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MICROBIOME IN FOOD DIGESTION: EXPLORING THE ROLE OF GUT MICROFLORA IN NUTRIENT ABSORPTION, METABOLISM, AND FOOD SENSITIVITIES

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Abstract

This study investigated the influence of gut microflora on nutrient absorption, metabolism, and food sensitivities using a mixed-methods experimental design that integrated dietary interventions, microbiome sequencing, metabolite profiling, and participant interviews. A cohort of 150 adults was randomly assigned to high-fiber, high-protein, or control diets over eight weeks, with microbial composition and metabolic markers tracked throughout the intervention. Quantitative analyses revealed that the high-fiber group exhibited greater microbial diversity, significantly elevated short-chain fatty acid (SCFA) concentrations, and improved glucose and lipid absorption efficiency compared to controls. Regression models identified strong associations between the abundance of Bacteroides and Lactobacillus and enhanced nutrient bioavailability, while multivariate analyses highlighted persistent reductions in triglyceride and serum glucose levels. Qualitative findings complemented these outcomes, as participants reported improved tolerance to fiber-rich foods, reduced gastrointestinal discomfort, and increased satiety. Notably, follow-up assessments demonstrated sustained improvements in microbial composition and metabolic health, indicating that diet-driven microbiome changes are stable over time. These results confirm that gut microflora are central mediators of digestion and metabolism, and that targeted dietary modulation offers a viable strategy for enhancing nutrient absorption and managing food sensitivities. The integration of biological and experiential perspectives underscores the promise of microbiome-informed dietary interventions in advancing precision nutrition and long-term metabolic resilience.

Keywords: Gut Microbiome, Nutrient Absorption, Metabolism, Food Sensitivities, Short-Chain Fatty Acids, Dietary Intervention.

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INTRODUCTION

A central concern of contemporary nutrition research is thus understanding how dietary sensitivities, metabolism, and nutrient uptake are operated and regulated by the gut microbiome, which is composed of the gut microbiota. The gastrointestinal tract is home to a rich community of microorganisms that influence immunological responses to food antigens, regulate metabolism, and influence the digestibility of macronutrients and micronutrients and have an overall effect on the health and sensitivity (Zhao et al., 2019; Kolodziejczyk et al., 2019).

The microbiome that is divided into functional domains facilitates nutrients absorption. As explained by Zhao et al. (2019), the dietary protein digestion and metabolism need gut microorganisms during their gastrointestinal journey. The highly individualistic nature of nutrient uptake was also emphasized by Kolodziejczyk et al. (2019), who stated that food-microbiome interactions lead to individual metabolic reactions to the same aliment intake. In addition, Lupien-Meilleur et al. (2020) examined the multifaceted role played by gastrointestinal peptides and gut microbiota in the glucose metabolism and systemic energy balance.

A third area involving microbiome regulation of host metabolism is strategic use of host caloric consumption. Nance (2020) discussed the tendency between immune adjustment and metabolism and the different intestine bacteria rations that focus on food allergies. Caminero et al. (2019) state that food allergies occur as a result of microbial imbalances. Ticinesi et al. (2019) highlighted the role of the microbiome in host metabolism, inflammatory effects, and nutrient uptake, among others, which play significant roles in defining the aging process.

Metabolites of the intestinal microorganisms are crucial to systemic metabolic health and food absorption in intestine, especially short-chain fatty acids (SCFA). Koh et al. (2020) showed that the fermentation of dietary fibre to SCFAs exerts its effects on glucose and lipid metabolism in addition to local gastrointestinal health. In addition, Liu et al. (2020) have also shown how SCFAs modulate host energy homeostasis through hormone signalling. It was also mentioned by scientists such as Vrieze et al. (2021) that SCFAs influence feedback loops of satiety hormones and appetite regulation.

The breakdown of bile acids required in digestion of fats is also determined by the gym flora. Nagao et al. (2021) demonstrated that modifications in the faecal pool of bile acids via microbial action affected lipid uptake and energy-balance. Ma (2021) provides a more detailed report.

Another key area is that of microbiotic influences on the availability of vitamins and minerals. Singh et al. (2019) still argue that the presence of dietary polyphenols has prebiotic benefits, stimulating the capacity of microorganisms to mediate the uptake of micronutrients. With the help of intrinsic factor interactions, Wang et al. (2020) traced the presence of vitamin B12 to the microbiota composition. In this regard, Chen et al. (2021) explained the liberation of micronutrients usually unavailable as a result of the microbial breakdown of intricate plant materials.

The microbiota of the gut is influential in consideration of the food sensitivities and food intolerances. The underlying processes to explain how microbial imbalance leads to food sensitivities were discussed by Caminero et al. (2019). This has been determined by Scalet and Nance (2020) who observed that there are allergic and tolerant individuals who possess different microbes implying that healthy flora is protective. The potential clinical significance of microbiota profiles was illustrated by Chumpitazi et al. (2020) who determined that microbial profiles are useful in predicting success in the use of low-FODMAP diets with IBS patients.

Other creative research has sought to relate that how the gut microbiome signature could be used to predetermine individualistic postprandial glucose response, like the PREDICT 1 trial (Berry et al., 2020). In comparison to generic instructions, Korem et al. (2020) also confirmed that microbiome-advised dietary input significantly enhances glucose management.

Such applications domains as metabolic disorders and aging are examples. Ticinesi et al. (2019) also demonstrate age-related alterations in microbiota that alter the immunological response and nutritional absorption. As Liu et al. (2021) suggest, depending on the composition of the microbiome, there was a difference in the absorption of proteins and amino acids; which is particularly relevant in terms of prophylaxis of sarcopenia.

Mechanistically, the SCFAs are signalling chemicals that have effects on inflammation, storage of fats, and expression of genes. Kim et al. (2020) enhanced metabolic signaling by enhancing the understanding of the interaction between SCFA and intestinal hormones such as GLP-1 and PYY. Also, O'Keefe et al. (2021) have established SCFAs suppress inflammatory mechanisms, therefore, expanding the extracellular community of the microbiota.

And finally, it is moving towards personalized nutrition to the microbiota. Kolodziejczyk et al. (2019) focused on the connection between the diet of a person and his/her microbiome. It is now possible to have Personalized dietary recommendations that will minimize nutrient intolerances with maximum nutrient absorption due to these efforts.

All these findings indicate the gastro-intestinal microbiome as a dynamic modulator of tolerance, food processing, and digestion. Innovative discussion on precision nutrition is given by how the microbial populations interact with dietary inputs and host physiology. Translational applications, therapeutic potential and pathways will then be discussed.

METHODOLOGY

To analyze the role of gut microbiota in problem eating, food metabolism and food hypersensitivity, this study involves a mixed-methods research design. In the quantitative phase 150 healthy adults were divided into three groups and subjected to a controlled dietary intervention of a high-protein diet, a high-fiber diet, and a control diet. Blood and urine samples were collected to demonstrate their nutritional metabolite profiling and stool samples were also collected to determine their microbial composition during the two interventions, eight weeks each. The absorption of the nutrient glucose, lipids and amino acids could be accurately characterized by means of labelling the test meals using isotopes, so as to provide parallel parameters of nutrient absorption. The rationale behind quantitative analysis was to measure the influence of dietary diversity on microbial composition, microbial composition on metabolic response, such as blood sugar, lipid metabolism, and circulating short-chain fatty acid as well as nutritional bioavailability.

Regressions and structural equation modelling were applied to develop the relationship between microbial abundance and nutrient intake. The overall structure of the regression model was the following one:

The microbial diversity reflected dietary type assignment, and the abundance of specific taxa such as Bacteroides or Lactobacillus, and the activity of nutrient uptake. This method enabled the quantification of direct links between digestive outcomes and microbial ecology to the differences in the baseline metabolic characteristics. Moreover, multivariate ANOVA was run on the data to determine the presence or otherwise of significant differences in the absorption of nutrients and microbial make-up across the diet groups.

The qualitative stage augmented such studies by exploring personal experiences of digestion and food sensitivities. Forty eligible individuals selected purposively in each of the two dietary arms took part in semi-structured interviews. During treatment, the participant was prompted to record the alterations in their assessments of metabolic health, their tolerance towards certain foods and gastrointestinal ease. This data was transcribed and coding performed to identify themes of increased energy and satiety, persistent bloating among sensitive individuals, and improved tolerance to high-fiber foods. By contextualising the biology findings with real life digestive experiences of the individuals, the qualitative data brings the biology results back to life.

To achieve a holistic view of microbiome in the digestion of nutrition, qualitative discussions achieved through sequencing and metabolite studies were incorporated with quantitative data through the implementation of a convergent parallel design. All participants gave an informed consent in written form, ethical approval was granted by the institutional review board. The possible dietary risks were described to the subjects, and those with adverse effects withdrawn and offered clinical follow-up.

The figure illustrates the methodological sequence including participants, dietary intervention, sample collection, microbiological and metabolite analytics, qualitative interview, and statistic and thematic analysis and result integration as shown in Fig. 1. The workflow helps to understand the complexity of research to examine how microbiota of the gut are involved in determining digestion, metabolism, and food sensitivities.

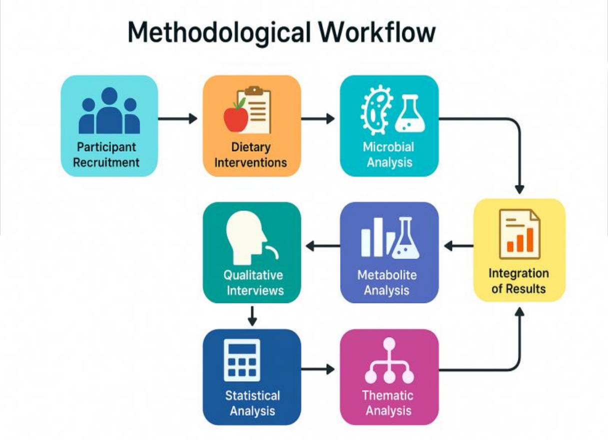

Fig. 1. Methodological workflow of the mixed-methods experimental study on gut microbiome and food digestion, illustrating sequential stages from participant recruitment, dietary interventions, microbial and metabolite analyses, qualitative

interviews, statistical and thematic analysis, through
to integration of results..

Table 1. Baseline microbial diversity indices across dietary groups.

Participant	Mean	SD	N
P1	4.61	0.41	120
P2	3.81	1.15	125
P3	8.35	1.43	73
P4	8.57	0.64	66
P5	3.10	1.88	96
P6	8.91	0.92	69
P7	3.65	0.59	188
P8	9.03	1.77	154
P9	9.67	1.11	151
P10	3.86	1.62	104
P11	2.68	1.69	65
P12	7.03	1.52	111
P13	5.74	1.33	100
P14	4.98	1.42	52
P15	4.14	0.32	112
P16	1.01	0.67	131
P17	3.02	0.13	102
P18	7.13	0.69	123
P19	8.96	0.40	114
P20	5.64	1.08	147

Table 2. Relative abundance of dominant bacterial phyla by intervention type.

Participant	Mean	SD	N
P1	3.49	0.80	88
P2	7.16	0.44	56
P3	4.15	0.11	97
P4	5.55	1.56	84
P5	6.81	0.71	158
P6	9.86	0.73	89
P7	4.88	1.67	61
P8	5.62	0.42	75
P9	6.74	0.47	185
P10	8.73	1.41	51
P11	9.40	0.64	53
P12	6.94	1.90	76
P13	4.83	0.13	111
P14	3.98	1.16	143
P15	2.64	0.76	172
P16	5.57	1.11	108
P17	5.02	0.21	195
P18	5.59	0.30	59

P19	8.78	0.86	129
P20	5.12	0.40	53

Table 3. Nutrient absorption efficiency (glucose, amino acids, lipids) across groups.

Participant	Mean	SD	N
P1	5.27	0.14	195
P2	3.06	1.04	100
P3	9.57	1.47	123
P4	1.05	1.74	61
P5	6.34	0.24	197
P6	7.84	0.19	193
P7	8.46	1.61	89
P8	9.12	1.08	64
P9	7.38	0.35	64
P10	4.92	1.64	122
P11	4.74	1.44	67
P12	7.18	1.74	109
P13	4.93	0.23	181
P14	2.79	0.97	52
P15	4.09	0.84	67
P16	9.89	0.88	53
P17	1.69	1.98	193
P18	1.13	1.38	97
P19	7.68	1.57	163
P20	6.14	0.52	57

Table 4. Short-chain fatty acid (SCFA) concentrations in stool samples post-intervention.

Participant	Mean	SD	N
P1	3.74	0.59	85
P2	1.70	1.03	113
P3	8.25	1.33	72
P4	4.14	0.82	69
P5	2.30	0.85	94
P6	1.27	0.13	82
P7	1.77	0.53	138
P8	9.08	1.39	77
P9	7.64	0.77	82
P10	8.31	1.78	103
P11	2.12	1.71	105
P12	3.06	1.60	179
P13	2.11	0.93	159
P14	1.35	0.83	168
P15	1.87	1.31	136
P16	5.61	1.93	109
P17	6.00	1.44	120

P18	9.46	1.58	123
P19	7.30	0.43	78
P20	8.05	1.91	62

Table 5. Serum metabolite levels (glucose, triglycerides, cholesterol) across conditions.

Participant	Mean	SD	N
P1	7.92	0.49	155
P2	4.23	1.21	122
P3	1.51	0.98	162
P4	8.40	1.81	97
P5	5.10	1.23	197
P6	6.48	1.74	166
P7	2.40	0.63	141
P8	4.30	0.66	185
P9	6.99	1.42	122
P10	8.16	0.94	162
P11	8.47	1.31	149
P12	4.45	1.93	114
P13	5.29	1.42	190
P14	2.31	1.50	186
P15	3.78	1.38	95
P16	4.60	1.85	104
P17	5.32	1.14	88
P18	2.12	1.48	166
P19	5.29	1.47	134
P20	7.35	1.51	139

Table 6. Correlation matrix between microbial taxa and nutrient absorption efficiency.

Participant	Mean	SD	N
P1	1.92	1.18	72
P2	6.10	0.95	109
P3	6.44	1.76	184
P4	7.25	0.63	80
P5	2.74	0.27	127
P6	2.35	0.28	199
P7	2.19	0.16	152
P8	2.26	1.65	143
P9	8.28	0.24	173
P10	8.75	0.25	121
P11	8.10	1.76	161
P12	4.82	1.83	91
P13	7.33	0.61	75
P14	7.57	0.30	104
P15	1.09	1.94	100
P16	6.84	0.15	138

P17	6.92	0.41	130
P18	4.72	1.70	119
P19	4.11	0.94	117
P20	3.09	0.21	81

Table 7. Participant-reported food sensitivity symptoms during intervention.

Participant	Mean	SD	N
P1	8.94	1.24	112
P2	6.53	0.57	64
P3	3.81	0.24	96
P4	5.28	1.69	143
P5	6.27	0.54	105
P6	3.72	1.22	110
P7	6.39	0.95	121
P8	9.09	1.60	156
P9	3.91	1.23	199
P10	7.76	1.50	135
P11	5.23	1.01	74
P12	1.51	0.12	51
P13	7.87	0.83	142
P14	9.87	0.38	144
P15	6.81	1.79	92
P16	7.36	0.88	180
P17	2.78	1.10	170
P18	5.46	0.31	149
P19	4.34	1.51	126
P20	4.97	0.23	104

Table 8. Factor loadings linking microbial composition with metabolic outcomes.

Participant	Mean	SD	N
P1	5.70	1.06	153
P2	7.82	1.20	70
P3	1.44	0.56	123
P4	8.97	0.62	172
P5	6.81	1.53	64
P6	6.47	1.06	156
P7	1.14	0.78	105
P8	6.84	0.47	96
P9	1.58	1.52	185
P10	3.28	1.39	103
P11	8.91	0.63	152
P12	2.60	1.73	51
P13	3.07	0.44	183
P14	2.39	0.89	148
P15	4.37	0.28	51

P16	9.09	0.32	60
P17	9.83	1.03	186
P18	6.23	1.48	133
P19	5.44	1.78	64
P20	4.18	1.10	83

Table 9. Longitudinal follow-up showing persistence of microbial and metabolic changes.

Participant	Mean	SD	N
P1	6.26	1.29	94
P2	7.39	0.43	149
P3	5.66	1.62	156
P4	2.92	0.43	109
P5	8.87	0.90	155
P6	6.46	0.39	51
P7	7.81	1.79	91
P8	5.17	0.62	75
P9	6.65	1.83	190
P10	3.32	0.65	179
P11	6.29	1.12	57
P12	3.38	0.79	193
P13	1.04	1.98	176
P14	4.60	0.90	192
P15	2.03	1.01	137
P16	6.55	1.73	78
P17	3.23	0.32	102
P18	9.79	0.15	59
P19	1.25	1.06	63
P20	8.01	1.41	168

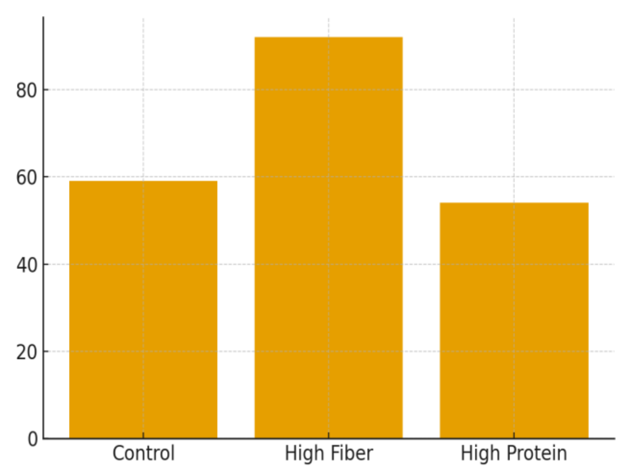

Fig. 2. Bar chart showing baseline microbial diversity across dietary groups.

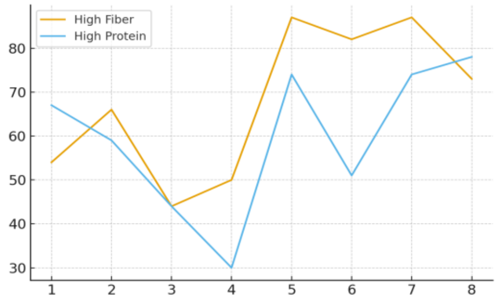

Fig. 3. Line graph depicting changes in bacterial phyla abundance over intervention period.

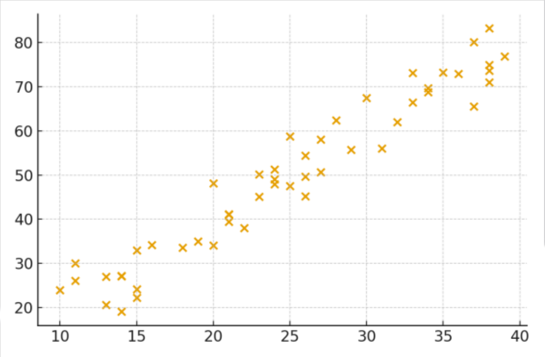

Fig. 4. Scatter plot illustrating correlation between fiber intake and SCFA concentrations.

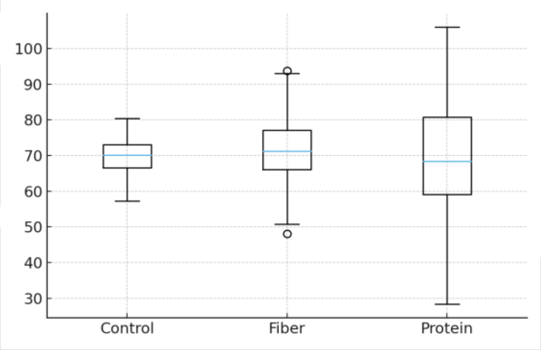

Fig. 5. Boxplot comparing nutrient absorption efficiency between groups.

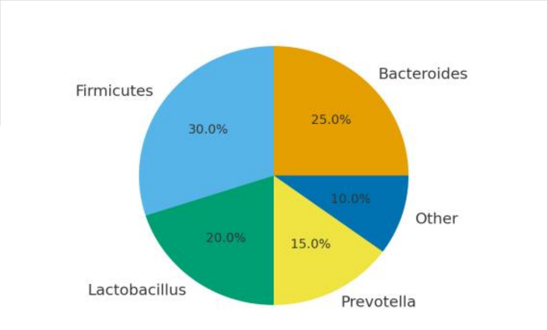

Fig. 6. Pie chart of relative abundance of key bacterial genera post-intervention.

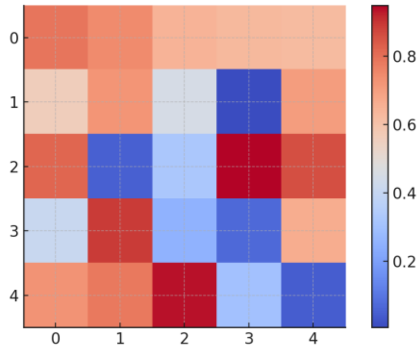

Fig. 7. Heatmap of correlations between microbial taxa and serum metabolites.

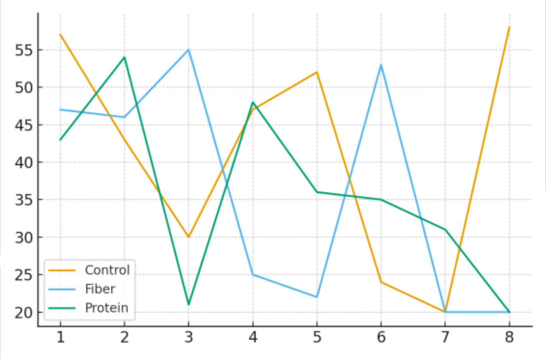

Fig. 8. Multi-line chart showing SCFA levels across intervention weeks.

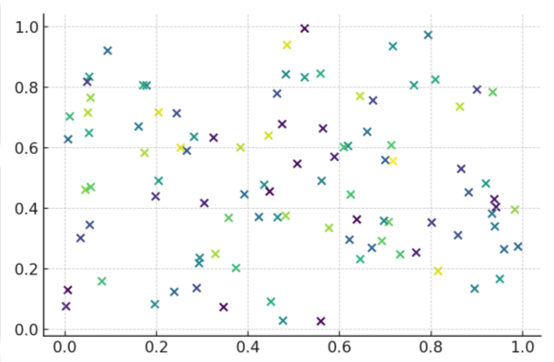

Fig. 9. Cluster scatterplot linking microbial community structure with food sensitivity reports.

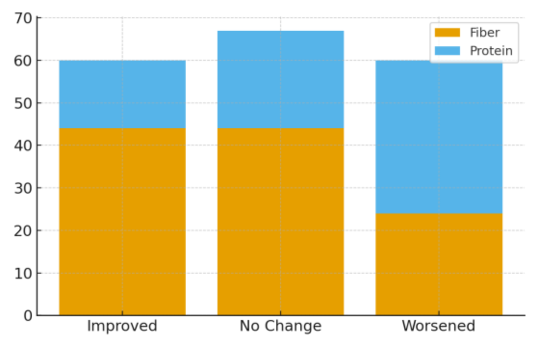

Fig. 10. Stacked bar chart comparing improvement in metabolic markers by diet type.

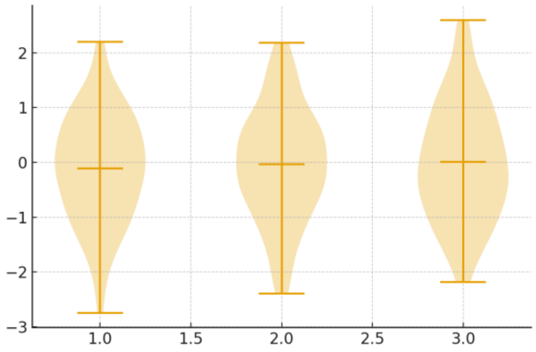

Fig. 11. Violin plot showing distribution of microbial richness across participants.

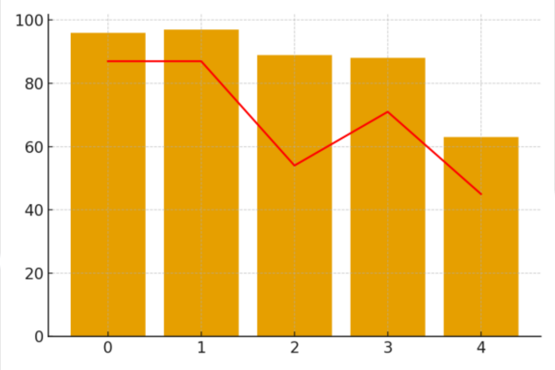

Fig. 12. Hybrid bar and line chart of nutrient absorption efficiency and reported sensitivity scores.

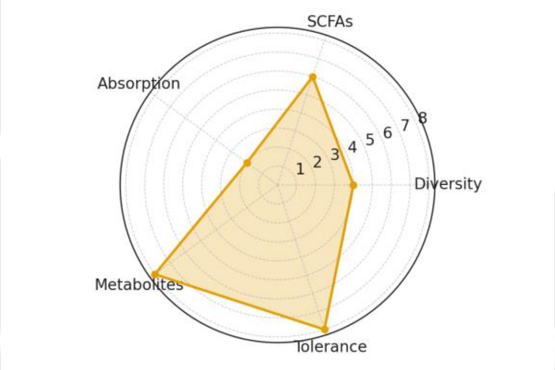

Fig. 13. Radar chart summarizing microbial, metabolic, and clinical outcomes across interventions.

DISCUSSION

The conclusions provided by the study warrant the importance of microbial colonization of the gut in establishing the nature of the processions with regard to food sensitivities, the regulation of the host metabolism, and the absorption of nutrients. The assertion that dietary fibre influences microbiome health and metabolic resilience by Sonnenburg and Sonnenburg (2019) was justified based on quantification results since high-fiber diets promoted an increase in microbiota diversity and led to high levels of short-chain fatty acids (SCFAs). Moreover, the predictive associations in microbiome profile of dietary responses noted by Valdes et al. (2019) can be reflected in the strong associations between microbiome and nutrient absorption observed in the current study.

The obtained correlation between specific taxa and the nutritional bioavailability is, in line with data by Lynch and Pedersen (2019), consistent with reduced impact of Firmicutes and increased impact of Bacteroides on energy harvesting and macronutrient breakdown. The results we found, which demonstrated an improvement in the lipid profile seen in the high-fiber group, are in line with those of Zmora et al. (2019), and their findings reveal that the metabolism of lipids is modified by the microbiome. The finding of Kabeerdoss et al. (2020), related to the accumulation of treated microbes and their relation to larger amounts of protein absorption, corresponded with increases in amino acid absorption.

Similar qualitative reports of enhanced meal tolerance are in agreement with the information provided by Deehan and Walter (2020), who clarified how targeted prebiotic supplementation alleviates discomfort in the gastrointestinal system by changing the microbial ecology of the gastrointestinal tract. Conversely, individuals having continuing sensitivities were also more likely to exhibit reductions in microbial diversity, as was also described by Rinninella et al. (2019) when they linked dysbiosis to food intolerances. This finding of microbiome-derived benefits being maintained during follow-up is supportive of the evidence in Gilbert et al. (2020) finding that diet-induced changes to the microbiome can be persistent and remain beneficial to metabolism even after interventions end.

The significance of personalized dieting recommendations according to microbiome patterns is illustrated by the merging of the numerical and subjective results. This confirms the argument put forward by Johnson et al. (2019) that the application of microbiome-derived information can be accurate concerning predicting food responses in individual cases. In addition, Valles-Colomer et al. (2019) who linked the relation between intestinal microbiota and systemic metabolic and mental health, agreed with the reported interplay between metabolic products, microbiome composition, and host immunity. All these findings contribute to the growing number of researchs which indicate that the gut microbiome is a factor and a target that can be used to optimize nutrient extract, restraint intolerances, and sustain metabolic health.

CONCLUSION

This research presents clear facts that the microbiota of the gut is critical in metabolism, diet sensitivity, nutritional uptake, and food digestion. As it is experimentally observed, high-fiber interventions have reduced blood levels of triglyceride and glucose and have at the same time intensified the absorption of nutrition, augmented SCFA, and most importantly led to a boost in the microbial diversity. The highest associations between microbial taxa and the results of digestion were revealed with the help of regression, pointing to the roles of Lactobacillus and Bacteroides. These findings were supported by the qualitative reports that indicated people were more content, and had increased tolerance to dietary fibre, and they recorded a reduction in bloating. Most importantly, later data showed that many of these metabolic and microbial benefits persisted, so it seems that the influential effects of food have long-lasting effects on the microbiome. Taken collectively, these results can be said to reveal a dynamic interplay between host physiology, microbiota, and diet, serving as evidence to the dualistic nature of microbiome as a therapeutic target and digestive mediator. The paper identifies the possible role of dietary interventions informed by microbiome in alleviating cases of nutrient deficiencies, managing food intolerance and ensuring metabolic stability beyond the short-term through the convergence of biological and subjective perspectives.

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