



JOURNAL ON COMMUNICATIONS

ISSN:1000-436X

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The Gendered Gut: Women's Historical Food Practices and the Technological Revolution in Microbiome Nutrition

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Abstract

The human microbiome of the gut has become one of the most important players in the regulation of metabolic, immune, and nutritional processes, with a wealth of studies showing how dietary intake influences microbial communities within the body. Traditional diets based on foods gathered, prepared, and fermented by women could be one explanation for the diversity of the ancestral human microbiome. Conventional fermented foods and plant-centric diets ensured that individuals were constantly exposed to microbes and their metabolic products, including short chain fatty acids, which are crucial for intestinal and immunological homeostasis. Modern research in microbiome biology, however, has added to this knowledge base the idea of the “microgenderome” to emphasize the importance of biological sex and diet-specific behaviour influenced by gender in the development of microbiology. At the same time, innovations such as shotgun metagenomics, multi-omics and machine learning-driven precision nutrition modeling have transformed studies on diet-microbiome relationships. Nevertheless, there still exists several difficulties in terms of methodology, such as high-dimensional computational noise, overfitting in machine learning models, insufficient validation by mechanisms, as well as severe population biases favouring the Western industrialized populations. This review attempts to critically analyse the connection between the traditional dietary behaviours of females and the development of their gut microbiota, as well as the use of novel technological solutions in precision nutrition.

Key words: Gut microbiome, Women’s food practices, Traditional diets, Fermented foods, Precision nutrition.

Introduction

The human gut microbiota has been recognized as a key determinant of metabolic, immune, and nutritional balance, thereby defining human beings as superorganisms, which consist of both the host as well as the microbiota [1]. Trillions of microorganisms existing in the gut help with digestive processes, production of vitamins, and maintenance of the intestinal barrier function. Evidence is accumulating to demonstrate that changes in the microbial makeup, known as dysbiosis, have been linked with obesity, inflammation, metabolic syndrome, and neuropsychiatric conditions [2]. On the other hand, the shift from fibre-rich ancestral diets to processed foods has played an instrumental role in bringing about a significant reduction in microbial diversity and metabolism within humans [2,3]. Traditionally, the food habits of people depended on the sex-specific labour division, especially in the earlier stages of human civilization when women were responsible regarding the collection of plants, cooking, and fermentation of foods [4,5]. The consumption of traditional fermented foods made from cereals, milk, and vegetables provided humans with a healthy microbial exposure, as well as other beneficial metabolites such as short chain fatty acids (SCFAs) [6]. Thus, such food processing techniques in the home could well have been instrumental in establishing ancestral microbial ecology over many generations. The notion of the “microgenderome” which has gained more attention in recent times is an example where sex and gender differences in diet may affect gut microbiota [7]. The new technologies, especially the emergence of shotgun metagenomics, multi-omics analysis, and machine learning precision nutrition models, have transformed research on the diet-microbiota interaction [5]. These tools have made it possible for researchers to analyse microbiota taxonomy and function, as well as dietary-specific microbes, more precisely than ever before. But there are still serious challenges, including population bias towards Western populations, noisy computation associated with high dimensionality, and lack of mechanism for microbial interactions seen. This review attempts to discuss the relationship among women’s traditional food habits, microbial evolutionary patterns, and the new technological tools being applied to precision nutrition. Though there is increasing literature available on gut microbiota, fermented foods, and precision nutrition, all these topics have been explored individually. This review brings an interdisciplinary approach into consideration by incorporating food practices of women from the past with contemporary scientific approaches such as that of the microgenderome. Unlike the hypothesis generation in previous work, which proposes clear cause-and-effect relations, this review highlights current literature, reveals knowledge gaps,

and suggests that current technologies such as shotgun metagenomics, multi-omics, and machine learning could assist in further exploration of these theories.

Deconstructing the “Historical” Baseline: Fermentation and Dietary Ratios:

Studies from anthropologists and nutritionists have indicated that the dietary intake of our ancestors was far more varied and fibrous in comparison to contemporary industrialized food habits. The hunter-gatherer tribes depended largely on wild greens, tubers, nuts, fruits, and naturally occurring fermentable sources, which could contribute complex polysaccharides for microbial development in the gut environment [3,4]. In these communities, women played a vital role in the collection of edible plants and the processing of food at home, thus affecting dietary quality and the exposure to microorganisms [4]. The shift from the forager mode to agricultural practices made the consumption of domestic crops, pulses, and fermented foods even more important [8]. Fermentation of food was one of the early uses of biotechnology by man and became crucial for establishing microbial ecology (Figure 1). Due to the fermentation process using milk products, grains, vegetables, and legumes, there was a rise in the number of lactic acid bacteria, which led to better food preservation and increased nutrient absorption and utilization [6,8]. Furthermore, fermented food is also part of the production process of short-chain fatty acids, such as acetate, propionate, and butyrate. These SCFAs are vital for gut barrier integrity and control of inflammation and metabolism in the body [9]. Microbial metabolic products are now considered crucial components that link dietary habits and metabolic health. It is worth noting that a lot of the fermentation and food processing activities performed by humans had their roots in the domestic labor practices of females in various societies in history. Fermentation of curds, cereals, vegetables, and the diet of mothers might have resulted in repeated transfer of beneficial microorganisms across successive generations. It is, however, difficult to understand the microbial composition of ancestral foods. The research into the human microbiome makes heavy use of contemporary hunter-gatherers as proxies for the past, even though there is significant divergence between the two in terms of environmental influence, antibiotics, and sanitation. This must be considered when drawing correlations between ancient practices regarding food preparation and consumption by women with modern-day microbiology. This modern environment of industrial food production has brought about even greater complexity to these evolutionary associations. Consumption of ultra-processed food high in refined sugar content, saturated fats, and preservatives has been linked to low microbial diversity and microbial metabolism [2]. At the same time, decreased consumption of naturally fermented food products and

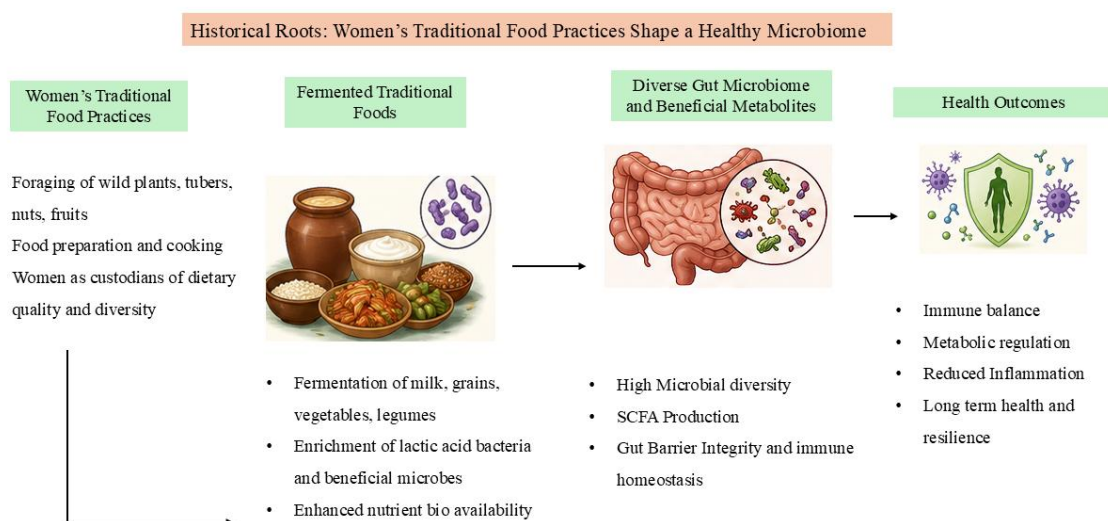
environmental microbes might also lead to an increase in the number of diseases caused by dysbiosis, such as obesity, inflammation, and metabolic syndrome [3]. Based on these facts, it can be maintained that ancient nutrition systems established by women can help understand how to preserve and use microbiomes for future interventions.

The “Microgenderome”: Biological Reality or Confounding Variable?

Due to recent discoveries in the field of microbiomes, the notion has been emerging that there is a strong likelihood that biological sex plays a vital role in determining the composition and metabolism of the gut microbiome, resulting in the introduction of the idea of microgenderome [10]. It is known that males and females are distinguished by several differences associated with their microbiome, which are more noticeable post-puberty, and such differences appear to be due to the action of hormones on microbes [11]. Oestrogen and testosterone are considered to indirectly affect the distribution of microbes through their ability to influence immune signalling, bile acid metabolism, and gut physiology [10,11]. Animal model experiments also prove the existence of hormonal-gut microbiome interaction. For instance, mice experiments that involved castration proved to produce significant changes in gut microbiome composition and bile acid synthesis, changes which can partly be restored through hormonal treatment [12]. Furthermore, transplantation of the microbiota from males into germ-free females leads to metabolic and immunological alterations, indicating that the microorganisms may play a role in determining sex differences in physiology [13]. Such results prove that, besides being a passive bacterial community, the gut microbiome is also an endocrine-related system able to interact with hormones in the body. In addition to metabolic function, growing evidence points towards the impact of biological sex, hormones, immune function, diet, and environment on the composition of the gut microbiota. Nevertheless, quantifying the contribution of each determinant is difficult due to the interaction between these factors and differences among study samples. Many studies have documented the link between the gut microbiome and illnesses such as auto-immune diseases, depression, obesity, and schizophrenia in women; however, much of the evidence presented is purely observational in nature and cannot be considered a causal relationship [13-15]. Thus, there is a need for further studies to better understand the role of these variables in influencing female gut microbiome composition. Despite this evidence, however, methodological weaknesses in the field of study have continued to hinder understanding of the microgenderome paradigm. Studies involving human populations have tended to be based on cross-sectional designs that do not properly address various confounding factors like dietary habits, social environment,

medication use, and antibiotic use. Separating out the influence of biological sex from gender-based behavioural influences is especially difficult in nutrition microbiome studies. However, diets, cultural eating patterns, stress levels, and availability of health services may also differ between the two sexes, thus posing a risk of independent influence on microbial profiles aside from hormonal regulation. Therefore, despite the biological plausibility of the idea of microgenderome, extensive longitudinal and multiracial studies will need to be conducted to determine whether the microbiological variations seen are primarily a result of hormone levels or gender-specific behaviours. In addition to this, even though many investigations have identified correlations between the gut microbiota composition and biological sex, diet, and health status, these relationships are not always reproducible among various populations. Factors such as differences in methodology, sampling sizes, dietary practices, medication intake, geographical location, analysis techniques, and many more cause great variability, preventing the discovery of universal microbiome profiles. Thus, all the current results should be viewed with caution, and further longitudinal investigations among varied populations are necessary. Moreover, the sexual dimorphism among microbes is not limited only to the gut microbiota but also to the reproductive tract microbiome of females. The latter has significant importance for female reproduction and immune defence, besides its significance in the transfer of maternal and fetal microbes [16,17]. Both gut and reproductive tract alterations in microbiome composition have been shown to be associated with metabolic disorders and inflammation due to obesity, implying an even wider impact of interactions between hosts and their microbiomes on females [18]. Historical diet behavior and sexual distinctions are key aspects from both biological and cultural perspectives in order to understand gut microflora; however, analysis of such complicated processes is possible with the help of novel techniques. Modern developments in the areas of shotgun metagenomics, multi-omics, and machine learning create new chances to study the effects of historical diet behavior, fermentation and sex-specific diets on microflora.

Figure 1. Conceptual framework illustrating the relationship between traditional women-associated food practices, including plant collection, food preparation, and fermentation, and their potential influence on dietary fibre intake, microbial exposure, short-chain fatty acid (SCFA) production, gut barrier integrity, immune regulation, and metabolic homeostasis. The figure summarizes proposed mechanisms discussed in this review and should be interpreted as a conceptual model rather than direct causal evidence.



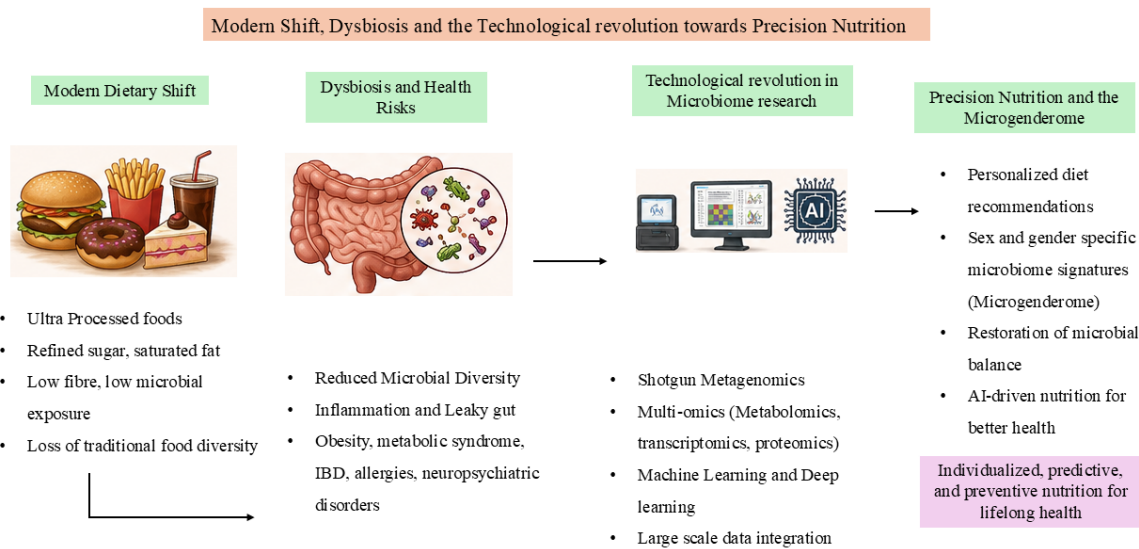
As illustrated in Figure 1, traditional dietary practices may influence host health through multiple interconnected mechanisms involving microbial exposure, dietary fibre fermentation, SCFA production, and host metabolic responses.

Technological Bottlenecks: Metagenomics and Machine Learning

The shift from 16S rRNA gene sequencing to more advanced next generation sequencing approaches, especially shotgun metagenomics, has revolutionized microbiome studies by making it possible to analyze not only the taxonomic make-up but also the functional potential of the microbiome [19,20]. While 16S rRNA sequencing offers information about taxonomy only, shotgun metagenomics allows to identify about the microbial genes and their functional roles [21]. This is particularly critical in examining the historical dietary patterns since the functional attributes of microbes rather than their taxonomic classification play a role in the metabolic effects of foods with high levels of fiber and fermentation. Thus, through the advances in DNA sequencing, it becomes possible to test historical dietary hypothesis through the examination of traditional food preparation practices in light of the metabolic roles of microbes. The incorporation of multi-omics technology into microbiome research has enabled increased scope of analysis in the field. Alongside metagenomics, metabolomics, transcriptomics, and proteomics can help to explore functional pathways of microorganisms and host-microbiome interaction mechanisms [19]. More advanced methodologies are also available for assessing an individual's nutritional intake by analysing the DNA remnants of consumed foods in stool samples, which serves as an alternative to the

subjective and error-prone food frequency questionnaires commonly used [22]. This advancement has greatly benefitted the emerging concept of precision nutrition through enhanced capabilities for correlating diet with microbial metabolism. On the other hand, Machine Learning (ML) algorithms have become necessary tools for the evaluation of the high levels of complexity associated with microbiome-related data (Figure 2). Various models such as Random Forests, Support Vector Machines (SVM), and classifiers using neural networks are being utilized in the identification of diseases, predicting the body's reaction to certain diets, and in personalized nutrition [23,24]. Such computational methods attempt to find the microbial markers responsible for obesity, heart-related diseases, inflammatory conditions, and metabolic syndromes. With the incorporation of microbial composition along with diet and clinical information, ML methods could be used to provide personalized nutrition. However, there are still many obstacles that prevent microbiome research from being used in practical applications within clinical practice and nutrition. Microbiome data have a high dimensionality, sparsity, and noise, which makes feature selection and results reproducibility a problem [24]. Curse of dimensionality means that the number of microbe parameters far outweighs the sample size. Moreover, the absence of standardized procedures for sampling, DNA extraction, sequencing technologies, bioinformatics analysis and dietary intake assessments adds to the variability [25]. Different methodologies and different reference datasets are some of the factors that make comparison between the independent studies difficult. Another major problem associated with the use of machine learning is the lack of equal distribution in terms of population data on the microbiome, since samples from Western industrialized countries are much more represented than diets of traditional population from South Asia, Africa, Latin America and other regions [6]. Consequently, most predictive machine learning models might not be able to correctly characterize the intricacies of interactions between the diet and microbiome of people outside Western societies. Therefore, future studies on microbiomes need to involve a greater variety of subjects and employ computational approaches as well as methods for validating mechanisms.

Figure 2. Conceptual overview of how modern microbiome technologies, including shotgun metagenomics, multi-omics, and machine learning, can be integrated to investigate diet-microbiome interactions and support precision nutrition. The framework highlights technological applications for analysing microbial composition, functional pathways, dietary signatures, and personalized nutritional interventions.



As illustrated in Figure 2, it summarizes how contemporary sequencing technologies and computational approaches can be used to evaluate historical dietary hypotheses and translate microbiome data into precision nutrition strategies.

Conclusion:

The existing evidence indicates that the historically women-oriented tradition of eating plant-based diets and fermenting foods might have been an important factor in the creation of diets favoring diverse gut microbiota. But, the link between historically known practices and the composition of the ancestors microbiomes lacks direct evidence, and many of the assumptions should be regarded as believable hypotheses. The development of modern technologies such as shotgun metagenomics, multi-omics, and machine learning can be considered a great chance to test the hypothesis with the help of dietary, microbiome, and functional data. Currently, there is enough scientific literature proving the link between diet and gut microbiota. Future directions of research should thus aim at studies involving longitudinal cohort design using varied samples, validation techniques, and application of computational biology to different diets. Knowledge of the relationship between the history of foods used by different populations and their metabolism is likely to offer great information that can help create effective and scientifically informed nutrition solutions.

ACKNOWLEDGMENT

We thank the Department of Science and Technology, Government of India, for providing support through the Fund for Improvement of S&T Infrastructure in Universities and Higher Educational Institutions (FIST) program (Grant No. SR/FIST/College-/2020/943):

CONFLICTS OF INTEREST/COMPETING INTERESTS

No Conflict of Interest

ETHICS APPROVAL

Not applicable

CONSENT TO PARTICIPATE

Not applicable

WRITTEN CONSENT FOR PUBLICATION

Not applicable

AVAILABILITY OF DATA AND MATERIAL

Not applicable

CODE AVAILABILITY

Not applicable

AUTHOR CONTRIBUTION

PR- Conception, writing original draft; PV- Reviewing and Editing Manuscript; ML-Reviewing and Editing Manuscript

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