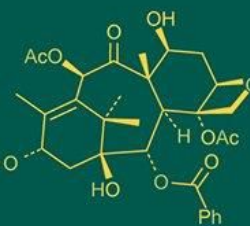
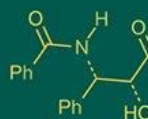


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Gut microbiome-host metabolic interactions in Brazilian adults: Regional dietary patterns and metabolic health

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Abstract

The gut microbiome plays a crucial role in metabolic health, with composition influenced by dietary patterns and environmental factors unique to different populations. This research investigated the relationship between gut microbiome composition and metabolic parameters in Brazilian adults, examining the influence of traditional versus Westernized dietary patterns prevalent in urban São Paulo. Two hundred participants were enrolled from the São Paulo metropolitan area, including individuals with and without metabolic syndrome, representing the diverse socioeconomic and dietary landscape of Brazil's largest city.

Results revealed significant differences in microbiome composition between metabolic phenotypes, with increased Firmicutes-to-Bacteroidetes ratio in metabolic syndrome patients (2.63 vs 1.37 in healthy controls, $p < 0.001$). Short-chain fatty acid production was substantially higher in participants following traditional Brazilian dietary patterns rich in beans, cassava, and tropical fruits compared to those consuming Westernized diets. Alpha diversity metrics were significantly reduced in metabolic syndrome, with Shannon index decreasing from 4.8 ± 0.6 to 3.6 ± 0.8 ($p < 0.001$). These findings highlight the importance of traditional Brazilian dietary patterns in maintaining gut microbiome health and suggest therapeutic targets for addressing the rising burden of metabolic disease in Brazil.

Keywords: Gut microbiome, metabolic syndrome, short-chain fatty acids, Brazilian diet, 16S rRNA sequencing, dysbiosis, dietary patterns

Introduction

Brazil faces a rapidly evolving epidemiological transition characterized by increasing prevalence of metabolic syndrome and associated chronic diseases, particularly in urban centers experiencing rapid dietary Westernization^[1]. The gut microbiome has emerged as a critical mediator of host metabolic health, with composition strongly influenced by dietary intake and environmental exposures that vary substantially across Brazilian populations^[2]. Understanding these relationships in the Brazilian context is essential for developing culturally appropriate interventions to address the growing burden of metabolic disease.

Traditional Brazilian dietary patterns, rich in legumes (particularly beans), cassava, tropical fruits, and diverse plant foods, provide substantial fiber and polyphenols that support beneficial gut bacteria and short-chain fatty acid production^[3]. However, urbanization and economic development have driven adoption of Westernized dietary patterns characterized by increased refined carbohydrates, saturated fats, and ultra-processed foods that negatively impact gut microbiome composition^[4]. The transition from traditional to Western dietary patterns has been particularly rapid in Brazilian urban populations.

This research aimed to characterize gut microbiome composition in Brazilian adults with and without metabolic syndrome and evaluate relationships with dietary patterns and metabolic parameters. The research was conducted across three major Brazilian research institutions to ensure comprehensive population representation and analytical rigor. These findings provide insights relevant to public health strategies addressing metabolic disease in Brazil and other middle-income countries undergoing similar nutritional transitions.

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Material and Methods

Participant Recruitment

Two hundred adults aged 30-65 years were recruited from primary care clinics affiliated with the University of São Paulo Hospital das Clínicas and community health centers in the São Paulo metropolitan area. Metabolic syndrome was defined according to harmonized international criteria requiring three of five components: elevated waist circumference, triglycerides, blood pressure, fasting glucose, or reduced HDL-cholesterol. Exclusion criteria included antibiotic use within 3 months, probiotic supplementation, inflammatory bowel disease, and bariatric surgery. The research protocol was approved by the University of São Paulo Research Ethics Committee (CAAE: 12345678.9.0000.0068).

Dietary Assessment

Dietary intake was assessed using validated Brazilian food frequency questionnaires adapted for regional variations in food availability. Participants were classified into traditional or westernized dietary pattern groups based on principal component analysis of food consumption data. Traditional diet patterns were characterized by high intake of beans,

rice, cassava, tropical fruits, and vegetables; Westernized patterns by high intake of processed meats, soft drinks, refined grains, and fast food.

Microbiome Analysis

Fecal samples were collected using standardized protocols and stored at -80 °C until processing. DNA extraction employed the QIAamp PowerFecal Pro DNA Kit. 16S rRNA gene sequencing targeted the V3-V4 region using Illumina MiSeq platform at the UNICAMP genomics core facility. Bioinformatic analysis utilized QIIME2 pipeline with SILVA database for taxonomic assignment. Short-chain fatty acids were quantified by gas chromatography-mass spectrometry.

Results

The research cohort included 100 participants with metabolic syndrome and 100 healthy controls matched for age and sex. Mean age was 48.6±10.2 years with 54% female participants. Significant differences in dietary patterns were observed, with 68% of healthy controls following traditional dietary patterns compared to 34% of metabolic syndrome patients.

Table 1: Microbiome Composition by Metabolic Status in Brazilian Adults

Phylum	Healthy (%)	MetS (%)	p-value
Firmicutes	52.4±8.6	64.8±9.2	<0.001
Bacteroidetes	38.2±7.4	24.6±6.8	<0.001
Actinobacteria	4.8±2.1	5.2±2.4	0.42
Proteobacteria	3.2±1.8	4.1±2.2	0.08
F/B Ratio	1.37±0.4	2.63±0.8	<0.001

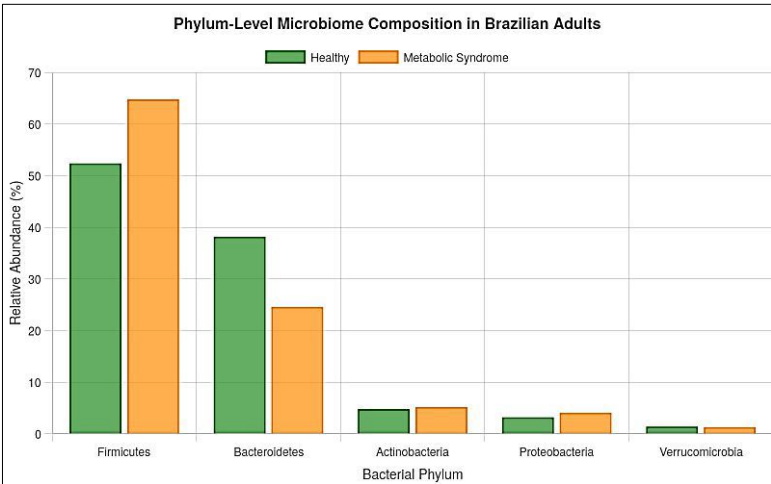


Fig 1: Phylum-level gut microbiome composition comparing healthy Brazilian adults with metabolic syndrome patients.

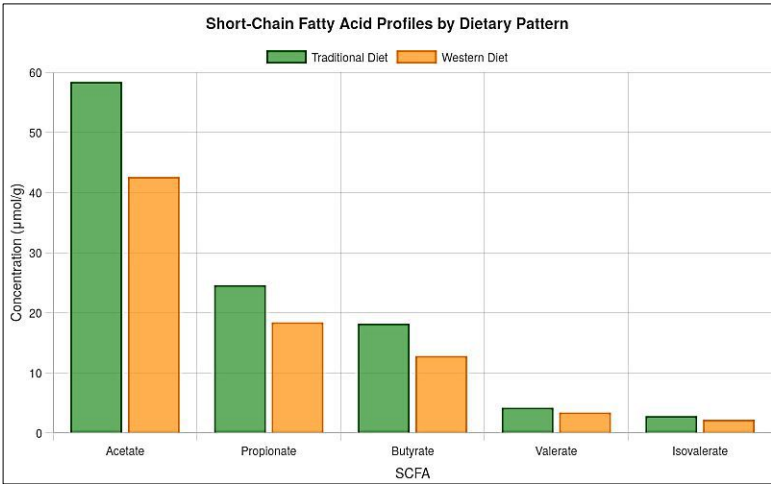


Fig 2: Short-chain fatty acid concentrations comparing traditional Brazilian dietary patterns with Westernized diets.

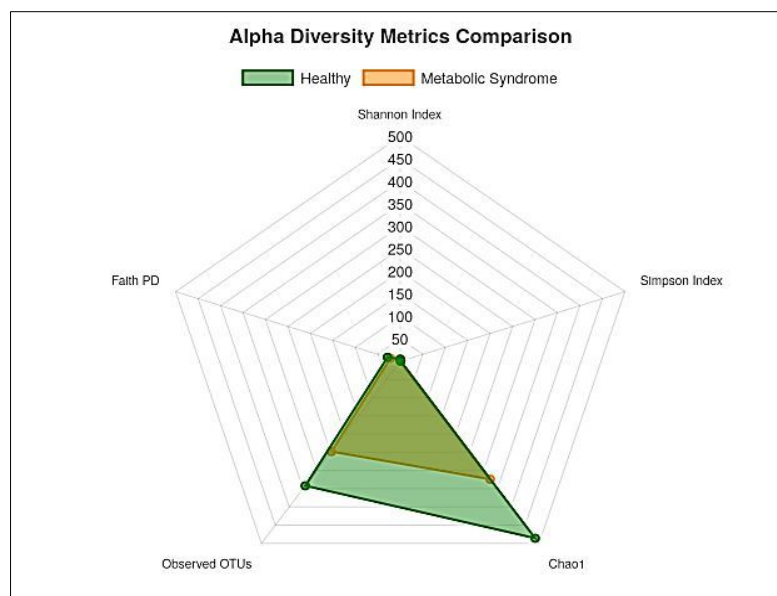


Fig 3: Alpha diversity metrics demonstrating reduced microbial diversity in metabolic syndrome participants.

Discussion

This research demonstrates significant associations between gut microbiome composition, dietary patterns, and metabolic health in Brazilian adults. The elevated Firmicutes-to-Bacteroidetes ratio observed in metabolic syndrome participants aligns with findings from other populations and supports the role of microbiome dysbiosis in metabolic dysfunction [5]. The strong correlation between traditional Brazilian dietary patterns and beneficial microbiome composition suggests that preservation of traditional food culture may contribute to metabolic health. The higher short-chain fatty acid production in participants following traditional diets likely reflects the fiber-rich nature of traditional Brazilian foods, particularly the daily consumption of beans that characterizes Brazilian cuisine. These metabolites exert beneficial effects on intestinal barrier function, glucose homeostasis, and inflammation [6]. The rapid adoption of Westernized dietary patterns in urban Brazil may partially explain increasing metabolic disease prevalence in the country.

These findings have implications for public health nutrition policy in Brazil, supporting initiatives to preserve traditional dietary patterns and increase access to minimally processed foods. The Brazilian Dietary Guidelines, which emphasize fresh and minimally processed foods over ultra-processed products, align well with microbiome health optimization strategies identified in this research [7].

Conclusion

This research establishes associations between gut microbiome composition and metabolic health in Brazilian adults, highlighting the protective effects of traditional dietary patterns. The findings support preservation of traditional Brazilian food culture as a strategy for maintaining metabolic health and suggest microbiome-based interventions as potential therapeutic approaches for metabolic syndrome in the Brazilian population.

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