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Review Article

Microbial Consortia: Synergistic Effects on Plastic Degradation and Enzyme Production

*[1]Aminat Olamide Shokunbi, [2]Ogochukwu Mercy Ezeh, [3]Deborah Pelumi Fadipe, [4]Ayobami Samson Olanrewaju, [4]Olabisi Oluwaseun Badru, [5]Chinechendo N. Eze, [6]Loveth Chinwendu Iwuala

About Article

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About Author

[1] Instituto Politécnico Nacional-Centro de Biotecnología Genómica, Mexico

[2] Department of Biological Sciences, Georgia State University, Atlanta, Georgia 30303, USA

[3] Department of Biology, Illinois Institute of Technology Chicago, Illinois, USA

[4] Department of Industrial Chemistry, University of Ibadan Opposite Agbowo Shopping Complex, Ibadan, Nigeria

[5] Department of Biology, University of Louisiana at Lafayette Lafayette, LA, USA

[6] Department of Chemistry and Biochemistry, University of Oklahoma, Norman, OK 73019, USA

Contact @ Aminat Olamide Shokunbi
shokunbi.o.aminat@gmail.com

ABSTRACT

Growing interest in biological degradation as a sustainable mitigation strategy is a result of the fact that plastic pollution is still one of the most persistent environmental threats. Through cooperative metabolism and complementary enzyme production, microbial consortia—diverse communities of bacteria, fungi, or both—have shown synergistic capacities to break down otherwise resistant plastics, outperforming single isolates. The enzymatic or oxidative activity of one organism in mixed cultures can release substrates for other organisms, speeding up the depolymerization and mineralization of polymers like polyethylene, polyethylene terephthalate, and polystyrene. More thorough degradation pathways are made possible by these consortia's support of diverse enzymatic repertoires, such as laccases, cutinases, and multicopper oxidases. Although previous research has listed strains and enzymes that break down plastic, this review synthesizes in a novel way how particular metabolic interactions within consortia promote superior plastic biodegradation. We discuss the significance of enzyme complementarity and cross-feeding, highlight recent research that demonstrates co-occurrence and functional cooperation, and pinpoint important design guidelines for scalable, consortium-based bioremediation. Future waste management solutions are informed by these insights into both the ecology of natural plastispheres and engineered microbial systems.

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1. INTRODUCTION

Plastics made from petroleum are now everywhere because they are strong, cheap, and can be used in many ways. According to Danso *et al.* (2019), Geyer *et al.* (2017), and Lebreton and Andrady (2019), global output recently reached 400 million tons (Danso *et al.*, 2019; Geyer *et al.*, 2017; Lebreton & Andrady, 2019). Mismanaged plastic garbage piles up in landfills and natural areas on a huge scale (Jambeck *et al.*, 2015; Ragaert *et al.*, 2017). Researchers have already found tiny pieces of microplastic in almost every habitat, from the deep sea to the snow in the Alps and the ice in the Arctic (Amaral-Zettler *et al.*, 2020; Bergmann *et al.*, 2019). Conventional plastics like polyethylene (PE), polypropylene (PP), polystyrene (PS), and polyvinyl chloride (PVC) are difficult to break down by nature; therefore, they can stay in oceans and soils for decades to millennia (Andrady, 2011; Danso *et al.*, 2019). The pollution that results, which ranges from visible trash to microplastics, is catastrophic for ecosystems and human health. Plastic waste lasts a long time because it breaks down slowly in the environment, but not at all by living things. Over time, it builds up and breaks down into microplastics (Andrady, 2011; Barnes *et al.*, 2009).

Microbial biodegradation could be a way to help the environment. Recently, there have been many reports of bacteria and enzymes attacking synthetic plastics. Such evidence gives us hope for biological waste treatment. Indeed, various bacteria and fungi capable of attacking synthetic polymers have been isolated over the past decades (Khan & Majeed, 2019; Massot *et al.*, 2022). For example, the discovery of *Ideonella sakaiensis*—a bacterium that can almost completely degrade poly(ethylene terephthalate) (PET) by secreting specialized enzymes—demonstrated that microbes can adapt to metabolize even highly recalcitrant plastics (Yoshida *et al.*, 2016). However, most single strains show only limited breakdown efficiency for strong polymers like PE and PP, which don't have bonds that can be easily broken down by water and stay mostly intact when acted on by one type of microbe (Andrady, 2011; Danso *et al.*, 2019). No singular enzyme has been identified that effectively depolymerizes these polyolefins (Danso *et al.*, 2019), underscoring a deficiency in biodegradation capacity when organisms operate independently.

But in nature, plastics don't usually come into contact with single microbes. Instead, they become home to a variety of communities (the "plastisphere") where many microorganisms live on the surface of the trash (Amaral-Zettler *et al.*, 2020; Zettler *et al.*, 2013). These microbial consortia can work together to break down polymers by using different metabolic processes that a single species couldn't do on its own. One organism in the community may oxidize or soften the plastic surface, allowing others to break it down even more, or various members may break down intermediate products in order. These kinds of synergistic interactions can speed up and increase the rates and amounts of degradation (Massot *et al.*, 2022; Skariyachan *et al.*, 2022). In addition, consortia can make a wider range of enzymes, such as esterases, oxygenases, and laccases, that can break down diverse chemical bonds in complicated plastic combinations. Microbial consortia have become a potential way to break down resistant polymeric wastes more fully than single isolates by using the combined catalytic abilities and metabolic cooperation of different species.

This article aims to provide a comprehensive overview of current progress in the biodegradation of plastics by microbial consortia. We investigate the synergistic depolymerization of significant synthetic plastics by mixed microbial communities and the variety of enzymes they provide, and we review pertinent studies and the mechanisms that facilitate these interactions while also proposing future strategies to improve consortium-based bioremediation of plastic waste.

2. LITERATURE REVIEW

Researchers have identified a wide array of bacteria involved in partial plastic breakdown. Various bacterial taxa, such as *Pseudomonas, Rhodococcus*, *Bacillus*, and *Streptomyces*, are known to colonize and gradually degrade polyethylene, polyurethane, and other polymers (Khan & Majeed, 2019; Carmen, 2021; Danso *et al.*, 2019). Many fungi, particularly saprotrophic molds such as Aspergillus, Penicillium, Fusarium, and white-rot basidiomycetes, can degrade resistant plastics by secreting powerful oxidative and hydrolytic enzymes (Ibrahim *et al.*, 2024; Sangale *et al.*, 2019). Fungi frequently infiltrate polymer matrices through mycelial development, generating extracellular laccases, peroxidases, and cutinases that catalyze polymer degradation (Ibrahim *et al.*, 2024; Wei & Zimmermann, 2017). Bacteria thrive in biofilms on plastic surfaces, where they can use the products of initial oxidation and break down the material even more with enzymes that are stuck to the surface (Danso *et al.*, 2019; Zettler *et al.*, 2013). Even though these strains can break down plastic, their innate ability to do so is usually limited. For instance, even the best polyethylene-degrading isolates (usually *Rhodococcus* or *Pseudomonas* spp.) only lose a few percent of their weight over weeks to months of incubation (Danso *et al.*, 2019; Dubey & Thalla, 2025). This lack of performance has led to the study of multi-species communities to get better degradation results.

The Plastisphere and Natural Consortia: Plastics quickly form complex biofilm communities in the environment called the "plastisphere." These communities consist of bacteria, fungi, algae, and protists embedded in extracellular polymeric substances. Research has shown that these natural groups of organisms include types that can break down plastic additives and oligomers that leak from the polymer, as well as types that start the slow breaking of polymer bonds. For example, researchers have found that marine plastisphere communities have bacteria that break down hydrocarbons (like Alcanivorax and Halomonas) and fungi that break down lignocellulose, living together on polyethylene debris. This suggests that they break down polymer fragments and waxes on the plastic surface at the same time (Ibrahim *et al.*, 2024; Zettler *et al.*, 2013). Certain bacteria that live together in soil can greatly speed up the breakdown of polymers. Chigwada *et al.* (2023) enhanced indigenous landfill soil consortia on low-density polyethylene (PE) and recorded a weight decrease of around 22–56% in PE films within 90 days, significantly greater than the minimal weight loss reported from any one isolate within those consortia (Chigwada *et al.*, 2023). These results show that in a mixed community, one member can do an initial oxidative step (like adding oxygen functional groups to an inert carbon chain) (Chigwada *et al.*, 2023; Zampolli *et al.*, 2023), which makes the plastic easier for other community members to break down with depolymerase enzymes. The consortium's combined metabolic toolkit broadens the spectrum of chemical linkages that can be targeted and inhibits the buildup of obstructive intermediates via cross-feeding.

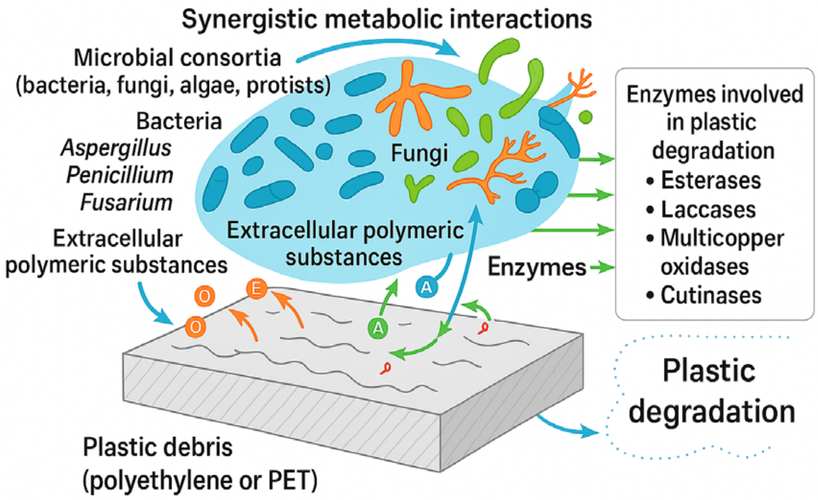

Figure 1. A schematic depiction of microbial consortia (the plastisphere) inhabiting plastic trash and collaboratively decomposing polymers.

Researchers have increasingly engineered or chosen specific microbial consortia to evaluate synergistic effects on plastic breakdown. A striking example comes from the waxworm (*Galleria mellonella*) gut microbiota: Lou *et al.* (2022) isolated a two-member consortium—a yeast (*Meyerozyma*) and a bacterium (*Serratia*)—that together degraded nearly 16% of a polyethylene film within one month, whereas each organism alone achieved substantially less degradation (Lou *et al.*, 2022). The bacteria in this pair were discovered to upregulate a multicopper oxidase gene during co-culture, which means that the yeast made the bacterium make enzymes that are useful for breaking down polymers (Lou *et al.*, 2022). Similarly, mealworm larvae that only eat plastic depend on the bacteria in their guts. When antibiotics are used to kill these bacteria, the breakdown of polystyrene and polypropylene stops. This experiment shows that a collection of gut microbes works together to break down plastic in the body. These natural groups led to the creation of lab consortia. Maheswaran *et al.* (2023) showed that a synthetic group of four different microorganisms (two bacteria and two fungi) could work together to break down PET film by about 29% over two months. No single strain could do more than 10% of the same thing in the same amount of time (Maheswaran *et al.*, 2023). In that group, each organism worked on breaking down a different portion of PET. For example, one fungus created an enzyme that helped break down PET, while a bacterium exploited the terephthalic acid that was released to help break down more PET (Maheswaran *et al.*, 2023). This division of labor shows how combining organisms with different metabolic tasks can make the process of turning polymers into harmless end products more complete.

2.1. Enzymatic complementation in mixed cultures

Microbial consortia not only broaden the spectrum of metabolic processes utilized on plastics but also frequently demonstrate increased overall enzyme production rates. Microorganisms can induce enzyme production in each other during co-culture via signaling or by alleviating catabolite repression. For example, growing a ligninolytic fungus and a bacterium that breaks down plastic together can provide a more diverse mix of enzymes that work together on a polymer surface (Sangale *et al.*, 2019; Zampolli *et al.*, 2023). Zampolli *et al.* (2023) recently described two laccase-like multicopper oxidases from a *Rhodococcus* strain that may start the oxidative cleavage of polyethylene chains (Zampolli *et al.*, 2023). You can see a group of bacteria working together to form hydrophilic scission sites in the PE, which makes it simpler for an esterase or lipase from another microbe to break down those oxidized chains. A number of studies show that mixing bacteria and fungi causes more plastic weight loss than using either one on its own. This is because the enzymes work together and break down metabolic bottlenecks (Chigwada *et al.*, 2023; Ibrahim *et al.*, 2024). These results from both environmental and laboratory consortia underscore that microbial communities are intrinsically equipped to address the intricacies of polymer degradation via cooperative metabolism and mutualistic enzyme complementation.

3. METHODOLOGY

This narrative review was compiled by examining research publications (2015–2025) concerning the microbial degradation of plastics by consortia, identified using databases (Web of Science, Scopus) with keywords such as "plastic biodegradation," "microbial consortium," and "enzyme production." The focus was on peer-reviewed research illustrating multi-microbe interactions in polymer degradation. We incorporated both experimental studies on consortium-mediated plastic degradation and pertinent reviews to document methodological advancements.

The experimental procedures in the papers evaluated generally consist of enhancing microbial communities on target polymers as the exclusive carbon sources and assessing degradation performance. For instance, consortia have been derived from environmental samples through prolonged incubation with polymer films or powders, followed by repeated transfers to a fresh medium to isolate polymer-degrading members (Salinas *et al.*, 2023; Su *et al.*, 2023). Weight loss measures of plastic films, spectroscopic study of changes in polymer functional groups (e.g., FTIR), and chromatography to find breakdown products (monomers or CO$_2$) are all ways to evaluate polymer degradation (Taghavi *et al.*, 2021). Microbial community profiling (16S/ITS rRNA gene sequencing) and metagenomic analysis are utilized to identify consortia members and the catabolic genes expressed during degradation (Salinas *et al.*, 2025; Su *et al.*, 2023). Moreover, enzyme assays (for hydrolases, oxidases, etc.) are conducted on isolated strains or culture supernatants to associate certain enzymatic activity with the observed polymer degradation (Salinas *et al.*, 2023; Zampolli *et al.*, 2023). These integrated methodologies yield a comprehensive understanding of the relationships between consortia makeup, metabolic function, and enzyme production in relation to plastic biodegradation outcomes.

4. RESULTS AND DISCUSSION

Consortium Performance on Different Plastics: It has been shown that microbial consortia work better than single strains on a number of plastics. Mixed cultures have been notably helpful on PET, where only certain enzymes, like PETase, can break it down. For example, a specific group of Sarcina, *Bacillus*, and two fungi caused the PET film to lose about 30% of its weight in 8 weeks. This amount is much more than the best single isolate from that group, which only lost 10% of its weight (Maheswaran *et al.*, 2023). Another study found that a consortium made from natural compost could break down not just PET but also polypropylene and polystyrene in a sample of mixed plastic trash. The results showed that the consortium could work with a wide range of substrates that monocultures couldn't (Salinas *et al.*, 2025a). Researchers have also looked into engineered synthetic consortia. Bao *et al.* (2023) created a two-strain bacterial consortium to completely mineralize PET hydrolysate. One strain of *Pseudomonas* putida broke down terephthalic acid, and the other broke down ethylene glycol. Together, they turned PET waste into biomass and useful bioproducts more quickly than a single strain could do both (Bao *et al.*, 2023). These examples show that splitting up the metabolic task between different bacteria can get around problems that happen when one organism is breaking down something. Table 1 shows some research that compares how well microbial consortia break down different forms of plastic compared to individual strains.

Table 1. Comparative efficacy of microbial consortia vs individual strains in plastic degradation

Plastic Type	Consortium Composition	Degradation Performance	Enzymes/Mechanisms Highlighted
PET	*Sarcina*, *Bacillus*, two fungi	29% PET film loss in 8 weeks	PETase, laccases, synergistic hydrolysis
PE	Landfill soil bacteria + fungi	22–56% LDPE loss in 90 days	Oxygenases, esterases, and oxidative pre-treatment
PET hydrolysate	Engineered *Pseudomonas* putida strains	Complete mineralization of monomers	Aromatic compound catabolic pathways (terephthalate, EG)
PE	*Meyerozyma* (yeast) + *Serratia* (bacterium)	16% PE film loss in 30 days	Multicopper oxidase, enzyme induction via co-culture
Mixed plastics	Compost-derived bacteria and fungi	Broad-spectrum degradation observed	Cutinases, lipases, laccases, and syntrophic interactions

Researchers have demonstrated even more significant enhancements on polyolefins such as PE and PP, which are very inert polymers (Dubey & Thalla, 2025; Maheswaran *et al.*, 2023). Individual soil bacteria usually only break down a few percent of PE over a few months (Danso *et al.*, 2019), but communities of different types of bacteria can break down these polymers a lot more. A recent study utilizing landfill wastewater showed that a consortium of three distinct microorganisms degraded polyurethane film sufficiently to liberate quantifiable monomers (adipic acid and 1,4-butanediol) within a mere 48 hours (Su *et al.*, 2023). A recent finding shows that a specific strain of *Bacillus* bacteria from the deep sea may decompose polyester-based polyurethane, indicating that robust single-organism processes may be augmented through synergistic interactions with other species (Gui *et al.*, 2023; Su *et al.*, 2023). Similarly, consortia on PE have lost tens of percent of their weight; for example, a landfill soil community took away over 50% of an LDPE sample in three months. Likewise, indigenous bacteria extracted from landfill leachate significantly improved the breakdown of polypropylene microplastics (Dubey & Thalla, 2025). Sarkhel *et al.* (2019) documented that a marine-derived bacterial-fungal consortia destroyed approximately 29% of the polyethylene film within two months, without any chemical pre-treatment (Sarkhel *et al.*, 2019). In contrast, pure cultures of recognized PE-degraders, such as *Rhodococcus opacus* or Brevi*bacillus* strains, typically yield less than 10% weight loss over equivalent durations. The huge increase in degrading efficiency shows that heterogeneous communities really do work together. The prevailing hypothesis regarding polyolefins posits that an initial member of the group initiates the degradation of the robust carbon framework, potentially through the release of reactive oxygen species or enzymes that adhere to surfaces. This process subsequently enables other enzymes from distinct microbes to further decompose the polymer chain (Zampolli *et al.*, 2023). Lou *et al.* (2022) observed the upregulation of an oxidase in a PE-degrading consortium exclusively during co-cultivation of the two species, rather than in isolation (Lou *et al.*, 2022). So, the community setting can start metabolic pathways that stay dormant in axenic culture, which directly speeds up the breakdown of polymers.

4.1. Synergistic degradation mechanisms

In-depth studies of community-driven plastic biodegradation uncover multiple synergistic pathways. One way this happens is through metabolic division of labor, when one organism's intermediate metabolites are used up quickly by another. This collaborative process stops those intermediates from building up (which may stop further polymer hydrolysis) and moves the equilibrium toward more complete degradation (Bao *et al.*, 2023; Maheswaran *et al.*, 2023). There are kinds of bacteria that break down PET. One type breaks it down into two simpler compounds, and other bacteria quickly consume these molecules. This process makes the PETase enzyme perform better (Bao *et al.*, 2023; Yoshida *et al.*, 2016). Co-aggregation and biofilm formation are two more ways that enzymes from different species might work together. In a mixed biofilm, enzymes from different species can act on the polymer surface sequentially. Fungal hyphae in consortia can promote surface erosion by breaking up or oxidizing the polymer, which lets bacterial cells get deeper and find new polymer connections (Ibrahim *et al.*, 2024; Sangale *et al.*, 2019). The end product is a more effective attack on the plastic than either could do on their own. A third mechanism involves signaling that activates genes and stimulates their expression. Occasionally, when a second microbe is present, it makes the first bacterium respond to stress or substrate in a way that boosts its enzyme output. As mentioned before, co-culturing with yeast caused a *Serratia* sp. to grow to produce more of a laccase-like oxidase, which speeds up the breakdown of polyethylene (Lou *et al.*, 2022). Consortium members can also share growth ingredients or get rid of harmful by-products, which makes the microenvironment more suitable for long-term degrading activity (Massot *et al.*, 2022; Su *et al.*, 2023).

Even though these results are promising, there are still problems that need to be solved before microbial consortia can be completely used for large-scale plastic biodegradation. Numerous consortia evaluated in laboratories operate under optimum conditions (e.g., pre-treated plastics, regulated temperature and pH, supplemented nutrients) that may be challenging to recreate in natural environments or waste management facilities (Evode *et al.*, 2021; Karlsson *et al.*, 2018). Also, not all combinations of degraders work together to break down polymers better than the best single strain. In certain circumstances, competition or hostility in a mixed culture might make the breakdown process slower. So, it's important to find strains that really work together. There is also the issue of full mineralization: consortia often only proceed as far as intermediate oligomers or monomers, which may still need more treatment even though they are smaller. For instance, a consortium may depolymerize PET into terephthalic acid; however, if no member is capable of fully metabolizing

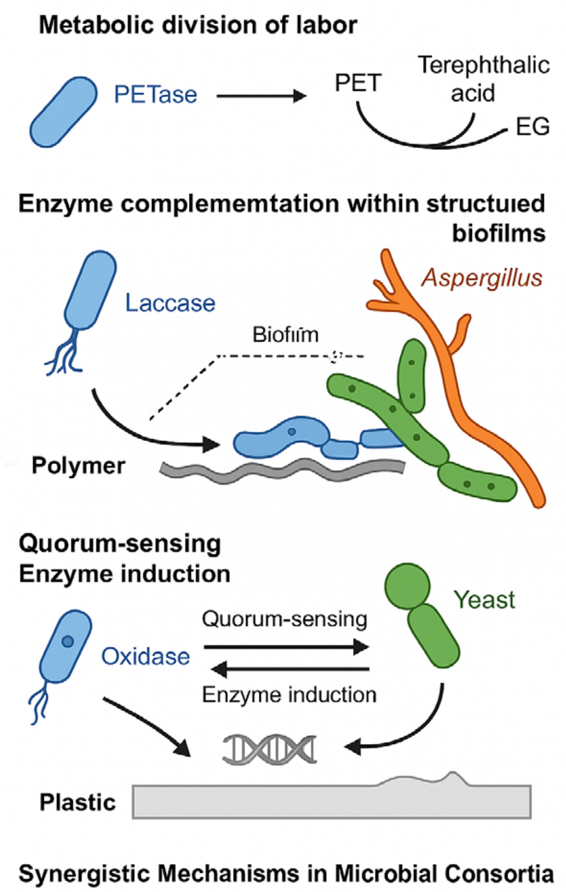

Figure 2. Diagram of synergistic mechanisms in microbial consortia, illustrating metabolic division of labor, enzyme complementation in biofilms, and quorum-sensing-driven enzyme induction during plastic degradation.

terephthalate, the process halts (Danso *et al.*, 2019). Future research is concentrating on either enhancing consortia with supplementary metabolic functions (by bioaugmentation or genetic engineering) or amalgamating biological processes with physicochemical pretreatments. Mild pretreatments such as low-dose UV or thermal aging can introduce functional groups that "prime" the plastic for microbial attack (Karlsson *et al.*, 2018), potentially reducing the overall time to achieve biodegradation. In parallel, synthetic biology is being applied to design microbial communities with defined composition and communication systems that maximize cooperative enzyme production while minimizing competition (Bao *et al.*, 2023; Massot *et al.*, 2022). As research progresses, it is essential to evaluate the performance of the consortium on actual plastic waste streams, which frequently comprise mixed polymers, additives, and biofilms, under ambient environmental conditions. Still, the research we have now strongly suggests that microbial communities with several strains could be a good way to speed up the breakdown of plastic contaminants that are hard to get rid of.

4.2. Future directions and practical implications

The progress of research on microbial consortia creates several new ways to better manage plastic trash. One immediate goal is to take consortia-driven biodegradation from small-scale trials to large-scale industrial processes. Bioreactor designs can be improved to keep mixed cultures alive in situations when working together is more important than competing (for example, by co-immobilizing complementary microorganisms in biofilms or on carrier materials) (Massot *et al.*, 2022). Maintaining the stability and activity of consortia in non-sterile waste streams that change over time will be crucial. This may require adding critical nutrients regularly or using sequential bioprocessing, where various microbial communities are used for different polymers. Another intriguing approach involves designing or incorporating functions specific to the needs of consortia. Synthetic biology methods can add new catabolic genes to consortium members or make communication circuits that improve synergistic degradation pathways (Bao *et al.*, 2023). For example, designer communities could be made where one bacterium is engineered to make a high-activity PETase, another is engineered to take up terephthalate well, and a third is engineered to make a biofilm matrix for stability. Together, these three bacteria would make a beneficial plastic-degrading assembly.

Simultaneously, the identification of innovative plastic-degrading strains and enzymes continues to be a priority. Metagenomic and pangenomic investigations of microbial communities from plastic-dense habitats (such as landfills, composts, and ocean plastics) are expected to reveal previously unidentified enzymes that consortia may utilize (Massot *et al.*, 2022; Skariyachan *et al.*, 2022). Computational modeling and machine learning are becoming useful for figuring out which combinations of organisms might have complementary metabolic profiles for breaking down polymers (Skariyachan *et al.*, 2022). These in silico methods, when used with high-throughput screening of environmental consortia, can speed up the process of finding the best multi-species teams for certain forms of plastic. Also, using moderate pretreatment technologies along with biodegradation could make the whole process more efficient. Low-energy ultrasound, UV irradiation, or oxidative aging are examples of physical or chemical pretreatments that can “pre-weather” plastics to make them more biodegradable. After that, consortia can more easily attack the weakened polymers (Karlsson *et al.*, 2018). This type of integrated strategy could help fill the present gap, since consortia rarely reach full mineralization on their own.

Lastly, when putting microbial consortia to work to clean up plastic trash, safety and rules must be taken into account. Using naturally occurring consortia from local habitats instead of genetically modified strains may make it easier to get regulatory approval and lower ecological dangers. One possible use is to speed up the decomposition of agricultural films and packaging debris by adding specialized consortia to waste composting facilities or soil biopiles. In the long run, the information learned from consortia research could also help with the design of new polymers that break down more easily on their own. For example, they could include bond structures that known enzymes can break or add co-metabolizable additives to attract and keep degrading communities (Shi *et al.*, 2024). Combining new materials, bioprocess engineering, and the amazing ability of microbial populations to break down things, it may be possible to greatly reduce plastic pollution in a way that is good for both the economy and the environment.

5. CONCLUSION

Microbial consortia have become a strong model for overcoming the problems that occur with single-organism plastic biodegradation. Consortia can break down polymers more thoroughly and release a larger range of degradative enzymes than isolated strains because they take advantage of the metabolic variety and cooperative interactions of several microorganisms. In the last ten years, many proof-of-concept studies have shown that synergistic communities can break down tough plastics like PET, PE, and PU at much faster rates, turning them into usable intermediates and even complete mineralization in some cases. There are still problems like process scalability, incomplete degradation, and community stability, but new ideas in enrichment techniques, metabolic engineering, and process integration are quickly solving these problems. The utilization of microbial consortia is a very promising aspect of a long-term solution to plastic pollution that works well with better plastic design, recycling, and waste reduction. Ongoing research and development in this interdisciplinary domain will be essential for converting laboratory achievements into practical bioremediation and recycling initiatives, advancing us toward a circular plastic economy in which microbial communities are crucial for degrading and enhancing the value of plastic waste.

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