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Breaking down the plastics paradox: polymer degrading microorganisms

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Plastic's unique qualities, which make it appealing for daily usage, also endanger the sustainability of the global community. The main benefit of plastics is that they are sturdy, long-lasting, and non-reactive. As a result, the production of plastic garbage has exponentially increased, but due to its non-biodegradable nature, a threat to the environment is now identified on a global scale. The existing abiotic ways of getting rid of these wastes (incineration, landfilling, and recycling) are extremely expensive, unsustainable, and burdensome to the environment. In light of this, current attention has been drawn more to the possibilities for biological systems to break down plastics made from synthetic materials. A number of polymer-degrading microorganisms have been identified in various sources like garbage, mines, dumping yards, and other extreme environments. The microbial enzymes and their mode of action are also being investigated, in view to developing a recombinant microbial strain or enzyme for a sustainable approach to getting rid of plastic. The present review aims at studying all these efforts and draw a meaningful conclusion for breaking down the plastic paradox.

Keywords: Polymer, Biodegradation, Microorganisms, Microbial enzymes, Sustainability.

INTRODUCTION

One of the most pressing environmental issues today is the buildup of plastic garbage leading to 'White Pollution', which globally affects all living forms, natural ecosystems, and the economy. Plastics are man-made polymers with an enormous number of applications. Due to their pliability, endurance, and ability to withstand erosion, plastics are excellent materials for a variety of applications. Forty percent of the over 400 Mt of plastics manufactured are utilized in single-use applications, producing a sizable quantity of trash. The environmental harm is caused by the buildup of garbage made of polystyrene, polyethylene, polypropylene, polyvinyl chloride, polyurethane, and polyethylene terephthalate. The molecular structures of major polymers are presented in Fig. 1. There is a lot of study being done on their potential for degradation through biotic and abiotic processes. The majority of current waste management practices include abiotic processes like: recycling, burning for energy recovery, and buildup in landfills, causing more harm to the environment [1].

Moreover, the worldwide ecology and the health of living things are negatively impacted by the increasing amount of micro-nano plastics in the natural ecosystem. Through trophic transfer, ingestion, and inhalation, micro-nano plastics penetrate the agroecosystem, flora, fauna, and human body, causing blood vessel obstruction, infertility, and aberrant behaviors [2]. Therefore, using a cutting-edge method to remove micro-nano plastics from the natural environment becomes essential. In light of this issue, it is essential to find alternatives that are environmentally responsible options, like biodegradation instead of conventional dumping. Microbial remediation is viewed as a greener solution among the several micro-nano plastics remediation techniques now in use [3]. In order to build an efficient and sustainable approach to managing plastic trash, an eco-friendly strategy is required. This approach takes advantage of the potential of various microbial species to degrade these polymers [4].

Polymer-degrading microorganisms

Polymer-degrading microorganisms are a group of microbes that have the ability to break down various types of polymers, such as plastics and synthetic materials, into simpler compounds. These microorganisms play a crucial role in the natural biodegradation of polymers, helping to reduce environmental pollution caused by plastic waste [5]. There are several types of polymer-degrading microorganisms, including bacteria, fungi, and some types of algae. They possess specific enzymes that can target and cleave the chemical bonds present in polymers, breaking them down into smaller molecules that are potential sources of energy and nutrients for the microorganism [6].

It is important to fully comprehend how these microbes work to lessen the amount of plastic in the environment. Microorganisms can decompose a polymer either aerobically or anaerobically.

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Microorganisms may utilize these polymers as a source of energy by releasing some extracellular enzymes. Numerous enzymes, including PETase, cutinases, hydrolases, and bacteriophilic enzymes thought to be involved in the breakdown of plastics, have been identified from bacteria. The first and crucial step is the adherence of microbes to the surface of the polymer. There are anchor peptides on the surface of these enzymes that work in the linking of enzymes with the polymer [7]. Enzymes catalyze the bioremediation process and convert large polymers into small inorganic molecules that can be utilized by microbes as a source of carbon and energy [8].

Studies that focus on the structural study of relevant enzymes and the reaction pathways to achieve desired outcomes have been carried out to optimize efficient enzymatic conditions for the breakdown of plastics. It is important to choose an appropriate microbe for plastic degradation that targets various types of polymers. Additionally, they can aid in the creation of better enzymes to handle the problems associated with plastic waste [9].

Assessment of bioremediation

In a study conducted on microbial degradation of polymers, it was observed that the anaerobic incubation of polymers with some bacterial strains resulted in structural changes in the raw and deteriorated polymers. It has been analyzed through the use of Fourier-transform infrared spectroscopy (FTIR), thermo-gravimetric analysis (TGA), X-ray diffraction (XRD), and contact angle research. The polymer-degrading bacteria *Brevundimonas* and *Sphingobacterium* served as catalysts for the succeeding aerobic treatment's stimulation of the PBAT/PLA polymers' breakdown by thermophilic anaerobic degradation. Under thermophilic circumstances, the physical breakdown of the PBAT/PLA polymer was noticed [10].

Apitius *et al*. (2019), immobilized polymer-degrading enzymes producing microorganisms to effectively reduce long-lasting plastics. In order to specifically adhere entire cells to the surface of polymers, polymer-binding peptides were used as adhesion promoters. To increase the binding strength of peptides that bind to polymers, guided development of such peptides for *Escherichia coli* surface display scanning method was designed. By immobilizing entire cells on polymer beads, the cell surface screening technique enabled the enrichment of better binding peptides from a culture broth. It is possible to employ this method of cell display screening to improve adhesion peptides in order to direct and immobilise organisms to polymer surfaces (like PP) and to break down certain types of plastic in a targeted manner [11]. Ji *et al*. (2023) developed a procedure for locating and creating anchor peptides that were specially designed to act as non-catalytic binding sites for synthetic polymers. In order to increase the effectiveness of biocatalytic plastic recycling processes, the found anchor peptides have the potential to attach to plastic-degrading enzymes [12].

The fracturing stimulation process revealed challenges related to the effectiveness of the oxidative breaker when addressing oil and gas reservoirs marked by low permeability and temperature. This circumstance resulted in the accumulation of polymer blockages and subsequent decreases in production rates. To tackle this issue, researchers conducted a microbial-assisted experiment aimed at eradicating the polymer-caused congestion within fractures, with the goal of augmenting oil yields. The findings confirmed the viability of alleviating polymer blockages within these reservoirs by utilizing native microorganisms. Additionally, these findings carried noteworthy implications, as they laid the foundation for a crucial approach in enhancing oil recovery [13]. Scanning electron microscopy, Fourier transform infrared spectroscopy, and contact angle measurements were applied to determine the degree of microplastics' biodegradation in deeper strata than river [14]. Grivalský *et al.* (2018) revealed that nonisothermal chemiluminescence, which examines the polymer surface's momentary oxidation state, is a good tool to observe the biodegradation dynamics on polymeric film, while Ecoflex agar is able to choose advantageous bacteria that can break down polymers [15].

Polymer-degrading bacteria and their sources

Plastics are naturally broken down by enzymatic, aerobic, or anaerobic biodegradation due to the bacterial and fungus communities that live in garbage or abandoned plastics. Through a variety of approaches, bacteria, and fungi having the capacity to degrade polymers are identified. *Arthrobacter sp., Bacillus* sp*., Rhodococcus* sp*., Microbacterium* sp*., Phanerochaete* sp*., Pseudomonas* sp*., Staphylococcus* sp*.,* and other particular bacterial and fungal species specifically break down polymers at the appropriate rate and duration. In addition to improving agricultural crop productivity and surface and subsurface water quality, polymer decomposition by microbes modifies soil properties, ecology, ecosystem, and characteristics. It reduces the release of polymers from the industry and limits contamination in the soil layer. It will eventually aid in maintaining the ecosystem and natural resources [16].

Polymer biodegrading microorganisms have been identified from a broad range of habitats, including polluted soil, water bodies (such as rivers, lakes, and oceans), compost heaps, waste disposal sites, wastewater (WW) streams, municipal sludge, municipal solid waste (MSW), plastic dump yards, and even from the guts of certain organisms like insects and worms [17].

Water bodies

Microplastics are generated in various environments by physical and chemical disruption processes that break down plastic debris. Since microplastics may be transported anywhere in the globe by wind or ocean currents, they can even travel to the most distant parts of our planet. As a result, they are found in practically every habitat. Interest in the field of microbial ecology has increased with the discovery that this special substrate can facilitate microbial spread. On the growth, movement, persistence, and ecology of microorganisms, microplastics have synergistic effects [18, 19]. In a study conducted by Kumar *et al*., epiphytic bacteria associated with five different marine macroalgae (*Sargassum, Ulva, Padina, Dictyota*, and *Pterocladia* sp.), that were obtained from India's central west coast, were examined for their cultivable diversity and polymer-degrading ability. Using 16S rRNA gene sequence analysis, 238 bacteria were identified and subjected to degrading polymer (cellulose, pectin, xylan, and starch) activities. Out of the 360 total strains that were isolated, purified, and conserved, xylanase activity made up 61.3% of the polymer hydrolysis potential, whereas amylase, cellulase, and pectinase activity made up 59.7%, 58.8%, and 52.2% of the total, respectively [20].

Bacteria and fungi isolated from the marine environment have been used to biodegrade synthetic polymers made from discarded plastic bottles. By using characterization techniques including weight loss, FTIR, SEM, and XRD, the deteriorated polymer films were thoroughly assessed. According to the findings, in a period of 6 weeks, the polymers from waste samples from plastic bottles degraded by 35% when treated with bacterial strains and by 22% when treated with fungal strains. Different criteria were used to analyze the data, including temperature, pH, and inoculum dose concentration [21]. Longitudinal gradients of river sediments were examined and the microplastics and associated microbial populations were discovered by Niu *et al*. in 2021. The average quantity of microplastics increased from the upper levels to the lower levels of sediment, where smaller microplastic particles predominated. Microplastics deteriorated faster in deeper layers, according to contact angle measurements, scanning electron microscopy, and Fourier transform infrared spectroscopy-attenuated total reflectance research [13].

Wastelands/ garbage soil

Polymer-degrading and thermophilic bacteria, *Acidicaldus* and *Granulicella*, were identified by Kohler *et al.* from a copper slag deposit. *Povalibacter*, a less prevalent but intriguing bacterium that breaks down polymers, was also discovered in soil specimens taken from the collection of pre-industrial mines. A single sample of industrial mining waste has been chosen for 16S rRNA analysis and identification. The findings demonstrated the presence of soil bacterial communities in soil samples from historic copper mine sites, which may provide a prospective source for microorganisms with important metabolic properties [22].

From waste soil, Patil (2018) identified four bacterial species and two fungus species. *Pseudomonas putida, Bacillus amylolyticus, Pseudomonas fluorescence* and *Bacillus firmus* were recognized as bacterial species. In a 30-day examination of the effectiveness of *Bacillus sp*. separated from waste dirt on the degradation of commercially available plastic carrying cases made of low-density polyethylene (LDPE) in shaker culture, it was shown that the bacteria reduced the plastic by up to 32%. [23]. Applying a polymer film-based examination method, PLA-degrading bacteria were collected from digester sludge, and the isolates were later identified as *Bacillus sp*. MYK2 and *Pseudomonas sp*. MYK1 by 16S rRNA analysis. An agar plate with a PLA film on it was infected with the associated biofilm during sludge addition on PLA granules, which were carried out by serially transferring a subculture into a new medium for 40 days. With the help of 3D optical microscopy, it was confirmed that isolates physically deteriorated the PLA sheet [24].

Chronically, plastic dump sites rich in LDPE may be used as a crucial resource of polymer degrading bacteria. Using biochemical tests and gram-staining techniques, the bacteria that break down polythene at soil waste sites were found. The decomposition using mineral salt media (MSM) in bags made of polythene using a weight determination technique beneath laboratory circumstances (inside the lab) was used for 30 days and demonstrated to be effective by *Klebsiella pneumonia, Pseudomonas aeruginosa, Micrococcus* sp*, Bacillus* sp*., Arthobacter* sp*.,* and *Pseudomonas* sp. The weight loss method, FTIR, and SEM were used to measure

the decomposition of polythene in separate studies [25-28].

Potential bacterial strains identified from waste disposal sites in Uttaranchal, India, as well as others from specially created dirt beds included maleic anhydride, glucose, and minute particles of plastic. Based on their capacity for using high- and low-density polyethylenes (HDPE/LDPE) as a major carbon source, isolates were screened. The degradation of consortium-treated HDPE was confirmed by simultaneous thermogravimetric-differential thermogravimetric-differential thermal analysis (TG-DTG-DTA) and Fourier transform infrared spectroscopy (FTIR), which showed that it was significantly worse than that of LDPE and considerably worse than that of untreated samples [29-31]. LDPE biodegradation effectiveness of possible microbial consortia for polymer degradation was evaluated in relation to the effects of a pair of nanoparticles, specifically superparamagnetic iron oxide nanoparticles (SPION), nano barium titanate (NBT), fullerene-60. Using Fourier transform infrared spectroscopy (FTIR), thermogravimetric-differential thermo gravimetric-differential thermal analysis (TG-DTG-DTA), scanning electron micrographs (SEM) and other methods, it was demonstrated that LDPE degrades in many steps when exposed to nanoparticles. The study emphasized the importance of interactions between bacteria and nanoparticles, which had a significant impact on the biodegradation processes [32, 33].

The progressive response of various bacterial consortia made up of *Pseudomonas sp.* strains Rb10, Rb11, *Bacillus* sp. strain Rb18 and *Ps.* sp., Rb13, *Lysinibacillus* sp. strain Rb1, and *Ps.* sp. was tested for degradation of PET, PHB, cellophane-like polymers. When these composites were treated with a bacterial consortium, significant alterations in the link strength, external morphology, and conductivity be situated discovered. Once compared to copolymer, these alterations in mixes were far more pronounced. The prospective isolates not only survived, but the variety of the bacteria increased significantly throughout the course of the whole incubation period [34-38]. There are reports on thermophilic, alkaliphilic, halophilic, and psychrophilic bacteria's biodegradation of typically manufactured plastics in both natural and laboratory environments. The majority of the information addresses two key issues: the degradation of different artificial polymers is expected to be facilitated by extremophilic microorganisms and their enzymes, and any potential effects can extremophiles have on emerging technology for combating pollution [39].

An efficient method for selecting microbes adapted to degrading polyethylene (PE) and polypropylene (PP) was established and size of the polymer breakdown by separated populations of bacteria from wasteland was evaluated. The isolates included seven bacterial strains with PE degradation potential (three *Priestia megaterium, Enterobacter ludwigii, Klebsiella pneumoniae, Chryseobacterium* sp. *Ps. fluorescens*), seven varieties of fungi with PE degradation potential (two *Lecanicillium* spp., *Trichoderma* sp. and four *Fusarium* spp.,), seven different bacterium strains (two *Enterobacter* spp. and five *Serratia marcescens*) and six different fungal varieties (*Penicillium* spp., *Fusarium* spp., and four *Aspergillus* spp.,) had the ability to break down PP. Analysis using scanning electron microscopy (SEM) demonstrated that a biofilm was present [40].

Genes coding the intracellular lipases LIP1 and LIP2, which are produced by the bacteria *Pseudomonas chlororaphis* PA23 were identified. Following incubation with LIP1 and LIP2, Gel permeation chromatography (GPC) examination revealed a reduction within the polymers' molecular mass. The polymer-degrading activity of the enzymes was also seen in polymers based on petroleum including polyethylene succinate (PES) and poly (-caprolactone) (PCL) [41]. From Chinese forest soil, Gram-negative, short rod-like strain that is capable of degrading different polymers was found. According to the examination of the 16S rRNA gene sequence, this particular strain had 99.3% higher similarity rates with *P.alcaliphila* NBRC 102411T, 99.2% with *P. mendocina* NBRC 14162T, and 99.0% with *P. oleovorans* NBRC 13583T [42].

Acinetobacter sp., *Escherichia coli*, and *Brevibacillus* sp. were isolated from industrial effluent and employed independently to track the breakdown of five synthetic polymers that are not biodegradable. All three strains have a greater than 75% degradation rate for the aforementioned polymers [43]. In landfills, *Bacillus megaterium* and *B. cereus* were isolated and tested for their capacity to break down polycarbonate (PC) polymers. By looking at the growing trajectory, clean area development, amylase & lipase creation, AFM, and FTIR, it was possible to assess the isolates' capacity for biodegradation. It was discovered that isolates had highly promising PC biodegradation abilities [44].

PET is a polymer that is widely utilized in plastic items, and its build up in the environment has raised

concerns throughout the world. A significant amount of PET-containing plastic materials due to an accretion in the atmosphere being a non-degradable contaminant, is posing serious threats to the survival of numerous endangered species and so endangering the ecosystem and biodiversity. A bacterium known as *Ideonella sakaiensis* has drawn notice for its unusual capacity to degrade and consume a kind of plastic known as polyethylene terephthalate (PET). A group of scientists from Japan's Kyoto Institute of Technology found this bacterium in 2016. It was given the name "*Ideonella sakaiensis*" since it was identified from soil samples taken at Sakai City PET bottle recycling facility. Debris made of polyethylene terephthalate (PET) are extremely durable and hence pose a long-term environmental burden. However, existing recycling initiatives are still not sustainable. A potential fix is two newly identified bacterial enzymes that selectively break down PET. First, PET is transformed hooked on mono-(2-hydroxyethyl) terephthalate (MHET) by *Ideonella sakaiensis*PETase, a consensus /-hydrolase fold enzyme with a well-characterized structural fold [45-59].

It was demonstrated that MHETase serves as exo-PETase by hydrolyzing the created PET pentamer based on structural studies and biochemical investigations. The experiments further showed that MHETase possesses hydrolysis activity against the PET film produced by termini, illustrative of the enzyme's exo-PETase activity. An MHETaseR411K/S416A/F424I variant with increased BHET activity was engineered, showing improved PET film degrading activity [60, 61].

Other sources

Tachibana *et al.* studied the microbiota of washed-rind cheeses from Japan and identified a bacterium similar to a marine inhabitant; *Alcanivorax dieselolei*, from one of the cheeses Muchuri. It is crucial to look into the microorganisms in fermented foods' capacity to hydrolyze polymers since the usage of biodegradable polymers for food packaging is growing in popularity [62].

The Greater wax moth gut microbiota was investigated using a culture-dependent methodology. In the GWM gut, nine bacterial and one microalgal species were identified by 16S-rDNA sequencing. They degrade low-density polyethylene, 2-methyl phenanthrene, and polycyclic aromatic hydrocarbons [63].

Role of fungi in polymer degradation

Marine fungi may also exhibit a significant role in the decomposition of complex organic matter in the ocean. An advanced research has shown that certain marine fungi, such as *Zalerion maritimum*, have the capacity to break down polyethylene [64]. As their sole supply of carbon, certain fungal strains use these plastic polymers to create environmentally benign carbon compounds. It has been discovered that a number of fungi may effectively and successfully break down a variety of plastic polymers. The following processes make up the biodegradation mechanism: biodeterioration, fragmentation, assimilation, and mineralization [65].

Fungi play a pivotal role in the biodegradation of polymers, as evidenced by their secretion of various enzymes including cutinase, lipase, proteases, and lignocellulolytic enzymes. They can also effectively break down plastics when exposed to specific pro-oxidant ions. Through enzymatic oxidation or hydrolysis, high molecular mass polymers undergo fragmentation into lower molecular mass polymers, leading to the introduction of functional groups that enhance polymer hydrophilicity. The quality of plastics begins to deteriorate within a short span. Specific well-known fungal species demonstrate efficient plastic breakdown, aiding in the degradation process by colonizing plastic materials. Combining photodegradation and thermo-oxidative processes with biodegradation, as suggested by multiple studies, accelerates the disintegration of plastic materials [66, 67].

Based on the literature that is currently accessible, a list of all the fungi that have been identified as degrading plastic, and remarks were made regarding the main fungal groups. In addition, 395 strains were used to analyze the evolutionary relationships of the fungus responsible for decomposing plastic. It was confirmed that polymer-decomposing fungi are found in eleven classes in the fungal phyla Ascomycota. The majority of plastic degraders in the kingdom of fungi are members of the Eurotiomycetes [68].

Although lignocellulose developed by plants is resistant to deterioration, fungi eventually learned to use it as a source of food. It may be helpful to consider the methods used to examine lignocellulose breakdown, including advanced microscopy, genomic, and post-genomic investigations (such as gene expression analysis). Based on known limits on biological lignocellulose breakdown, such as the necessity of physiochemical pretreatments for biofuel generation, potential limitations on biological plastic degradation might be expected. Although lignocellulose and plastics share many

characteristics, such as being mixtures of hydrophobic polymers with amorphous and crystalline regions and needing hydrolases and oxidoreductases to break them down, plastics differ significantly from lignocellulose in that they lack hydrolyzable C-C or C-O bonds, which gives them a higher degree of recalcitrance. Thus, the breakdown of lignocellulose by fungi can help to understand the degradation mechanism of fungi [69].

A study conducted in the vicinity of Lake Zurich in Switzerland unveiled a diverse array of fungal species thriving within the accumulated waste. Among these fungi, four saprotrophic species—namely *Cladosporium cladosporioides, Penicillium griseofulvum, Xepiculopsis graminea*, as well as a single plant pathogenic species, *Leptosphaeria* sp., exhibited the ability to degrade polyurethane. A number of different fungi that didn't grow on plastic waste were also examined. Of them, only two litter-saprotrophic fungi that can break down polyurethane were *Agaricus bisporus* and *Marasmius oreades* [70]. In a screening process, researchers utilized thirty fungal strains that had been isolated from terrestrial environments in Korea. Their objective was to assess the degradation potential of polymers such as polylactic acid (PLA) and polycaprolactone (PCL). This assessment involved observing the formation of a distinct clear zone around fungal colonies on agar plates that contained emulsified PLA or PCL. Five of them showed promising biodegradation outcomes. These were identified as *Apiotrichum porosum, Fusicolla acetilerea, Talaromyces pinophilus, Purpureocillium lilacinum,* and *Penicillium samsonianum* [71]. The printed circuit board, or PCB, is a crucial component of electronic waste. PCB is a secondary metal reservoir because of its abundant metallic content, which includes base, valuable, and poisonous metals. To safeguard the environment and preserve natural resources, PCB recycling is essential. *Aspergillus* species were used to try to bioleach certain metals from desktop PCB, The capacity of *Aspergillus niger* to produce organic acids helped in the bioleaching, which led to its selection. *Aspergillus nomius* was reported to degrade LDPE [72-74].

Role of algae in polymer degradation

Polyethylene (PE), a polymeric material produced from the basic building block ethene (C2H4), frequently obstructs sewer pipelines, agricultural land, rivers, canals, and oceans. Recently, it has been demonstrated that various algae can colonize PE surfaces using polymeric carbon and are widely accessible and relatively simple to separate. Using this group of organisms to biodegrade PE will probably help achieve a number of environmental objectives, including reducing carbon emissions and bioprospecting for products with added value. The ability to degrade PE was discovered in algae including *Anabaena spiroides, Navicula pupula, Oscillatoria subbrevis, Phormidium lucidum, Scenedesmus dimorphus* [75, 76].

In the era of plastic pollution, plants have been written off as a system that is unaffected by micro and nanoplastics, however, recent research shed light on how plastics interact with plants and explains how using plants' capacity to take up plastic particles can help get rid of plastics from water and soil systems. Due to their small size, microplastics often cannot be absorbed by plant root systems; nevertheless, some investigations suggest they may penetrate through stomata into the plant tissue while nanoparticles have been reported to travel from plant roots through the xylem to higher plant sections. However, through enzyme-facilitated breakdown processes, algae can be employed to break down polymers suspended in the water bodies [77].

Recombinant microorganisms for polymer biodegradation

Due to its intricate chemical composition, polystyrene is regarded as being both highly resistant to breakdown and non-biodegradable. The suspected enzymes that break down polystyrene come from a white-rot fungus that can break down the material. Eight *T. reesei* strains were successfully created, and the enzyme activity of the culture supernatants was checked. Several polymers had their ability to degrade tested, and gas chromatography-mass spectrometry and high-performance liquid chromatography were used to find degradation products. Although biodegradation was not observed with these recombinant strains, it was a stepping stone for further research [78].

Recently, a potential PETase-like enzyme called *Ideonella sakaiensis*PETase (IsPETase) has been discovered for entirely depolymerizing this polymer into its constituent parts. Three changes in the IsPETase active site were identified to increase its PET-degrading activity, based on the structure of cutinases and lipases being similar to the IsPETase 3D structure. The S238Y mutant which is close to the catalytic triad, had a 3.3-fold higher degrading activity than the wild-type enzyme. It's significant to note that this structural alteration boosted the enzyme's ability to degrade highly crystallized (around 31%) PET, which is used in commercial soft drink bottles. Additionally, a microscopic examination revealed that IsPETase works better under mechanical stress on the substrate surface.

These findings signify a significant step forward in the pursuit of a comprehensive and sustained degradation of PET contamination [79].

Insufficient soluble expression level of *Ideonellasakaiensis*PET hydrolase (IsPETase) prevents its efficient use in the biodegradation of PET. A variety of approaches were used to methodically investigate the IsPETaseMut, an active mutant of IsPETase ever discovered, expressed itself in *E. coli.* The higher product formation caused by NusA-IsPETaseMut PET decomposition over two weeks is more likely to be a result of the latter two catalytic qualities of the enzyme when combined. By combining the two mutations, IsPETaseS121E/D186H/S242T/N246D variant was created. Contrary to IsPETaseWT, which lost activity within a day at 37 °C, the quadruple version kept PET degradation activity going for 20 days. As a result, the activity was 58 times higher than it was for IsPETaseWT [80, 81]. To aid in a better understanding of the involvement of microorganisms, genes, enzymes, and biodegradation pathways in plastic mineralization, a thorough appraisal of the biotechnological and molecular development in plastic biodegradation is required [82]. Environmental safety is a prime concern for scientists globally. Through the use of living organisms, such as bacteria, fungi, and plants, bioremediation processes can efficiently break down and remove various contaminants from soil, water, and air. Nowadays research is also focusing on the development of alternative materials of nonbiodegradable polymers. Recently, biocarbon (BC) has come to be recognized as a sustainable filler for polymer nanocomposites made from biomass. The in-question nanocomposites have prospective uses in energy storage, heat-resistant coatings, and electrical conductivity [82]. Through value addition, pea peel waste has been effectively used to create biodegradable film. The latter showed good surface thickness, water solubility, and tensile strength. Therefore, a biodegradable film may replace synthetic plastic with the benefits of recovering energy, and contributing to a sustainable environment and development [83].

CONCLUSION

In conclusion, bioremediation is a strong and effective strategy for protecting the environment and eradicating pollution. A sustainable method, bioremediation, uses natural processes to break down contaminants. It decreases the need for dangerous chemicals and the production of extra trash. Bioremediation frequently turns out to be more affordable than conventional clean up techniques. It may be used for a variety of environmental cleaning operations since it uses fewer resources and can be scaled up. Numerous contaminants, including hydrocarbons, heavy metals, pesticides, and other dangerous compounds, can be treated *via* bioremediation. Due to its versatility, different forms of pollutants may be addressed in specialized ways. Table 1 summarizes some of the polymer-degrading microorganisms isolated from different sources, and the types of polymers they are degrading.

In addition to removing contaminants, bioremediation can enhance ecosystems' general health. The regenerated habitat may thrive with increasing biodiversity when natural microorganisms are used. Bioremediation helps to improve public health, lower exposure to dangerous compounds, and avert potential long-term health problems by removing contaminants from polluted locations. By helping to comply with legal requirements and international obligations to reduce pollution, bioremediation is in line with the concepts of sustainable development and environmental conservation.

Challenges

However, significant obstacles still stand in the way of the practical use of bioremediation. The particular circumstances that each contaminated site provides might determine how effective bioremediation is. For best outcomes, specific procedures and thorough site analyses are required. It may take persistence for bioremediation to be effective because it is sometimes a lengthy process. To get the intended result in some situations, additional methods or long-term monitoring may be required. It is essential that the public be made aware of and comprehend the advantages and safety of bioremediation. To increase confidence in this environmentally beneficial method, clear communication and education are required.

In spite of these difficulties, bioremediation is nevertheless a useful tool for the effort to create a cleaner and healthier environment. We can maximize the potential of bioremediation by continuously developing research, using technical advancements, and encouraging cooperation between researchers, policymakers, and communities.

Table 1. A list of polymer-degrading microorganisms.

Microorganisms	Source	Polymer	Ref.
Bacteria			
BrevundimonasSphingobacterium		Polylactide (PLA), Poly (butylene adipate-co-terephthalate) (PBAT)	[10]
Bacillus sp., Rhodococcus sp., Pseudomonas sp., Staphylococcus sp., Arthrobacter sp., Microbacterium sp., Phanerochaetesp	Plastic dumping yard	Polypropylene (PP), Low-density and linear low-density polyethylene (LDPE, LLDPE), Polyvinyl chloride (PVC), High-density polyethylene (HDPE), Polystyrene (PS), Expandable PS (EPS), Polyethylene terephthalate (PET)	[16], [19]
Acidicaldus,Granulicella, Povalibacter	Copper Slag Deposit	Polyvinyl alcohol	[22]
Bacillus amylolyticus, Bacillus firmus, Pseudomonas putida, Pseudomonas fluorescence	Garbage soil	Low-density polyethylene	[23]
Pseudomonas sp., Bacillus sp.	Digester Sludge	PLA	[24]
Klebsiella pneumonia, Pseudomonas aeruginosa, Micrococcus sp, Bacillus sp., Arthobacter sp., Pseudomonas sp.	Plastic dumpsites	Low-density polyethylene (LDPE)	[25], [26], [27], [28]
Pseudomonas sp., *Bacillus sp.Lysinibacillus sp*.	Culture	PET, PHB, Cellophane	
Priestia megaterium strains, Klebsiella pneumoniae, Pseudomonas fluorescens, Enterobacter ludwigii, Chryseobacterium sp. Fusarium spp., two *Lecanicillium spp*., *Trichoderma*	Wasteland	Polyethylene (PE)	[40]
Serratia marcescen sEnterobacter spp.) *Aspergillus spp. ,Fusarium oxysporum, Penicillium granulatum*	Wasteland	Polypropylene (PP)	[40]
Pseudomonas chlororaphis, Pseudomonas alcaliphila, Pseudomonas mendocina, *Pseudomonas oleovorans*	Forest Soil	Polyhydroxyalkanoates (PHAs), polylactic acid (PLA), and Para-nitrophenyl (pNP) alkanoates, Poly (-caprolactone) (PCL) Polyethylene succinate (PES)	[41], [42]
Acinetobacter sp., Escherichia coli, *Brevibacillus sp.*	Industrial Effluent	Maleic acid propane-1, 2 diol glycerol co-polyester, Maleic acid phthalic acid propane-1, 2 diol glycerol co-polyester, Maleic acid phthalic acid butan-1	[43]
Bacillus cereus, Bacillus megaterium	Landfills	Polycarbonate (PC)	[44]
Ideonellasakaiensis	Soil from Sakai City	Polyethylene terephthalate (PET).	
Alcanivoraxdieselolei	Washed rind cheese	Poly(3-hydroxybutyrate) (P(3HB))	[62]
Bacillus circulans, Enterococcus faecalis, Microbacteriumzaea, ExiguobacteriumaestuariiAgrobacterium sp., Sphingomonaspseudosanguinis, Sphingobiumyanoikuyae Acinetobacter radioresistens	Greater wax moth gut	Low-density polyethylene, 2-methyl phenanthrene, Polycyclic aromatic hydrocarbons	[63]
Fungi			
Aspergillus nidulans, A. flavus, A. glaucus, A. oryzae, A. nomius, Penicillium griseofulvum, Bjerkanderaadusta,	Marine plasisphere	Plastics	[66], [67]

Phanerochaetechrysosporium, Cladosporium cladosporioides, Pleurotus abalones, P. ostreatus, P.eryngii, Agaricus bisporus			
Ascomycota, Mucoromycota		Plastics	[68]
Cladosporium cladosporioides, Xepiculopsisgraminea, *Penicillium griseofulvumLeptosphaeria sp Agaricus bisporusMarasmiusoreades*	Plastic waste	Polyurethane	[70]
Apiotrichumporosum, Fusicollaacetilerea, Talaromycespinophilus, Purpureocilliumlilacinum, Penicillium samsonianum	Terrestrial settings in Korea	Polymers polylactic acid (PLA), Polycaprolactone (PCL)	[71]
Aspergillus nomius	Culture	Low-density polyethylene (LDPE)	[74]
Algae			
Sargassum, Ulva, Padina, Dictyota, and*Pterocladia sp*.	Water bodies	Cellulose, Pectin, Xylan, Starch	[20]
Phormidium lucidum, Oscillatoria subbrevis, Scenedesmus dimorphus, Anabaena spiroides, Navicula pupula	Culture	Polyethylene (PE)	[75], [76]

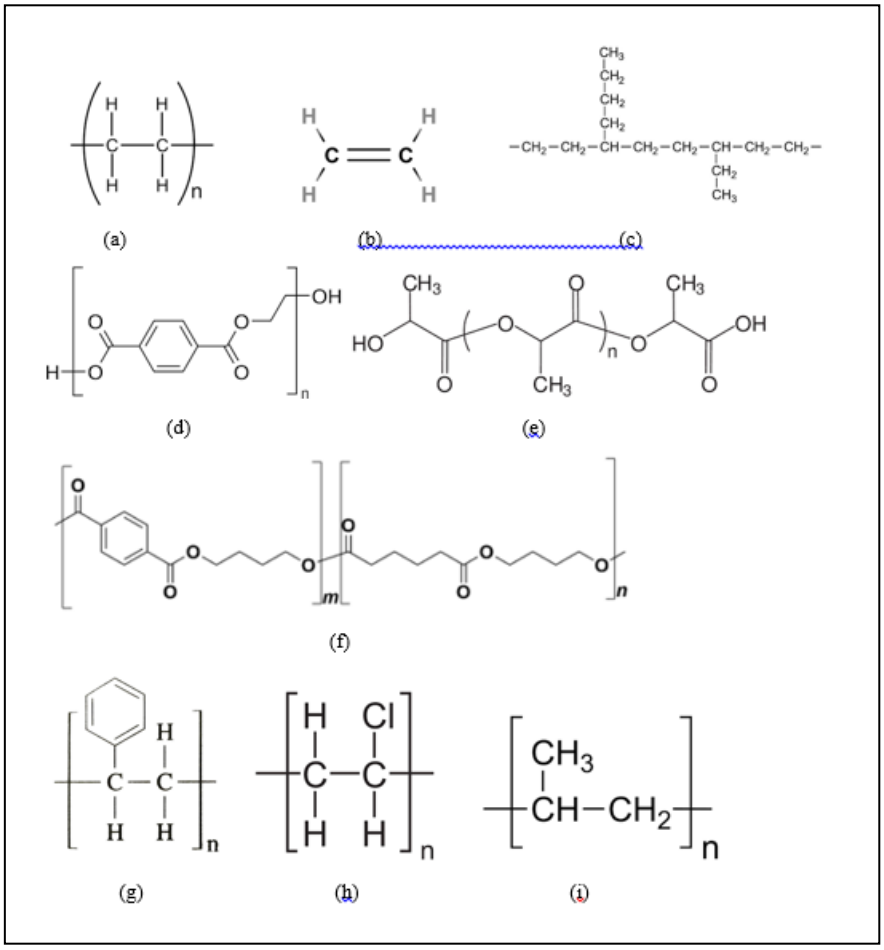

Fig. 1. Molecular structures of few polymers polluting the planet. a) Polyethylene (PE), b) Low-density polyethylene (LDPE), c) High-density polyethylene (HDPE), d) Polyethylene terephthalate (PET), e) Polylactide (PLA), f) Poly (butylene adipate-co-terephthalate) (PBAT), g) Polyurethane, h) Polyvinyl chloride) i) Polypropylene (PP)

REFERENCES

1. J. A. Verschoor, H. Kusumawardhani, A.F. Ram, J. H. de Winde, *Front. Microbiol.*, **13**, 821629 (2022).
2. N. Bostan, N. Ilyas, N. Akhtar, S. Mehmood, R.U. Saman, R.Z. Sayyed, S. Pandiaraj, *Env. Res.*, 116523 (2023).
3. Y. Zhou, M. Kumar, S. Sarsaiya, R. Sirohi, S. K. Awasthi, R. Sindhu, M. K. Awasthi, *Sci. Total Environ.,* 802, (2022).
4. S.S. Ali, T. Elsamahy, E. Koutra, M. Kornaros, M. El-Sheekh, E. A. Abdelkarim, J. *Sci. Total Environment*, **771,** 144719 (2021).
5. A. Amobonye, R. Bhagwat, S. Singh, S. Pillai, *Sci. Total Env.*, **759**, 143536 (2021).
6. N. Delangiz, S. Aliyar, N. Pashapoor, K. Nobaharan, B. A. Lajayer, S. Rodríguez-Couto, *Chemosph.*, **294**, 133709 (2022).
7. Y. Ji, Lu, Y. H. Puetz, U. Schwaneberg, *Methods in Enz.,* **648,** 271 (2021).
8. A. Elahi, D. A. Bukhari, S. Shamim, A. Rehman, *J. of King Saud Uni.-Sci.*, **33**(6), 101538. (2021).
9. Z. Cai, M. Li, Z. Zhu, X. Wang, Y. Huang, T. Li, M. Yan, *Microorg.*, **11**(7), 1661 (2023).
10. W. Peng, Z. Wang, Y. Shu, F. Lü, H. Zhang, L. Shao, P. He, *Biores.Tech.*, **343,** 126079 (2022).
11. L. Apitius, K. Rübsam, C. Jakesch, F. Jakob, U. Schwaneberg, *Biotch Bioeng.*, **116**(8), 1856 (2019).
12. Y. Ji, Y. Lu, H. Puetz, U. Schwaneberg, *Methods in Enz.,* **648,** 271 (2021).
13. L. Niu, Y.Li, Y. Li, Q. Hu, C. Wang, J. Hu, H. Zhang, *Water Res.*, **188,** 116449 (2021).
14. Q. A. Da, G. L. Lei, C. J. Yao, X. H. Qu, C. C. Chu, *Int. Field Explor. Devel.Conf.* **141** (2021).
15. T. Grivalský, J. Rychlý, L. Rychlá, M. Bučková, L. Kraková, A. Puškárová, D. Pangallo, *J. of Polym. Env.*, **26,** 680 (2018).
16. A. Sharma, V A. Nampoothiri Devadas, P. P. Nair, C. Manpoong, B. D. Kartha, *Curr.Green Chem.*, **9**(1), 3 (2022).
17. A. P. Asiandu, A. Wahyudi, S. W. Sari, *J. of Env. Treat.Tech.*, **9**(1), 148 (2021).
18. S. Dey, A. K. Rout, B. K. Behera, K. Ghosh, *Env. Microb.*, **17**(1), 1 (2022).
19. I. Wojnowska-Baryła, K. Bernat, M. Zaborowska, *Int. J. of Env. Res. and Pub.Health*, **19**(20), 13223 (2022).
20. P. Kumar, A. Verma, S. S. Sundharam, A. K. Ojha, S. Krishnamurthi, *Microorg.*, **10**(12), 2513 (2022)
21. R. Sarkhel, S. Sengupta, P. Das, A. Bhowal, *J. of Polymer Res.*, **27,** 1(2020).
22. J. M. Köhler, N. Beetz, P. M. Günther, F. Möller, J. Cao, *Microorg.*, **9**(7), 1422 (2021).
23. R. C. Patil, *J. Env. Sci.*, **6**(4), 33 (2018).
24. N. ISLAM, J. O. Geonwoong, J. U. N. G. Sokhee, *Proceeding KSBB Spring Meeting and Int. Symposium* 2023.
25. M. Yadav, S. Manderia, S. Singh, M. Deva, *Nature Env. Poll. Tech*., **21**(1) (2022).
26. R. Naaz, W.A. Siddiqi, *Polym.Biomater. Bioeng.*, **87** (2022).
27. P. Satheeshkumar, M. Gopal, *Int. J. Mech.Eng.*, **6,** 981 (2021)
28. M., Wróbel, S. Szymańska, T. Kowalkowski, K. Hrynkiewicz, *Microbiol. Res.*, **267**, 127251 (2023).
29. A. Satlewal, R. Soni, M.G.H. Zaidi, Y. Shouche, R. J. Goel,*J. of Microb. Biotech.*, **18(**3), 477 (2008).
30. A. Kapri, M. G. H. Zaidi, A. Satlewal, R. Goel, *Int. Biodet.Biod.*., **64(**3), 238 (2010).
31. R., Soni, A. Kapri, M. G. H. Zaidi, R. Goel, *J.Biol. Biotech.,* **20**(6), 1032 (2010).
32. A. Kapri, M. G. H. Zaidi, R Goel, R. *J. of Microb. Biotech.*, **20**(6), 1032 (2010)
33. A. Sah, A. Kapri, M. G. H. Zaidi, H. Negi, R. Goel, *J. of Microbio. Biotech.***20(**5), 908 (2010).
34. S. Raghuwanshi, M. G. H. Zaidi, S. Kumar, R. Goel, *J. of Polym. Env*., **26,** 2661 (2018).
35. P. Debbarma, D. C. Suyal, M. G. H. Zaidi, A. Yadav, Y. Shouche, R. Goel, *Res.Sq.*, (2022).
36. R. Goel, P. Jayal, H. Negi, P. R. Saravanan, & M. G. H. Zaidi, *Int. J. of Env. Waste Manag.*, **13**(4), 348 (2014).
37. S. Raghuwanshi, T. Agarwal, A. Yadav, M. G. H. Zaidi, Y. Shouche, R. Goel,*Chem. Ecol.*, **32**(6), 583 (2016).
38. P. Debbarma, S. Raghuwanshi, J. Singh, D. C. Suyal, M. G. H. Zaidi, R. Goel, *3Biotech***7** (178), 1 (2017).
39. N. Atanasova, S. Stoitsova, T. Paunova-Krasteva, M. Kambourova, *Int. J. Mol.Sci.*, **22**(11), 5610 (2021).
40. N. Mohanan, C. H. Wong, N. Budisa, D. B. Levin, *Front. Bioeng. Biotechnology.*, **10**, 854298 (2022).
41. N. Mohanan, C. H. Wong, N. Budisa, D. B. Levin, *Int. J. of Molecular Sci*, **24**(5), 450 (2023).
42. S. Zhou, Y. Wang, H. Xia, D., Liu, S. Chen, F. Li, *Int. J. of Systematic and Evolutionary Microbiology*, **70**(5), 3049 (2020).
43. S. Akther, G. K. Paul, S. Mahmud, M. S. Hossain, M. A. Saleh, S. Zaman, M S. Uddin, *Adv. Biotechnology Exp. Ther*, **5,** 487 (2022).
44. M. Arefian, A. Tahmourespour, M. Zia, *Archives of Env. Protection*, **46**(1), 14 (2020).
45. G. J. Palm, L. Reisky, D. Böttcher, H. Müller, E. A. Michels, M. C. Walczak, G. Weber, *Nature Communications,* **10**(1), 1717 (2019).
46. R. P. Magalhães, H. S. Fernandes, S. F. Sousa, *Catalysis Science and Technology*, **12**(11), 3474 (2022).
47. S. I. Hachisuka, T. Nishii, S. Yoshida, *Applied and Env.Microbiology*, **87**(18), (2021).
48. M. H. Weiland, *Mechanistic Enzymology: Bridging Structure and Function.* Bridging Structure and Function 161 (2020).
49. J. S. Poulsen, J. L. Nielsen, *J. of Proteomics*, **279**, 104888 (2023).
50. H. F. Son, I. J. Cho, S. Joo, H., Seo, H. Y. Sagong, S. Y. Choi, K. J. Kim, *ACS Catalysis*, **9**(4), 3519 (2019).
51. B. Alfieri, M. Alfieri, M. Kelly, S. Kilcoyne, L. Poprik, A. Sanyal, J. Pousont, *FASEB*, 36 (2022).
52. C. Liu, C. Shi, S. Zhu, R. Wei, C. C. Yin, *Biochemical and Biophysical Research Commu.*, **508**(1), 289 (2019).

53. W. Maity, S. Maity, S. Bera, A. Roy, *Applied Biochemistry and Biotechnology*, **193**, 2699 (2021).
54. Q. Yin, S. You, J. Zhang, W. Qi, R. Su, *Bioresource Technology*, **364**, 128026 (2022).
55. S. Yoshida, K. Hiraga, I. Taniguchi, K. Oda, *Methods in Enzymology*, **648**, 187 (2021).
56. H. Seo, S. Kim, H. F. Son, H. Y. Sagong, S. Joo, K. J. Kim, *Biochemical and Biophysical Research Commun.*, **508**(1), 250 (2019).
57. Y. Joho, V. Vongsouthi, M. A. Spence, J. Ton, C. Gomez, L. L. Tan, A. Ardevol, *Biochemistry*, **62**(2), 437 (2022).
58. S. Feng, Y. Yue, M. Zheng, Y. Li, Q. Zhang, W. Wang, *ACS Sustainable Chemistry and Eng.*, **9**(29), 9823 (2021).
59. H. Y. Sagong, H. F. Son, H. Seo, H. Hong, D. Lee, K. J. Kim, *J. of Hazardous Materials*, **416**, 126075 (2021).
60. H. Y. Sagong, H. Seo, T. Kim, H. F. Son, S. Joo, S. H. Lee, K. J. Kim, *ACS Catalysis*, **10**(8), 4805 (2020).
61. I. Karunatillaka, L. Jaroszewski, A. Godzik, *Proteins*, **90(**2), 504 (2022)
62. Y. Tachibana, K. Kageyama, M. Suzuki, H. Koshigumo, H. Takeno, Y. Tachibana, K.I. Kasuya, *Polymer Degradation and Stability*, 160, 264 (2019).
63. S. S. Saikia, B. K. Borah, G. Baruah, Rokozeno, M. K. Deka, *Folia Microbiologica*, **67**,133 (2022).
64. E. Zeghal, A. Vaksmaa, H. Vielfaure, T. Boekhout, H. Niemann, *Frontiers in Marine Science*, **8,** 738877 (2021).
65. S. Varshney, V. Gupta, A. N. Yadav, R. K. Rahi, D. K. Neelam, *J. of Applied Biology and Biot.*, **11**(3), 61 (2023).
66. M. Srikanth, T. S. R. S. Sandeep, K. Sucharitha, S. Godi, *Biores. Bioprocessing*, **9**(1), 42 (2022).
67. Y. Du, X. Liu, X. Dong, Z. Yin, *Comput. Struct.Biotech.*, **20,** 975 (2022).
68. A. H. Ekanayaka, S. Tibpromma, D. Dai, R. Xu, N. Suwannarach, S. L. Stephenson, S. C. Karunarathna, *J. of Fungi*, **8**(8), 772 (2022).
69. P. Daly, F. Cai, C.P. Kubicek, S. Jiang, M. Grujic, M.J. Rahimi, I. S. Druzhinina, *Biotechnology Advances*, **50**, 107770 (2021).
70. I. Brunner, M. Fischer, J. Rüthi, B. Stierli, B. Frey, *PLOS ONE*, **13**(8) (2018).
71. S. K. Lee, L. N. Ten, K. Das, Y. H. You, H. Y. H. Y. *Mycobiology*, **49**(3), 285 (2021).
72. A. Trivedi, S. Hait, *Energy, Environment, and Sustainability, Springer*, 271 (2020).
73. M. Osman, S. M. Satti, A. Luqman, F. Hasan, Z. Shah, A. A. Shah, *J. of Polymers and the Env.*, **26,** 301 (2018).
74. E. Munir, R. S. M. Harefa, N. Priyani, D. Suryanto, *Earth and Env.Sco., IOP Conf. Ser.* **126** (1) 012145, (2018).
75. P. Sarmah, J. Rout, *Advances in Cyanobacterial Biology*, 333 (2020).
76. W. Y. Chia, D. Y. Y. Tang, K. S. Khoo, A. N. K. Lup, K. W. Chew, *Env. Sci. and Ecotechnology*, **4,** 100065 (2020).
77. E. Karalija, M. Carbó, A. Coppi, I. Colzi, M. Dainelli, M. Gašparović, F. Martinelli, *J. Hazard. Mater.***438**, 129450 (2022).
78. D. C. La Grange, I. S. Pretorius, M. Claeyssens, W. H. Van Zyl, *Applied and Env. Microbiology*, **67**(12), 5512 (2001).
79. M. E. Sevilla, M. D. Garcia, Y. Perez-Castillo, V. Armijos-Jaramillo, S. Casado, K. Vizuete, L. Cerda-Mejía, *Polymers*, **15**(7), 1779 (2023).
80. L. Aer, Q. Jiang, I. Gul, Z. Qi, J. Feng, L. Tang, *Env. Research*, **212**, 113472 (2022).
81. H. F. Son, S. Joo, H. Seo, H. Y. Sagong, S. H. Lee, H. Hong, K. J. Kim, *Enzyme and Microbial Tech.*, **141,** 109656 (2020).
82. A. Priya, K. Dutta, A. Daverey, *J. of Chemical Tech. & Biotech.*, **97**(2), 381 (2022).
83. L. Liu, M. Xu, Y. Ye, B. Zhang, *Science of the Total Env.*, **806,** 151312 (2022).
84. R. Saleheen, M. G. H. Zaidi, S. Mehtab, K. Singhal, *Renewable Energy for Sust.Growth Ass.*, **305** (2022).
85. D. V. Upasana, M. G. H. Zaidi, A. K. Shukla, *Pharm. Innov.***11**(6), 2396 (2022).