Sustainable Food Technology

ROYAL SOCIETY OF CHEMISTRY

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From waste to resource: microbial pathways for sustainable food production

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Despite the increasing global production of food, a significant proportion is wasted, leading to severe environmental harm, economic losses, and exacerbated social inequalities. Food waste occurs at every stage of the food supply chain, from agricultural production to household consumption and has emerged as a critical challenge in achieving sustainability and effective resource management. In this context, understanding the role of microbial ecosystems in the degradation, transformation, and valorization of food waste has become increasingly important. The benefits and advantages of using microorganisms in food production are covered in this review. Both humans and animals can receive nutrients directly from microbes, which can be utilised as substitute food sources. Furthermore, bacteria facilitate crop yield and agri-food production with greater flexibility and diversity. In order to support plant growth, microbes serve as natural nitrogen fixators, mineral solubilizers, nano-mineral synthesisers, and inducers of plant growth regulators. In addition, they are active organisms that break down organic compounds, remove pollutants and heavy metals from soils, and act as soil-water binders. Furthermore, microorganisms living in the rhizosphere of plants release biochemicals that are safe for both the environment and the host. These biochemicals can be used as biocides to manage illnesses, infections, and pests in agriculture. Thus, the utilisation of microorganisms for sustainable food production should be taken into account.

Sustainability spotlight

Transforming waste into valuable resources is a cornerstone of sustainable development. This work highlights the pivotal role of microbial ecosystems in converting food waste and by-products into essential components for sustainable food production. By leveraging microbial pathways, this approach not only minimizes environmental impact but also enhances resource efficiency, supports circular food systems, and contributes to global food security. The integration of microbial technologies paves the way for innovative, eco-friendly solutions that reduce waste, conserve natural resources, and promote a resilient and sustainable food future.

1. Introduction

The world's population has risen to over 78 billion people, and by 2023, 2037, and 2057, it is predicted to reach 80, 90, and 100 billion people, respectively.[1,2] In their quest for more food, people are clearing forests to acquire more farmland, which inadvertently impacts the agricultural and food supply production by exacerbating climate change.[3] The world's food and climate crises are made worse by the growing demand for meats, which in particular speeds up the consumption of grains and the generation of greenhouse gases by animals, such as carbon dioxide and methane. Finding sustainable and alternate sources of nutrient-dense food is necessary to end this vicious cycle.[4] The sustainable food supply of the future will rely on microorganisms. Microorganisms double their biomass far faster than mammals and plants, with doubling times as short as tens of minutes. For instance, *Saccharomyces cerevisiae* takes 90 minutes, while *Escherichia coli* and *Bacillus subtilis* take roughly 20–30 minutes.[5] Furthermore, compared with crop/livestock farming, microorganism culture uses less water and land and emits less carbon dioxide and other greenhouse gases per unit of biomass produced. Furthermore, the biomass of many microorganisms is nutritionally equivalent to or superior to various meats due to its high protein content (up to 70% of the dry cell weight), vitamins, antioxidants, and bioactive substances.[6,7] The microbial system includes different bacteria, fungi, archaea and microorganisms that support natural decomposition and convert food waste into compost, biofuels, bioplastics and biofertilizers.[8] Bacteria and fungi in organic waste are adapted to break down carbohydrates, proteins, lipids and lignocellulose in food waste.[9] How biodegradation

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proceeds and converts pollutants partly depends on the synergy and competition among microbes, the availability of nutrients, and environmental factors such as temperature, pH and moisture.[10] Microbes can manage waste degradation even where there is no oxygen, so waste can be treated with composting, anaerobic digestion and bioelectrochemical technologies. From a systems biology perspective, microbial ecosystems present in food waste are very active in metabolism, genetic mixing and chemical solutions, which encourages studies focused on using them to better manage waste sustainably.[11] Additionally, modern techniques such as metagenomics, transcriptomics, proteomics and metabolomics have revealed the microbial manufacturing centers responsible for the mechanisms that govern manage waste transformation.[12] In addition, connecting synthetic biology and microbial engineering has allowed the creation of microorganisms or groups of microorganisms that can break down given contaminants or produce desired substances efficiently.[13] Because many nations are tightening their laws on waste and greenhouse gas emissions, there is an increasing focus on using microbial technologies that are in line with the principles of circular bioeconomy.[14] When compared with waste landfilling or burning, it is better to use a microbial system that is cheaper and more easily adjustable.[8] Besides protecting nature and conserving resources, using microbes to manage food waste contributes to food security by returning nutrients and enriching the soil, thereby completing the cycle from food production to waste.[15] Based on this, the current study is focused on developing an approach for the sustainable conversion of waste into useful products using microbes. In addition, this study discusses and highlights various microbial pathways for sustainable food production.

2. Limitations and challenges of microbial consortia in traditional practices

Conventional microbial methods for food waste management, which are dependent on naturally occurring microbial populations, face numerous constraints that impede effective food waste processing. A significant difficulty is the insufficient metabolic diversity within these communities, which restricts their capacity to digest complex organic compounds, such as lignocellulose and lignin.[16] These fibrous compounds exhibit resistance to microbial degradation, especially under conventional conditions, and typically require specialised microbial consortia for successful decomposition.[17] Moreover, natural microbial populations may exhibit sensitivity to variations in environmental parameters, including pH, temperature, and moisture levels.[18] In FW situations, these variables can fluctuate significantly, hindering unenhanced microbial populations from maintaining effective degradation rates.[19] This diversity may result in protracted decomposition, offensive odours, and potential hazards from infections if conditions permit their proliferation. Moreover, indigenous microbes are not consistently capable of neutralising pathogens or poisons found in FW.[20] In the absence of regulated settings and specific microbial varieties, the hazards posed by pathogens may persist, thereby restricting the safety and agricultural efficacy of the composted material. AD, another prevalent FW management method, encounters constraints with natural microbial populations. The methanogenesis phase, responsible for methane production, frequently constitutes the rate-limiting step, as indigenous bacteria may be deficient in effective methanogens or a well-balanced microbial community to maximise methane output.[21] The effective management of food waste presents a significant challenge, as conventional composting and recycling techniques are increasingly inadequate for handling substantial amounts produced globally.[22] Engineered microbial solutions offer a novel method for improving the biodegradation rate of organic waste and tackling scaling challenges in food waste management systems. Metabolic engineering and synthetic biology enable the construction of microbial consortia to enhance the decomposition of lignocellulosic and other intricate organic compounds included in food waste, resulting in accelerated biomass degradation and diminished byproduct accumulation. This method not only reduces greenhouse gases, specifically methane and carbon dioxide but also produces important byproducts, such as biogas and nutrient-rich fertilisers, which can enhance bioenergy generation and soil vitality. Engineered microorganisms can be refined to operate effectively under many environmental circumstances, enabling them to treat multiple organic waste streams with minimal intervention. This customisation facilitates a continuous, high-capacity waste management process that is scalable to diverse operational sizes, ranging from local to industrial levels. The incorporation of these microbial solutions into current waste treatment systems can diminish the need for substantial physical enhancements, rendering these biotechnological approaches economically and logistically feasible. The scalability of engineered microbial solutions offers substantial progress in diverting food waste from landfills, facilitating the shift towards a sustainable and circular bioeconomy while mitigating the ecological consequences of food waste disposal.

3. Sources and classification of food waste

Food waste is a critical global problem, involving the loss or disposal of food that is safe to be consumed but is discarded along the food supply chain, including production, post-harvest processing, processing, distribution, retailing, and consumption.[23] Food waste sources can be categorized into three broad groups, namely, agricultural production, food processing and manufacturing and the consumption phase at households and food service industries. Food waste in the agricultural industry comes about as a result of inefficient harvesting methods and pests, climatic factors, and non-commercial aesthetic standards of crops that have not been accepted into commerce because of size, shape or color.[24] Poor storage facilities, infrastructure, poor transportation networks, and poor preservation facilities in developing nations also contribute to post-harvest losses, with the supply chain in developing countries prone to being fragmented and inefficient.[25]

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Food processing and manufacturing: wastes are made through cutting, peeling, oversupply, and ruinage during processing, and through food that cannot pass quality control criteria. Furthermore, factories can end up throwing away quite large quantities of by-products, including peels, husks, and seeds, which could be valuable, but they are frequently unused efficiently. At the distribution and retail level, food waste is largely motivated by logistical wastefulness, food overstock, poor handling, wrong packing and high aesthetic requirements that result in edible but cosmetically pristine food being thrown away. Supermarkets and grocery stores commonly discard food that is just shy of their so-called indicator dates, such as best-before or sell-by dates, which may have nothing to do with edibility. Finally, improper storage, misinterpretation of food labels, over-prioritizing, overcooking and failure to take advantage of the leftover food, especially in high-income countries where food is relatively cheap and in abundance at the consumer level, contribute to waste.[24] Restaurants, cafeterias, and catering services are a part of the food industry that also results in significant food waste by producing too much food, inefficient portion sizes, and customer demand estimations. This food waste may be categorized as avoidable or may avoid food waste and waste that is impossible to avoid. Avoidable waste of food is food that used to be edible but was nevertheless discarded, including uneaten meals, expired products, and leftovers. It is also conceivable that food waste can be avoided, such as items that some individuals may eat and others may not, such as bread crusts or potato skins. Unavoidable food waste refers to those parts of foods that people do not traditionally eat, like eggshells, banana peels, bones, and ground coffee, and some of them can be valorized as bioenergy or composted.[26] Food waste may also be categorized based on its biodegradability and composition, *e.g.*, in fruit and vegetable waste, meat and fish waste, cereal and grain waste and dairy waste, with each having different properties, influencing their treatment and possibly recycling or energy recovery. Additionally, food waste may be identified in terms of origin: whether it is pre-consumer waste, which happens before the consumer interacts with the food, or post-consumer waste, which also happens beyond the point of purchase, *i.e.*, after the food is purchased and when it is consumed.[27] Pre-consumed wastes, such as agricultural wastes and on-farm processing wastes, form potential reusable industrial processes or animal feeds, while post-consumer wastes usually offer challenging processes because they are contaminated and mixed food items.[28] Food scraps can also be categorized based on their physical properties as solid or liquid, where liquid food scraps contain food scraps, such as soups, sauces, and milk residuals,

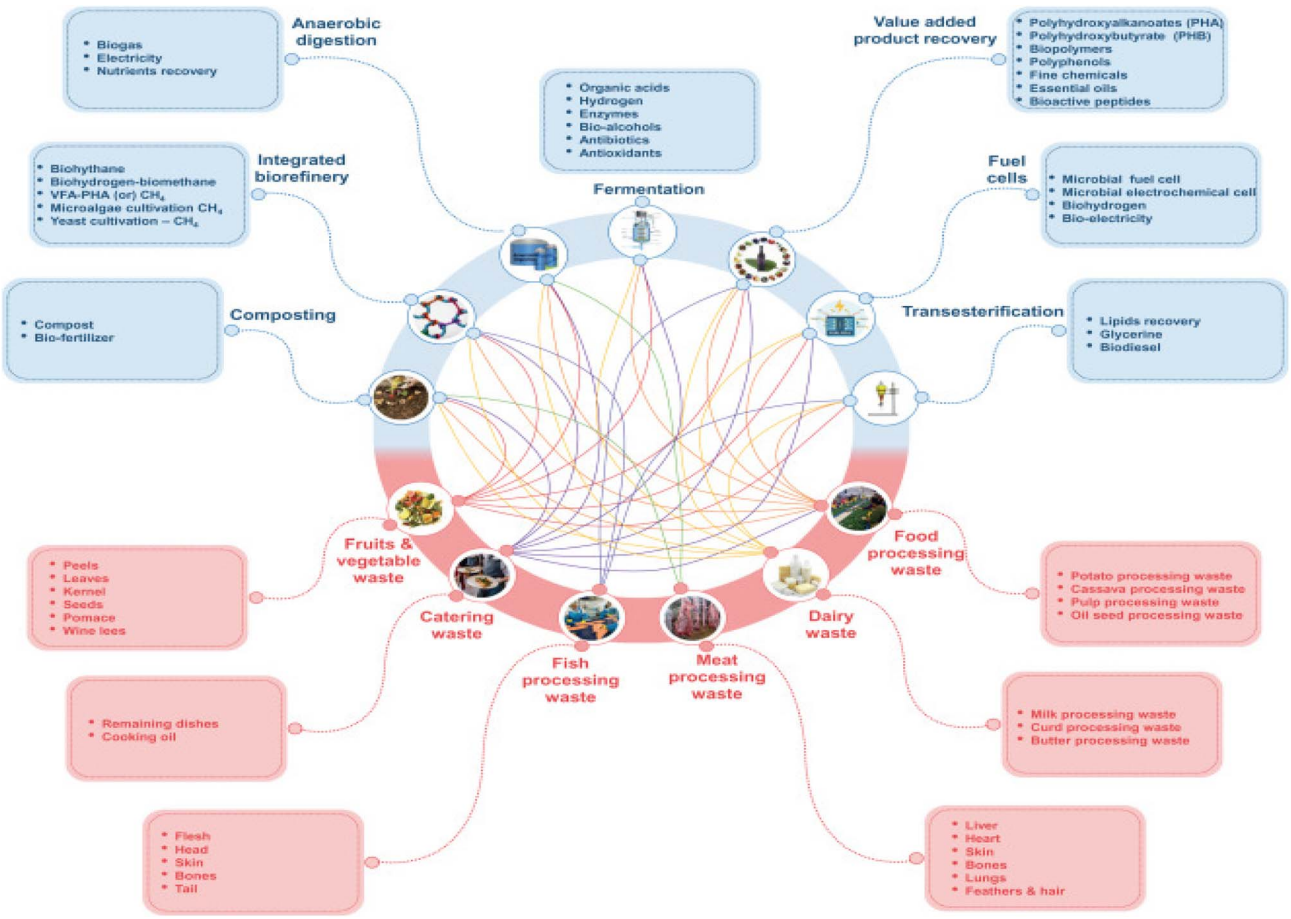

Fig. 1 Routes and sources of food waste.[30]

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which have unique handling and treatment procedures. Understanding the causes and types of food waste is essential for developing highly targeted waste reduction action plans, improving the efficiency of the food system, minimising environmental damage, and achieving sustainability along the entire food chain.[29] The need for interventions that reduce the enormous amount of food wasted worldwide, as well as the difficulties associated with food security issues, environmental degradation, and economic loss, includes policy reforms such as improving harvesting practices, improving cold chain logistics, lowering cosmetic standards, educating consumers, and enacting laws that encourage food donation and recycling (Fig. 1).

4. Characteristics of sustainable food production

Problems associated with traditional agricultural methods can be classified into two categories: (1) wildlife depletion to increase arable land and (2) intense land use. Consequently, sustainable food production has been proposed as a means of reducing dependence on traditional agriculture. Sustainable food production must be analysed comprehensively and structured to enhance three elements concurrently: economic, social, and environmental.[31] Consequently, in order to offer a novel methodology (*e.g.*, gene editing techniques) or to capitalise on a new opportunity (*e.g.*, intelligent food packaging), judgements must be evaluated across all three dimensions.[32] Fig. 2 illustrates the structural framework for the construction of a sustainable food production system. The food supply chain utilising blockchain technology (BCT) is integrated into three elements of sustainability: environmental, social, and economic. Six themes under the sustainable food system framework are categorised as follows: (1) resilience and resource efficiency; (2) sustainable and healthy diets; (3) circular economy; (4) profitability and efficiency; (5) sustainable supply chains and fair trade; and (6) transparency, traceability, and trust. The circular economy, as an emerging issue, significantly contributes to reducing resource consumption, eliminating waste, sustaining economic development, and facilitating

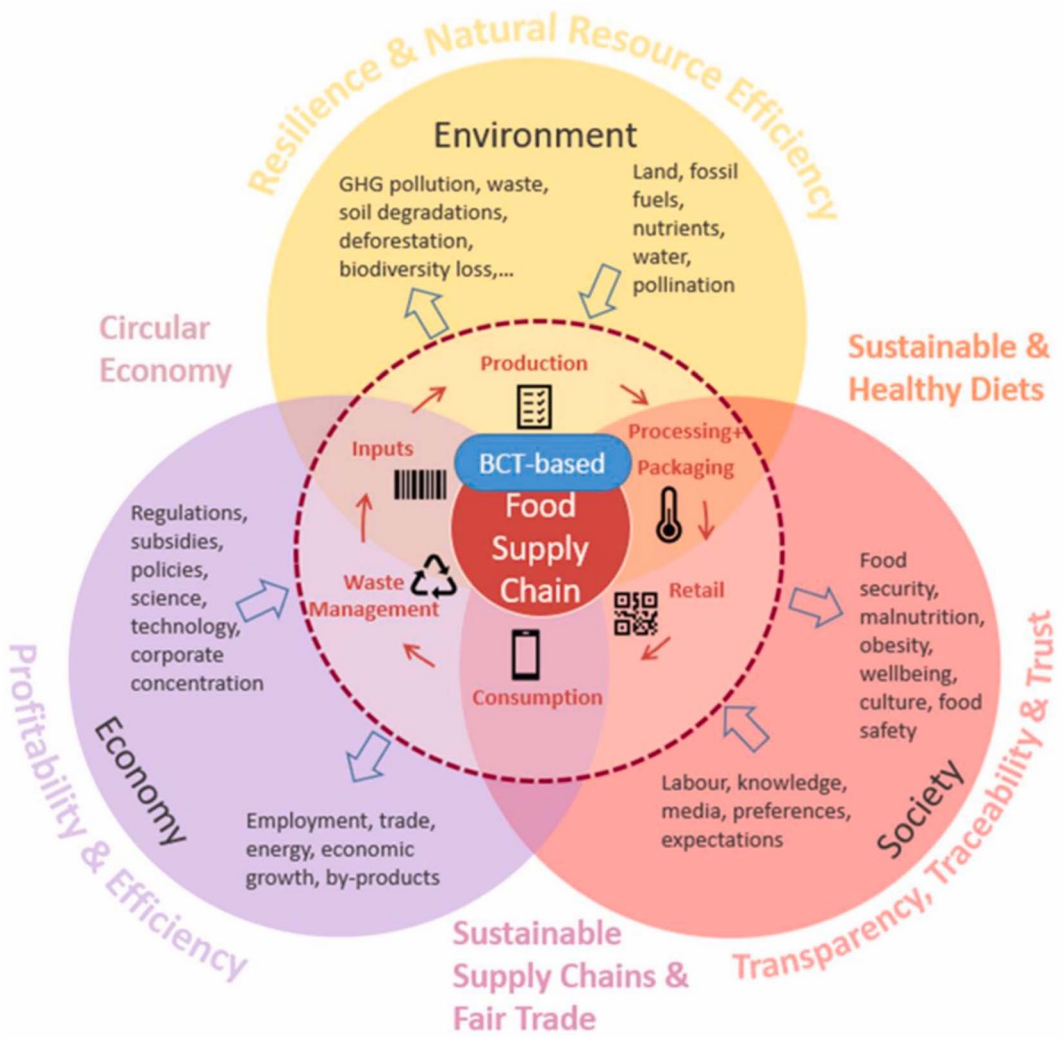

Fig. 2 Block chain technology for sustainable food technology and some of its key elements.[31]

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recycling, reuse, remanufacturing, and reclamation in a closed system.[33,34] Furthermore, life cycle assessment can be utilised to facilitate decision-making and comprehensively examine the environmental consequences of developing technologies from "cradle to grave" within the sustainable food production system.[35] Despite ongoing advancements, the fundamental attributes of sustainable food production merit greater scrutiny in light of the increasingly intricate issues in food production.[36]

5. Microbial diversity in food waste ecosystems

There is a wide variety and complex nature of microbes in waste food ecosystems that work together to deal with and turn into valuable materials: the organic material in waste streams.[37] They both assist in the degradation of food waste and in keeping by-products such as compost, digestate and other valuable materials well-developed and stable.[38] The types of microorganisms involved in food waste degradation are influenced by the chemical composition of the waste, its response to parameters such as pH and temperature and its physical characteristics.[39] Initially, most of the decays are done by bacteria, especially Firmicutes, Bacteroidetes, Proteobacteria, and Actinobacteria, which are observed in both the presence and absence of oxygen. Besides, in these groups, genera including *Bacillus*, *Clostridium*, *Pseudomonas*, *Lactobacillus*, and *Streptomyces* are important for hydrolysis, acid formation, and interactions that support the breakdown of organic materials.[39] The decomposition of complex polysaccharides, lignocellulosic materials, and recalcitrant proteins greatly depends on fungi of the filamentous type and yeasts.[37] The main fungal genera in food waste treatment are *Aspergillus*, *Penicillium*, *Rhizopus*, *Mucor* and *Saccharomyces*, and they all produce strong extracellular enzymes called cellulases, amylases, lipases and proteases that are useful in breaking down organic compounds.[38] Hyphae help to physically change the waste's structure so that bacteria can reach it, and the right amount of moisture is maintained. In anoxic environments, like biogas digesters, the archaea *Methanosaeta*, *Methanosarcina*, and *Methanobacterium* play a crucial role in the last stages, transforming volatile fatty acids and hydrogen into methane and carbon dioxide. They collaborate with fermentative and acetogenic bacteria steadily to sustain bioenergy production.[40] In microbial fuel cells (MFCs), some bacteria such as *Geobacter*, *Shewanella*, and *Desulfuromonas* transfer electrons from waste to the anode, facilitating energy generation and aiding in waste treatment.[41] Numerous protozoans and other eukaryotic microorganisms inhabit food waste environments, contributing to the regulation of microbial populations and the maintenance of system stability. Biofilms, aggregates of bacteria encased in self-produced gels, are commonly observed in food waste treatment, as these formations provide separation, communal metabolism, and adaptability to environmental variations.[42] In compost piles, microbial types change from mesophilic in the initial phase to thermophilic as temperatures increase and revert to mesophilic decomposers during the curing process.

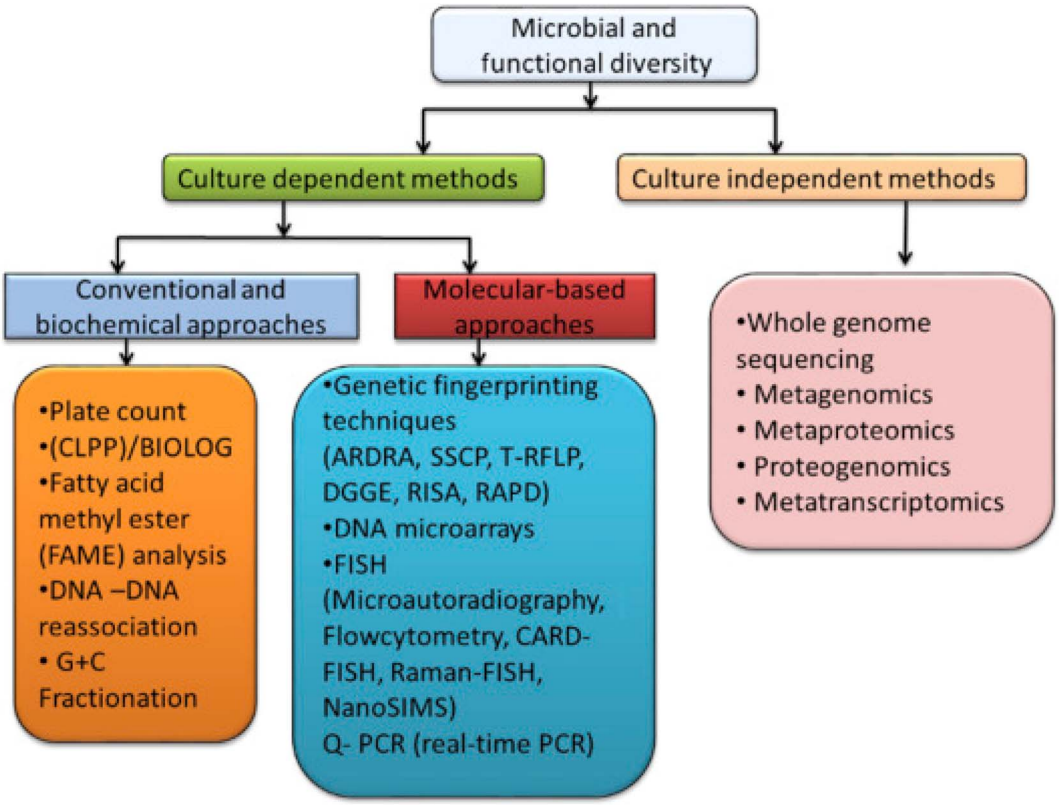

Fig. 3 Microbial diversity in food systems.[50]

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These include *Thermus* and *Thermoactinomyces*, which are heat-resistant bacteria, as well as *Thermomyces* and *Myceliophthora*, which are fungi utilised in the high-temperature processing of lignin and cellulose.[43] Advanced techniques, including 16S and 18S rRNA sequencing, internal transcribed spacer (ITS) profiling, and metagenomic analysis, have provided fresh insights into the diversity of bacteria in food waste and their functions.[44] Microbial communities, identified by high-throughput sequencing, exhibit activity and site-specific uniqueness and are influenced by the materials employed, their geographical location, and local operational procedures.[45] Shotgun metagenomics and transcriptomics enhance our comprehension of metabolic capabilities, regulatory mechanisms, and stress resilience within the microbial community.[46] Integrative omics, such as metabolomics and proteomics, are increasingly frequently employed in microbial ecology to investigate microbial activity beyond their taxonomic classifications, as shown in Fig. 3. By comprehending these elements, creating microbial consortia can achieve many outcomes in food waste treatment, like rapid decomposition, inhibition of pathogenic bacteria, or enhanced biogas production.[47] Understanding microbial variety is essential for biosafety and hygiene, as it helps assure the absence of harmful organisms, such as *Salmonella*, *Listeria*, *Escherichia coli*, or *Aspergillus flavus*, in food waste.[48] Regulating microbial populations involves utilising beneficial species while suppressing detrimental ones. In summary, the breakdown of food waste and its conversion into beneficial products relies on microbial diversity, which provides the necessary mechanisms and microorganisms for efficient organic matter decomposition.[49] Manipulating these microbes enables researchers and practitioners to enhance food waste treatment efficacy, foster sustainability, and contribute to the development of a robust circular bioeconomy.

6. Ecological interactions and microbial community dynamics in food waste treatment systems

Interactions among microorganisms in food waste ecosystems are complex, dynamic, and essential for the effective management of food waste. Interactions such as synergism, mutualism, commensalism, rivalry, antagonism, and predation influence the structure, functionality, and stability of the microbial communities involved in food waste processing (Fig. 4).[51] Nutrients are abundantly available yet unevenly distributed in food waste habitats, which prompts many bacterial species to collaborate and compete, resulting in behaviors that are unattainable individually.[52] During the breakdown of complex materials, it is very important because step one begins with primary degraders breaking large polymers like cellulose, hemicellulose, proteins and lipids into smaller ones that the second group takes over.[53] For example, *Clostridium thermocellum* hydrolyzes cellulose into glucose, which *Lactobacillus* species ferment into organic acids and alcohols, and these are then provided to methane-producing organisms in an anaerobic system. When microbes depend on each other, their waste helps fuel the growth of other groups.[54] When composting and

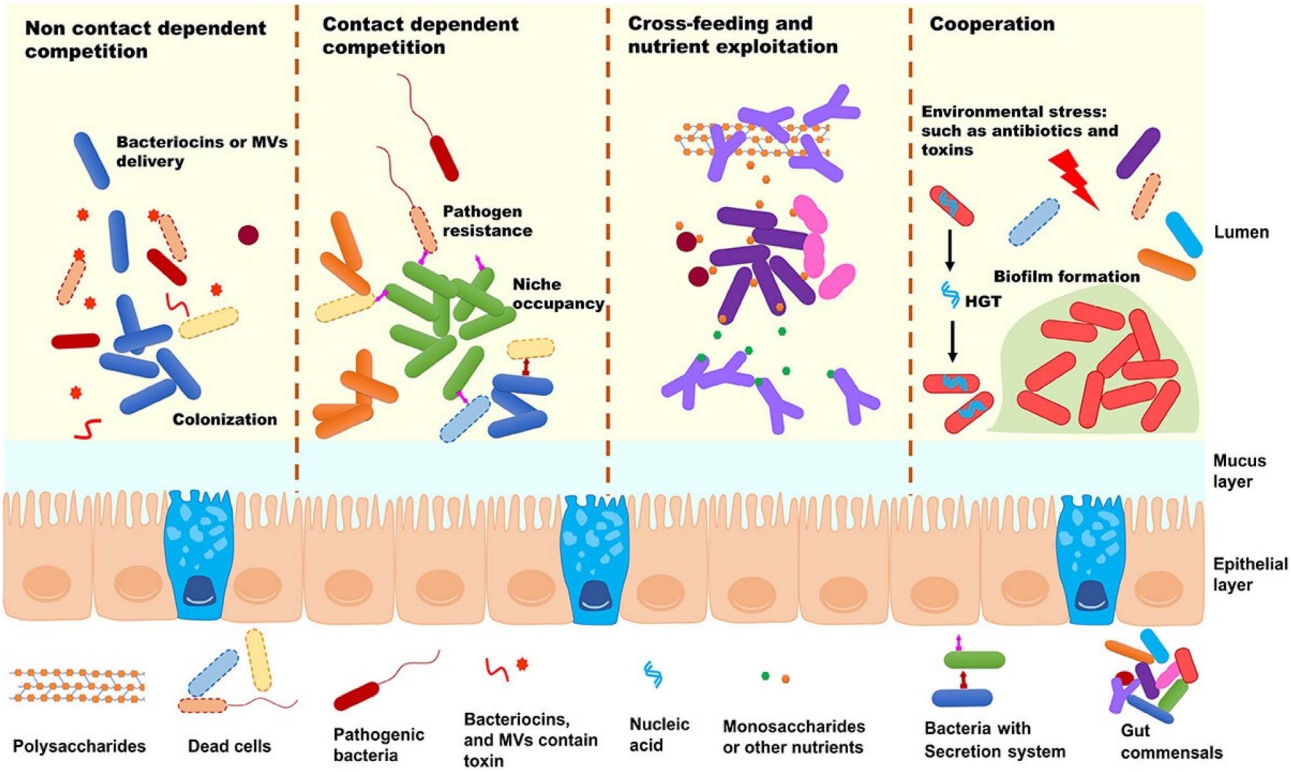

Fig. 4 Illustration of ecological interactions among the microbial species.[65]

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anaerobically digesting waste, the connection between different types of microorganisms ensures that they break down the materials properly. Mutualism exists in biofilms, as microorganisms grow together, exchange and use enzymes, exchange genes and are guarded by EPS.[55] Microbial fuel cells (MFCs) operate by allowing *Geobacter sulfurreducens* to depend on fermentative bacteria to supply reduced materials, thus ensuring a continuous stream of electrons to the anode. Additionally, when composting aerobically, thermophilic fungi help create air spaces and aid oxygen flow, which encourages aerobic bacteria to grow and become active. Community composition and variety are often adjusted when some species better compete for resources such as carbon, nitrogen or micronutrients.[56] Opportunistic microbes can take the lead under some conditions, but as time goes on and treatment conditions remain stable, more specialized species can take over. Microorganisms often use bacteriocins, antibiotics and secondary metabolites to help control the types of organisms in their environment. Thanks to such microbial conflict, unwanted microbe growth in composting or fermentation can be limited, increasing the safety and hygiene of the results. Bacteria in mixed cultures significantly help one another by using the metabolic residue created by another, without harming their hosts.[57] Predation occurs in microbial ecosystems related to food waste though it is less understood. Natural population control comes from protozoa and bacteriophages, which consume certain bacteria and affect the breakdown of nutrients and their recycling.[58] By applying our understanding of ecology, we may enhance the functionality of designed systems, maintain microbial stability, and prevent consortium failure.[59] Anaerobic digesters depend on maintaining a balanced population of acid- and methane-producing bacteria; allowing one group to overpower the other can lead to an accumulation of volatile fatty acids and a decrease in pH, which adversely affects methane generation. Process parameters such as temperature, pH, hydraulic retention time, and the type of waste utilised can be modified to enhance favourable reactions and mitigate detrimental ones.[60] Advancements in systems biology and microbial ecology, facilitated by high-throughput sequencing, metagenomics, and bioinformatics, have revealed networks and co-occurrence patterns that influence alterations in microbial populations within food waste ecosystems.[61] This software identifies the most critical species, key creatures, and necessary pathways for the community's functionality and resilience. Such insights facilitate the construction of artificial consortia that are better equipped to adapt to or withstand shifting environments. Moreover, microbes possess mechanisms for DNA exchange, known as horizontal gene transfer (HGT), and utilise quorum sensing to collectively respond to environmental stressors.[62]

Using certain microbes for bioaugmentation depends on knowing how these strains interact with microbes already in the environment.[63] Overall, the way microbes influence one another supports the full breakdown of food waste and determines how safe and effective the end products are. Using ecological engineering, synthetic biology and process optimization greatly helps in creating sustainable food waste management technologies that are strong and friendly to the environment.[64] In short, interactions between microbes in food waste greatly display nature's power and usefulness and act as a useful guide for recycling and new environmental solutions.

Microbial community changes in different waste treatment systems are important for the balance, stability and outcome of various means of waste management, and these changes differ based on whether the system is aerobic (like composting), anaerobic (for example, anaerobic digestion) or mixed with air and water (*e.g.*, microbial fuel cells and bio-electrochemical systems). Such changes mean that microbial consortia alter in composition, shape and power over time due to what substances are provided, the setting, system parameters and the way different microbes affect one another.[1,66] The initial, hungry mesophilic bacteria in composting are *Bacillus*, *Pseudomonas* and Actinobacteria, which decompose sugars and proteins. When temperatures rise because of microbial activity, *Thermus*, *Streptomyces*, *Aspergillus* and *Mucor* become dominant, they focus on breaking down tough materials, such as cellulose and lignin. As compost matures, mesophilic microbes are reintroduced, which supports humification and stabilization processes.[67] This pattern is necessary for nutrient recycling and stopping pathogens, influenced by how much and what kind of compost is aerated, the level of moisture, the carbon to nitrogen (C/N) ratio and what types of organic materials are composted. Instead, the microbes in anaerobic digestion are divided into separate groups within the system.[68] These bacteria called hydrolytic and fermentative, such as *Clostridium*, *Bacteroides* and *Hydrogenobacter*, help the process by breaking up complex compounds into simple molecules and volatile fatty acids.[69] They are further processed by acetate-consuming bacteria such as *Syntrophomonas* and *Syntrophobacter*, which team up with various methanogenic microbes, mainly *Methanosaeta*, *Methanosarcina* and *Methanobacterium*, to produce methane and carbon dioxide. Any problems, such as a growth in VFA or ammonia inhibiting the microorganisms, can interfere with methane formation within anaerobic systems.[70]

Higher stability in anaerobic systems often leads to a decrease in microbial diversity because specialized roles appear and redundancy among bacteria decreases. Conversely, microbial fuel cells (MFCs) and various bio-electrochemical systems build up special collections of bacteria, among which are *Geobacter*, *Shewanella* and *Pseudomonas*. They build biofilms on electrodes and depend on electron transfer outside the cell to generate electricity when they oxidize organic wastes from food. Under selective conditions, the community in MFCs develops better electron transmitters, and how they function depends greatly on the type of substrate, electrode and MFC design used.[71] Besides, MFCs usually feature microbial communities that have fermentative species producing reduced compounds, such as acetate, hydrogen or lactate, which are used by electroactive bacteria, thus assisting their groups to work together. Anaerobic membrane bioreactors (AnMBRs), dark fermentation systems and microbial electrolysis cells are linked types, and the microbes in these systems are selected to generate specific products, such as biohydrogen, volatile fatty acids or concentrated effluent, intended for further use. Such

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systems are influenced by the hydraulic retention time, organic load rate and nutrient addition, which impact the kinds of bacteria and their functions.[72]

Moreover, changes in temperature, salinity, heavy metals, antibiotics and traces of oxygen in the environment can impact the community of microbes by causing changes in populations, their ability to cope or the system failing, relying on how adaptable and resilient the microbes are. Advancements in 16S rRNA gene sequencing, shotgun metagenomics and metatranscriptomics now make it possible for us to watch these changes occur from moment to moment.[73] Studies using metagenomic techniques have shown that archaea in anaerobic digesters handling food waste respond to raised ammonia levels by having *Methanoculleus* take over from *Methanosaeta*.[74] Subsequent research utilising network analysis has identified specific species and microorganisms termed keystone taxa and hub microbes, which frequently exert a significant influence on community stability and functionality.[75] Upon comprehending these dynamics, specialised microorganisms are introduced to enhance treatments at underperforming stages, such as incorporating cellulolytic bacteria to facilitate hydrolysis and hydrogenotrophic methanogens to augment methane production when VFA levels increase.[76]

Another objective is to establish designer consortia by utilising synthetic biology, which can operate efficiently and maintain durability under diverse stress settings. Mixtures of engineered *E. coli* and *Clostridium* strains have been established to produce increased butyrate and ethanol from liquid food waste.[77] Biostimulation, which involves manipulating environmental variables to enhance native microbial activity, influences community formation. Altering pH, oxidation state, or introducing supplements benefits certain microbes, thereby inhibiting bacteria such as sulfate-reducing bacteria that deplete resources from beneficial methanogens in anaerobic settings.[78] The selection of inoculum influences the early community and affects the speed of digestion initiation and its sustained stability; digesters utilising adapted sludge commence operation more rapidly and exhibit superior performance.[79] Comparing systems from cross-ecosystems reveals that in aerobic systems, there is more microbial diversity resulting from changing oxygen levels and differences in habitats, as illustrated in Fig. 5, but in anaerobic systems, there is less diversity and more species that help one another or rely on each other. Overall, the behavior and composition of microbes in food waste treatment systems are determined by environmental, process, substrate and ecological factors.[80] If these dynamics are well understood, treatment systems can be made more efficient and microbial communities can be strategically built to help reduce waste, conserve resources and preserve the environment.

7. Metabolic pathways for food waste decomposition

Microbial communities break down food waste by involving numerous metabolic routes that turn complex compounds into simple compounds, energy and biogas, compost, organic acids and biofuels.[81] These kinds of metabolic processes occur depending on the surrounding conditions and which microbes are involved. According to the conditions related to oxygen, such as composting, microorganisms oxidize organic substances to make carbon dioxide, water, heat and more microbes, as depicted in Fig. 6(a) and (b). Initially, amylases, cellulases, proteases and lipases break down the big polysaccharides, proteins and lipids into glucose, amino acids and fatty acids outside the cell.[82] Microorganisms take up monomers and break them down through glycolysis, the tricarboxylic acid cycle and oxidative phosphorylation, producing ATP and completely oxidizing monomers into carbon dioxide.[83] By comparison, anaerobic decomposition takes place where oxygen is not present, such as in anaerobic digesters and in landfills, and employs a more complicated and multi-stage biochemical process with several diverse groups of cooperating microorganisms.[84] Hydrolysis, acidogenesis, acetogenesis and methanogenesis are the major stages of the anaerobic digestion (AD) process. As in aerobic systems, hydrolysis breaks down food waste polymers into monomers using enzymes. Short-chain volatile fatty acids (VFAs), alcohols, hydrogen and carbon dioxide are produced as acidogenic bacteria ferment these monomers.[85] These acetogenic bacteria turn the intermediates into acetic acid, more carbon dioxide and hydrogen, which become the main food for the final methanogenic bacteria.[86] Methanogens such as *Methanosarcina* and *Methanobacterium* perform methanogenesis using either acetoclastic

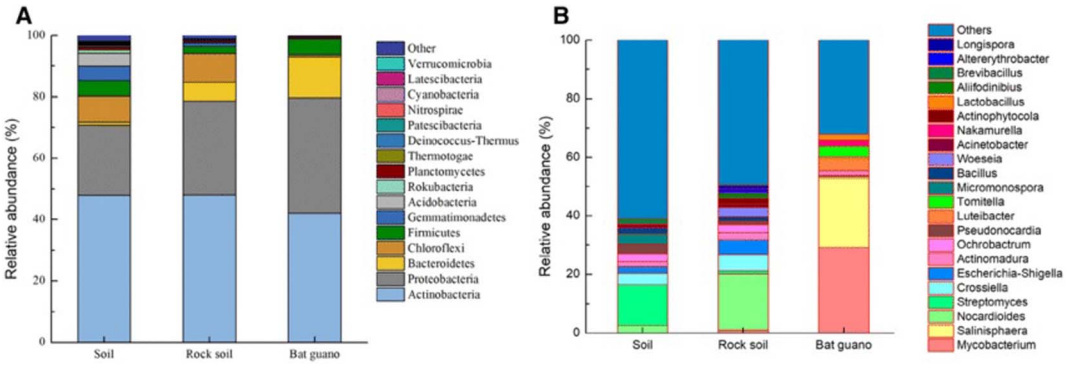

Fig. 5 Microbial diversity and relative abundance of various microbes.

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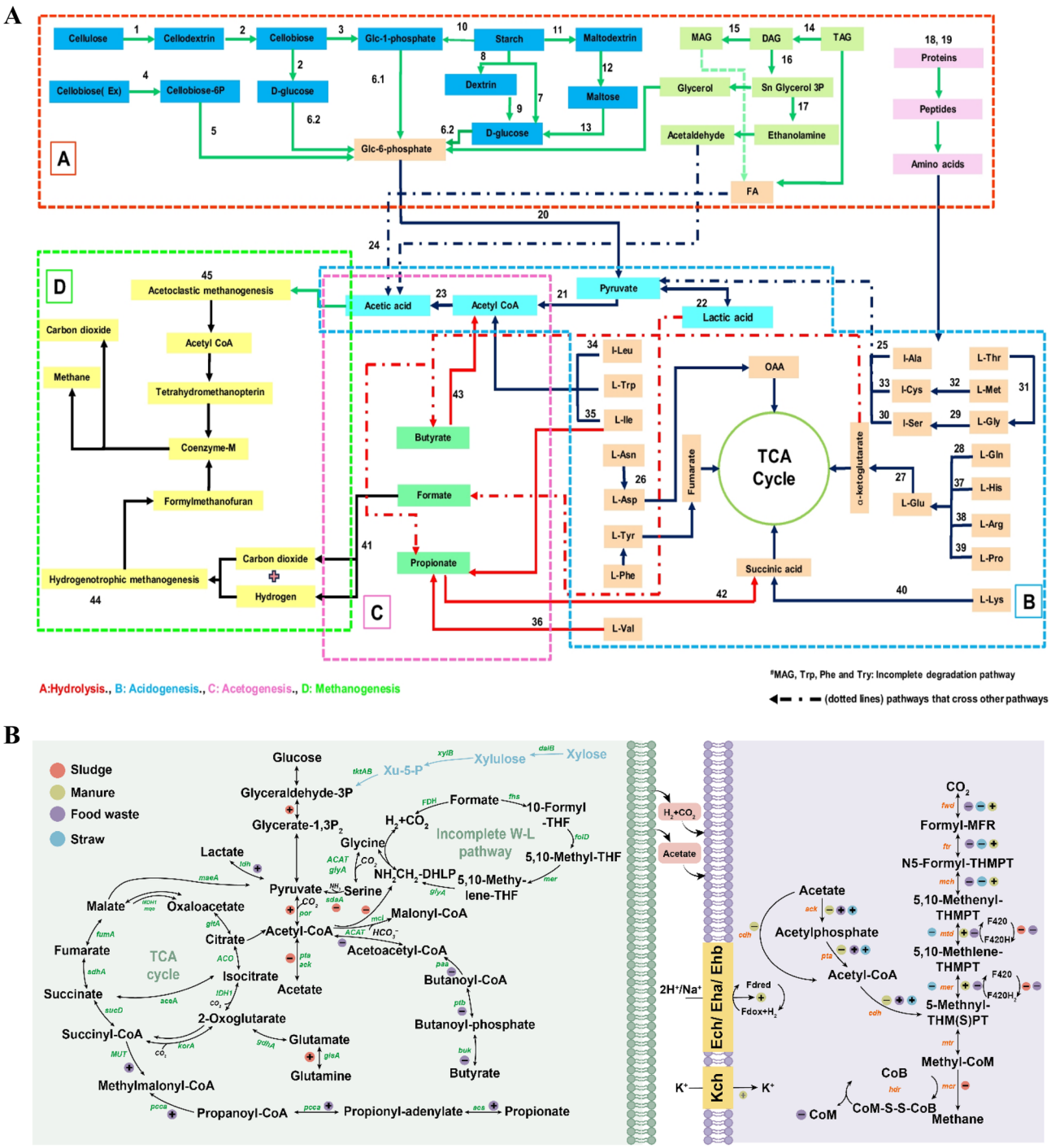

Fig. 6 (a) Metabolic pathway of food waste degradation.[94] (b) Anaerobic metabolic pathway of food waste degradation.[95]

methanogenesis, which changes acetate directly to methane and CO_2 or hydrogenotrophic methanogenesis, which breaks down H_2 and CO_2 into methane. Achieving efficiency in this process is best done by keeping a good balance between the microorganisms involved and the necessary environmental conditions, like neutral pH, proper temperature, low levels of ammonia and enough time for the process.[87] Apart from regular aerobic and anaerobic methods, alternative pathways are now recognized because they can help us use food waste to create bio-energy and chemicals. Among them are fermentation processes that yield ethanol, butanol, lactic acid and succinic acid, and these are carried out by bacteria, such as *Zymomonas mobilis*, *Clostridium acetobutylicum* and *Lactobacillus plantarum*.[88] The enzymatic and microbial degradation of lignocellulosic constituents in fibrous waste yields fermentable sugars, which subsequently undergo reactions to produce bioethanol or organic acids. In microbial fuel cells (MFCs), electroactive microorganisms decompose organic molecules and transfer

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electrons directly or *via* mediators to an anode.[89] The activities utilise specific metabolic pathways, notably the citric acid cycle, and incorporate specialised electron transport chains capable of transferring electrons beyond the cell.[90] The heat produced by microbes helps raise the temperature, which allows thermophilic microbes to degrade tough or lignin-rich materials in the compost pit.[91] During composting, the microorganisms in the community use different metabolic processes: first oxidative breakdown, then mineralization and finally stabilizing the substances.[92] The presence of secondary metabolites in soil, such as organic acids and phenolics, also has effects on which microbes gain advantage and how nutrients become available.[93]

Recent studies of food waste decomposition show that metagenomics reveals both the taxonomic composition and the functional potential of microbial communities during composting or anaerobic digestion. For example, composting stages (mesophilic, thermophilic, maturation) show shifts in dominant taxa (*e.g. Bacillus* and *Cellulomonas*) and in genes encoding carbohydrate-, protein-, and lipid-degrading enzymes; glycoside hydrolase (GH) families are particularly enriched in the early to mid composting stages.[96] Transcriptomics work is less frequent but growing: metatranscriptomic reviews highlight the active expression of microbial enzymes (CAZymes and amino acid metabolism) during food fermentation and nutrient breakdown, showing how genes for hydrolysis and fermentative processes are regulated in response to substrate type.[97] Proteomics confirms which enzymes are actually being produced and functional; for example, in fermented products, changes in proteolytic enzymes correspond to protein hydrolysis and flavor and texture evolution. Proteomics helps identify peptidases and other hydrolases responsible for the breakdown of complex proteins in food waste.[98]

Metabolomics, including untargeted metabolite profiling, tracks downstream small molecules: sugars, amino acids, volatile fatty acids (VFAs), antibiotic compounds, and intermediates like phenazines. A recent study integrating metagenomics and metabolomics of an anaerobic digestion and composting system treating organic municipal solid waste (OFMSW) elucidated the persistence and alteration of antibiotic resistance genes and antibiotic compounds during waste processing, highlighting distinct metabolic and chemical profiles at each treatment stage.[99] Collectively, multi-omics integration elucidates the process: hydrolysis → fermentation → VFA synthesis → methanogenesis or aerobic stabilisation, while identifying inefficiencies or risks (*e.g.*, buildup of certain metabolites and persistence of antibiotic resistance). These findings facilitate the optimisation of waste treatment (temperature, inoculants, and feedstock composition) to improve decomposition, biogas production, and safety.

During composting, the breakdown of organic matter in the feedstock mass is facilitated by hydrolytic enzymes, which include cellulases and β-glucosidases that depolymerize cellulose and glucosides, respectively. Hydrolytic enzymes degrade waste lignocellulosic compounds into polyphenols, polysaccharides, monosaccharides, aldehydes, and acids, which are synthesized by microbial communities at different composting stages. Metabolites produced from lignocellulose degradation are polymerized into humic substances based on humic formation theories, which play an essential role in compost quality. Some particular CAZyme genes detected at different stages of the composting metagenome are summarised (Fig. 7). A comparison of carbohydrate-active enzyme encoding genes against the CAZy database showed that out of annotated glycoside hydrolase (GH) families, sequences affiliated with GH2, GH3, GH20, GH29, and GH43 indicate the primary role of bacteria in hydrolysis of polysaccharides during the initial and mesophilic stages of composting. Other GH families affiliated with GH103 and GH13 genes are relatively more abundant in the thermophilic stage, which is associated with the functional activity of hemicellulose degradation and cleavage of α-glycosidic linkage containing substrates like starch, than in other stages of composting. The thermophilic stage also shows the richness of the sequences of glycosyl transferase (GT) families, like GT4 and GT51 genes, that are associated with the synthesis of peptidoglycan of the bacterial peptidoglycan layer, which might support germination for the establishment of a new bacterial community after the dormant state of bacteria.

8. Use of metagenomic tools to investigate microbial communities in waste

Metagenomic tools have become pivotal in elucidating the structure and functional dynamics of microbial communities in FW systems.[100] Through the direct sequencing of environmental DNA, metagenomics enables a comprehensive and unbiased characterization of both cultivable and non-cultivable microorganisms, thereby overcoming the inherent limitations of culture-based methods.[101] This approach is particularly relevant to FW environments, which are microbiologically complex and characterized by diverse substrates that support the heterogeneous microbial consortia involved in the decomposition and transformation of organic matter. High-throughput sequencing (HTS) platforms, including 16S rRNA gene amplicon sequencing and shotgun metagenomics, allow for fine-scale taxonomic resolution and functional annotation of microbial genes.[102] These methodologies have been successfully applied to monitor microbial succession and metabolic capabilities during composting, revealing key microbial taxa and enzymatic pathways that vary with the composting stage and environmental parameters. Such insights are instrumental in refining operational parameters to enhance the degradation efficiency and stability of compost systems.[66] Moreover, metagenomics has elucidated the functional roles of microbial taxa in AD processes, highlighting the influence of additives like activated carbon on microbial composition and metabolic activity.[103] These amendments modulate microbial syntrophy and electron transfer, leading to improved CH4 yields and process stability. Functional gene profiling derived from metagenomic datasets further allows for the identification of genes encoding key enzymes in hydrolysis, acidogenesis, acetogenesis, and methanogenesis—pathways central to biogas production.[104] To complement sequencing data, computational tools such as

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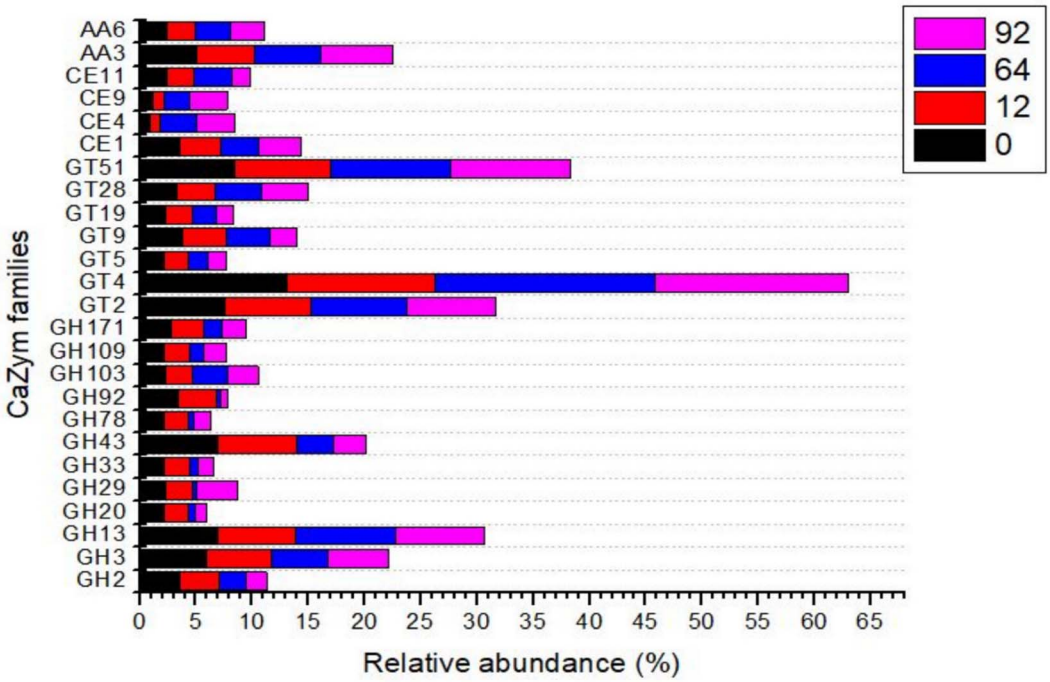

Fig. 7 Metagenome annotation for CAZyme families.[96]

QIIME (Quantitative Insights into Microbial Ecology) and PICRUSt (Phylogenetic Investigation of Communities by Reconstruction of Unobserved States) are used to predict metabolic potential from taxonomic data, facilitating a system-level understanding of microbiome functionality.[105] These advancements support the rational design of microbial consortia and the development of precision microbial management strategies to optimize FW valorization through composting, AD, and the production of bio-based compounds. Table 1 presents the Next-Generation Sequencing (NGS) approaches for microbial community profiling in various composting substrates.

9. Factors influencing microbial activity in food waste degradation

The biodegradation of food waste is highly sensitive to multiple physicochemical and biological parameters. Fig. 8 shows different parameters that affect food waste biodegradation.[123] The C : N ratio is widely recognized as a critical factor, with composting studies reporting that maintaining a ratio between 25 : 1 and 30 : 1 maximizes microbial activity and heat generation, while C : N values below 20 : 1 can result in ammonia volatilization rates exceeding 1.5 g NH_3–N per kg dry matter and strong odor emissions.[124] In anaerobic digestion (AD), protein-rich food waste often causes elevated total ammonia nitrogen (TAN) concentrations; values above 3000 mg L^{-1} have been shown to inhibit methanogenesis by more than 40%, necessitating co-digestion with high-carbon bulking agents such as straw or paper to dilute nitrogen loading.[125] Moisture content around 55–60% is considered optimal in composting, with levels above 70% reducing porosity and oxygen diffusion, leading to anaerobic conditions and incomplete degradation. Similarly, aeration rates of 0.3–0.6 L air per min per kg dry matter have been reported to sustain aerobic conditions while preventing excess heat or water loss.[126] Temperature profiles strongly affect microbial succession: thermophilic composting at 55–65 °C accelerates organic matter decomposition by up to 30% faster than mesophilic regimes, while in AD, biogas yields of 480–520 mL CH_4 per g VS are commonly reported under mesophilic conditions but may decline by 20–25% when TAN or VFAs accumulate at high loading rates.[127] Operationally, maintaining an organic loading rate (OLR) below 3 g VS per L per day is critical for the mono-digestion of food waste, as exceeding this threshold often leads to VFA accumulation above 2000 mg L^{-1}, triggering pH drops below 6.5 and process inhibition. Multi-omics analyses further show that under such stress, methanogen populations (*e.g.*, *Methanosaeta*) can decline by 50–70%, while acidogenic bacteria proliferate, reinforcing instability.[128] Mismanagement of these parameters not only reduces efficiency but also generates odors (NH_3 > 20 ppm, H_2S > 5 ppm) and leachate rich in COD (>20 000 mg L^{-1}), which compromise environmental safety; however, interventions such as biochar addition at 5–10% w/w have been shown to reduce NH_3 emissions by 30–40% and buffer VFAs to restore methanogenic activity. Collectively, these numerical findings underscore that precise control of feedstock properties, environmental conditions, and microbial ecology is essential for transforming food waste into stable compost or high-yield biogas while minimizing environmental impacts.[129]

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Table 1 Next generation sequencing (NGS) approaches for microbial community

Compost substrate	Sequencing approach	Target	Key findings	NGS platform	Reference
Food waste and wastewater	Amplicon, 16S (V5–V9)	Bacteria	116 OTUs; 16 genera	Roche 454	106
Maize straw	Amplicon, 16S (V3–V4), ITS (fungi)	Bacteria, fungi	8535 Bacterial OTUs (24 phyla); 412 fungal OTUs (1 phylum)	Roche 454	6
Spent mushroom waste	Amplicon, 16S (V5–V8)	Bacteria	19 Phyla, 33 classes, 48 orders, 85 families, 129 genera	Roche 454	107
Green waste & barley grain	Amplicon, 16S (V1–V2)	Bacteria	20 Bacterial genera across phases	Roche 454	108
Olive mill waste	Amplicon, 16S (V4–V5)	Bacteria	10 Dominant genera (meso/thermo stage); 8 genera in maturation	Roche 454	109
Food waste & cattle manure	Metagenomic, *de novo* assembly	Bacteria, virus	Proteobacteria (~65% reads); 5 pathogens; phages (mainly insect viruses)	Ion torrent	110
Chicken manure	Amplicon, ITS	Fungi	526 OTUs; 4 fungal phyla	Illumina	111
Maize straw	Amplicon, 16S (V3–V4)	Bacteria	16 Phyla; 4 phyla represented 92.2% of sequences	Illumina	112
Rice husk and dewatered sludge	Amplicon, 16S (V4–V5)	Bacteria	29 OTUs; 11 bacterial genera	Illumina	113
Sewage sludge (gelatin, municipal)	Amplicon, 16S (V3), 18S, ITS	Bacteria, fungi	8 Bacterial and 2 fungal phyla detected	Illumina	37
Food waste	Amplicon, 16S (V4)	Bacteria	5 Dominant phyla; >40 bacterial species	Illumina	114
Corn straw & cow manure	Amplicon, 16S, ITS	Bacteria, fungi	272 Bacterial OTUs; 321 fungal OTUs	Illumina	115
Food waste	Amplicon, 16S (V3–V4)	Bacteria	29 Bacterial strains detected	Illumina	114
Paper mill sludge	Amplicon, 16S (V3–V4)	Bacteria	Dominance of proteobacteria, firmicutes, bacteroidetes; key degraders enriched	Illumina	116
Vegetable waste	Amplicon, 16S (V4), ITS	Bacteria, fungi	35 Bacterial genera and 9 fungal genera; succession driven by the composting stage	Illumina	117
Municipal solid waste compost	Amplicon, 16S (V3–V4)	Bacteria	12 Bacterial phyla; actinobacteria and firmicutes are dominant in the thermophilic stage	Illumina	99
Coffee husk	Amplicon, ITS (fungi)	Fungi	Ascomycota dominant (>70%); key lignocellulose degraders identified	Illumina	118
Tea waste	Amplicon, 16S (V4), ITS	Bacteria, fungi	*Bacillus*, *Pseudomonas*, and *Aspergillus* enriched during active degradation	Illumina	119
Brewery spent grain	Amplicon, 16S (V3–V4)	Bacteria	*Lactobacillus*, *Bacillus*, and Actinobacteria are predominant	Illumina	120
Cassava peels	Amplicon, 16S (V4), ITS	Bacteria, fungi	Cyanobacteria and firmicutes are abundant; *Fusarium* spp. key lignocellulose degraders	Illumina	121
Sugarcane bagasse	Amplicon, 16S (V3–V4)	Bacteria	Firmicutes and actinobacteria are dominant in the thermophilic phase	Illumina	122

10. Biotechnological applications of microbial consortia in food waste valorization

Using microbial groups to change food waste into valuable products fits well with the ideas of circular bioeconomy and sustainability.[131] Teamwork among different microbial groups is more helpful than a single group for transforming complex substances, such as food waste.[132] Using these assemblages, food waste can be made into different valuable bioproducts, including biofuels (such as biogas, biohydrogen, and bioethanol), bio-based chemicals (such as volatile fatty acids, lactic acid, and succinic acid), biological fertilizers, and proteins from live cells and bioplastics.[58] Anaerobic digestion is a highly developed use of microbes where groups of hydrolytic, acidogenic, acetogenic and methanogenic microbes help digest waste and make biogas rich in methane.[133] New methods in microbiome engineering have improved how much biogas is produced from waste by properly setting operations using co-digestion and using particular strains, such as hydrogenotrophic methanogens, to boost methane production in the presence of high levels of ammonia. Decomposition by dark fermentation occurs when *Clostridium*, *Enterobacter* and *Bacillus* species dominate the microbial community, turning food waste carbs into biohydrogen, which is environmentally friendly. These groups of bacteria are encouraged to produce energy under chosen pH and temperature levels, which increases the

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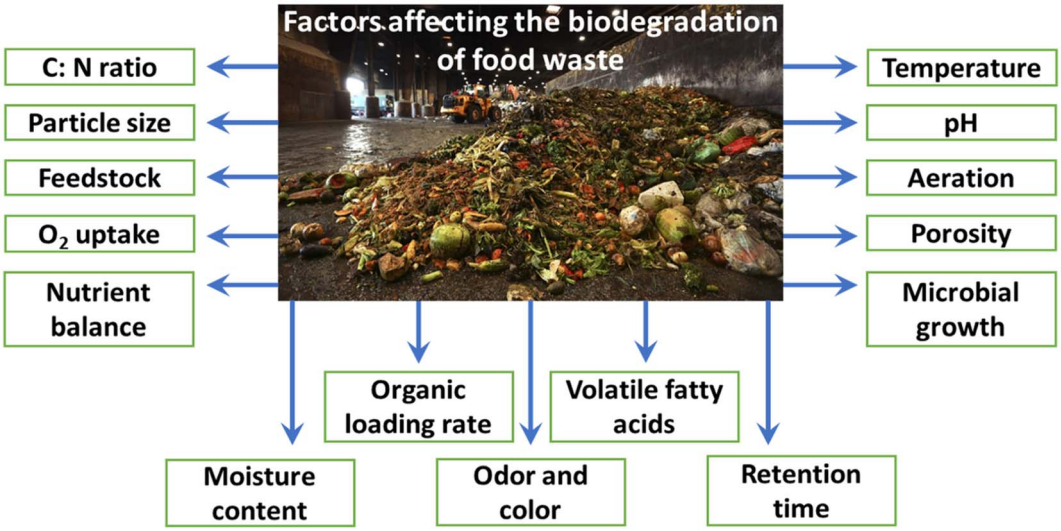

Fig. 8 Effects of various parameters on the biodegradation of food waste.[130]

amount of hydrogen and lowers the chances of other bacteria turning hydrogen into methane.[134]

The use of electroactive bacteria in microbial fuel cells (MFCs) turns food waste's chemical energy into electricity.[135] *Geobacter* and *Shewanella* communities can form conductive films on the anode surface, and healthy anode growth relies on acetate or hydrogen supply from fermentative microbes. Consortia often benefit from stability and improvement when researchers use evolution, change the substrate and modify the electrode. Producing volatile fatty acids (VFAs) *via* acidogenic fermentation is another notable use of this process. With acetic, propionic and butyric acids, downstream manufacturing turns them into biodegradable plastics, solvents and fuels.[136] To promote the production of certain acids by microbial consortia, pH, the time VFA is retained, and the organic material fed can be adjusted. Using tailored groups of microorganisms, integrated biorefineries are now popular to maximize resource reuse by breaking down VFAs, biohydrogen, and gas out of food waste in a row. Besides, microbial consortia are involved in producing polyhydroxyalkanoates (PHAs), which are made from renewable sources. PHA production can be achieved with MMCs from food waste digestates grown in feast–famine cycles if given suitable carbon.[137]

Besides being sources of energy and materials, microbial groups are used to make biofertilizers and soil conditioners from food waste. Stabilization of organic waste and improvement in nutrient access and microbe diversity in agricultural soil are possible when composting, vermicomposting and aerobic digestion are practiced with microorganisms.[138] The use of plant growth enhancing bacteria (PGPR) as part of these consortia can help the compost become even more valuable for crops.[139] A new area of interest is making single-cell protein (SCP) from waste products by mixing microbial communities that contain yeasts (like *Candida*, *Saccharomyces*), fungi (like *Aspergillus* and *Rhizopus*) and bacteria (such as *Methylobacterium* and *Corynebacterium*).[140] Such proteins help to address food waste and the lack of protein in food resources for animals and humans. It is now possible to build "synthetic communities" of bacteria using synthetic biology and metabolic engineering to create key products. Special teams made up of *Escherichia coli* and *Clostridium acetobutylicum* have been designed to help with better butanol production, and some others include algae and bacteria to achieve both carbon capture and bioenergy generation. Because of spatial organization, resource organization and strength against changing conditions, such groups succeed better.[141]

Besides, biotechnology uses microbial consortia for the oxidation and detoxification of food processing waste that may carry xenobiotics, heavy metals and synthetic additives. Microbial biofilms, enzymes and redox components in consortia can degrade persistent pollutants, which assists in environmental remediation. Similarly, bio-electrochemical systems that rely on microbial teams can fix carbon dioxide and recover nutrients from food waste effluents, so this becomes a way to produce products without using any carbon.[142] Achieving success with these applications necessitates precise monitoring and management of microbial communities, achievable through high-throughput sequencing, metagenomic analysis, metabolomics, and software tools. Mixing omics technologies with machine learning helps forecast the way consortia work, which leads to improved manufacturing and the ability to scale up.[143]

Moreover, people are focusing on applying microbial consortia at a larger scale to turn food waste into useful products. In Europe, Asia and North America, companies and researchers are producing modular bioprocessing units, so they can be put in places such as cities, food plants and farms. The purpose of these systems is to make valuable energy and useful materials from waste local food and to avoid having a large environmental impact. Despite what they can offer, there are still many problems, such as stable performance in changing raw material situations, rules for products extracted from waste and public opinions about using garbage resources.[144] Moreover, microbial

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ecology, bioprocess engineering and systems biology are quickly reducing these gaps (Fig. 9).

10.1 Biosafety risks of engineered microbes in food waste valorization

The deployment of engineered microbes through synthetic biology, such as modified *Escherichia coli*, *Saccharomyces cerevisiae*, or *Pseudomonas putida*, offers major advances in converting food waste into biofuels, organic acids, bioplastics, and nutraceuticals, but it also raises significant biosafety concerns. Engineered strains often carry enhanced metabolic pathways and heterologous enzymes, increasing the risk of horizontal gene transfer (HGT) to environmental microbiota, which potentially spreads synthetic operons or resistance markers. Laboratory studies have shown that plasmids and transposons remain highly active in mixed communities, with transformation frequencies in soil and wastewater as high as 10^{-6}–10^{-3} per recipient cell. Additionally, genetically modified bacteria exhibiting enhanced substrate utilisation, such as cellulase-overproducing *E. coli* or lipid-accumulating *Yarrowia lipolytica*, may surpass indigenous species in nutrient-abundant waste streams, thereby disrupting ecological equilibrium. These concerns underscore the necessity for sophisticated biosafety techniques that go beyond traditional sterilisation methods.[146] Genetic biocontainment strategies encompass kill switches that induce cell death in response to particular signals, exemplified by the "Deadman" and "Passcode" systems. Synthetic auxotrophy serves as an additional protection, which is illustrated by recoded *E. coli* depending on *para*-aminophenylalanine (pAF) and cannot thrive outside of supplemented conditions. Metabolic addiction circuits, linking growth to the availability of waste-derived substrates, further limit proliferation outside reactors. Complementary process-level controls, such as closed-loop bioreactors, effluent sterilisation, encapsulation of engineered microorganisms in hydrogels, and membrane bioreactor (MBR) systems, introduce physical barriers while improving productivity. These stratified defences integrate genetic, biochemical, and engineering precautions for efficient containment.[147] Regulatory frameworks strengthen biosafety supervision. The Cartagena Protocol on Biosafety (2000) establishes precautionary rules for the management of living modified organisms (LMOs) on an international scale. In the United States, the EPA TSCA Biotechnology Rule (1997) and NIH Guidelines mandate risk evaluations and delineate biosafety levels (BSL-1 to BSL-4). The EU Directive 2009/41/EC requires risk-based classification and containment of genetically modified microbes, while OECD and ISO 35001:2019 offer standardised biosafety guidelines.[148] Current rules must adapt to advancements in synthetic biology, including genome recording, CRISPR gene drives, and xenobiology. Systems utilizing unusual base pairs (UBPs) or extended genetic codes may diminish horizontal gene transfer (HGT) potential while posing challenges to current regulatory frameworks.[149]

The secure utilization of modified microorganisms in food waste valorization necessitates a multi-tiered defense strategy: molecular protection, process-level containment, and

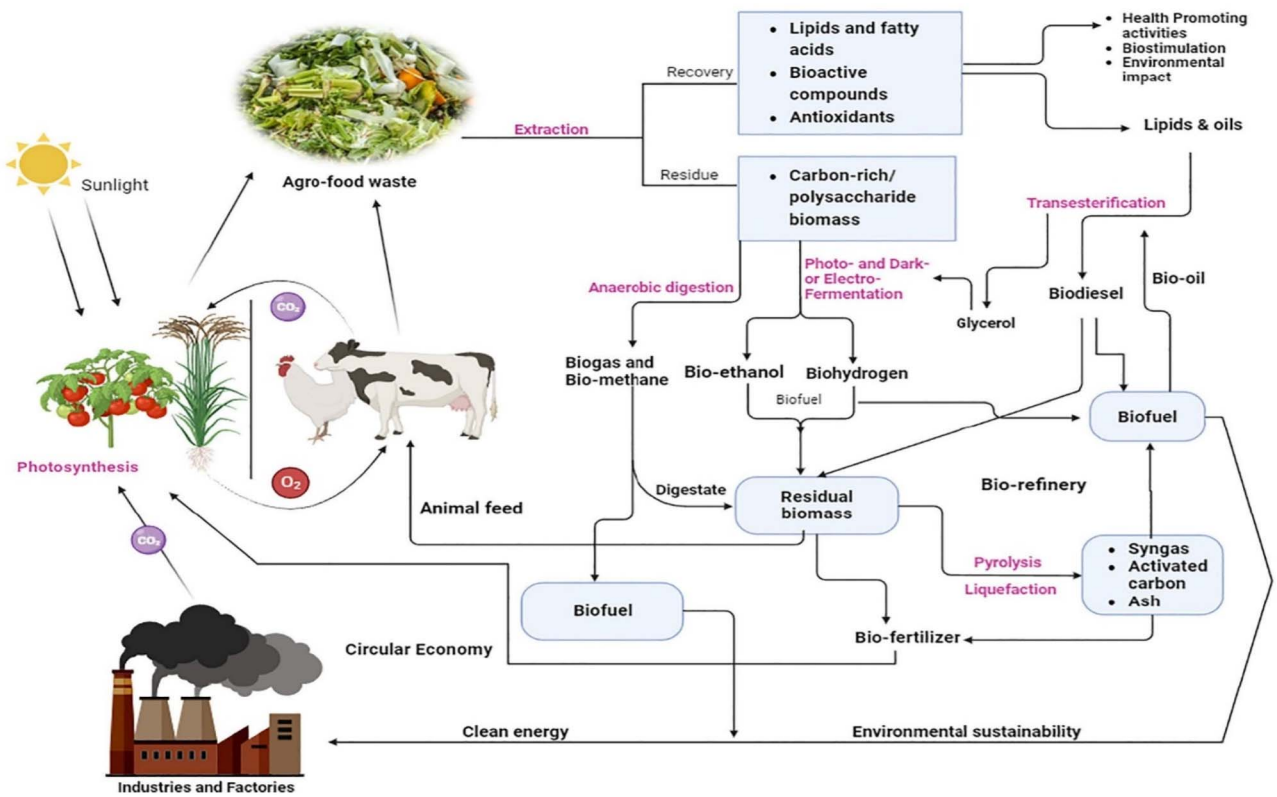

Fig. 9 Valorization of food waste using biotechnological approaches.[145]

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Table 2 Biosafety risks and their mitigation strategies

Biosafety risk	Description	Mitigation strategies	References
Gene transfer	Engineered microbes may transfer modified genes to native microorganisms, potentially creating novel pathogens or spreading antibiotic resistance	Use genetic safeguards (*e.g.*, kill-switches and auxotrophy); limit use of mobile genetic elements; employ CRISPR-based containment	146
Pathogen or toxin release	Improper containment could allow engineered microbes to escape into the environment, releasing pathogenic organisms	Strict biosafety protocols; bioreactor containment; use of non-pathogenic chassis organisms; regular monitoring	147
Antibiotic resistance	Some engineered strains or their hosts may carry resistance genes, contributing to the development and spread of antibiotic resistance in food chains	Avoid antibiotic resistance markers; replace with alternative selection methods (*e.g.*, auxotrophy and fluorescent tags)	148
Harmful metabolites	Fermentation by engineered microbes may produce undesirable biomolecules (*e.g.*, histamine, biogenic amines, or toxins) that pose risks to human/animal health	Metabolite profiling; strain engineering to block unwanted pathways; quality control testing of end-products	149
Unforeseen ecological impacts	Introduction of engineered microbes into food waste environments could disrupt microbial communities and ecosystems, leading to unintended ecological consequences	Conduct ecological risk assessments; employ closed-loop systems; use microbes with limited environmental survivability	150

compliance with international biosafety regulations. Incorporating these criteria with efficiency reporting is essential for regulatory approval, public confidence, and sustainable integration into the circular bioeconomy (Table 2).[150]

11. Case studies: microbial food production

Recent advancements in microbial biotechnology illustrate the conversion of food waste into high-value products *via* various microbial routes, as evidenced by numerous global case studies.[151] Lactic acid production from domestic food waste utilizing *Lactobacillus plantarum* in South Korea attained yields of 65–75 g L^{-1} with over 90% conversion efficiency, providing a substrate for biodegradable polymers and food additives.[152] Unibio A/S in Denmark has successfully commercialised single-cell protein (SCP) production by cultivating *Methylococcus capsulatus* on methane sourced from anaerobically digested food waste, yielding biomass with over 60% protein content as a substitute for fishmeal and soy.[153] In India, consortia of *Clostridium butyricum* and *Enterobacter aerogenes* effectively fermented fruit and vegetable waste into biohydrogen, achieving yields of up to 2.1 mol H_2 per mol glucose equivalent under optimised conditions, which highlights the promise of waste-to-energy bioprocesses. In the dairy industry, whey waste in Italy has been utilised for the cultivation of probiotic strains, including *Lactobacillus rhamnosus* and *Bifidobacterium bifidum*, attaining biomass concentrations of up to 10^{11} CFU mL^{-1} and generating economical probiotic cultures for functional foods. Large-scale anaerobic digestion plants such as Borås Energy in Sweden treat ~30 000 tons of food waste annually, yielding biogas with ~70% methane content to power ~4000 households while generating nutrient-rich digestate for agricultural reuse.[154] Furthermore, Chinese pilot studies have demonstrated that mixed microbial cultures can transform canteen food waste into polyhydroxyalkanoates (PHA), with yields reaching 20–30% of cell dry weight, presenting sustainable alternatives for bioplastic production.[144] Collectively, these case studies highlight the transformative potential of microbial pathways in shifting food waste from an environmental burden to a critical resource for sustainable food production and circular bioeconomy advancement.

12. Recent advances, challenges, and future prospects in microbial food waste conversion

Significant advancements in biology, especially in systems biology, synthetic biology, metabolic engineering, and environmental biotechnology, have markedly improved the efficiency and product diversity of microbial food waste conversion. A significant advancement is the utilization of multi-omics methods, including genomics, transcriptomics, proteomics, and metabolomics, which provide a comprehensive analysis of microbial populations. These techniques elucidate essential genes, constraints, and species relationships, illuminating collaborative processes, such as methane production and the nitrogen cycle. Metaproteomics and metabolomics offer immediate insights into essential chemicals and pathways, facilitating the optimization of digestion and product synthesis.

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Synthetic biology and metabolic engineering enhance microbial performance by increasing inhibitor tolerance, optimising substrate absorption, and facilitating novel metabolic pathways. CRISPR-based engineering has enabled the production of high-value chemicals, including polyhydroxyalkanoates (PHAs), butanol, and lactic acid. Engineered microbial consortia, optimised for robustness and self-regulation, are progressively utilised to oversee intricate waste bioconversion. Enhancing biology, reactor innovations, such as two-stage anaerobic digesters, membrane bioreactors, and microbial electrochemical systems, facilitate meticulous regulation of microbial retention, nutrient equilibrium, and hydraulic parameters. Intelligent monitoring utilising biosensors, IoT devices, and AI-driven analytics enhances process stability by anticipating microbial stress, projecting yields, and facilitating proactive interventions.

Co-digestion systems, which integrate food waste with agricultural waste or wastewater, improve nutritional equilibrium and biogas production. Extremophilic microorganisms broaden the spectrum of treatable waste, while their integration with carbon capture and utilization (CCU) technology facilitates carbon-neutral or carbon-negative systems. Demonstration projects in Europe, Asia, and North America have already exhibited microbial biorefineries that generate electricity, fertilizers, enzymes, and bioplastics. Policy initiatives, such as landfill diversion incentives and carbon credits, further promote commercialization.

Notwithstanding the advancements made, obstacles persist. Variability in food waste—attributable to seasonality and origin—impacts microbial efficacy, while pollutants such as pesticides, heavy metals, and preservatives interfere with metabolism and heighten safety issues. Microbial consortia may become destabilized under stress, complicating the stability of reactors in the long run. Transitioning from laboratory to industrial scale introduces engineering challenges in heat transmission, mass movement, and homogeneous nutrient distribution. From an economic perspective, sophisticated reactors and the subsequent recovery of products such as PHAs or hydrogen are expensive, while more affordable options like composting and landfilling continue to be competitive. Market constraints encompass uneven product quality, consumer skepticism, and regulatory ambiguity, especially concerning genetically altered bacteria and waste-derived goods.

Anticipating the future, interdisciplinary approaches are essential. Modular, decentralized processing systems designed for local waste streams may lower expenses and enhance adaptability, particularly in urban environments and the food sector. The amalgamation of automation, sensors, and machine learning facilitates self-regulating systems, while the integration of omics with digital twins enhances predictive control. Progress in synthetic biology persists in producing robust microbial strains, while insights from natural ecosystems may inform the development of resilient synthetic consortia. The investigation of "microbial dark matter" has potential for discovering new enzymes and methods for waste valorization. Ultimately, policy frameworks must evolve to provide biosafety rules, standardized protocols, and economic incentives. Enhancing multidisciplinary capability across academia, industry, and government is essential for establishing microbial food waste valorization as a fundamental component of the circular bioeconomy.

13. Conclusion

Currently, environmental damage, insufficient resources and food insecurity make food waste a serious concern and, simultaneously, an opening for sustainable growth. It is now possible to turn food waste into helpful resources with the help of microbial ecosystems. It discusses microbial communities and their roles in breaking down food waste and producing biofuels, biofertilizers, bioplastics, and similar products using composting, anaerobic digestion, and similar processes. The increase in omics, metabolic engineering, and systems biology has made it easier to understand how microbes interact, so efficient and stable bioprocesses can be designed. Better bioreactor design, real-time checking, and AI increase the feasibility of scaled applications. Even now, issues like feedstock variability, microbial instability, extracting the product successfully, cost concerns, and rules and views from society remain. Seeing microbial ecosystems as active and connected groups makes it possible to improve their functions with directed measures. Engineering the microbiome and creating specific consortia make the process work better. Using microbial fuel cells and nutrient recovery systems along with MBRs adds additional help to the environment and economy. Modular and flexible technologies created for each area are better for regions with fewer resources and lower incomes. People need to be involved and learn, and both the public and private sectors must work together for adoption. Strong policies with clear directions, incentives and infrastructure are essential. Working with microbes that have not been studied and using AI for prediction creates exciting new areas. By exploiting the value of microbes, food waste can contribute to circular economies and better development step by step, turning waste into wealth.

Author contributions

All authors worked on concept, writing and proofreading.

Conflicts of interest

There are no conflicts to declare.

Data availability

The data supporting the findings of this study are available from the corresponding author upon reasonable request.

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