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REVIEW ARTICLE

Microbial Technologies in Waste Management, Energy Generation and Climate Change: Implications on Earth and Space

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Abstract | Microbes are important decomposers of organic waste. By decomposing organic waste and using it for their growth, microbes play an important role in maintaining ecosystem's carbon and nitrogen cycles. An ecosystem's microbial shift may disturb it's carbon/nitrogen cycle as a result of any climate change or humanitarian factors, but heat produced by various instruments and greenhouse gases contribute significantly to global warming which in turn may be related to microbial shift of ecosystems. To reduce greenhouse gas emissions and global warming, innovative clean energy production methods must be employed to develop fuels with minimal greenhouse effect. Biofuels, such as bioethanol, provide clean energy with less carbon dioxide emissions. For the production of bioethanol, it is always recommended to use microbes that are capable of decomposing complex organic matter (cellulose, lignin, hemicellulose). Some microbes can efficiently decompose complex organic matter due to the presence of genetic machinery that produces cellulases and β-glucosidase. The membrane transporters are also important for microbes in uptake of simple sugars for metabolism and ethanol production. Microbial technologies are addressing the future needs for not only organic waste management but also clean energy/bioethanol production. However, the role of these technologies on space missions and extraterrestrial settings needs to be explored to improve long term space missions.

1 Introduction

Modern society produces a significant amount of food and organic waste. An estimated third of food intended for human consumption goes to waste through the food supply chain[1], accounting for approximately $750 billion in production costs. As per previous reports, over 46% of global solid waste is organic waste[2]. The United States produces 71 million tons of organic waste derived from food waste and yard trimmings, contributing to 28% of the country's total municipal solid waste stream[2]. Environmental policies promote the use of organic waste and their management practices to produce energy and reduce greenhouse gas emissions[2]. Food waste contains complex carbohydrates (starch, cellulose, and hemicellulose)[3], which are resistant to degradation. However, organic waste can be managed by valorization through anaerobic digestion, composting, and mulching to produce useful products[2, 4]. In anaerobic digestion, the decomposition of organic matter occurs in the absence of oxygen, while composting is a process that facilitates the aerobic decomposition of organic matter. These management practices also depend upon the composition of the organic waste and its decomposition during composting and anaerobic digestion[2]. The organic waste management strategies

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end up in methane production and organic products, which can be used as fertilizers. The properties of a microbe to decompose a specific material depend on its genetic machinery, which is meant for production of several enzymes. These enzymes play essential roles in the decomposition of complex organic materials (cellulose, starch, and lignin) to simple carbohydrates/sugars which are further utilized by microbes for their growth and metabolic activities. Additionally, the uptake systems and specific membrane transporters of microbe play important roles in intake of simple carbohydrates/sugars into the cell which after metabolism fermentation produces several useful end products like ethanol. More specifically, during fermentation and decomposition processes, the fungal/ bacterial cellulases hydrolyze cellulose into oligoglucans, and cellobiose is further converted to glucose by β-glucosidase[5]. This review discusses the organisms used in managing organic wastes and their functional properties. Moreover, we discussed the expected role and potential applications of microbial based technologies in addressing global change. Microbes are closely related to soil decomposition processes, therefore, are also thought to play an important role in the carbon (C) cycle and climate change. Consequently, changes in the microbial composition of an ecosystem are expected to affect the C cycle, the nitrogen (N) cycle, and soil productivity, all of which may be related to climate change. Despite having insufficient evidence, global warming is considered to play a role in changing biodiversity, however, the present review article also highlights factors other than global warming that are contributing to microbial diversity and other biodiversities in ecosystems. Current lacunae in literature, challenges to study climate change in the natural ecosystem, and future prospects for understanding the factors affecting climate change and biodiversity are highlighted in this article.

2 Microbes and Their Characteristics in Complex Organic Matter Degradation

Microbes, including bacteria, fungi, and yeasts, play critical roles in decomposing organic matter and the global carbon cycle as the primary decomposers of litter and wood[6]. Fungi are primary decomposers of organic material in terrestrial ecosystems[7]. Wood decaying fungi are traditionally classified as white rot or brown rot[8]. White rot fungi are characterized by their capability to degrade all components of plant cell walls, including lignin[8]. In contrast, brown rot fungi evolved selectively to target carbohydrates and leave behind lignin largely intact and unused[7,8]. The lignin decomposition mechanisms were first uncovered in "white rot" fungi, which produce carbohydrates by degrading lignin. The brown rot adaptation of fungi is supported by mechanisms that release reactive oxygen species (ROS) that attack wood structures[7]. A recent study of carbohydrate-active enzymes (CAZYs) families has shown that a temporal regulatory shift of lignocellulose-oxidizing genes was reported during the early stages of brown rot compared to white rot[7]. Thus, the modulated expression of ROS-generating genes could have played a pivotal role in brown rot adaptation[7]. A recent study on 34 fungal isolates reported that fungi's decomposition ability varies from stress-tolerant, poorly decomposing fungi to fast-growing, competitive fungi that rapidly decompose wood. The fungal communities of fast-growing fungi decompose wood more quickly[6]. Fungal growth rate (hyphal extension rate) is reported as the strongest predictor of fungal-mediated wood decomposition rate under laboratory conditions. However, the decomposition rate correlates negatively with moisture niche width (an indicator of drought stress tolerance) and with the production of nutrient-mineralizing extracellular enzymes[6].

Most organisms require water for survival but fungi can perform decomposition and nitrogen transformations even in droughts[9]. The functions of C-and N-acquisition in drought are performed by inducing an increase in frequencies of fungal functional genes related to ammonium transporter, amino acid permease enzyme, chitinases, and cellulose-targeting AA9 genes[9]. In other words, we can say that in drought, the fungal species that contain these genes get enumerated. The fungi having these genes may better adapted to harsh environments like drought[9]. Furthermore, fungal degradation of cellulose and plant cell walls can also be enhanced by increasing the availability of nitrogen. In bacteria, analysis of functional traits revealed species-specific properties to degrade β-glucans can serve as predictive functions for efficient cellulose decomposition[10]. A recent study has categorized fungal gene family domains encoding for enzymes responsible for N uptake and organic matter decomposition. Ammonium transporter and nitrate transporter genes were considered responsible for the uptake of inorganic N, whereas amino acid permease was deemed critical to the uptake of organic N. However, there were two categories for the decomposition of organic matter, the genes involved in the decomposition of cellulose (genes coding for cellobiohydrolase, β-glucosidase and lytic polysaccharide monooxygenase) and the genes involved in the decomposition of lignin (lignin peroxidase)[11]. The following section discusses the impact of these functional characteristics of microbes on solid waste management and production of biofuels.

3 Solid Waste Management for Global Energy/Biofuel Generation

As a common biofuel, bioethanol is used to overcome the greenhouse gas emissions. However, the greenhouse gases released during the fermentation process of producing bioethanol should be considered when discussing clean energy. Several substrates can be used in ethanol production, such as molasses, starch-based substrates, sugar sorghum cane extract, lignocellulose, and others[12]. There are several strategies which are implemented to optimize ethanol production, shorten fermentation time, and reduce process cost[13]. Use of solid and other waste materials containing organic matters are best employed to generate bioethanol. A recent study has evaluated the ability six wood-decay and compost-inhabiting ascomycetes in bioethanol production where *Fusarium oxysporum* had shown potential for maximum bioethanol production and yield of 2.47 g/L and 0.84 g/g[14]. To meet the future energy demands, similar strategies can be implemented in space. Space associated fungal species and other microbes may be best implemented to clean the closed environments like International Space Stations (ISS) by decomposing the generated waste along with production of biofuels[15].

4 Ecosystems Balance, Climate Change and Biodiversity

Microorganisms consume and produce the key greenhouse gases CO_2, CH_4, and N_2O, which contribute to global warming[16]. The abilities of microbes are not limited to only decomposing complex carbon sources/ organic matter and metabolizing them to form useful endproducts but these abilities are the cause of their close connection with global/climate change. Understanding the mechanisms controlling the accumulation of soil carbon is critical to not only predicting the Earth's future climate but also remedial measures. There are evidences that soil's microbial signatures play key roles in carbon storage[17]. As per theoretical prediction, presence of Ectomycorrhizal and ericoid mycorrhizal (EEM) fungi in soils increases carbon storage capacity. As per global data sets, ecosystems dominated by EEM-associated plants contains 70% more carbon per unit nitrogen than soil in ecosystems dominated by arbuscular mycorrhizal (AM)-associated plants[17]. Although the effect of global change on fungi is still insufficient but there are evidences that warming and physical changes can nutrient availability and cycling by microbes, which will have unknown cascading effects on the environment[18,19].

There are many hypotheses and assumptions about the role of microbes in climate change and ecosystem balance. However, the cause-or-effect relationship between microbes and climate has yet to be clarified. Marine biodiversity is claimed to be affected by climate warming at a global scale[20]. However, the effect of factors other than global warming/climate changes on marine biodiversity are not considered. Marine diversity of pelagic species might be significantly impacted due to fishery activities (including tourism and snorkeling) rather than warming[21–23]. There are many assumptions, but until now, there has been no controlled experiment to validate the effects of proposed temperature shifts/climate change on the diversity, mortality, and survival of pelagic species or microbial diversity. Water pollution is not even considered when global warming is cited as for affecting diversity. In temperate rivers, the change in biodiversity is noticed due to river fragmentation and the introduction of non-native species[24]. Biodiversity questions in connection to climate change or global warming need re-iteration and carefully investigated before reaching conclusions so that factors other than global warming should also be considered to protect the planet earth. There is evidence that factors other than global warming/climate change are contributing significantly to the decline of marine biodiversity. These factors are human activities, water pollution, and the fishery industry[22–24]. Global warming/climate change affects microbial and other biodiversity[25]. However, uncontrolled human activities seem to have a far greater impact on the marine environment than a minor increase in temperatures. In contrast to the lack of significant evidence that a minor degree increase in temperature is lethal for marine life and biodiversity, other factors and humanitarian activities need to be taken into consideration in order to resolve the mechanistic insights about global warming related biodiversity shift and its relationship to C/ N cycles. Insights into factors causing changes in biodiversity will help to design microbial remedies for reversing climate change and related issues such as drought, soil productivity, and changes in biodiversity.

Moreover, literature is also scarce regarding the role of microbes on ecosystem balance and climate change. Still, there are clues that microbial communities are related to productivity and health outcomes of flora/ fauna of a territory[16]. A recent study reported that the richness of fungal decomposers is positively associated with ecosystem stability worldwide. In addition, the richness of soil decomposers was reported to be positively linked with higher resistance of plant productivity in response to extreme drought events. Notably, the presence of fungal plant pathogens is negatively linked to plant productivity. Thus, maintaining the richness of soil decomposers may act as a buffer against extreme climate events like drought, with the suggestion of promoting stable plant production over time in global ecosystems[26]. The study also provides clues about the strategies to be followed for growing plants in adverse conditions and encouraging efficient efforts in plant production on ISS and extraterrestrial worlds. As per recommendations of the study, use of microbial richness of decomposers in the soil/ Mars and Lunar regolith may open up opportunities for improving plant production in drought conditions on earth and extraterrestrial worlds. The change in microbial communities of an ecosystem may have been impacted because certain microbial communities adapted higher temperatures are supposed to be predominantly abundant than the previous microbiome. In the natural habitat conditions, it may be impossible to detect the determining factor that impacts biodiversity. Still, some controlled experiments can validate the effect of each element expected to be involved in climate change. Therefore, factors, global warming/climate change, water/ ecosystem pollution, or humanitarian activities (fishery, tourism and snorkeling) in context to biodiversity need to be studied by using controlled experiments. Considering humans are the significant carriers/ spillers of the microbiome[27], thus, a change in the microbial shift in the human-exposed ecosystem is expected. Marine phytoplankton perform half of the global photosynthetic CO_2 fixation and half of the oxygen production[28,29]. Moreover, microorganisms have important roles in carbon and nutrient cycling, agriculture, animal and plant health[28], thus, a microbial shift in the ecosystems may have huge impact on these processes. After conducting more focused studies and continuous monitoring of microbial shifts in specific ecosystem/ marine worlds, specific microbial remedies may help improve the microbial balance if the change in microbial diversity is considered the cause rather than the consequence of human activities and global warming. To get closure look on the effect of climate change or humanitarian activities, there is need to regularly monitor marine water samples for microbial and total biodiversity by using advanced next-generation sequencing techniques along with analyzing the chemical composition of water by using metabolomics techniques. To achieve these objectives, sample preservation/storage strategies must be employed and correlations between shifts in chemical composition with biodiversity needs to be established for validation of factors affecting biodiversity, along with establishing the cause or consequence relation between them.

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Author contributions

AMC conceptualized and wrote the article. KV and NKS also partially conceptualized and edited the article. All authors read and approved the final manuscript.

Declarations

Conflict of interest

The authors declare that they have no competing interests.

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Dr. Atul Munish Chander is a biomedical scientist with extensive experience in microbial sciences, bioinformatics techniques as well as genomic data analysis, fungal taxonomy, microbial genomics, gut microbiome, food and nutrition biotechnology, metagenomics, comparative genomics of probiotics and infectious microbes/ pathogens. Moreover, he has extensive experience in designing and conducting clinical studies and clinical trials. In his work at JPL, he has contributed to the description of two novel fungal genera from the spacecraft assembly facility (SAF), as well as the description of ten unknown fungal/ yeast species. He has also gained extensive experience in evaluating the effect of space radiation and microgravity on living systems (bacteria, fungi, yeast, and invertebrate animals/ *Caenorhabditis elegans*). He has been exploiting microbial potential to life support technologies and real life problems on earth and space sciences.

Dr. Nitin Kumar Singh 10+ years of research in Microbiology encompasses Microbial taxonomy, Microbial Genomics, Metagenomics, and Microbial ecology study, analysis, and interpretation. He is specialized in working on pathogenic microbes found in hospital environments / clean rooms (SAF) to understand how microbes adapt to become more pathogenic under anthropogenic pressures. His work on Acinetobacter sp. and Bacillus anthracis clad has helped in the taxonomic resolution of both the genus. He has played a crucial role in describing 14 novel bacterial species from various environments. He has been involved in the Genomic and Metagenomic analysis of various projects like ISS-MO, ISS-MOP, CASIS, IMPAS, SPACE-X, JPL-SAF, HEPA and MARS 2020. His work has helped narrow down ISS's dominant microbial population and establish its genomic identity through metagenome resolved genomes. He has been part of the team which described three novel species from ISS, including a novel genus. He is a member of the current JPL's; Team A, COVID-19 analysis team, murine model study, Tardigrade, and Diatom genome analysis, Human genome analysis, and MAG-based ecological descriptions. He has been instrumental in the implementation of BIG-DATA analysis, ML, AI, and visualization leading to the corelational analysis of all the studies conducted at BPPG.

Dr. Kasthuri Venkateswaran is the Senior Research Scientist at JPL and supports the Biotechnology and Planetary Protection Group. His 47+ years of research encompasses marine, food, and environmental microbiology. He has applied his research in molecular microbial analysis to better understand the ecological aspects of microbes, while conducting field studies in several extreme environments such as deep sea (2,500 m), spacecraft missions (Mars Exploration Rovers), assembly facility clean rooms, and the space environment in Earth orbit (ISS). Also, he provides expertise for non-NASA programs such as commercial agencies (Boeing – airline cabin air measurement) and medical industries (tissue and organ transplants processing). The bioinformatics databases generated by Venkat's team are extremely useful in the development of biosensors which will provide information about the spacecraft surfaces and enclosed habitats in an attempt to determine forward contamination as well as develop countermeasures (advance cleaning and sterilization technologies) to control the problematic microbial species.