Original Article

Impact of Ketogenic Diet on Gut Microbiota Composition and Short-Chain Fatty Acid Production in Central Indian Adults: A Case-Control Study

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Abstract

Background: The ketogenic diet (KD) has become widely accepted to treat metabolic disorders, but the processes on the composition of gut microbiota and metabolic output are not sufficiently described regarding non-Western populations. Gut microbiome has a decisive impact on health including immunity, metabolism, and systemic inflammation by generating short-chain fatty acids (SCFAs) and altering the gut-brain axis. The aim behind conducting this study is to judge the effect of an 8-week ketogenic diet on the diversity of gut microbiota, taxonomic and functional metabolic alterations in healthy Central Indian adults relative to a standard Indian diet (SID). **Material and Methods:** The case-control study involved 264 healthy adults (132 in KD group, 132 in control group) aged between 18-50 years having BMI, 18.5-29.9 kg/m 2 during Index Medical College between January 2023 and December 2024. The KD diet included 70, 20, 10 percent carbohydrates, fat, and protein respectively whereas the controls were fed on conventional Indian diet (55-60 percent carbohydrates, 20-25 percent fat, 15-20 percent protein). At baseline and weeks 8, stool samples underwent 16S rRNA gene sequencing (V3-V4 region, Illumina MiSeq) of the samples. Q IIME2 and DADA2 pipelines were used to analyze alpha diversity (Shannon index), beta diversity (PCoA), taxonomic abundance, and Firmicutes/Bacteroidetes (F/B) ratio. **Results:** alpha diversity (Shannon index: 3.45±0.38 to 3.12±0.35, p< 0.001) was significantly reduced in the KD group after 8 weeks, yet negligibly different in controls (3.44±0.39 to 3.43±0.38). Analysis of beta diversity showed that there was extensive community reorganization in the KD group (PCoA distance 0.28+0.07) compared to controls (0.04+0.02, p<0.001). KD taxonomically led to higher relative Firmicutes (52.1 6.5% to 58.3 6.8% p< 0.001) and lower Bacteroidetes (40.3 5.9% to 34.1 5.7% p< 0.001) and raised the F/B ratio relative to 1.29 -0.21 to 1.71 -0.25 (p< 0.001). There were no significant changes in taxonomic shifts in the control group. The KD group had specific improvement of Akkermansiamuciniphila and Parabacteroides. The alpha diversity was negatively associated with diet adherence in the KD group (r=-0.31, p<0.001) but not the control groups. **Conclusion:** 8-week ketogenic diet results in thorough gut microbiota restructuring and cannot be deemed healthy in Indian adults, such as diversity reduction, F/B ratio rise, and selective enrichment of fat-metabolic taxa. Although this has the potential to promote ketogenic metabolism and some other health-promising effects, the decrease of microbial diversity is a factor that should be taken seriously in the long-term use of KD. These discoveries offer new information on how microbiomes respond to KD in a non-Western ethnic with unique baseline dietary habits.

Keywords: Microbiota, ketogenic diet, gut microbiota, 16S rRNA sequencing, Firmicutes, Bacteroidetes, Indian population.

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Introduction

The human gut microbiota is a complicated ecosystem of trillions of microorganisms which are crucial to the metabolism and immune process of those hosts and their general well-being.[1] It is a microbial community that responds greatly to dietary interventions where the macronutrient composition is an evident main factor in microbiome structure and functions.[2] The ketogenic diet (KD) which has an extremely low carbohydrate (less than 50g12 with decreasing threshold) content (usually less than 50g per kilocalorie or 5-10% of calories), high-fat content (70-80%), and moderate protein content (15-20%), has become a treatment dietary intervention in several conditions in addition to its use in refractory epilepsy.[3]

Although metabolic and neurological implications of KD have been seriously studied, the effect it imposes on the composition of gut microbiota is a still developing field of research. The severe decrease in the carbohydrate content of the diet, which serves as the key nutrient of most intestinal bacteria, and the rise in the quantity of fat consumption radically changes the nutritional environment of the intestinal context.[5] This movement may possibly advantage microbes with lipid and ketone-body metabolic potential and decrease those relying on fermentable carbohydrates.[6]

Recent findings have shown that KD may have a great influence

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in changing the microbiome composition of the gut in patients with epilepsy and animal models.[7,8] Nevertheless, the majority of studies on the topic have been carried out in Western cohorts or non-clinical groups, creating a significant knowledge gap because of microbiome reactions to KD within the context of healthy people belonging to non-Western groups. The gap is especially wide concerning Indian populations, as the baseline patterns of diets are usually characterized with a high proportion of carbohydrates in the form of grains and legumes, putting the microbiome composition at a specific starting point relative to the Western cohorts.[9]

The gut microbiota affects the host physiology in several ways, including generation of short-chain fatty acids (SCFAs) like butyrate, propionate, and acetate, which act as energy source to the colonocytes and regulators of the immune activity.[10] Also, microbial diversity is typically viewed as an indicator of ecosystem reliability and well-being and lower diversity is correlated with different diseasey conditions.[11] It is important to know how KD influences these parameters within the Indian context to come up with safe, effective, and culturally appropriate dietary interventions.

The particular demographic traits of India, including genetic predispositions, the traditional studies of a high-carbohydrate diet, and the unique burden of diseases necessitate the analysis of the KD effects in the given population instead of generalizing it on the body of research in the West.[12] Increasing use of KD in the urban settings of India in weight management and metabolic health is an indication of the urgency of the research.

The objective of the study was to assess in detail the effects on intestinal microbiota diversity, taxonomic profiles and functional modifications of an 8-week ketogenic diet in healthy Central Indian adults through superior 16S rRNA sequencing and bioinformatic studies. The hypothesis of our research was that KD would cause profound changes to the microbiome structure, as compared to a typical Indian diet, which might have an impact on the ecology of microorganisms and on host health.

Materials and Methods

Study Design and Setting: This is a prospective case-control study, which was carried out at the Department of Physiology, Index Medical College Hospital and Research center, Indore, Madhya Pradesh, India, in the period of January 2023 to December 2024. The protocol used was validated by the Institutional Ethics Committee and the study followed in the Declaration of Helsinki. Each participant signed an informed consent.

Participant Recruitment and Selection: The eligibility of the study was done on adults aged 18-50 years who presented themselves in the outpatient departments of General Medicine and Physiology. A literature did not identify large effect sizes (Cohen d=0.5) of microbiota response to dietary intervention, so sample size was computed at alpha=.05 and power=.80 (264 (132 per group) with dropout =0.10).

Inclusion Criteria:

- Age 18-50 years
- BMI 18.5-29.9 kg/m²
- Willing to follow assigned diet for 8 weeks
- Able to provide informed consent
- No antibiotic use in preceding 3 months

Exclusion Criteria:

- Known gastrointestinal disorders (IBD, celiac disease, peptic ulcer)
- Diabetes mellitus requiring insulin
- Chronic use of medications affecting gut function
- Pregnant or lactating women
- Immunocompromised status
- Recent probiotic or prebiotic supplementation

Dietary Interventions

Ketogenic Diet Group (n=132): Monitored KD followed by the participants was 70 percent fat, 20 percent protein, and 10 percent carbohydrates. Culturally appropriate, such as ghee, coconut oil, nuts and seeds, paneer, non-starchy vegetables, eggs, fish, and chicken were used to create individualized meal plans. Strict avoidance was in grains, sugars, legumes and starchy vegetables. A structured induction period on a 3-day basis was introduced.

Ketosis checking was conducted twice per week on the capillary blood 1-3 mmol/L of 2,4-dihydroxybutyrate (FreeStyle Precision Neo) using handheld meters. Indian food composition databases were used to analyze weighed food records (detailed 3-day weighed) collected bi-weekly.

Control Group (n=132): The participants were free of any exercise and were on a regular Indian diet (SID) as per ICMR-NIN ratios: 55-60 percent carbohydrates, 20-25 percent fat, 15-20 percent protein. Whole grains (rice, roti), lentils (dal), vegetables, fruits, dairy, moderate fats/oils were the diet. Biochemical food diaries were taken after every two weeks to ensure compliance.

Stool sample collection and processing: A baseline (T0) and 8 weeks (T1) DNA/RNA shield tubes were collected and 2 hours following collection stored at -80 o C. Standardized collection kits and instructions were given to the participants to make the sample intact.

DNA Extraction and 16S rRNA Gene sequence: Microbial DNA was isolated by means of the QIAampPowerFecal Pro DNA Kit (Qiagen) according to the instructions. NanoDrop spectrophotometry was used to measure the DNA concentration and purity. Amplification of the V3-V4 hypervariable region 16S rRNA gene hypertrophic to hypermuscular spine was carried out with universal primers (341F: 5' -CCTACGGGNGGCWGCAG -3', 805R: 5' -GACTACHVGGGTATCTAATCC -3').

The Illumina MiSeq platform was used to prepare libraries and sequence them using paired-end sequencing (2×300 bp). The depth of sequencing was normalized to make sure that enough diversity is covered to analyze it.

Bioinformatic Analysis: Raw sequence data were analyzed with QIIME2 (version 2021.4) pipeline. The filtration of quality, denoising, and chimera were done with DADA2. The amplicon sequence variants (ASVs) became generated and taxonomically categorized with the assistance of the SILVA 138 reference database.

Alpha Diversity: Acceptance number was estimated by Shannon diversity index, which was used to measure diversity within-

sample using rarefied ASV tables.

Beta Diversity: Principal coordinates analysis (PCOA) using Bray, Curtis dissimilarity was run to depict cross between-sample community variation.

Taxonomic Analysis: Relative abundance of bacterial phyla and genera was done. Microbiome dysbiosis was measured by firmicutes/ Bacteroidetes (F /B) ratio.

Differential Abundance: LEfSe (Linear discriminant analysis Effect Size) and DESeq2 were applied to find taxa that were found to be significantly enriched or depleted among the groups and after 5 days.

Statistical Analysis: Data were compared and investigated in SPSS version 28.0 and R statistical software version 4.1.0. Mean+SD were used to express the continuous variables as well as compare the variables with independent t-tests or Mann-Whitney U tests according to the normality (Shapiro-Wilk test). Historical t-tests or Wilcoxon signed-rank tests were used to evaluate changes within populations. The relationship between parameters of diet adherence and microbiota was tested by Pearson or Spearman correlation coefficients. p<|human|>The statistical significance level was p less than 0.05. The false discovery rate (FDR) is another correction method that was utilized to perform multiple testing corrections on taxonomic comparisons.

Results

Baseline Characteristics

Both groups were well-matched at baseline with no significant differences in age, sex distribution, BMI, or microbiota parameters (all p>0.05), confirming adequate randomization and comparability.

Table 1: Baseline demographic and microbiota characteristics showing no significant differences between groups

Variable	KD Group (n=132)	Control Group (n=132)	p-value
Age (years)	34.6±7.8	34.1±8.0	0.62
Sex (M/F)	68/64	70/62	0.78
BMI (kg/m²)	25.1±2.8	25.0±2.9	0.85
Alpha diversity (Shannon)	3.45±0.38	3.44±0.39	0.84
F/B ratio	1.29±0.21	1.29±0.20	0.99

Table 2: Changes in alpha diversity (Shannon index) after 8-week intervention

Group	Baseline	8 weeks	Change	p-value	Effect Size (d)
KD	3.45±0.38	3.12±0.35	-0.33±0.18	<0.001	0.91
Control	3.44±0.39	3.43±0.38	-0.01±0.17	0.82	0.03
Intergroup comparison of change scores: p<0.001, Cohen's d=1.78					

Changes in Alpha Diversity: The KD group demonstrated a significant reduction in alpha diversity with a mean decrease of 0.33 units in Shannon index (p<0.001), representing a large effect size (Cohen's d=0.91). In contrast, the control group showed virtually no change (-0.01 units, p=0.82). The intergroup difference in change scores was highly significant (p<0.001) with a very large effect size (d=1.78).

Table 3: Beta diversity changes based on Bray-Curtis dissimilarity and Principal Coordinates Analysis

Comparison	PCoA Distance	p-value (PERMANOVA)
KD: Baseline vs 8 weeks	0.28±0.07	<0.001
Control: Baseline vs 8 weeks	0.04±0.02	0.45
Between groups at 8 weeks	0.35±0.09	<0.001

Beta Diversity Analysis: Beta diversity analysis revealed substantial community restructuring in the KD group, with significant separation between baseline and 8-week samples (PCoA distance 0.28±0.07, PERMANOVA p<0.001). Control group samples showed minimal community shift (0.04±0.02, p=0.45). At 8 weeks, microbiota composition differed markedly between KD and control groups (distance 0.35±0.09, p<0.001), indicating distinct microbial communities.

Table 4: Changes in relative abundance of major bacterial phyla

Phylum	Group	Baseline (%)	8 weeks (%)	Change (%)	p-value
Firmicutes	KD	52.1±6.5	58.3±6.8	+6.2±4.2	<0.001
	Control	52.0±6.6	51.8±6.7	-0.2±3.8	0.74
Bacteroidetes	KD	40.3±5.9	34.1±5.7	-6.2±4.1	<0.001
	Control	40.2±5.8	40.0±5.9	-0.2±3.5	0.71
F/B Ratio	KD	1.29±0.21	1.71±0.25	+0.42±0.18	<0.001
	Control	1.29±0.20	1.28±0.21	-0.01±0.15	0.82
Actinobacteria	KD	4.8±2.1	4.9±2.2	+0.1±1.5	0.68
	Control	4.7±2.0	4.7±2.1	0.0±1.4	0.98
Proteobacteria	KD	2.1±1.3	2.0±1.2	-0.1±0.9	0.51
	Control	2.2±1.4	2.1±1.3	-0.1±0.8	0.46

Taxonomic Composition Changes at Phylum Level

The most striking taxonomic change in the KD group was the

reciprocal shift between Firmicutes and Bacteroidetes. Firmicutes increased from 52.1±6.5% to 58.3±6.8% (+6.2%, p<0.001), while Bacteroidetes decreased from 40.3±5.9% to 34.1±5.7% (-6.2%, p<0.001). This resulted in a significant elevation of the F/B ratio from 1.29±0.21 to 1.71±0.25 (p<0.001). The control group showed no significant changes in any phylum.

Genus-Level Differential Abundance

LEfSe analysis identified 23 genera significantly altered in the KD group (LDA score >2.0, FDR-adjusted p<0.05).

Notable enrichments included:

- Akkermansia (LDA=3.8, p<0.001): Increased 2.8-fold
- Parabacteroides (LDA=3.2, p<0.001): Increased 2.1-fold
- Roseburia (LDA=2.9, p=0.002): Increased 1.7-fold
- Coprococcus (LDA=2.6, p=0.004): Increased 1.5-fold

Significant depletions included:

- Prevotella (LDA=3.6, p<0.001): Decreased 3.2-fold
- Bifidobacterium (LDA=2.7, p=0.001): Decreased 1.9-fold
- Faecalibacterium (LDA=2.5, p=0.003): Decreased 1.6-fold.

Table 5: Correlation analysis between dietary adherence markers and microbiota changes

Variable Pair	KD Group (r, p)	Control Group (r, p)
Adherence vs Δ Alpha diversity	-0.31, 0.001	0.02, 0.82
Adherence vs Δ F/B ratio	0.35, <0.001	-0.03, 0.74
Adherence vs Δ Akkermansia	0.28, 0.002	0.01, 0.91
Blood β-HB vs Δ Alpha diversity	-0.33, <0.001	N/A
Blood β-HB vs Δ F/B ratio	0.37, <0.001	N/A

Correlation Between Diet Adherence and Microbiota Changes: Higher adherence to KD (assessed by food logs and ketone monitoring) correlated negatively with alpha diversity changes (r=-0.31, p=0.001) and positively with F/B ratio elevation (r=0.35, p<0.001). Blood β-hydroxybutyrate levels showed similar associations, suggesting dose-dependent microbiome effects of ketogenic metabolism. No such correlations existed in the control group.

Discussion

The present research has given extensive space of facts that an 8 weeks ketogenic diet has a massive and systematically imposed effects on the gut microbiota composition in healthy Central Indian adults. The trend defining the main results associated with impaired alpha diversity, increased F/B ratio, selective enrichment of fat-utilizing taxa, and loss of carbohydrate-utilizing bacteria are all expected in minimizing macronutrient dynamics, and provide new knowledge in the context of the Indian population.

Reduced Microbial Diversity Under Ketogenic Diet

The 25.5 percent decrease in Shannon diversity index (= -33; p= 0.001) in our KD group is among the most coherent results of the KD researches reported in different populations.[13,14] These decreases are probably indicative of the disappearance of dietary substrates (complex carbohydrates, fiber) that promote the proliferation of many bacterial species, especially Bacteroidetes phylum polysaccharide-lysis-specific species.[15]

Although decreased diversity can typically be perceived as a negative factor in the itis dysbiotic case, the functional role in KD situations can vary. High-fat, low-carbohydrate dieting that causes severe selective pressure seems to prefer specialized microbes that can metabolize lipids and ketone bodies, which can be viewed as an adaptive and not pathological change.[16] There are however reservations about the long term resilience as there are normally more resistant to perturbation and colonization of pathogen by diverse ecosystems.[17]

Significantly, the fact that we found a correlation between the reduction of diversity and diet adherence (r=-0.31, p=0.001) and blood ketones (r=-0.33, p<0.001) indicates that such effect is conditioned by metabolic condition of ketosis itself and not by diet changes. This dose-response effect enhances causal induction.

Elevated Firmicutes/Bacteroidetes Ration

The rise in F/B ratio: 1.29 to 1.71 (Δ=+0.42, p<0.001) is a significant change in the structure of the gut ecosystem. The ratio has been widely researched in its role as a value of metabolic health, but its meaning is context-specific.[18] Other studies have attributed high F/B ratios to obesity indicating increased energy harvest capacity,[19] though our KD subjects had better metabolic markers with the resultant high F/B ratios.

Substrate availability seems to be the mechanistic driver. Firmicutes consist of a large proportion of species that degrade fats (e.g., Roseburia, Coprococcus) that create well in a high fat environment with Bacteroidetes being mostly plant polysaccharide fermenters not found in KD.[20] It is interesting to note that the state of F/B ratio increased in our Indian cohort (Δ= +0.42) was more pronounced than in Western KD literature (usually 0.2-0.3) perhaps due to higher levels of consuming carbohydrate in the traditional Indian diet.

Selective Enrichment of Akkermansia and Parabacteroides

The Akkermansiamuciniphila enrichment (2.8-fold) is the most remarkable finding. This degradative mucin bacterium has become a useful microbe related to a higher metabolic well-being, better gut barrier activity, and decreased inflammation.[22,23] It has been found to be enriched in epilepsy patients and mice when enriched with KD where it can potentially mediate therapeutic effects through several different pathways such as; GABA generation and immune regulation.[24]

The 2.1 fold enhancement in the increase of the Parabacteroides species also agrees with the previous KD research and can be attributed to the ability of this genus to use the bile acids and fatty acids found to be increased with high fat feeding.[25] At least the two genera were found to be involved in better glucose metabolism and less adiposity, which might help KD to benefit metabolically.

Depletion of Carbohydrates-Fermenting Taxa: The huge

changes in Prevotella (3.2-fold), Bifidobacterium (1.9-fold), and Faecalibacterium (1.6-fold) show the exclusion of their main food. Prevotella species are specific to the complex carbohydrate fermentation and are generally enriched in the populations of the plant-based diet.[26] Their reduction during the presence of KD is naturally anticipated but it is further lessening, as Prevotella plays a role in the production of SCFA.

Equally, it can be noted that a decrease in Faecalibacteriumprausnitzii - which is among the most abundant and useful human gut bacteria - is of concern considering its vital function in the production of butyrate, integrity of the gut barrier, as well as, immunity control.[27] This species cannot die without the presence of complex carbohydrates and so its depletion in the presence of KD is predictable but can be a serious issue over the long term conditions of the gut.

The immune homeostasis could be affected by the Bifidobacterium decrease because such genus promotes the development of regulatory T cells and the synthesis of anti-inflammatory compounds.[28] All of these findings collectively indicate that KD enhances the fuel via depletion of some beneficial microorganisms and at the same time depletes others with proven health-promoting effects.

Comparison with western population

I find that our results are similar and different at the same time as Western KD studies. The trend of shifts, decreased diversity, increased F/B ratio, Akkermansia enrichment, are similar in all populations.[29,30] But the magnitude of some changes seems to have been more in our Indian group especially increase in F/B ratio and depletion of Prevotella.

It is likely that these differences are useful reflections of whole and discrete baseline microbiota compositions that are formed by traditional high-carbohydrate Indian diets. The Western population should possess the low background Prevotella and high background Bacteroides, which may affect the degree of microbiome restructuring in the context of KD.[31] This highlights the need to conduct population-wide microbiome studies instead of making blanket assumptions about the response of different populations to dietary interventions.

Implications for SCFA Production and Gut Health

Although the concentrations of the SCFA were not determined in this share, the implication of these taxonomic changes is evident. Such decrease in fiber-fermenting bacteria (Prevotella, Faecalibacterium, Bifidobacterium) in combination with scarce carbohydrate food is probably to decrease the overall production of SCFA, notably butyrate.[32] This could impair the energy provision of colonocytes and intestinal resistant mechanisms in the long-term.

Nevertheless, the ketone bodies might partially reimburse themselves, because 2-hydroxybutyrate may also act as the alternative energy source of colonocytes and was found to decrease inflammation through the HDAC inhibition.[33] Moreover, other productive enriched taxa such as Akkermansia generate propionate and other metabolites which have a positive action.[34] The overall functional effect needs to be researched using metabolomic studies.

Clinical and Nutritional implications.

These results have a number of practical implications. First, the microbiome reorganization that takes place at a considerable scale in 8 weeks indicates that the changes in the gut ecosystem are rapid in KD, which may underlie positive as well as negative outcomes observed during the adaptation. Second, the adherence / ketosis / microbiome shift correlation suggests that patients who are more adherent to the KD have more significant effects-data which can be used in clinical guidelines.

Third, the decline of the beneficial bacteria such as Faecalibacterium and Bifidobacterium implies possible countermeasures. Low-carbohydrate fiber supplements (e.g. inulin, psyllium) could be useful to keep populations of commensal beneficial effectors intact and also to keep ketosis intact.[35] Instead, one can think about targeted probiotic supplementation.

Fourth, the results highlight that close attention should be paid to monitoring over long terms of KD since the decreased microbial diversity and the taxonomical depletion can have implications that are not immediately seen in short-term research. Regular checking of the microbiome would inform individual modification to achieve maximum metabolic and gut ecosystem well-being.

Strengths and Limitations

The strength of this study was thought to be the fact that the sample size (n=264) was relatively large, the design was a prospective study, there was a complete microbiome profiling based on validated methods (16S rRNA sequencing), and the population was understudied. The strict monitoring of adherence to the diet by monitoring food records, as well as objective measurements of ketones, enhance confidence in fidelity to intervention.

The limitations involve the 8-week period that are unlikely to study the long-term adaptation and reversibility of changes. Metagenomic sequencing or metabolomics would provide more mechanistic information, whereas the application of 16S rRNA sequencing only gives compositional, and not functional, information. We never measured SCFA outputs, which prevented functional repercussions interpretation. Single center design can be a problem in generalizability to the diverse regions of India and the varied dietary practices. Lastly, although we used recent antibiotic use as a confounding factor, we have not evaluated detailed medication records or stress levels that could also have an effect on microbiota.

Future Research Directions

Further research that would examine more prolonged KD intervention (6-12 months) should be conducted to evaluate the adaptation and stability of the microbiome. Changes would be reversible, which would be explained through post-diet recovery studies. Combined approaches to metabolomics (SCFAs, bile acids, ketones) and metagenomics would provide a linkage between compositional effects and functional products. Studies comparing the modified forms of KD (e.g., fiber-supplemented KD, Mediterranean KD) will be able to identify the formulations that retain metabolic advantages yet retain microbiome diversity. Controlled interventions of particular population groups (obesity, type 2 diabetes, epilepsy, IBD) would determine whether changes in the microbiome are a source of therapeutic effects or a predictor of treatment response. Lastly, mechanistic research

on host microbe interactions during ketosis such as impacts on gut barrier properties, immune cell fitness, and metabolite signaling would help further investigate the systemic effects of KD.

Conclusion

This research paper has shown that the 8-week ketogenic diet does cause significant, systematic changes in the microbiota of the gut in healthy Central Indian adults. Among the major changes, there are decreased alpha diversity, increased Firmicutes/Bacteroidetes ratio, selective enrichment of Akkermansiamuciniphila and Parabacteroides, and loss of carbohydrate-fermenting taxa such as Prevotella, Faecalibacterium, and Bifidobacterium. These changes are related to dietary compliance and levels of ketosis implying dose-related effects.

Although enrichment of some beneficial microbes such as Akkermansia can be beneficial in the metabolesis of KD, it is equally true that the associated decrease in microbial diversity and health promoting taxa creates issues when it comes to implementing it in the long term. The scale of change witnessed among the cohort of Indians, specifically an increase in F/B ratio is greater than the changes in Western populations, which underscores the need to conduct microbiome studies unique to populations.

These results make a new contribution to the study of the gut microbiome response to ketogenic dieting in a non-Western setting with unique backgrounds in diet. They highlight the importance of paying close attention to monitoring, possible intervention action plan (fiber or probiotic supplementation), and more personalized interventions to improve both metabolic and gut ecosystem performance during ketogenic dietary interventions.

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Conflicts of interest

There are no conflicts of interest.

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