq (R 4.4.1), evaluating the effects of BMI with covariates.

Results: BMI was associated with altered KEGG pathways related to teichoic acid biosynthesis and vitamin B6 metabolism. The teichoic acid biosynthesis pathway produces key structural components of Gram-positive bacterial cell walls that maintain cell wall integrity and mediate host-microbe interactions, while the vitamin B6 metabolism generates pyridoxal-5'-phosphate, an essential cofactor involved in amino acid metabolism, cell wall biosynthesis, redox balance, and bacterial metabolite production. Additionally, the interaction between BMI, *Necator americanus* infection, and alcohol misuse influenced the monobactam biosynthesis, penicillin and cephalosporin biosynthesis, and nicotinate and nicotinamide metabolism pathways. We believe this is primarily driven by alcohol misuse as these pathways are differentially abundant in a model solely testing the interaction between alcohol misuse and parasite infection as well.

Conclusions: Our findings suggest that, among people with TB, BMI is independently associated with altered gut microbial metabolic pathways, which may influence microbial utilization and production of host nutrients. Understanding how BMI interacts with other host factors to influence microbial metabolism may provide insight into how infectious disease processes alter nutrient metabolism as well as host nutritional status and have implications for clinical management.

Funding Sources: No external funding

Current Developments in Nutrition 10 (2026) 109084
<https://doi.org/10.1016/j.cdnut.2026.109084>

P40-16-26 High Protein Nutrition Shake with Pea Protein and a Mixed Fiber Blend Enhances Prebiotic Impact in an in vitro Colon Model

Erin C Lamb¹, Vanessa Millovich¹, Peter Azmi², Jonas Ghyselinck², Christina J Valentine¹

¹ Kate Farms, United States

² ProDigest, Belgium

Objectives: The aim of this in vitro study was to evaluate the effects of a pea-protein, plant-based high-protein nutrition shake (PPPB HPNS) on colonic microbial fermentation, microbial metabolic pathways, and microbial community composition in healthy adult donors. Previous examination with in vitro pea protein-based formula (PPBF) resulted in significant pre- and probiotic effects. We hypothesized that the inclusion of a mixed fiber blend within a high-protein matrix would also uniquely enhance colonic fermentation compared to a previously reported colonic fermentation of pea protein plant-based formulas with a lower quantity of protein and fiber.

Methods: Fecal samples from ten healthy adult donors were inoculated in a Colon-on-a-plate® (CoaP) system and treated for 48 hours with a PPPB HPNS containing 25 g of yellow pea protein and 6 g of a mixed fiber blend including agave inulin, gum acacia, fiber intrinsic to the pea protein, and oat hull fiber. A parallel system was used as a negative control (NC). At the 48-hour mark, the test arm (PPPB HPNS) had fermentation activity measured by change in pH, production of gas, short chain fatty acids (SCFAs), branched chain fatty acids (BCFAs), and ammonium. The measured SCFAs included acetate, propionate, and butyrate. LA-REIMS metabolic fingerprinting assessed broad changes in microbial metabolic output at 48 hours.

Results: All results are compared against the negative control. The PPPB HPNS promoted significant increases in SCFAs acetate (+32%), propionate (+42%), and butyrate (+11%). The pH significantly decreased in the PPPB HPNS (pH 6.6) and median gas production increased by 32%. BCFA and ammonium production increased by 16% and 18%, respectively. Untargeted LA-REIMS metabolic fingerprinting detected significant differences in metabolite signatures in PPPB-HPF compared with the control.

Conclusions: In this in vitro colonic fermentation model, PPPB-HPNS treatment significantly increased a prebiotic impact. A nutrition shake with high protein and fermentable fiber could be an important adjunct to therapy in patients experiencing dietary gaps to improve the microbiome. Future studies are needed in vivo.

Funding Sources: This research was funded by Kate Farms, Inc.

Current Developments in Nutrition 10 (2026) 109085
<https://doi.org/10.1016/j.cdnut.2026.109085>

P40-17-26 Diabetes Modifies Gut Microbial SCFA Recovery Patterns After COVID-19: An Exploratory Metabolomic Study

Bukola T Lawal¹, Thunnicha Ondee¹, Krit Pongpirul¹

¹ Chulalongkorn University, Thailand

Objectives: COVID-19 disrupts the gut microbiome, but recovery of microbial metabolites may depend on host metabolic