



Microbiome Conflict: From the Food Chain to the Host Gut

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ABSTRACT

The process of food fermentation has improved the safety qualities of raw materials and produced novel foods with improved organoleptic properties. The scientific community has taken notice of the empirical finding that certain items might have a health benefit. To determine which of these compounds might be effective against particular diseases, several researches have been carried out in both animal and human hosts. Despite the growing body of research, regulatory agencies have only approved a relatively small number of items as functional meals. This problem may be greatly exacerbated by inconsistent data and a lack of thorough preclinical characterization of functional products. The improved accessibility of omics platforms and bioinformatics methods for thorough data analysis nowadays can help with the systematic investigation of microbe-microbe, microbe-matrix, and microbe-host interactions and offer insightful information about maximizing their positive impacts. Food science still has difficulties integrating these platforms, but with concerted efforts and cross-disciplinary cooperation, a new age in the discipline might be on the horizon.

Keywords: Probiotics, *Lactobacilli*, Fermentation, Functional foods, Multi-Omics

INTRODUCTION

The development of fermented foods and their occupational uses

The idea of fermented meals dates back to the days when our forefathers were attempting to extend the shelf life of raw ingredients and enhance their safety. As they provide a hostile environment for disease proliferation and can preserve their quality attributes at room temperature, fermented foods and beverages are in fact more resistant to deterioration. Therefore, fermentation is a type of bio-preservation. Notably, fermentation techniques were developed on every continent. The production of fermented foods from meat, wheat, and dairy using lactic acid bacteria, moulds, and yeasts was primarily practiced in Europe, Australia, and North and South America, while root vegetables and milk were primarily consumed on the African continent. For the production of alcoholic beverages like sake and fish sauce, ancient populations in Asia used vegetables, soybeans, grains, and fish as substrates. Although raw material preservation is already a thing of the past thanks to modern science, fermented foods are nevertheless religiously consumed. There are two reasons for the increased attraction of fermented foods. Intake of these foodstuffs has been intuitively related to consumers' wellbeing. First, raw material fermentation can provide unique textures and aromas that add to the hedonistic value of food.

Functional foods or nutraceuticals are terms used to describe fermented foods that are believed to have health benefits for the consumer. These meals may either include probiotic microbes or have been fortified with vitamins and bioactive substances like phytochemicals. Because health and disease prevention are becoming increasingly popular in Westernized nations, consumer interest in these products has sharply increased in recent years. Studies on the impact of functional foods on animal and human health, however, are scarce, frequently unclear, and occasionally even inconsistent. Because of this, regulatory frameworks have placed tight regulations about which products can bear this mark. In order to regulate the expanding market demands and safeguard consumers from fraud, Japan was the first nation to put legal frameworks in place in 1991. As a result, the sale of functional foods in Japan now requires the "Food for Specified Health Uses" (FOSHU) approval, which is granted by the Japanese Ministry of Health, Labor, and Welfare. 1071 items were granted FOSHU approval in 2020. However, the European Food Safety Authority has only approved a far smaller number of functional foods in Europe.

From this vantage point, we will critically examine the current state of fermented functional food products and offer fresh perspectives for a thorough assessment of their potential health advantages for consumers. The ability to systematically analyse the composition and functional characteristics of fermented goods as well as their impact on customers has been made possible by recent advancements in omics and their expanded accessibility. Their inclusion in research on food science, however, is still difficult.

The fermentation process, deconstructed

A material decomposes into a simpler substance during the fermentation process. More specifically, fermentation is a type of anaerobic metabolism that occurs when the temperature and pH are just right, without the presence of molecular oxygen. Complex carbohydrates, which are found in meat, grains, legumes, fish, vegetables, and fruits and can be broken down to create alcohols, carbon dioxide, ammonia, fatty acids, and other chemicals, are the substrates for these reactions. Autochthonous or allochthonous bacteria and fungi that can use raw materials as energy sources are typically the catalysts of these processes. Typically, consortia of microbes, known as starting cultures, are introduced specifically in particular raw materials. Numerous bioactive substances found in fermentation byproducts improve the foods' nutritive and functional profiles. In preclinical studies, lactis was found to lower obesity-related biomarkers. Active phenolic compounds and antibacterial chemicals like bacteriocins are two other compounds of interest. Exopolysaccharides, short chain fatty acids, and vitamins can all be made by lab. However, it's important to keep in mind that these substances are typically present in trace amounts, making it challenging to predict whether healthy populations will benefit from them. Phytic acid, a metal-chelating chemical that functions as an anti-nutrient, is one hazardous substance that bacteria may metabolize and inactivate, which is another significant component of fermentation. The composition of the microbial population is crucial because these chemicals may be created through chain reactions in which multiple bacterial or fungal species take part.

A stable, yet dynamic, microbial ecosystem can be found in fermented foods

Due to the presence of stable populations, the microbial ecology of fermented goods is rich. The stability of its composition must be guaranteed during production and storage since the influence of this microbial fingerprint on the organoleptic and functional aspects of the products is crucial. Additionally, regulatory agencies require the stability of populations as a safety requirement for novel functional items. Organoleptic properties may change or even spoil as a result of changes in these dynamics or the development of alien species. In fact, unstable ecological dynamics may result in the extinction of other populations in favour of the growth of productive lineages. The phrase "food microbiome" refers to the homeostatic makeup of these food matrices. Conventional culture-based techniques can be used to study the organization of these groups. However, the development of next-generation sequencing tools has made this process simpler and given researchers the chance to investigate uncultivable strains as they are being produced and stored. Recent evidence suggests that next-generation sequencing platforms may be more effective than traditional methods in this setting for identifying rotting bacteria.

Probiotics are live bacteria that can enter the intestine and benefit the host when given in adequate amounts. Some inhabitants of the food microbiome fall under this category. WHO first recommended the definition, which Hill later revised? Consuming probiotics may alter the host's immune system or gut microbiome, and various studies suggest that they may have beneficial benefits on digestion, nutrient absorption, and allergy avoidance in people who are more vulnerable to developing allergies. Probiotics are typically isolated from dairy or non-dairy food products, as well as from human or animal interior cavities.

Probiotics have been domesticated in particular food matrices due to their long history of usage in fermentation. On that basis, because of their increased genetic variety, lactobacilli can adapt to a wide range of environmental niches. Based on their ability to ferment substances, lactobacilli species can be classified as facultative, obligatory heterofermentative, or obligate homofermentative. Their ability to use amino acids from the environment and preferred carbohydrate pathways.

primarily hexose are the basis for this differentiation. What happens, though, when we attempt to introduce a new strain of interest in well-established food microbiomes? This subject is extremely pertinent to the functional food sector.

Conflict between microbiomes

When consuming fermented goods, the host microbiomes known unknown" microbiome interacts with the microbiome of the food matrix. The interactions that follow are really interesting, but we might not be able to fully grasp their scope. Due to its tremendous complexity and host specificity, the gut microbiota cannot be completely recreated in vitro. As a result, it is challenging to model something we are unfamiliar with. More levels of complexity are added by the host's genetics, way of life, ethnicity, age, and pathophysiology, all of which can have a significant impact on the composition and function of the microbiome. To examine the evolutionary connections and dynamics among microbiome inhabitants, some crude models have already been developed. To investigate evolution following mice's mono- or co-colonization with other microbes, Baroso-Batista developed a mouse model. It was demonstrated that the evolutionary patterns varied depending on the situation and that particular genes and metabolic pathways were chosen to facilitate the adaption. These investigations could aid in our comprehension and forecasting of the phenotypic changes that an eaten strain might experience as it moves from the microbial communities of food to those of the gut. Host characteristics can impact ecological interactions in the same situation. It was demonstrated, more particularly, that younger mice applied different evolutionary pressures to the strains than their more senior counterparts.

These investigations demonstrate that a variety of environmental parameters that affect the metabolic characteristics of newcomer strains and consequently modify their activity in this new environment are necessary for the integration of external strains into a microbiome niche. Importantly, computational methods have been created for the spatiotemporal investigation of these interactions, assisting in the comprehension of the complex interactions occurring in complex microbial communities and creating an ideal environment for interdisciplinary cooperation.

Beginning of a new era

The study of microbial consortia, regardless of their origin, has benefited from the meticulous characterization of the gut microbiome during the past few decades and the thorough exploration of its structure and function as well as its impact on the host. The development of next-generation sequencing technology and the introduction of effective computational pipelines to evalu-

-atethe obtained data allowed for the study of the human microbiome. Due to growing consumer demand, there are now an exponentially growing number of fermented products on the market. Even though these items have been empirically used for their purported health-promoting characteristics, clinical claims about functional foods are rarely made. This phenomenon is significantly influenced by data disparity and the inability of preclinical discoveries to be translated to the clinic. Indeed, results about the impact of certain probiotics or their bioactive metabolites should be cautiously interpreted and verified in animal models and in human volunteers because preclinical studies that use cellular models do not account for the biological complexity of the organisms. For instance, in vitro studies of intestinal colonization fall short because they do not account for how the probiotic strain interacts with the host's immune system and commensal bacteria in the gut.

The joint activity of many strains is rarely investigated in vitro, which has an important impact on how well the mechanism of action of multispecies supplementation is understood before it is used in clinical investigations. Concerning animal studies, the mouse gut microbiota's structural variations and lack of the degree of variety seen in human hosts could both result in artifacts, underscoring the need for more reliable models. Additionally, because single strains or strains given as supplements are typically used in mechanistic investigations in animal models, the impact of the food matrix itself is disregarded.

Last but not least, preclinical testing is frequently skipped, leading to the testing in clinical trials of numerous new functional items including single or multi-strain consortia without prior knowledge of their mode of action. This method gives the impression that strains are chosen at random to provide positive results. The analytical rigour of the studies could also be seriously compromised by other methodological problems with the measurement of outcomes, such as qualitative parameters or self-reported outcomes. Met-analyses could solve this issue, but because there are typically only a few studies with the same experimental setup that are available, conducting met-analyses can be problematic.

CONCLUSION

Consumers prefer functional items because of their improved organoleptic qualities and potential health advantages. There is still limited transferability of research findings in the clinical setting despite the abundance of in vitro and in vivo data on their health-promoting characteristics that is currently available. The inconsistency of the clinical data that now supports the beneficial effects of these products also emphasises the need for greater research on their biological effects. In line with this, characterization of bioactive substances and metabolic byproducts found in the food matrix may reveal their biological potential and encourage tailored supplementation. In order to identify antagonistic connections and trophic networks produced by strains and open the door to more effective therapies, the study of population dynamics—the interaction between probiotic microbes, hosts, and food microbiome—is crucial. The achievement of this goal may be aided by the use of multi-omics platforms, the relevant interpretation of clinical data derived from high-quality studies, and appropriate outcome measurements.