

Review

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Review

The Plastisphere in Saline Ecosystems: Quorum Sensing, Halotolerant Fungi and Microplastic Degradation Pathways

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Abstract

Plastic pollution has generated a novel anthropogenic habitat, the plastisphere, where microorganisms colonize and establish complex biofilms on the surfaces of synthetic polymers. Although considerable progress has been made in describing plastisphere microbial diversity, the ecological mechanisms linking community assembly, microbial communication, and polymer biodegradation remain poorly understood, particularly in saline ecosystems. Here, we review current knowledge on plastisphere formation in marine, estuarine, hypersaline, and other saline environments, emphasizing the ecological roles of quorum sensing (QS), halotolerant fungi, and microbial interactions in regulating biofilm development and microplastic degradation. We discuss how environmental factors characteristic of saline habitats, including osmotic stress, ultraviolet radiation, nutrient limitation, and high ionic strength, shape plastisphere succession and influence microbial physiology. Particular attention is given to halotolerant fungi, whose oxidative and hydrolytic enzymes—including laccases, peroxidases, cutinases, esterases, and lipases—complement bacterial metabolism during polymer transformation. We further examine recent evidence demonstrating that QS coordinates microbial attachment, extracellular polymeric substance production, biofilm maturation, extracellular enzyme secretion, and metabolic cooperation, thereby linking microbial communication with biodegradation efficiency. Based on current evidence, we propose an integrative ecological framework in which abiotic weathering, environmental filtering, quorum sensing, bacterial–fungal interactions, and extracellular enzymatic pathways constitute successive and interconnected processes governing plastisphere functioning in saline ecosystems. Finally, we identify major knowledge gaps and highlight future research priorities, including the integration of multi-omics approaches, synthetic microbial consortia, systems biology, and artificial intelligence for the discovery of novel plastic-degrading enzymes. By integrating microbial ecology, fungal biology, chemical communication, and environmental biotechnology, this review provides a systems-level perspective on the plastisphere and establishes a conceptual framework for understanding and enhancing microplastic biodegradation under saline conditions.

Keywords: plastisphere; microplastics; saline ecosystems; quorum sensing; halotolerant fungi; biofilms; microbial interactions; plastic biodegradation; extracellular enzymes; bacterial–fungal consortia

1. Introduction

Plastic pollution has emerged as one of the defining environmental challenges of the Anthropocene. Global plastic production has exceeded 400 million metric tons annually, and the persistence of synthetic polymers has resulted in their accumulation across virtually every ecosystem on Earth, from polar regions and abyssal plains to hypersaline lakes and coastal wetlands. Through continuous exposure to ultraviolet radiation, mechanical abrasion, chemical oxidation, and biological activity, larger plastic debris progressively fragments into microplastics (<5 mm) and nanoplastics, creating highly persistent particles that remain in aquatic environments for decades or even centuries [1,2]. Once regarded merely as inert pollutants, these particles are now recognized as biologically active substrates that profoundly influence microbial ecology, biogeochemical cycling, and contaminant transport [3].

The realization that plastic debris rapidly becomes colonized by diverse microbial assemblages has fundamentally reshaped our understanding of plastic pollution. Within hours of entering aquatic environments, polymer surfaces are coated by organic matter that promotes the attachment of bacteria, archaea, fungi, microalgae, protists, and viruses, leading to the establishment of complex biofilms collectively known as the “plastisphere” [4]. Rather than representing random microbial assemblages, plastisphere communities exhibit ecological succession, metabolic specialization, interspecific cooperation, and competitive interactions that differ markedly from those occurring in the surrounding water column [3,5]. Consequently, plastics have been increasingly recognized as novel anthropogenic ecological niches capable of supporting unique microbial networks while simultaneously acting as vectors for pathogens, antibiotic resistance genes, invasive microorganisms, and pollutant-associated metabolic processes.

Despite the rapid expansion of plastisphere research over the last decade, current knowledge remains disproportionately concentrated on marine bacterial communities rather than the total microbiological content of plastispheres in all saline environments. Most studies have focused on taxonomic diversity, biofilm succession, and bacterial metabolism associated with polyethylene (PE), polypropylene (PP), polyethylene terephthalate (PET), and polystyrene (PS), whereas microorganisms colonizing other types of plastic have received considerably less attention [6,7]. This taxonomic imbalance limits our ability to understand the plastisphere as a multispecies ecosystem in which interactions among bacterial, archaeal, fungal, and protistan communities may collectively influence biofilm stability, nutrient cycling, and polymer transformation [3,5]. Consequently, ecological processes emerging from interactions among different microbial groups remain substantially less understood than bacterial community composition itself.

This limitation becomes particularly evident in saline ecosystems. Oceans, estuaries, salt marshes, mangroves, hypersaline lakes, saline lagoons, and solar salterns constitute environmentally dynamic habitats characterized by high osmotic pressure, intense ultraviolet radiation, nutrient limitation, and pronounced physicochemical fluctuations. These environmental filters select microbial communities possessing specialized adaptive strategies, including osmolyte synthesis, extracellular polymeric substance (EPS) production, oxidative stress tolerance, and efficient extracellular enzymatic systems [8,9]. Such physiological traits are likely to influence both microbial colonization of plastic surfaces and the biodegradation potential of polymer-associated biofilms. Nevertheless, saline ecosystems remain substantially underrepresented in plastisphere studies despite functioning simultaneously as major sinks, transport corridors, and transformation hotspots for plastic debris.

Among the least explored components of saline plastisphere communities are halotolerant and halophilic fungi. Traditionally regarded as secondary colonizers in aquatic biofilms, these organisms are increasingly recognized as metabolically versatile decomposers capable of producing a broad spectrum of extracellular oxidative and hydrolytic enzymes, including laccases, manganese peroxidases, lignin peroxidases, cutinases, esterases, lipases, and unspecific peroxygenases [10,11]. Many of these enzymes have demonstrated the capacity to modify synthetic polymers or oxidize plastic-derived compounds [12], suggesting that fungi may contribute directly to polymer

weathering and biodegradation. Moreover, fungal hyphal networks provide physical scaffolds that facilitate bacterial dispersal, enhance spatial organization within multispecies biofilms, and promote metabolite exchange and metabolic cross-feeding between bacterial and fungal partners [13–15]. These interactions suggest that fungi play a far more central ecological role within the plastisphere than previously recognized. Nevertheless, compared with bacteria, fungal diversity, ecological functions, and enzymatic contributions to plastisphere functioning remain poorly characterized [3,16].

Equally overlooked is the role of microbial communication in regulating plastisphere assembly and function. Biofilm development is not simply the consequence of passive microbial attachment but is instead a highly coordinated process governed by cell-to-cell signaling mechanisms collectively known as quorum sensing (QS). Through diffusible signaling molecules—including acyl-homoserine lactones (AHLs), autoinducer-2 (AI-2), diketopiperazines, diffusible signal factors, farnesol, tyrosol, and other fungal signaling metabolites—microorganisms synchronize biofilm maturation, extracellular matrix production, nutrient acquisition, stress responses, horizontal gene transfer, and secretion of extracellular enzymes [17,18]. Emerging evidence suggests that QS also regulates microbial colonization of plastic surfaces and influences the expression of enzymes involved in polymer degradation [19,20]. However, the ecological significance of microbial signaling networks within plastisphere communities remains poorly understood, particularly regarding cross-kingdom interactions. Recent evidence demonstrates that quorum sensing can actively regulate plastisphere formation, biomass accumulation, extracellular polymeric substance production, and microbial community organization, indicating that microbial communication is an important component of plastisphere development [21]. Emerging evidence further indicates that the microplastisphere can function as a multi-kingdom microbial system comprising bacteria, fungi, protists, microalgae, and micrometazoans, with cross-kingdom connections contributing to community network complexity and stability [22]. These findings reinforce the need to move beyond bacteria-centered descriptions of the plastisphere toward an integrated understanding of interactions among its microbial components. Nevertheless, the mechanisms linking microbial signaling to cross-kingdom interactions and community-level ecological organization remain largely unresolved.

This represents an important conceptual limitation in current plastisphere research, as microbial community assembly, plastic–biofilm interactions, and polymer degradation have frequently been investigated through partially separated conceptual and methodological approaches [23,24]. Although increasing evidence links plastisphere community succession and microbial interactions to plastic transformation and degradation, the reciprocal relationships between biofilm organization and the physicochemical evolution of plastic substrates remain incompletely understood [24]. Far less attention has been devoted to understanding how microbial communication, cross-kingdom community assembly, and enzymatic activity jointly shape the ecological functioning of plastisphere biofilms, particularly under saline conditions. Consequently, the mechanistic links connecting quorum sensing, fungal ecology, biofilm organization, and microplastic degradation remain fragmented across multiple disciplines, limiting the development of an integrated framework capable of explaining plastisphere functioning in saline ecosystems [21–23].

In this review, we propose that quorum sensing constitutes a central regulatory mechanism linking microbial community organization to the biodegradation potential of saline plastisphere biofilms. We integrate current knowledge on plastisphere succession, halotolerant fungal ecology, bacterial and fungal quorum sensing, and polymer-degrading enzymatic pathways. From this synthesis, we develop a conceptual framework in which microbial communication mediates bacterial–fungal interactions and extracellular enzyme production, thereby influencing microplastic degradation in saline ecosystems. This framework connects microbial ecology, fungal biology, and chemical signaling to provide an integrated perspective on plastisphere functioning and identify priorities for future research.

2. Microplastics in Saline Ecosystems

2.1. Sources and Transport Pathways

Saline ecosystems constitute the ultimate environmental sink for a substantial proportion of the plastic waste generated worldwide. It is estimated that between 9 and 14 million metric tons of plastic enter aquatic environments annually through a combination of riverine discharge, wastewater effluents, urban runoff, atmospheric deposition, maritime activities, aquaculture, fisheries, and coastal tourism [25,26]. Rivers are recognized as the dominant transport pathways, carrying both primary microplastics—such as cosmetic microbeads and industrial resin pellets—and secondary microplastics produced through the fragmentation of larger plastic debris during environmental weathering.

Once introduced into saline environments, microplastics become incorporated into complex hydrodynamic transport networks. Ocean currents, tidal cycles, estuarine circulation, storm events, and seasonal river discharge redistribute particles across coastal and offshore ecosystems over spatial scales ranging from meters to thousands of kilometers. Atmospheric transport has also emerged as an important mechanism linking terrestrial and marine systems, allowing airborne microplastics to be deposited directly into remote marine environments, including polar oceans and isolated hypersaline lakes [27,28]. Saline ecosystems do not merely receive plastic pollution but actively transform its environmental behavior. Variations in salinity, ionic composition, suspended particulate matter, dissolved organic carbon, and biological activity influence particle aggregation, buoyancy, sedimentation, and biofilm development, thereby determining the residence time and ecological exposure of microplastics [29].

2.2. Environmental Fate Under Saline Conditions (Table 1)

The environmental fate of microplastics in saline ecosystems differs substantially from that observed in freshwater environments because of the unique physicochemical properties of seawater and hypersaline systems [30,31]. Elevated ionic strength compresses the electrical double layer surrounding particles, reducing electrostatic repulsion and promoting aggregation and heteroaggregation of microplastics with mineral particles, organic matter, and other suspended material [31]. Interactions with microbial extracellular polymeric substances (EPS) and biofilm development may further enhance particle aggregation and incorporation into organic aggregates [32,33]. Consequently, microplastics can become incorporated into marine snow, increasing aggregate settling velocities and facilitating their vertical transport from surface waters toward deeper waters and benthic environments [32–34]. Biofilm formation further modifies the physical properties and effective density of microplastic particles. Microbial colonization increases particle-associated biomass and can alter surface characteristics, including roughness, hydrophobicity, and electrostatic properties, thereby modifying particle–water and particle–particle interactions [35,36]. Biofouling can increase the effective density of originally buoyant polymers such as polyethylene (PE) and polypropylene (PP), potentially causing their descent from surface waters and contributing to their occurrence in deeper waters and sediments [3,35]. Because biofilm biomass itself changes through growth, decay, and ecological interactions, particle buoyancy may vary through time, potentially producing repeated vertical transitions rather than irreversible sinking [35]. Consequently, microplastics should be regarded as dynamic particles whose environmental trajectories are continuously reshaped by biological colonization and associated physicochemical transformations (Figure 1).

Weathering processes are also influenced by the physicochemical conditions of saline environments. Ultraviolet radiation, thermal oxidation, and mechanical abrasion progressively alter polymer surfaces, promoting chain scission, surface cracking, increased roughness, and the formation of oxygen-containing functional groups [30,37,38]. Water chemistry can further modulate the extent and characteristics of these physicochemical transformations [39]. Such weathering increases surface heterogeneity and may facilitate microbial attachment and subsequent biological transformation by

modifying surface chemistry and accessibility [39,40]. Abiotic and biological aging should therefore be regarded as interconnected processes rather than independent degradation pathways, highlighting the coupling between environmental weathering and microbial colonization.

2.3. Distribution Across Saline Ecosystems

Microplastics are now considered ubiquitous contaminants of marine environments, although their abundance, polymer composition, and particle morphology vary considerably among environmental settings [41]. In open-ocean environments, low-density polymers such as polyethylene (PE) and polypropylene (PP) dominate surface microplastic assemblages because of their positive buoyancy, whereas higher-density polymers, including polyesters, polyamide (PA), and polyvinyl chloride (PVC), tend to be relatively enriched in deeper waters and sediments [42,43]. Nevertheless, polymer density alone does not determine vertical distribution, as biofouling, aggregation, particle morphology, and hydrodynamic processes can substantially modify microplastic buoyancy and transport. Estuaries represent particularly dynamic environments where freshwater and marine processes interact, producing intense particle retention through estuarine turbidity maxima and flocculation processes. Consequently, estuarine sediments frequently exhibit some of the highest microplastic concentrations reported worldwide [44,45].

Mangrove forests and salt marshes function as efficient natural traps for microplastics owing to their complex vegetation structure, reduced hydrodynamic energy, and high rates of sediment accumulation [46,47]. Mangrove root systems and salt-marsh vegetation reduce water flow and enhance particle interception and sediment retention, promoting the accumulation and potentially long residence times of microplastics within these environments [46,47]. Retained particles also provide persistent substrates for microbial colonization, with plastisphere communities developing rapidly on microplastics deposited within salt-marsh sediments [48].

Hypersaline lakes and solar salterns represent comparatively understudied environments in plastisphere research, characterized by strong physicochemical selection pressures, including elevated salinity, evaporation, and intense solar exposure [49,50]. Such environmental gradients can influence both plastic-associated microbial community assembly and particle transformation, although their combined effects on plastisphere development remain poorly resolved. Recent evidence from salt-impacted aquatic systems indicates that salinity, light availability, nutrient conditions, and temperature can exert stronger influences on plastisphere community composition than polymer identity itself [51].

These contrasting habitats demonstrate that saline ecosystems are not environmentally homogeneous. Instead, they encompass a continuum of physicochemical conditions that strongly influence particle transport, microbial colonization, and the ecological functioning of the plastisphere.

2.4. Ecological Implications for Plastisphere Formation

The physicochemical dynamics governing microplastic transport ultimately determine the ecological opportunities available for microbial colonization. As particles move between surface waters, the water column, sediments, and benthic habitats, they encounter distinct microbial source communities and environmental conditions that drive biofilm assembly and succession [5,23,40,52]. Environmental filtering imposed by salinity, nutrient availability, oxygen concentration, ultraviolet radiation, temperature, and hydrodynamic stress acts simultaneously with polymer properties to shape plastisphere assembly [51,52]. Recent studies increasingly suggest that these environmental variables explain a greater proportion of microbial community variation than polymer type alone, challenging the traditional polymer-centric perspective of plastisphere ecology [3,5].

This ecological perspective emphasizes that microplastics should not be regarded simply as inert substrates but as mobile microbial habitats whose biological properties continuously evolve during environmental transport [3,5]. Plastisphere communities undergo ecological succession and environmental filtering, while polymer characteristics and physicochemical transformation simultaneously influence microbial community assembly and functional potential [3,6].

Consequently, understanding plastisphere ecology requires integrating environmental transport, polymer chemistry, microbial succession, and environmental selection within a unified ecological perspective. Such integration is particularly relevant in saline ecosystems, where salinity and other physicochemical gradients impose strong selective pressures on microbial colonization and community organization, potentially influencing microbial interactions and plastic transformation [5,48].

Table 1. Main characteristics of saline ecosystems, including major sources of microplastics, predominant polymers, environmental processes, and expected plastisphere characteristics.

Saline ecosystem	Major sources of microplastics	Predominant polymers	Dominant environmental processes	Expected plastisphere characteristics	Representative references
Open ocean	River discharge, shipping, fisheries, atmospheric deposition	PE, PP	Long-distance transport, UV weathering, biofouling, vertical mixing	Mature biofilms, high bacterial diversity, floating and sinking plastisphere	4, 5, 6
Estuaries	Urban runoff, wastewater effluents, rivers	PE, PP, PET, PS	Flocculation, tidal mixing, salinity gradients	Rapid microbial succession and high diversity	6, 54,
Mangrove forests	Riverine inputs, aquaculture, coastal litter	PE, PP, PET	Sediment trapping, organic matter accumulation	Stable biofilms and strong bacterial–fungal interactions	46, 56
Salt marshes	River discharge, atmospheric deposition	PE, PP, PET	Fine sediment deposition, periodic flooding	Persistent plastisphere communities	47, 48
Coastal lagoons	Wastewater, tourism, aquaculture	PE, PP, PS	Restricted circulation, eutrophication	Dense biofilms and active microbial metabolism	57, 58
Hypersaline lakes	Local anthropogenic activities, atmospheric deposition	PE, PP, PET	Extreme salinity, intense UV radiation, evaporation	Halophilic and halotolerant biofilms	51, 59
Solar salterns	Atmospheric deposition, industrial activities	PE, PP	Salt crystallization, evaporation, hypersalinity	Expected selection for halophilic and halotolerant plastisphere taxa	8. 60, 61

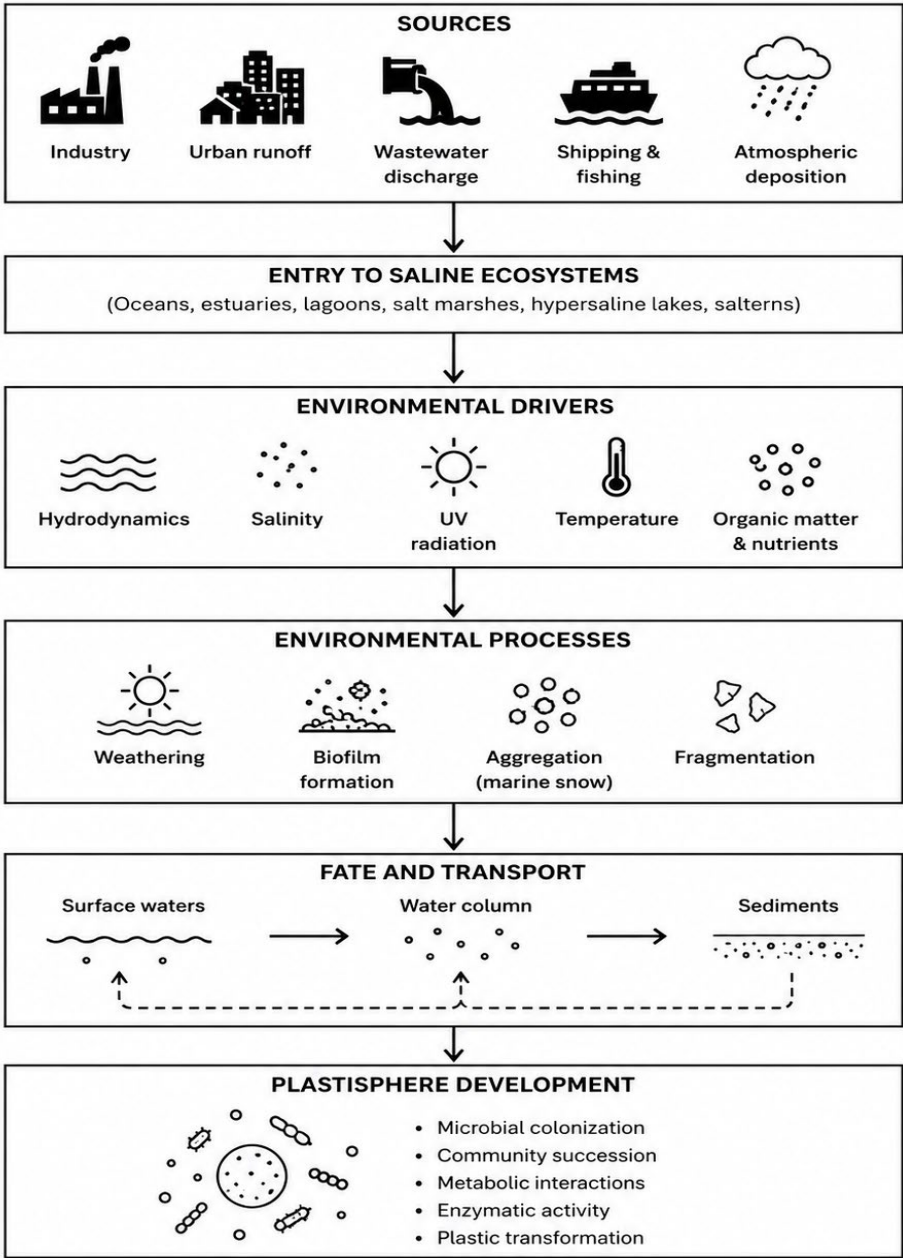


Figure 1. Environmental fate of microplastics in saline ecosystems and the initial stages of plastisphere development. Anthropogenic sources introduce microplastics into saline environments, where physicochemical drivers regulate weathering, transport, aggregation, and biofilm formation, ultimately determining microbial colonization and plastisphere establishment.

3. The Plastisphere as a Specialized Microbial Habitat

Plastic debris has traditionally been regarded as an inert substrate for microbial colonization. However, increasing evidence demonstrates that microplastics rapidly develop into biologically active habitats supporting structurally and functionally distinct microbial communities [3–5]. This colonized interface, known as the “plastisphere”, represents a novel anthropogenic microbial habitat in which microorganisms establish complex biofilms that differ from free-living communities in the surrounding environment [3–5]. Rather than being randomly assembled, plastisphere communities are shaped by ecological succession, microbial interactions, environmental selection, and the physicochemical properties of the polymer surface [5,62–64].

3.1. Biofilm Formation on Plastic Surfaces

The establishment of the plastisphere begins rapidly after plastic particles enter aquatic environments. Within minutes to hours, dissolved organic matter and biomolecules adsorb onto polymer surfaces, forming a conditioning film that modifies their physicochemical properties and influences subsequent microbial attachment [65,66]. This conditioning layer can modify surface hydrophobicity and electrostatic interactions, thereby influencing the initial stages of microbial adhesion and biofilm development [65,66].

Primary colonizers, predominantly bacteria, initially interact with conditioned surfaces through reversible physicochemical interactions, followed by more stable attachment mediated by cellular appendages, adhesion proteins, and extracellular polymeric substances (EPS) [7,67,68]. As colonization progresses, microorganisms produce increasingly complex extracellular matrices composed primarily of polysaccharides, proteins, extracellular DNA, and lipids, which stabilize the developing biofilm and promote cell–cell and cell–surface interactions [18,69,70]. The resulting matrix contributes to nutrient retention, metabolic cooperation, and protection against environmental stresses, thereby creating a structured microenvironment in which plastisphere communities can develop [69,70]. In saline ecosystems, ionic composition and salinity may further influence microbial attachment, EPS organization, and plastisphere community assembly. Salinity has been identified as an important environmental filter shaping plastic-associated microbial communities, sometimes exerting a stronger influence than polymer identity itself [6,63]. Consequently, plastisphere development in saline environments reflects the combined influence of surface conditioning, microbial succession, biofilm matrix formation, and environmental selection.

3.2. Ecological Succession Within the Plastisphere (Figure 2)

Plastisphere development is a dynamic ecological process characterized by temporal patterns of microbial succession [23,62,64]. Early colonization is frequently dominated by rapidly recruiting microorganisms capable of efficient attachment to newly available surfaces, with members of Alphaproteobacteria and Gammaproteobacteria commonly reported among pioneer bacterial communities [23,67,68]. As biofilms mature, community composition undergoes substantial turnover and taxonomic diversity may increase, incorporating Bacteroidota and other bacterial groups together with Archaea, fungi, protists, microalgae, and viruses [3,7,22,23]. These organisms occupy different ecological and trophic niches within the biofilm and may contribute to processes including primary production, organic matter decomposition, nutrient cycling, grazing, and polymer transformation [3,22,23]. The mature plastisphere can therefore develop into a spatially structured, multispecies microbial system characterized by diverse ecological interactions rather than functioning simply as a bacterial biofilm [3,22].

Plastisphere succession is not determined, however, by colonization time alone. Environmental conditions, including salinity, nutrient availability, temperature, and other physicochemical characteristics, can strongly influence microbial recruitment, community assembly, and succession [6,63,64,71]. Indeed, environmental conditions often exert stronger effects on plastisphere community structure than polymer identity, demonstrating that plastisphere development reflects the interaction between temporal succession, substrate properties, and environmental filtering [6,64,71].

3.3. Environmental Drivers of Community Assembly

The composition of plastisphere communities emerges from the interaction between polymer characteristics and environmental filtering. Polymer type influences initial microbial attachment through differences in surface roughness, hydrophobicity, crystallinity, additive composition, and susceptibility to environmental weathering. Nevertheless, an increasing number of studies indicate that environmental variables frequently exert stronger effects on microbial community composition than polymer chemistry alone [5,72,73]. Among saline ecosystems, salinity represents a strong ecological filter shaping microbial community composition and function [8]. Osmotic stress restricts

microbial colonization by favoring taxa possessing physiological adaptations such as compatible-solute accumulation, regulation of intracellular ion concentrations, oxidative-stress responses, and modifications of extracellular polymeric substances [59,74]. Within plastisphere communities, salinity can interact with other environmental variables to influence microbial recruitment and community organization [6,52,63]. Nutrient availability, dissolved oxygen, pH, suspended particulate matter, and hydrodynamic conditions may further modulate community assembly by affecting microbial growth, dispersal, and ecological interactions [3,52].

Plastisphere development, then, should be interpreted within the broader framework of microbial community ecology, in which deterministic processes such as environmental selection interact with stochastic processes including dispersal, ecological drift, and probabilistic colonization to shape community assembly [75,76]. Evidence from plastisphere studies indicates that community assembly reflects the combined influence of environmental filtering, substrate properties, colonization history, and stochastic processes rather than any single deterministic factor [3,77]. Plastisphere composition can therefore be understood as an emergent outcome of environmental selection, dispersal, succession, and biotic interactions operating simultaneously across spatial and temporal scales.

3.4. Functional Interactions Within Plastisphere Communities

The plastisphere is increasingly recognized as a highly interactive microbial system in which cooperative, competitive, and trophic interactions coexist [3,22,77]. Within multispecies biofilms, microorganisms can exchange metabolites, nutrients, signaling molecules, and extracellular products, generating interaction networks that influence resource utilization, community organization, and resilience [18,70,78]. Recent evidence from the microplastisphere further demonstrates that cross-kingdom associations contribute to network complexity and stability and support microbial food webs involving producers, decomposers, consumers, and symbionts [22]. Such ecological interactions may contribute to nutrient recycling, organic matter transformation, and functional organization within plastisphere biofilms.

Bacterial–fungal interactions provide an additional layer of ecological complexity. In multispecies microbial communities, fungal hyphae can provide three-dimensional surfaces for bacterial attachment and dispersal, while reciprocal metabolic exchanges can generate cross-feeding relationships between bacterial and fungal populations [15,79]. Although these mechanisms are well established in other microbial systems, their ecological importance within the plastisphere remains poorly resolved. Horizontal gene transfer further contributes to plastisphere adaptation; high cell densities and close physical proximity within biofilms create favorable conditions for genetic exchange [80]. Microplastic-associated biofilms have indeed been identified as potential hotspots for the transfer and dissemination of genes associated with antimicrobial resistance and other adaptive traits [80,81].

Collectively, these interactions support the consideration of the plastisphere as an ecologically integrated microbial consortium rather than simply a collection of independently colonizing species [3,22]. Such functional integration provides an ecological context in which microbial communication systems, including quorum sensing, can coordinate collective behaviors and influence biofilm development and extracellular product formation [21,82]. However, the extent to which quorum-sensing-mediated interactions regulate extracellular enzyme production and ultimately influence polymer biodegradation within natural plastisphere communities remains unresolved. Understanding these signaling processes would be an important step toward elucidating plastisphere functioning, particularly in saline ecosystems where environmental selection strongly influences microbial community assembly.

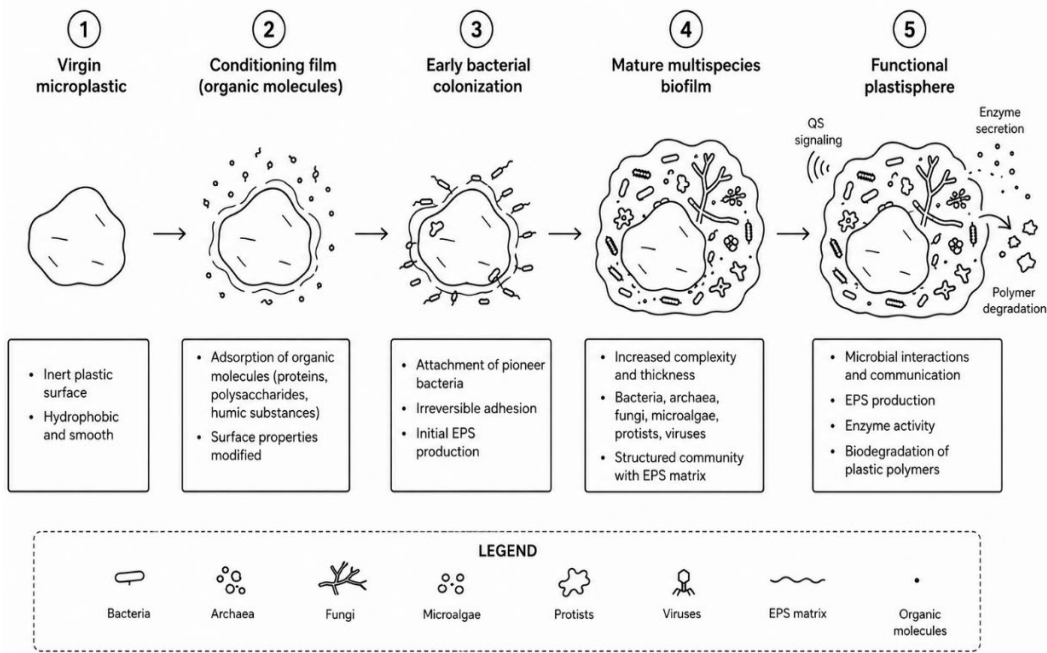


Figure 2. Formation and ecological succession of the plastisphere on microplastic surfaces.

4. Quorum Sensing as a Regulatory Network in the Saline Plastisphere

Microorganisms rarely function as isolated cells but rather engage in chemical communication that coordinates collective responses to changing environmental conditions [17,78,82]. Among these mechanisms, quorum sensing (QS) is one of the most extensively characterized forms of microbial communication, allowing cells to regulate population-level gene expression through the production, release, and detection of signaling molecules [17,83]. Although QS has historically been studied extensively in pathogenic and host-associated systems, it also plays important ecological roles in natural aquatic environments and surface-associated microbial communities, regulating processes associated with biofilm development, nutrient acquisition, secondary metabolism, and biogeochemical cycling [78,84,85]. Increasing evidence now indicates that QS is also relevant to microbial communities developing on microplastic surfaces [19,21,81].

Within the plastisphere, dense microbial populations embedded within extracellular polymeric substance (EPS) matrices create physicochemical conditions favorable to the accumulation, retention, and exchange of signaling molecules [18,19,70]. Recent evidence demonstrates that AHL-mediated QS can influence plastisphere formation, biomass accumulation, EPS production, microbial community organization, and functional activity, providing direct support for microbial communication as a regulatory component of plastisphere development [21]. QS signaling on microplastics has also been linked to changes in microbial metabolism and biofilm-associated functions, further supporting the view that plastic surfaces represent distinct signaling environments [81]. Nevertheless, the ecological importance of QS within natural plastisphere communities remains incompletely resolved, particularly regarding cross-species and cross-kingdom interactions, extracellular enzyme regulation, and their potential consequences for polymer biodegradation in saline ecosystems [19,21].

4.1. Principles of Quorum Sensing

Quorum sensing is based on the synthesis, release, accumulation, and perception of small signaling molecules known as autoinducers. As microbial populations increase, the local concentration of these molecules may reach a threshold that triggers coordinated changes in gene expression and collective behavior [17,82,83,86]. Different microbial groups employ diverse signaling

molecules. Gram-negative bacteria commonly use N-acyl-homoserine lactones (AHLs), whereas Gram-positive bacteria frequently rely on autoinducing peptides (AIPs) [17,83]. Autoinducer-2 (AI-2), produced through the LuxS pathway in numerous bacterial taxa, has been implicated in both intra- and interspecific communication, although its role as a universal bacterial signal is still debated because LuxS also participates in central metabolism [82,87]. Additional signaling compounds, including diffusible signal factors (DSFs), diketopiperazines (DKPs), quinolone signals, and indole derivatives, further expand the chemical diversity of microbial communication within environmental biofilms [78,88,89]. These signaling systems regulate numerous physiological processes relevant to plastisphere development, including surface attachment, motility, EPS production, biofilm maturation and dispersal, nutrient acquisition, stress responses, and extracellular enzyme production [78,82,90]. Quorum sensing may also influence horizontal gene transfer by modifying biofilm organization, cell proximity, and conjugation-related processes, thereby potentially affecting the dissemination of adaptive traits within densely colonized microbial communities [91,92]. Recent evidence that AHL-mediated signaling regulates plastisphere formation, biomass accumulation, EPS production, and microbial community organization provides direct support for the ecological relevance of these mechanisms on microplastic surfaces [21].

4.2. Bacterial Quorum Sensing in the Plastisphere

Bacterial communities represent major components of developing plastisphere biofilms, and increasing evidence indicates that quorum-sensing bacteria and their signaling molecules are widespread within plastic-associated microbial communities [19,21,93]. Several bacterial groups frequently detected in marine plastisphere communities, including members of the Rhodobacteraceae and Gammaproteobacteria, possess well-characterized quorum-sensing systems capable of regulating surface attachment, biofilm development, secondary metabolism, and extracellular product formation [78,84,93]. Indeed, multiple AHL molecules have been detected in bacterial isolates obtained from marine microplastic biofilms, supporting the concept of active QS-mediated communication within the plastisphere [93].

Recent experimental evidence provides direct support for a regulatory role of AHL-mediated signaling in plastisphere development. Exogenous AHL addition promotes microbial attachment, biofilm biomass accumulation, and EPS production on microplastic surfaces, activating genes associated with chemotaxis, flagellar motility, surface adhesion, and extracellular matrix formation [21]. QS-mediated regulation has also been associated with enhanced EPS secretion and horizontal gene transfer within microplastic biofilms, indicating that chemical signaling can influence both structural and functional properties of plastic-associated microbial communities [21,94]. More recent evidence further indicates that exogenous AHL signaling can redirect cellular energy metabolism toward EPS production and enhance biofilm-associated biogeochemical functions on microplastic surfaces [21].

However, disruption of AHL-mediated signaling through quorum-quenching approaches may substantially reduce plastisphere biofilm formation, biomass accumulation, and EPS production [21]. Experimental manipulation of QS and quorum quenching alters microbial community structure and assembly processes, indicating that chemical communication can actively contribute to plastisphere organization rather than simply emerging as a consequence of increasing biofilm density [21]. Collectively, these findings identify bacterial QS as an important regulatory mechanism in plastisphere development, although its ecological significance across different polymers, environmental conditions, and natural saline ecosystems remains incompletely understood.

4.3. Fungal Quorum Sensing and Cross-Kingdom Communication

Quorum sensing in fungi has received less attention than in bacteria, but there is increasing evidence that fungal communities employ chemical signaling to regulate population-dependent behaviors [95–97]. Molecules such as farnesol, tyrosol, phenylethanol, tryptophol, and other aromatic alcohols have been implicated in the regulation of fungal morphogenesis, filamentation, hyphal

growth, sporulation, stress responses, and biofilm development in several fungal taxa [95,96,98]. Within multispecies microbial communities, fungal hyphae can introduce an additional level of structural and ecological complexity by providing three-dimensional networks that facilitate bacterial attachment, spatial dispersal, and access to otherwise disconnected microhabitats [15,18,79]. Such “fungal highways” can increase bacterial dispersal and spatial intermixing, potentially enhancing opportunities for metabolic exchange and interspecific interactions [15]. Although these mechanisms are well established in other microbial systems, their significance within saline plastisphere communities remains largely unexplored.

Cross-kingdom chemical communication further increases the complexity of bacterial–fungal interactions. Bacterial quorum-sensing molecules, including AHLs, can alter fungal growth, morphology, and developmental transitions, whereas fungal signaling metabolites such as farnesol can interfere with bacterial quorum-sensing pathways, motility, virulence-related traits, and biofilm formation [15,99]. These reciprocal interactions demonstrate that bacterial and fungal signaling networks can intersect. Although direct evidence for such inter-kingdom signaling interactions within saline plastisphere communities is limited, the increasing recognition of the plastisphere as a multi-kingdom microbial system, together with evidence that cross-kingdom associations contribute to microbial network complexity and stability, provides a strong ecological basis for investigating such communication in plastic-associated biofilms [22]. Cross-kingdom signaling may represent an important mechanism influencing community organization and metabolic cooperation, although its role in extracellular enzyme production and polymer biodegradation in saline plastisphere communities remains to be studied.

4.4. Quorum Sensing Under Saline Conditions

Salinity can influence microbial communication through multiple physiological and physicochemical mechanisms. Changes in ionic strength and osmotic conditions affect cellular physiology, membrane properties, extracellular matrix composition, and biofilm organization, potentially modifying the production, transport, stability, and perception of quorum-sensing signals [100,101]. Experimental evidence from saline biofilms further demonstrates that salinity stress can alter AHL abundance and diversity and shift the balance between quorum sensing and quorum quenching [101].

Halophilic and halotolerant microorganisms possess multiple adaptations that enable growth and collective organization under osmotic stress, including compatible-solute accumulation, regulation of intracellular ion concentrations, modifications of membrane composition, and production of extracellular polymeric substances [8,102]. Within biofilms, high cell density and the extracellular matrix create spatially structured microenvironments that influence the transport, retention, and local concentration of quorum-sensing molecules [78,103,104]. The extracellular matrix and local hydrodynamic conditions can thus strongly modulate signal propagation and intercellular communication independently of cell density alone [104], while environmental variables common to saline ecosystems, including temperature, pH, nutrient availability, oxidative stress, and other physicochemical conditions, can further influence quorum-sensing systems by affecting signal synthesis, stability, transport, or receptor-mediated responses [78,100,105]. AHL stability itself is environmentally dependent, with temperature and pH influencing signal persistence and different AHL structures exhibiting distinct susceptibilities to degradation [100,105]. Consequently, quorum sensing should be regarded as an environmentally responsive regulatory process whose activity emerges from the interaction among population density, spatial organization, signal transport, and physicochemical conditions, rather than from cell density alone [78].

4.5. Ecological Implications for Plastisphere Functioning (Table 2)

The ecological significance of quorum sensing extends beyond cell-to-cell communication. By coordinating gene expression within microbial populations, QS can regulate processes relevant to plastisphere functioning (Figure 3), including biofilm maturation, extracellular product formation,

stress responses, nutrient acquisition, secondary metabolism, and microbial interactions [78,82,85]. Recent experimental evidence demonstrates that AHL-mediated signaling can directly influence plastisphere formation, EPS production, community structure, microbial interaction networks, and functional activity on microplastic surfaces [21]. Within multispecies plastisphere communities, chemical signaling may contribute to metabolic coordination among interacting microorganisms, although direct evidence for QS-mediated metabolic complementarity across bacteria, fungi, archaea, and microalgae remains very limited. High cell density, close physical association, and biofilm organization also create favorable conditions for horizontal gene transfer, and the plastisphere has increasingly been identified as an ecological hotspot for genetic exchange [80]. Such processes may facilitate the dissemination of adaptive traits, including genes associated with antimicrobial resistance, stress responses, and xenobiotic metabolism (Table 3), although direct links between QS-mediated horizontal gene transfer and the spread of plastic-degradation genes remain to be demonstrated.

Collectively, these observations support a conceptual model in which quorum sensing may function as an important regulatory interface linking plastisphere organization, microbial interactions, and metabolic responses. Rather than representing an isolated communication mechanism, QS can integrate information related to population density, environmental conditions, and community organization, thereby influencing collective microbial behavior [78]. We therefore propose that QS is a central regulatory mechanism connecting microbial community organization with the functional potential of plastisphere biofilms. This perspective provides the mechanistic foundation for examining how microbial communication may regulate extracellular enzyme production and, consequently, influence polymer transformation and biodegradation. Although microorganisms and extracellular enzymes associated with plastisphere communities have demonstrated substantial potential for polymer transformation, the extent to which these processes are regulated by QS within natural plastisphere communities is unresolved [19,21].

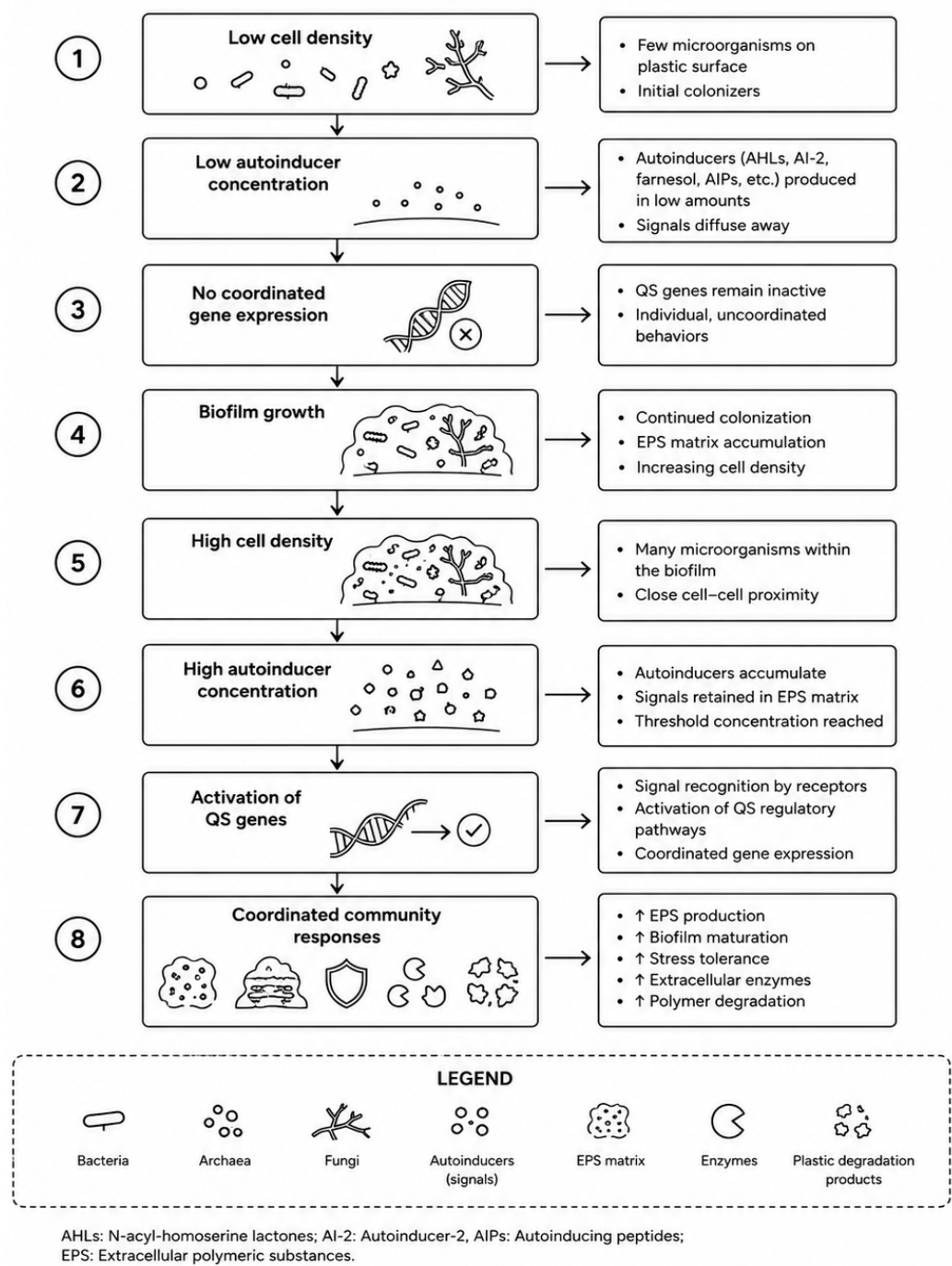


Figure 3. Quorum sensing as a regulatory network within the saline plastisphere.

Table 3. Major quorum sensing molecules and their potential ecological roles in plastisphere communities of saline ecosystems.

Signaling molecule	Major producers	Main physiological functions	Potential role in the plastisphere	References
N-acyl homoserine lactones (AHLs)	Gram-negative bacteria (Vibrio, Pseudomonas, Roseobacter, Alteromonas)	Biofilm formation, EPS production, motility, extracellular enzyme secretion	Promotes microbial attachment, biofilm maturation, and coordinated expression of plastic-degrading enzymes	17, 106, 107

Signaling molecule	Major producers	Main physiological functions	Potential role in the plastisphere	References
Autoinducer-2 (AI-2)	Gram-negative and Gram-positive bacteria	Interspecies communication, biofilm regulation, metabolic coordination	Facilitates communication among phylogenetically distinct members of the plastisphere	87, 108
Autoinducing peptides (AIPs)	Gram-positive bacteria (Bacillus, Staphylococcus, Enterococcus)	Biofilm development, competence, sporulation	Coordinates collective behavior of Gram-positive members within mature biofilms	86, 109
Diffusible signal factors (DSFs)	Xanthomonas, Stenotrophomonas, marine Proteobacteria	Biofilm dispersion, stress response, virulence regulation	Regulates biofilm architecture and microbial adaptation under environmental stress	110
Diketopiperazines (DKPs)	Diverse bacteria and fungi	Intercellular communication, biofilm regulation, modulation of AHL signaling	May enhance cross-species communication within mixed plastisphere biofilms	111
Indole	Escherichia coli, Vibrio, Pseudomonas and other Proteobacteria	Biofilm formation, oxidative stress response, persistence	Modulates bacterial physiology and interspecies interactions in nutrient-limited biofilms	112 113
Quinolone signals (PQS)	Pseudomonas spp.	Iron acquisition, oxidative stress, extracellular DNA release	Enhances mature biofilm stability and extracellular matrix organization	114, 115
Farnesol	Candida spp. and other yeasts	Hyphal inhibition, biofilm regulation, oxidative stress response	Regulates fungal development and bacterial–fungal interactions within plastisphere biofilms	116, 117
Tyrosol	Candida spp.	Cell proliferation, filamentation, biofilm formation	Accelerates fungal colonization during early biofilm development	117, 118
Phenylethanol and aromatic alcohols	Yeasts and filamentous fungi	Morphogenesis, sporulation, stress tolerance	May regulate fungal adaptation to saline biofilms and coordinate mixed microbial communities	117, 119
Putative archaeal signaling molecules	Halophilic archaea (Haloferax, Halobacterium, Haloarcula)	Biofilm formation, motility, environmental adaptation (still poorly understood)	Potential role in communication within hypersaline plastisphere communities remains largely unexplored	8

5. Halotolerant Fungi as Key Components of the Saline Plastisphere

Although bacteria have traditionally dominated plastisphere research, fungi are increasingly recognized as important components of aquatic biofilms because of their metabolic versatility, capacity for surface colonization, and ability to produce a broad range of extracellular enzymes [3,12,22]. In saline ecosystems, halotolerant and halophilic fungi are particularly relevant because they possess physiological adaptations that permit growth under elevated osmotic pressure, fluctuating salinity, nutrient limitation, and other environmental stresses characteristic of marine and hypersaline habitats [120–122]. These adaptations enable fungi to colonize diverse natural and anthropogenic substrates, including synthetic polymers, suggesting a potentially important role in plastisphere development and plastic transformation [12,124].

Compared with bacterial communities, however, fungal diversity and ecological functions within the plastisphere remain comparatively poorly understood [3,12,23]. Plastisphere research has historically emphasized bacterial community composition and prokaryotic metabolisms, whereas fungal colonization, interspecific interactions, and functional contributions to polymer transformation have received substantially less attention. Consequently, the ecological contribution of fungal communities to the organization and functioning of plastisphere biofilms, particularly in saline and hypersaline environments, remains incompletely resolved.

5.1. Diversity of Halotolerant Fungi in Saline Ecosystems

Halotolerant and halophilic fungi are widely distributed across marine and hypersaline habitats, including coastal environments, estuaries, mangroves, salt marshes, hypersaline lakes, deep-sea sediments, and solar salterns [11,120,124]. These communities are frequently dominated by representatives of Ascomycota and Basidiomycota, although fungi belonging to other evolutionary lineages are also present in aquatic environments [11,125,126].

Frequently reported marine and halotolerant fungal genera include *Aspergillus*, *Penicillium*, *Cladosporium*, *Alternaria*, *Aureobasidium*, *Hortaea*, *Wallemia*, and several yeast-forming taxa [11,120,124]. Several marine and terrestrial fungi, including species of *Aspergillus*, *Penicillium*, *Cladosporium*, and *Zalerion*, have demonstrated the capacity to colonize or transform synthetic polymers, highlighting their potential ecological relevance in plastic-associated microbial communities [12,123,127].

High-throughput sequencing has substantially expanded knowledge of fungal diversity in marine and extreme environments. Nevertheless, fungal components remain comparatively underrepresented in plastisphere studies, many of which have historically relied on bacterial 16S rRNA gene surveys rather than parallel characterization of bacterial and eukaryotic communities [3,23]. This methodological imbalance, together with limitations associated with fungal reference databases and cultivation of environmentally specialized taxa, suggests that fungal diversity and ecological functions within saline plastisphere biofilms remain incompletely characterized.

5.2. Physiological Adaptations to Saline Environments

Successful colonization of saline environments requires physiological adaptations that enable fungal cells to maintain homeostasis under osmotic and oxidative stress [120–122]. Halotolerant and halophilic fungi regulate intracellular osmotic balance through the accumulation of compatible solutes, particularly polyols such as glycerol, while coordinating ion transport and cellular signaling pathways that limit the physiological consequences of elevated extracellular salt concentrations [120,122,128,129].

Cell-wall and membrane remodeling represent additional components of fungal adaptation to salinity. Changes in membrane lipid composition, cell-wall structure, melanization, and extracellular material can increase resistance to osmotic stress, desiccation, oxidative damage, and radiation in extremotolerant fungi [121,122,124]. Many marine and extremotolerant fungi also exhibit considerable metabolic flexibility and produce diverse extracellular enzymes capable of utilizing

structurally complex carbon sources [11,12]. Such versatility may facilitate colonization of weathered plastic surfaces containing adsorbed organic matter, additives, and low-molecular-weight products generated during abiotic polymer weathering.

5.3. Fungal Contribution to Plastisphere Formation

Within multispecies biofilms, fungi can perform ecological functions extending beyond organic-matter decomposition. Filamentous hyphae generate three-dimensional networks that provide surfaces for bacterial attachment and facilitate bacterial movement between spatially separated microhabitats [15,79]. These so-called “fungal highways” can enhance bacterial dispersal and spatial connectivity and may therefore contribute to the structural organization of multispecies microbial communities. In the plastisphere, similar mechanisms could increase surface complexity and facilitate interactions among bacterial and fungal populations, although direct experimental evidence remains limited.

Fungal extracellular matrices can further contribute to adhesion, water retention, and structural stability within fungal and polymicrobial biofilms [69,130]. Such properties may be particularly relevant under fluctuating osmotic and hydrodynamic conditions. Their interaction with bacteria may involve reciprocal metabolic exchange, cross-feeding, modification of local physicochemical conditions, and exchange of growth-promoting compounds [15,79]. These interactions can generate metabolically interconnected communities capable of exploiting resources unavailable to individual populations. Their occurrence within the plastisphere provides a plausible mechanism through which fungi could influence bacterial community organization and substrate transformation. Chemical signaling adds another potential dimension to these interactions. Fungal signaling molecules such as farnesol and tyrosol regulate fungal biofilm development, while bacterial quorum-sensing molecules can modify fungal morphology and physiology, demonstrating that bacterial–fungal interactions may involve reciprocal cross-kingdom signaling [15,95,96,99]. Whether comparable signaling networks operate within natural saline plastisphere communities remains an important unresolved question.

5.4. Enzymatic Potential for Polymer Transformation

One of the most relevant functional characteristics of fungi is their capacity to secrete extracellular oxidative and hydrolytic enzymes capable of transforming structurally recalcitrant organic substrates. Enzymatic systems originally associated with the degradation of natural polymers can exhibit broad substrate specificity and have consequently been investigated for their capacity to modify synthetic polymers and polymer-associated compounds [12,131,132]. Fungal enzymes implicated in polymer transformation include laccases, lignin and manganese peroxidases, cutinases, esterases, lipases, and other oxidative or hydrolytic enzymes [12,132]. Depending on polymer chemistry, these enzymes may contribute to surface oxidation, hydrolysis of susceptible chemical bonds, and formation of lower-molecular-weight transformation products. Evidence of fungal-mediated plastic transformation has been reported for several polymers, including polyethylene and polyurethane, although degradation rates and mechanisms vary substantially among fungal species and polymer types [12,123,133].

Fungal and bacterial activities could act sequentially or synergistically during polymer transformation. Abiotic weathering can increase surface oxidation and alter polymer physicochemical properties, facilitating microbial attachment and subsequent enzymatic activity, while fungal oxidative processes may further modify polymer surfaces and generate compounds potentially accessible to other members of the microbial community [12,132]. Such interactions provide a plausible basis for complementary fungal–bacterial contributions to polymer turnover, although their importance within natural saline plastisphere communities remains to be experimentally demonstrated.

6. Knowledge Gaps and Future Directions

Our knowledge of aquatic fungi is still very limited, in part because of the inadequacy of current genetic databases [134], despite growing recognition of the ecological importance of fungi in these environments. Several fundamental questions remain unresolved. Fungal diversity and functional roles within plastisphere communities remain considerably less characterized than those of bacteria, particularly in saline and hypersaline environments [3,12]. This knowledge gap is especially pronounced in hypersaline lakes and solar salterns, where extremophilic fungal communities are known to occur but their association with plastic substrates remains largely unexplored [120–122]. Likewise, little is known about fungal quorum sensing and cross-kingdom signaling within environmental plastisphere communities, despite growing evidence that fungi employ chemical communication and interact extensively with bacterial populations in multispecies biofilms [15,96,97].

Another major limitation concerns the scarcity of functional studies. Plastisphere investigations have relied extensively on taxonomic and marker-gene approaches, which provide valuable information on community composition but limited insight into active metabolic processes and ecological interactions [3,12]. Integrating metagenomics with metatranscriptomics, metaproteomics, metabolomics, and culture-based experimentation should therefore provide a more comprehensive understanding of the metabolic activity and functional interactions occurring within plastisphere communities. Such approaches are particularly important because genomic potential alone does not demonstrate expression or activity of polymer-transforming enzymes, whereas transcriptomic and proteomic analyses can provide stronger evidence of active degradation pathways [135,136].

Future research should also prioritize the isolation and functional characterization of halotolerant fungal strains and their extracellular enzymes under environmentally realistic saline conditions. Marine fungi have already demonstrated potential for the transformation of synthetic polymers (Table 4), but evidence of complete biodegradation and the underlying enzymatic mechanisms remains limited for many polymer–fungus combinations [12,123]. The discovery of salt-tolerant polymer-active microorganisms and enzymes represents a particularly promising direction for environmental biotechnology, as recently illustrated by the identification of halophilic PET-degrading enzyme candidates from saline mangrove-associated microbial communities [137].

Collectively, current evidence indicates that fungi should no longer be considered peripheral components of plastisphere ecology. Their metabolic versatility, extracellular enzymatic capabilities, structural interactions with other microorganisms, and capacity to persist under saline conditions suggest that halotolerant fungi may represent functionally important members of saline plastisphere communities [12,15,79] (Figure 4). Determining the extent to which fungi regulate biofilm architecture, cross-kingdom interactions, extracellular enzyme production, and polymer transformation therefore represents an important priority for future plastisphere research.

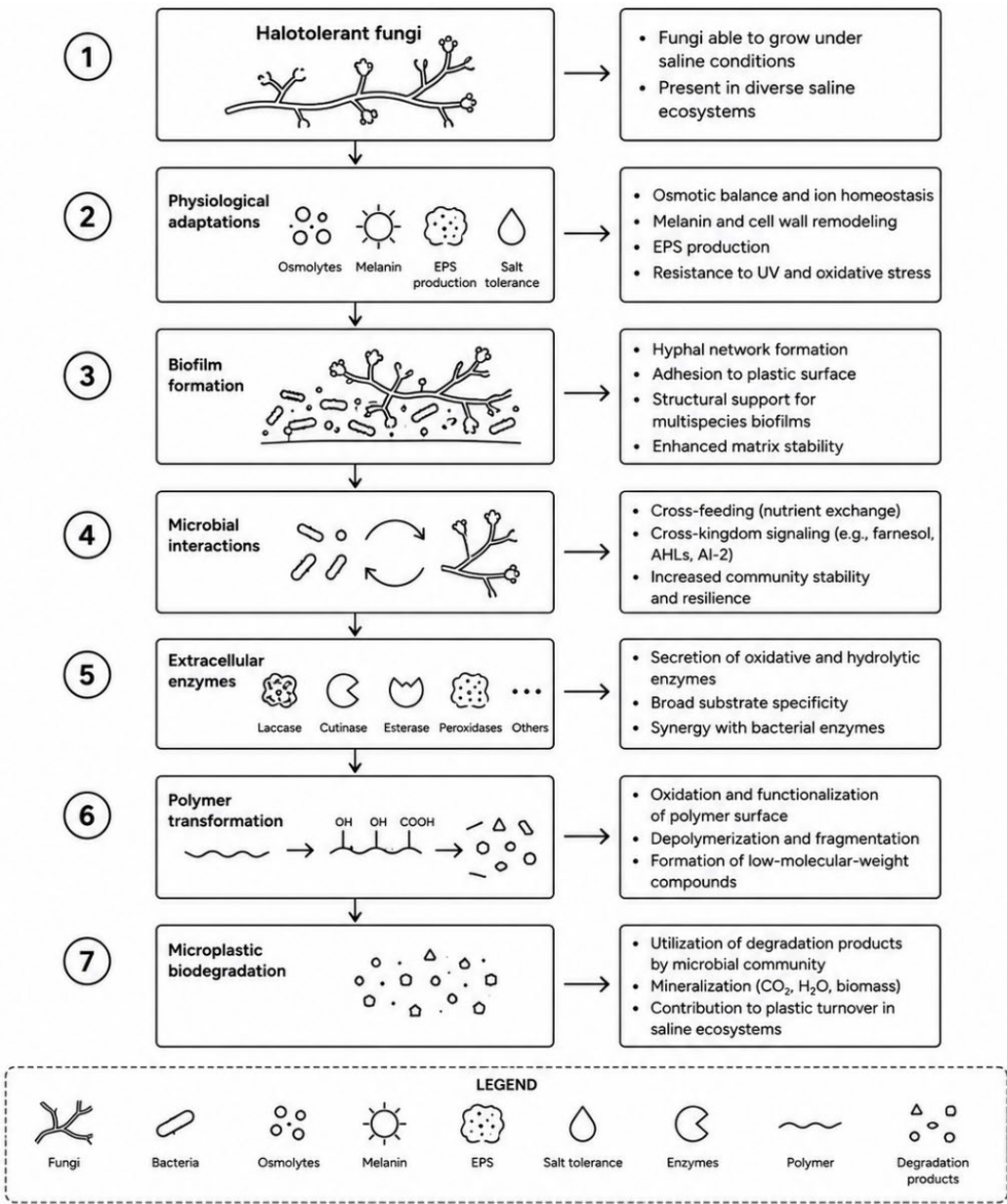


Figure 4. Ecological roles of halotolerant fungi in the saline plastisphere.

Table 4. Representative halotolerant fungi from saline ecosystems and their reported enzymatic potential for polymer.

Fungal taxon	Saline habitat	Main extracellular enzymes	Polymer or substrate	Potential ecological role in the plastisphere	Evidence level*	References
<i>Aspergillus sydowii</i>	Marine sediments, seawater	Laccase, esterase, lipase	Polyurethane (PU), aromatic hydrocarbons	Oxidative transformation of polymer-derived compounds; biofilm formation	Direct	10, 11
<i>Aspergillus terreus</i>	Coastal sediments	Cutinase, esterase, lipase	PET oligomers, aliphatic esters	Initial hydrolysis of ester-containing polymers	Direct	138, 139

Fungal taxon	Saline habitat	Main extracellular enzymes	Polymer or substrate	Potential ecological role in the plastisphere	Evidence level*	References
<i>Penicillium chrysogenum</i>	Marine sediments, estuaries	Esterase, laccase	Polyurethane (PU), polyethylene (PE)	Biofilm colonization and extracellular oxidation	Direct	133
<i>Cladosporium cladosporioides</i>	Mangroves, salt marshes	Laccase, peroxidase	Polyethylene (PE), lignin analogues	Polymer weathering and stabilization of multispecies biofilms	Indirect	10, 11
<i>Trichoderma harzianum</i>	Coastal soils, saline sediments	Cutinase, esterase, cellulase	Polyester-based polymers	Hydrolysis of ester bonds and synergistic interaction with bacteria	Direct	138
<i>Fusarium solani</i>	Marine sediments	Cutinase, lipase	PET model substrates	Surface oxidation and depolymerization of polyesters	Direct	138, 139
<i>Aureobasidium pullulans</i>	Marine biofilms, hypersaline habitats	Cutinase, esterase	PET oligomers, cutin	Early colonizer of hydrophobic surfaces; extracellular hydrolysis	Direct	140
<i>Debaryomyces hansenii</i>	Solar salterns, hypersaline lakes	Lipase, esterase	Hydrocarbon-derived compounds	Adaptation to hypersaline biofilms and carbon turnover	Indirect	120
<i>Hortaea werneckii</i>	Solar salterns	Oxidases, antioxidant enzymes	Aromatic compounds	Persistence under hypersaline conditions; candidate plastisphere colonizer	Potential	141, 142
<i>Wallemia ichthyophaga</i>	Hypersaline environments	Hydrolytic enzymes (poorly characterized)	Not yet demonstrated	Candidate extremophile for plastisphere colonization	Potential	143
<i>Marine fungal consortia</i>	Marine plastisphere	Laccases, peroxidases, esterases, lipases	PE, PET, PU, polymer additives	Cooperative biodegradation through multispecies biofilms	Potential/ Indirect	144, 145

6.1. Mechanisms and Enzymatic Pathways of Microplastic Degradation

The biodegradation of microplastics is a complex, multistep process that integrates abiotic weathering, microbial colonization, extracellular enzymatic depolymerization, intracellular assimilation, and ultimate mineralization. Rather than being mediated by a single microorganism or enzyme, plastic degradation generally results from the coordinated activity of multispecies biofilms in which bacteria, fungi, and other microorganisms perform complementary metabolic functions [147,156,158]. Within the plastisphere, these processes are further enhanced by high microbial

density, extracellular polymeric substances (EPS), and quorum sensing-regulated metabolic interactions, which collectively increase degradation efficiency and carbon utilization.

6.2. Polymer Weathering as a Prerequisite for Biodegradation

The intrinsic physicochemical properties of most synthetic polymers—including high molecular weight, hydrophobicity, crystallinity, and limited functional groups—render them highly resistant to microbial attack. Consequently, biodegradation is generally preceded by abiotic weathering, which represents the first and frequently the rate-limiting step in polymer transformation [1,146,147].

Exposure to ultraviolet (UV) radiation, thermal oxidation, mechanical abrasion, wave action, and reactive oxygen species progressively modifies polymer surfaces by introducing oxygen-containing functional groups such as hydroxyl, carbonyl, and carboxyl moieties. These reactions increase surface roughness, reduce polymer crystallinity, and enhance hydrophilicity, thereby facilitating microbial adhesion and enzymatic accessibility [37,146]. Weathering also generates cracks and pits that provide protected microhabitats for pioneer colonizers, accelerating plastsphere establishment. Saline environments introduce additional mechanisms that influence weathering. High ionic strength, repeated wetting–drying cycles, prolonged solar irradiation, and salt crystallization can intensify surface oxidation and mechanical fragmentation. Simultaneously, adsorption of dissolved organic matter forms conditioning films that promote microbial attachment, effectively coupling abiotic weathering with biological colonization [3,147].

6.3. Extracellular Enzymatic Depolymerization

Following successful colonization, microorganisms secrete extracellular enzymes that initiate depolymerization; intact polymers are too large to cross the cell membrane. Hydrolytic enzymes catalyze the cleavage of ester bonds in biodegradable polyesters such as polyethylene terephthalate (PET), polyurethane (PU), and polycaprolactone (PCL), whereas oxidative enzymes increase the susceptibility of more recalcitrant polymers such as polyethylene (PE) and polypropylene (PP) to subsequent degradation [147,148]. Among hydrolytic enzymes, PETase has become the best-characterized catalyst following its discovery in *Ideonella sakaiensis*. PETase hydrolyzes PET into mono(2-hydroxyethyl) terephthalate (MHET), with smaller amounts of bis(2-hydroxyethyl) terephthalate (BHET). MHET is subsequently hydrolyzed by MHETase into terephthalic acid (TPA) and ethylene glycol (EG), both of which are readily assimilated through central metabolic pathways [149–151]. Recent protein engineering efforts have substantially increased PETase thermostability and catalytic efficiency, highlighting its potential for industrial biorecycling applications [147,152,153].

Fungi contribute predominantly through oxidative and hydrolytic enzymes, including cutinases, esterases, lipases, laccases, manganese peroxidases, lignin peroxidases, versatile peroxidases, and unspecific peroxygenases; many of these act extracellularly [154]. These enzymes evolved primarily for lignocellulose degradation but display remarkable substrate promiscuity, enabling oxidation or hydrolysis of synthetic polymers and polymer-derived oligomers [148,155]. Cutinases are particularly effective against PET because of their ability to hydrolyze ester bonds, whereas laccases and peroxidases oxidize polymer surfaces, generating reactive intermediates that facilitate subsequent enzymatic attack. Polyolefins such as PE and PP remain among the most recalcitrant synthetic polymers because their carbon–carbon backbone lacks hydrolysable bonds. Their biodegradation therefore relies primarily on oxidative modification mediated by reactive oxygen species, alkane hydroxylases, monooxygenases, laccases, and peroxidases before smaller oxidation products become available for microbial metabolism [148,154].

6.4. Assimilation and Intracellular Metabolism

Following extracellular depolymerization, soluble intermediates are transported into microbial cells through specific membrane transport systems. Once internalized, these molecules are

incorporated into central metabolic pathways that convert polymer-derived carbon into cellular biomass and metabolic energy [139,147] (Table 5). The metabolism of PET degradation products has been particularly well characterized. Terephthalic acid (TPA) is oxidized through dioxygenase-mediated reactions to protocatechuate, which subsequently enters the β -ketoadipate pathway, one of the principal aromatic compound degradation routes in bacteria. Ethylene glycol is oxidized sequentially to glycolaldehyde, glycolate, glyoxylate, and ultimately acetyl-CoA, feeding directly into the tricarboxylic acid (TCA) cycle [149,151].

Comparable intracellular pathways have been proposed for oxidation products derived from polyethylene and polypropylene degradation, although these remain considerably less understood than PET metabolism. Current evidence suggests that β -oxidation-like pathways participate in the assimilation of short-chain oxidation products generated during extracellular polymer oxidation [157, 158].

6.5. Mineralization and Carbon Cycling

Complete biodegradation culminates in mineralization, during which polymer-derived carbon is converted into carbon dioxide, water, and microbial biomass under aerobic conditions or into methane and carbon dioxide under anaerobic environments [156,159]. However, complete mineralization of conventional plastics remains relatively rare under natural environmental conditions; degradation rates are often limited by polymer crystallinity, nutrient availability, oxygen concentration, and environmental temperature. Within plastisphere communities, mineralization generally represents a cooperative process involving multiple microbial populations rather than a single degrader. Intermediate metabolites released by one organism frequently become substrates for neighboring microorganisms, creating metabolically interconnected food webs that enhance carbon utilization efficiency [3,18]. Such trophic interactions contribute to local carbon cycling while simultaneously maintaining microbial diversity within mature biofilms.

6.6. Synergistic Degradation by Bacterial–Fungal Consortia

Accumulating evidence indicates that microbial consortia outperform individual isolates during plastic biodegradation because different taxa contribute complementary metabolic capabilities [157,158]. Within the plastisphere, filamentous fungi frequently initiate polymer oxidation through extracellular laccases, peroxidases, cutinases, and esterases while simultaneously increasing surface roughness through hyphal penetration and oxidative modification [148]. These structural changes facilitate bacterial attachment and increase the accessibility of hydrolytic enzymes to the polymer surface. Bacteria subsequently metabolize soluble oligomers and monomers released by fungal activity, completing depolymerization and intracellular assimilation pathways (Figure 5). This metabolic complementarity is further reinforced by biofilm organization and quorum sensing, which synchronize extracellular enzyme secretion, nutrient acquisition, stress responses, and collective resource allocation [17,18]. Consequently, biodegradation should be regarded as an emergent property of structured microbial communities rather than the isolated activity of individual species.

Although significant advances have been achieved in understanding PET degradation, the mechanisms governing biodegradation of polyolefins under environmentally relevant saline conditions remain poorly resolved. Future research integrating metagenomics, metatranscriptomics, metaproteomics, metabolomics, stable isotope probing, and single-cell approaches will be essential to identify active degraders, characterize functional enzyme networks, and quantify the contribution of bacterial–fungal consortia to carbon cycling within saline plastisphere communities [147,158].

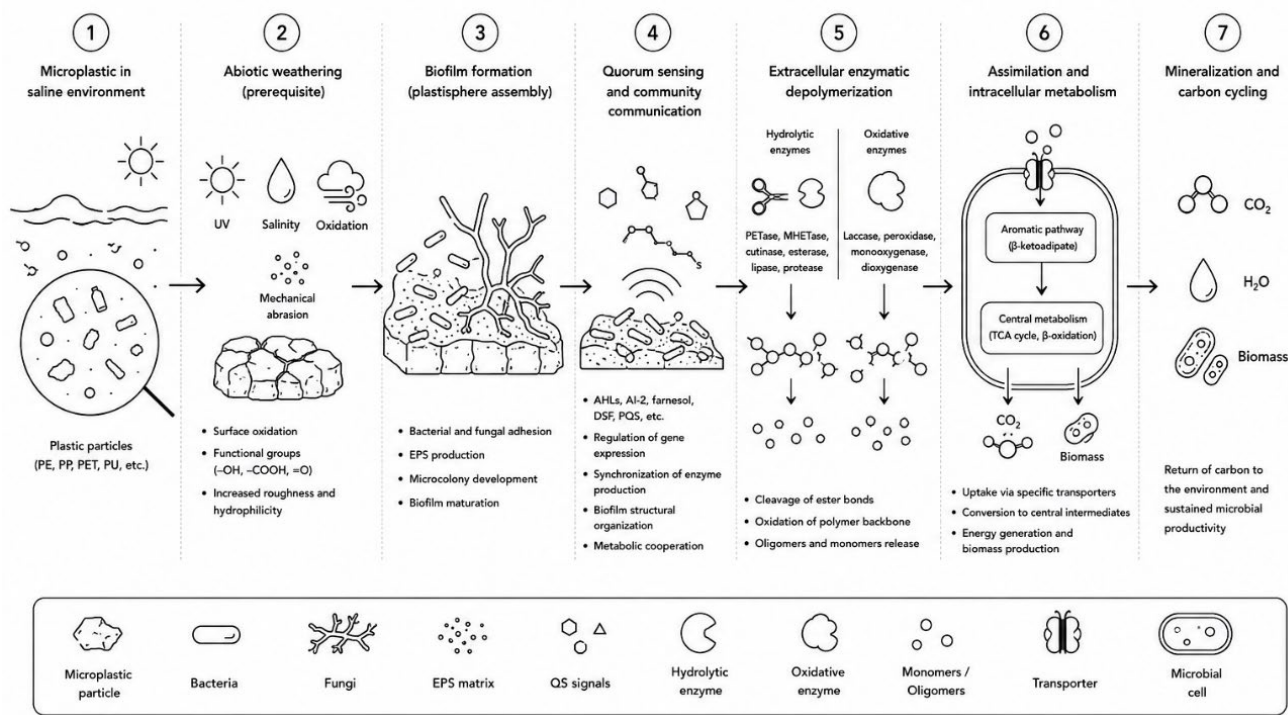


Figure 5. Integrated pathway of microplastic biodegradation within the saline plastisphere.

Table 5. Major enzymes involved in microplastic degradation, their microbial sources, target polymers, and catalytic functions.

Degradation stage	Enzyme	Predominant microbial group	Main producers	Target polymer(s)	Catalytic function	Main degradation products	Representative references
1. Surface oxidation	Laccase	Fungi	Trametes, Pleurotus, Aspergillus, Cladosporium	PE, PP, PET (surface), additives	Oxidation of aromatic and phenolic structures; introduction of oxygen-containing functional groups	Oxidized oligomers	155, 157
	Manganese peroxidase (MnP)	Fungi	Phanerochaete chrysosporium, Trametes versicolor	PE, PP, PU	Oxidative cleavage of C–C and C–H bonds	Oxidized polymer fragments	148, 155
	Lignin peroxidase (LiP)	Fungi	Phanerochaete chrysosporium	PE, PET (surface)	Oxidative depolymerization of aromatic structures	Aromatic acids, quinones	155, 157
	Versatile peroxidase (VP)	Fungi	Pleurotus eryngii, Bjerkandera adusta	PE, PP, PU	Oxidation of phenolic and non-phenolic substrates	Oxidized oligomers	155

Degradation stage	Enzyme	Predominant microbial group	Main producers	Target polymer(s)	Catalytic function	Main degradation products	Representative references
2. Polymer depolymerization	Unspecific peroxygenase (UPO)	Fungi	Agrocybe aegerita, Marasmius rotula	PE, PP, PET	Oxygen insertion into recalcitrant polymers	Alcohols, epoxides	148
	PETase	Bacteria	Ideonella sakaiensis	PET	Hydrolysis of PET ester bonds	MHET, BHET	149, 150, 151
	Cutinase	Bacteria and fungi	Thermobifida, Humicola, Fusarium, Aspergillus, Bacillus, Pseudomonas, Penicillium, Aspergillus	PET, PCL, PU	Cleavage of ester bonds	PET oligomers, TPA, EG	139, 147
	Esterase/Carboxylesterase	Bacteria and fungi	Pseudomonas, Penicillium, Aspergillus	PET, PU, PBAT	Hydrolysis of ester linkages	Organic acids, oligomers	147, 148
	Lipase	Bacteria and fungi	Candida, Aspergillus, Bacillus, Pseudomonas	PU, PLA, PCL	Hydrolysis of aliphatic esters	Fatty acids, alcohols	147, 148
3. Oligomer hydrolysis	MHETase	Bacteria	Ideonella sakaiensis, Alcanivorax, Pseudomonas, Rhodococcus	MHET	Hydrolysis of MHET	TPA, EG	149, 151
4. Assimilation of degradation products	Alkane hydroxylase (AlkB)	Bacteria	Pseudomonas, Rhodococcus	Oxidized PE and PP fragments	Oxidation of aliphatic hydrocarbons	Alcohols, aldehydes, fatty acids	156, 157
	Monooxygenases	Bacteria	Pseudomonas, Rhodococcus	Hydrocarbon intermediates	Hydroxylation reactions	Alcohols, ketones	147, 157
	Alcohol/Aldehyde dehydrogenases	Bacteria and fungi	Diverse taxa	Alcohols, aldehydes	Sequential oxidation to organic acids	Fatty acids, acetyl-CoA precursors	139, 147
5. Central metabolism and mineralization	Dioxygenases	Bacteria	Pseudomonas, Comamonas, Rhodococcus	Aromatic intermediates (e.g., TPA)	Aromatic ring cleavage	Protocatechuate, β -ketoadipate intermediates	151, 158
	β -Ketoacidipate	Bacteria	Diverse Proteobacteria	Protocatechuate, catechol	Conversion into TCA intermediates	Succinyl-CoA,	149, 151

Degradation stage	Enzyme	Predominant microbial group	Main producers	Target polymer(s)	Catalytic function	Main degradation products	Representative references
	pathway enzymes					Acetyl-CoA	
	β -Oxidation enzymes	Bacteria and fungi	Diverse taxa	Fatty acids derived from polymer oxidation	Sequential shortening of carbon chains	Acetyl-CoA	147, 156
	TCA cycle enzymes	All microorganisms	Bacteria, fungi and archaea	Acetyl-CoA	Complete oxidation and energy production	CO ₂ , H ₂ O and biomass	160, 161

Abbreviations: PET, polyethylene terephthalate; PE, polyethylene; PP, polypropylene; PU, polyurethane; PCL, polycaprolactone; PLA, polylactic acid; PBAT, poly(butylene adipate-co-terephthalate); MHET, mono(2-hydroxyethyl) terephthalate; BHET, bis(2-hydroxyethyl) terephthalate; TPA, terephthalic acid; EG, ethylene glycol.

7. Linking Quorum Sensing to Microplastic Biodegradation: An Integrative Ecological Framework

The plastisphere has traditionally been investigated from three largely independent perspectives: microbial community composition, biofilm ecology, and polymer biodegradation. However, recent advances indicate that these processes are mechanistically interconnected through microbial communication networks [162]. Among these, quorum sensing (QS) has emerged as a fundamental regulatory system capable of coordinating microbial attachment, biofilm maturation, extracellular polymeric substance (EPS) production, enzyme secretion, stress adaptation, and metabolic cooperation, thereby influencing both plastisphere assembly and microplastic degradation [17,18,86]. Recent experimental evidence further demonstrates that acyl-homoserine lactone (AHL)-mediated QS actively promotes plastisphere formation, increases biofilm biomass, stimulates EPS production, and enhances the transcription of genes involved in biofilm formation, chemotaxis, and flagellar assembly, establishing QS as a central driver of plastisphere development rather than merely a consequence of high microbial density.

The ecological significance of QS is particularly relevant in saline ecosystems, where microorganisms experience multiple environmental constraints, including osmotic stress, nutrient limitation, intense ultraviolet radiation, and fluctuating physicochemical conditions. Under these circumstances, coordinated community responses provide important adaptive advantages by optimizing resource allocation, regulating extracellular enzyme production, and improving resistance to environmental disturbances. Consequently, plastisphere biofilms should be regarded as self-organized microbial systems whose ecological functioning emerges from the interaction between environmental selection, interspecific cooperation, and chemical communication [3,18].

Although considerable progress has been achieved in identifying microorganisms capable of degrading synthetic polymers, comparatively little attention has been devoted to understanding how microbial communication regulates these processes. Most studies have investigated polymer-degrading microorganisms as isolated cultures, whereas degradation in natural environments is primarily performed by complex multispecies biofilms in which cooperative metabolism predominates [147,157]. Recent studies now suggest that QS regulates several ecological processes directly linked to biodegradation, including extracellular enzyme secretion, EPS synthesis, horizontal gene transfer, biofilm architecture, and metabolic specialization, thereby providing a mechanistic link between microbial ecology and polymer transformation. Based on these recent advances, we propose

that QS represents the central regulatory framework connecting microbial community assembly with the biodegradation potential of plastisphere biofilms in saline ecosystems. Rather than acting independently, environmental filtering, biofilm formation, bacterial–fungal interactions, and extracellular enzyme production constitute successive and interconnected processes that collectively determine the efficiency of polymer transformation.

7.1. Quorum Sensing Coordinates Biofilm Development

Biofilm formation on microplastic surfaces is a highly ordered ecological process that begins immediately after plastic particles enter aquatic environments. Adsorption of dissolved organic matter rapidly produces a conditioning film that alters surface physicochemical properties and facilitates the attachment of pioneer microorganisms [3,69]. Initial colonization is dominated by highly motile bacterial taxa capable of reversible adhesion through weak electrostatic and hydrophobic interactions. As colonization progresses, stronger attachment occurs through the production of adhesins, pili, flagella, and extracellular polymeric substances, resulting in the establishment of structured microbial biofilms [18,163].

Quorum sensing becomes increasingly important during this transition from reversible adhesion to mature biofilm formation. In Gram-negative bacteria, accumulation of N-acyl-homoserine lactones (AHLs) activates LuxI/LuxR regulatory systems, inducing coordinated expression of genes involved in EPS biosynthesis, biofilm maturation, motility, nutrient acquisition, and secretion systems [17,106]. Gram-positive bacteria employ autoinducing peptides (AIPs), whereas the LuxS/AI-2 system enables communication among phylogenetically distinct bacterial taxa, facilitating multispecies biofilm organization [86,87].

Recent investigations specifically addressing plastisphere communities have confirmed the ecological importance of these signaling pathways. Xu et al. (2023) [164] isolated multiple QS-positive bacterial strains from polypropylene and polyvinyl chloride biofilms and demonstrated that these microorganisms exhibit enhanced adhesion capacity, EPS production, and biofilm formation compared with non-QS isolates. The authors proposed that QS-regulated bacteria represent key pioneer colonizers responsible for initiating plastisphere development, thereby influencing subsequent community succession. This hypothesis has been experimentally validated by Wang et al. (2026) [21], who demonstrated that exogenous AHL supplementation significantly increased plastisphere biomass, extracellular polysaccharide production, and expression of genes involved in quorum sensing, bacterial chemotaxis, flagellar assembly, and biofilm formation. Conversely, inhibition of QS using AHL acylase markedly reduced biofilm formation and suppressed transcription of multiple pathways associated with plastisphere development, providing direct evidence that AHL-mediated communication actively regulates plastisphere assembly. Additional evidence indicates that AHLs influence not only later stages of biofilm maturation but also the earliest stages of microbial attachment [165]. Controlled laboratory experiments demonstrated that environmentally relevant concentrations of AHLs significantly enhance bacterial adhesion to multiple plastic polymers by stimulating EPS synthesis, increasing EPS hydrophobicity, and promoting bacterial chemotaxis toward plastic surfaces [21]. Importantly, this effect was observed across different polymer types and remained detectable even in natural river water and wastewater, suggesting that QS contributes to plastisphere formation under environmentally realistic conditions.

Within mature plastisphere biofilms, the EPS matrix further amplifies QS efficiency by reducing molecular diffusion and retaining signaling molecules near microbial cells. This creates a positive feedback mechanism in which increasing microbial density enhances signal accumulation, which in turn stimulates additional EPS production and biofilm development. Such feedback loops allow microbial communities to rapidly synchronize collective behaviors, increasing resilience against salinity fluctuations, ultraviolet radiation, oxidative stress, and hydrodynamic disturbance [18]. Saline ecosystems may further reinforce these processes. Elevated ionic strength alters electrostatic interactions within the EPS matrix, increasing biofilm cohesion and potentially prolonging the residence time of signaling molecules. At the same time, halotolerant microorganisms produce

abundant compatible solutes and extracellular polymers that stabilize both the biofilm structure and the signaling microenvironment [166]. Although direct experimental evidence remains scarce, these observations suggest that saline conditions may enhance QS efficiency by simultaneously promoting signal retention and biofilm stability, creating favorable conditions for cooperative metabolism and extracellular enzyme production.

Collectively, these findings indicate that quorum sensing should not be interpreted merely as a density-dependent communication mechanism but rather as the principal ecological regulator of plastisphere development. Through coordinated control of microbial attachment, EPS production, biofilm maturation, and community organization, QS establishes the structural and functional framework upon which extracellular enzymatic degradation and bacterial–fungal cooperation subsequently develop.

7.2. Regulation of Extracellular Enzyme Production by Quorum Sensing

One of the most important ecological consequences of quorum sensing (QS) is the coordinated regulation of extracellular enzyme production. Because the synthesis and secretion of hydrolytic and oxidative enzymes require substantial energetic investment, microorganisms have evolved regulatory systems that ensure these enzymes are produced only when population density is sufficiently high to maximize collective benefits. This strategy minimizes metabolic costs while maximizing substrate utilization, making extracellular enzymes classical examples of “public goods” within microbial communities [17,18,106]. Within the plastisphere, extracellular enzymes constitute the primary catalytic machinery responsible for polymer transformation. Since synthetic polymers are macromolecules that cannot be transported directly across the cell membrane, degradation must begin extracellularly through enzymatic depolymerization. Consequently, regulation of enzyme secretion becomes a critical determinant of biodegradation efficiency. Recent reviews increasingly recognize that QS represents one of the principal regulatory mechanisms linking microbial community development with polymer degradation [21,167], although direct experimental evidence remains limited for many environmental systems.

In Gram-negative bacteria, the LuxI/LuxR quorum sensing system regulates numerous extracellular enzymes, including proteases, lipases, esterases, cellulases, and chitinases. Activation of these pathways occurs after autoinducer concentrations exceed threshold levels, inducing coordinated transcription of genes involved in extracellular metabolism and biofilm maturation [17,106]. Similar regulatory systems have been described in Gram-positive bacteria through autoinducing peptides (AIPs), while the LuxS/AI-2 signaling pathway enables communication among phylogenetically distinct bacterial taxa, facilitating coordinated enzyme production within multispecies biofilms [86,87,168]. The plastisphere provides exceptionally favorable conditions for QS-mediated enzyme regulation. High cell density, restricted molecular diffusion within the extracellular polymeric substance (EPS) matrix, and prolonged physical association among microorganisms facilitate the accumulation of signaling molecules and synchronize gene expression throughout the biofilm. In this microenvironment, extracellular enzymes released by individual cells become accessible to neighboring microorganisms, allowing the entire community to benefit from collective enzymatic activity. Such cooperative metabolism substantially increases degradation efficiency compared with planktonic cells or monospecific cultures.

Experimental studies have begun to demonstrate this ecological relationship. QS-positive bacterial isolates recovered from marine microplastics exhibit significantly greater biofilm formation, EPS production, and extracellular hydrolase activity than QS-deficient strains, suggesting that signaling pathways contribute directly to plastisphere establishment and metabolic specialization [169]. Likewise, inhibition of AHL-mediated communication through quorum-quenching enzymes reduces biofilm biomass, suppresses extracellular polysaccharide production, and decreases transcription of genes associated with surface colonization and extracellular metabolism. These observations indicate that quorum sensing regulates not only microbial attachment but also the metabolic functionality of mature plastisphere biofilms.

The ecological significance of QS becomes particularly evident when considering the degradation of polyethylene terephthalate (PET). PET hydrolysis requires the coordinated secretion of PETases, cutinases, esterases, and MHETases, whose products subsequently enter intracellular catabolic pathways. Although the transcriptional regulation of PET-active enzymes remains incompletely understood, recent molecular studies suggest that degradation intermediates such as bis(2-hydroxyethyl) terephthalate (BHET) and mono(2-hydroxyethyl) terephthalate (MHET) function not only as metabolic substrates but also as signaling molecules capable of modulating the expression of PET degradation genes. In *Ideonella sakaiensis*, regulators associated with the MHETase operon appear to coordinate PET hydrolysis with downstream terephthalate metabolism, while transcriptomic analyses of marine *Vibrio* species indicate that PET-derived intermediates stimulate the expression of PET-active hydrolases under environmentally relevant conditions [20].

Fungal communities introduce an additional level of complexity to this regulatory network. Filamentous fungi secrete large quantities of oxidative enzymes, including laccases, lignin peroxidases, manganese peroxidases, versatile peroxidases, and unspecific peroxygenases, which initiate oxidation of recalcitrant polymers such as polyethylene and polypropylene [148,155]. Production of these enzymes is influenced by environmental signals, nutrient availability, oxidative stress, and fungal signaling molecules such as farnesol and tyrosol. Although the regulatory relationship between fungal quorum sensing and extracellular enzyme secretion remains less understood than in bacteria, studies on fungal biofilms strongly suggest that cell-density-dependent signaling contributes to the coordination of oxidative metabolism and extracellular enzyme production [97,170].

Within mixed plastisphere communities, bacterial and fungal enzymatic systems appear to operate synergistically rather than independently [171]. Oxidative enzymes secreted by fungi increase polymer hydrophilicity, introduce oxygen-containing functional groups, and generate surface defects that improve accessibility for bacterial hydrolases. Bacteria subsequently hydrolyze oxidation products into soluble oligomers and monomers that can be assimilated through central metabolic pathways. This sequential degradation process exemplifies metabolic complementarity; whereby different microbial groups perform distinct but interconnected biochemical reactions that collectively enhance polymer degradation efficiency.

Recent metagenomic and metatranscriptomic studies further support this integrative perspective [172]. Mature plastisphere biofilms are consistently enriched in genes associated with quorum sensing, extracellular hydrolases, oxidoreductases, transport systems, aromatic compound degradation, and central carbon metabolism [21,172–174]. Rather than functioning as isolated metabolic pathways, these genes form highly interconnected regulatory networks that respond dynamically to environmental conditions and substrate availability. Such observations reinforce the concept that polymer degradation is an emergent property of microbial communities rather than the physiological capability of individual species.

Collectively, current evidence supports a revised ecological model in which quorum sensing acts as a master regulatory system governing extracellular enzyme production within the plastisphere. By synchronizing enzyme secretion, coordinating metabolic specialization, and promoting cooperative resource utilization, QS maximizes the efficiency of polymer depolymerization while simultaneously strengthening biofilm stability. This integrated regulatory framework provides the mechanistic basis for understanding how structured microbial communities achieve levels of biodegradation that cannot be reproduced by isolated microorganisms, highlighting quorum sensing as a promising target for future biotechnological strategies aimed at enhancing microplastic degradation in saline ecosystems.

7.3. Cross-Kingdom Communication and Environmental Regulation in the Saline Plastisphere

Natural plastisphere biofilms are rarely composed of a single microbial group. Instead, they comprise phylogenetically diverse assemblages of bacteria, fungi, archaea, microalgae, and protozoa that continuously exchange metabolites, extracellular enzymes, signaling molecules, and genetic

material. Consequently, communication within the plastisphere extends beyond intraspecific bacterial quorum sensing and should be regarded as a complex cross-kingdom signaling network that contributes to community assembly, metabolic specialization, and ecological resilience [3,18].

Among eukaryotic microorganisms, fungi possess well-established quorum-sensing systems based on molecules such as farnesol, tyrosol, phenylethanol, and tryptophol. These compounds regulate morphogenesis, hyphal development, sporulation, oxidative stress responses, and biofilm formation in several fungal taxa, particularly *Candida*, *Saccharomyces*, *Aspergillus*, and filamentous marine fungi [96,116,117,175]. Evidence accumulated over the last decade demonstrates that fungal signaling molecules also influence bacterial physiology. Farnesol, for example, alters bacterial motility, extracellular polymer production, oxidative stress responses, and biofilm architecture in several Gram-negative bacteria, whereas bacterial AHLs modify fungal filamentation, enzyme secretion, and secondary metabolism [96,175]. These reciprocal interactions indicate that microbial communication within environmental biofilms is multidirectional rather than kingdom-specific, allowing bacteria and fungi to coordinate collective behaviors under changing environmental conditions.

Such interactions are likely to be particularly important in the plastisphere because bacterial and fungal communities perform complementary metabolic functions during polymer degradation. Filamentous fungi initiate oxidation of recalcitrant polymers through laccases, manganese peroxidases, lignin peroxidases, versatile peroxidases, and unspecific peroxygenases, thereby increasing polymer hydrophilicity and generating oxygen-containing functional groups that facilitate bacterial hydrolysis. In turn, bacteria assimilate oligomers and monomers released during fungal oxidation through PETases, cutinases, esterases, dioxygenases, and central carbon metabolic pathways [147,155,157]. The efficiency of this sequential degradation strongly suggests that communication between bacterial and fungal partners contributes to the coordination of extracellular enzyme production and substrate utilization. Environmental conditions characteristic of saline ecosystems further influences these communication networks. Salinity modifies osmotic balance, membrane permeability, extracellular polymer composition, and diffusion of signaling molecules, all of which affect quorum-sensing efficiency. High ionic strength also promotes the formation of compact extracellular polymeric matrices that retain signaling molecules within the biofilm, increasing their local concentration and prolonging signal persistence [18]. Consequently, saline environments may strengthen microbial communication by simultaneously increasing biofilm cohesion and reducing signal loss.

In addition to salinity, nutrient availability, dissolved organic matter, ultraviolet radiation, oxygen concentration, and hydrodynamic stress influence both the production and perception of quorum-sensing molecules. Nutrient limitation frequently stimulates cooperative metabolism by increasing dependence on extracellular enzymes, whereas oxidative stress induces regulatory pathways associated with antioxidant enzymes, compatible solute synthesis, and biofilm reinforcement [17,18,158]. These responses demonstrate that quorum sensing should be interpreted as an environmentally responsive regulatory system that continuously integrates physicochemical information with microbial physiology rather than functioning exclusively as a population-density sensor.

Despite these advances, knowledge concerning cross-kingdom signaling in saline plastisphere communities remains remarkably limited. Most available studies have focused either on bacterial quorum sensing or fungal communication under clinical conditions, whereas environmental interactions between halotolerant fungi and plastisphere-associated bacteria remain largely unexplored. Combining metatranscriptomics, metabolomics, stable-isotope probing, and single-cell analyses will be essential for identifying signaling molecules exchanged within natural plastisphere biofilms and determining how environmental gradients regulate these interactions.

7.4. An Integrative Ecological Framework Linking Quorum Sensing to Microplastic Biodegradation

Current evidence supports a conceptual shift in our understanding of plastisphere ecology. Rather than representing isolated biological processes, abiotic weathering, microbial colonization, quorum sensing, extracellular enzyme production, and polymer degradation constitute successive stages of a single self-organizing ecological network (Figure 6). In this framework, environmental drivers act as the initial selective forces determining microbial recruitment, while quorum sensing functions as the regulatory mechanism coordinating collective metabolic responses.

The process begins with abiotic weathering of plastic surfaces through ultraviolet radiation, oxidation, mechanical abrasion, and salinity-driven physicochemical transformations, which increase surface roughness and generate oxygen-containing functional groups [14,37]. These modifications facilitate attachment of pioneer microorganisms that subsequently establish structured biofilms through EPS production and irreversible adhesion [18,163]. As microbial density increases, signaling molecules accumulate within the extracellular matrix until threshold concentrations activate quorum-sensing regulatory circuits. This activation synchronizes transcription of genes involved in EPS biosynthesis, motility, chemotaxis, nutrient acquisition, oxidative stress tolerance, extracellular enzyme secretion, and horizontal gene transfer [17,106]. Recent global metagenomic analyses have shown that plastisphere communities are enriched in genes associated with AHL-mediated quorum sensing and biofilm formation, supporting the hypothesis that chemical communication is a defining feature of mature plastisphere communities [162,176].

Within this regulatory framework, fungi and bacteria perform complementary ecological functions. Oxidative enzymes secreted predominantly by fungi initiate polymer oxidation, whereas bacterial hydrolases catalyze depolymerization of oxidation products into soluble oligomers and monomers. Subsequent intracellular assimilation through β -oxidation, the β -ketoadipate pathway, and the tricarboxylic acid cycle converts polymer-derived carbon into microbial biomass, carbon dioxide, and dissolved organic carbon available to other members of the microbial community [147,149,151]. The framework predicts that biodegradation efficiency depends not only on enzyme diversity but also on the organization of microbial interaction networks. Disruption of quorum sensing through quorum-quenching enzymes, signal degradation, or environmental disturbances is thus expected to reduce extracellular enzyme production, impair metabolic cooperation, and decrease polymer degradation rates. Conversely, promoting stable communication networks within multispecies consortia may enhance biodegradation efficiency under environmentally relevant conditions, representing a promising strategy for future biotechnological applications. This community-centered perspective differs fundamentally from the traditional organism-centered view of plastic biodegradation. Instead of searching exclusively for “super-degrading” microorganisms, future research should prioritize understanding how microbial interactions, signaling pathways, and environmental conditions collectively regulate the functional performance of plastisphere biofilms. Such an ecological approach integrates microbiology, fungal biology, environmental chemistry, systems ecology, and biotechnology into a unified conceptual framework capable of explaining microplastic degradation in saline ecosystems.

This framework identifies several priorities for future research, including the characterization of quorum-sensing molecules in hypersaline environments, the identification of fungal signaling pathways regulating oxidative enzymes, the integration of multi-omics approaches with stable-isotope tracing, and the construction of synthetic bacterial–fungal consortia capable of reproducing the ecological functions observed in natural plastisphere communities. Addressing these questions will substantially improve our understanding of microbial communication and may ultimately enable the development of environmentally sustainable strategies for mitigating plastic pollution in saline ecosystems.

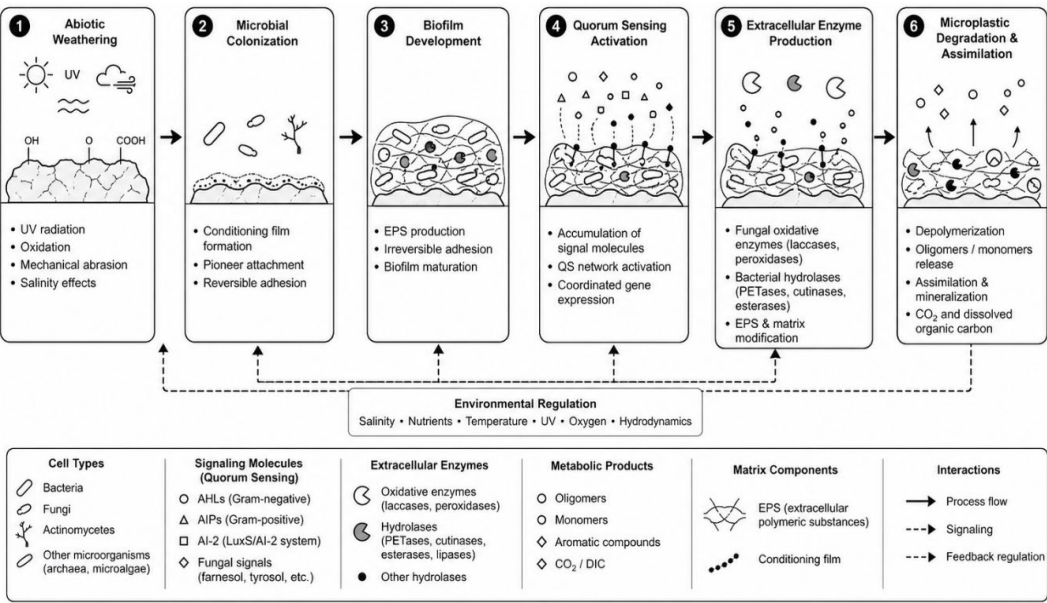


Figure 6. Integrative Ecological Framework Linking Quorum Sensing to Microplastic Biodegradation in Saline Ecosystems.

8. Future Perspectives and Research Priorities

Despite significant advances in plastisphere research over the past decade, our understanding of the ecological mechanisms governing microplastic degradation in saline ecosystems remains incomplete. Most current studies have focused on describing microbial community composition using taxonomic approaches, whereas considerably less attention has been devoted to identifying the functional interactions that regulate biofilm organization, microbial communication, and extracellular enzyme production. Consequently, future investigations should move beyond descriptive community analyses toward mechanistic studies integrating microbial ecology, molecular biology, enzymology, and environmental chemistry.

One of the highest priorities is the characterization of quorum sensing (QS) networks operating within natural plastisphere communities. Although AHL-mediated signaling has recently been shown to promote plastisphere formation and regulate biofilm development, the diversity, spatial distribution, and ecological functions of signaling molecules remain largely unknown, particularly in saline and hypersaline environments. Future studies should combine targeted metabolomics with metatranscriptomics and single-cell analyses to identify active signaling pathways and determine how environmental gradients such as salinity, nutrient availability, and ultraviolet radiation influence QS-mediated regulation of microbial metabolism. Recent findings suggest that QS may represent one of the principal regulators of plastisphere functioning, but its ecological significance has only begun to be explored.

Another important research frontier concerns halotolerant fungi. Compared with bacteria, fungal communities remain substantially underrepresented in plastisphere studies despite increasing evidence that they contribute to biofilm architecture, oxidative polymer modification, and extracellular enzyme production. The application of long-read sequencing, improved fungal reference databases, metaproteomics, and metabolomics will facilitate the identification of active fungal populations and their enzymatic contributions to polymer degradation. Isolation and physiological characterization of halotolerant fungal strains from hypersaline lakes, salt marshes, mangroves, and solar salterns should also be prioritized, as these environments likely harbor previously undescribed enzymes with high salinity tolerance and considerable biotechnological potential.

Progress in multi-omics technologies is expected to transform plastisphere research. While metagenomics has greatly expanded our understanding of microbial diversity, integrating

metatranscriptomics, metaproteomics, metabolomics, and stable-isotope probing will enable the identification of metabolically active microorganisms and quantify their contribution to polymer degradation under environmentally relevant conditions. These complementary approaches will facilitate reconstruction of metabolic networks linking quorum sensing, extracellular enzyme production, carbon assimilation, and microbial interactions within plastisphere biofilms. Coupling multi-omics with spatial imaging techniques, including fluorescence in situ hybridization (FISH), Raman microspectroscopy, and nanoscale secondary ion mass spectrometry (NanoSIMS), may further reveal the spatial organization of microbial interactions and substrate exchange at micrometer resolution.

Another promising area of research is synthetic microbial ecology. Most biodegradation studies still rely on single isolates, despite mounting evidence that polymer degradation is more efficient in multispecies consortia. Future research should therefore focus on designing synthetic bacterial–fungal communities that reproduce the ecological interactions observed in natural plastisphere biofilms. Such consortia could be optimized through systems biology, metabolic modeling, and adaptive laboratory evolution to enhance extracellular enzyme production, improve substrate utilization, and increase degradation efficiency under saline conditions. Integration of quorum sensing engineering and quorum quenching strategies may provide additional opportunities to regulate biofilm formation and enzymatic activity in a controlled manner.

Artificial intelligence and machine learning are also expected to play an increasingly important role in plastisphere research. Computational approaches have already accelerated the discovery of novel PETases, cutinases, esterases, and oxidoreductases through protein structure prediction, functional annotation, and enzyme engineering. Combining genomic databases with structural modeling and machine learning may enable rapid identification of previously unrecognized plastic-degrading enzymes from extremophilic microorganisms inhabiting saline ecosystems. Furthermore, ecological network analysis supported by artificial intelligence could improve prediction of microbial interactions, signaling pathways, and functional redundancy within complex plastisphere communities.

Finally, translating laboratory findings into environmentally relevant applications remains one of the greatest challenges. Most biodegradation experiments are performed under optimized laboratory conditions that differ substantially from natural saline ecosystems, where degradation rates are constrained by low nutrient availability, fluctuating salinity, temperature variability, and complex microbial interactions. Standardized experimental protocols, long-term mesocosm studies, and field-scale validation will therefore be essential to evaluate the ecological relevance of microbial degradation pathways and to assess the feasibility of developing sustainable bioremediation strategies based on naturally occurring plastisphere communities. Collectively, these research suggestions will support a transition from descriptive plastisphere ecology toward predictive and systems-level environmental microbiology capable of informing future biotechnological solutions for plastic pollution mitigation.

9. Conclusions

Microplastic pollution has created an unprecedented anthropogenic habitat that supports highly specialized microbial communities collectively known as the plastisphere. Although substantial progress has been achieved in characterizing the taxonomic composition of these biofilms, understanding of the ecological mechanisms governing their organization and functional performance remains limited. Throughout this review, we have highlighted that plastisphere development is not determined solely by polymer properties or microbial diversity but instead emerges from the dynamic interaction between environmental selection, microbial communication, and metabolic cooperation.

Saline ecosystems provide a unique framework for investigating these processes because high salinity, osmotic stress, ultraviolet radiation, and nutrient limitation impose strong environmental filters that select microorganisms with specialized physiological adaptations. Among these,

halotolerant fungi appear to play a far more significant ecological role than previously recognized by contributing to biofilm architecture, extracellular oxidative metabolism, and the initial transformation of recalcitrant polymers. Their interactions with bacterial communities expand the functional diversity of the plastisphere and create metabolically integrated consortia capable of exploiting complex synthetic substrates.

A central concept emerging from this review is that quorum sensing should be regarded as a key regulatory mechanism linking microbial community assembly with polymer biodegradation. Rather than functioning exclusively as a density-dependent signaling system, quorum sensing coordinates biofilm maturation, extracellular polymeric substance production, enzyme secretion, stress adaptation, and metabolic specialization. These coordinated responses optimize resource utilization within multispecies biofilms and enhance the efficiency of extracellular polymer transformation. Recent experimental evidence indicating that quorum sensing promotes plastisphere formation further supports this ecological perspective.

We therefore propose an integrative ecological framework in which abiotic weathering initiates polymer transformation, environmental filtering determines microbial recruitment, quorum sensing orchestrates community organization, bacterial–fungal interactions coordinate extracellular enzyme production, and complementary metabolic pathways ultimately drive polymer depolymerization, assimilation, and carbon cycling. Within this framework, microplastic degradation is interpreted not as the physiological capability of isolated microorganisms but as an emergent property of structured microbial communities. This conceptual shift has important implications for environmental microbiology and biotechnology. Future strategies should prioritize understanding microbial interaction networks, identifying signaling pathways that regulate extracellular metabolism, and developing synthetic bacterial–fungal consortia capable of reproducing the cooperative functions observed in natural plastisphere biofilms. Advances in multi-omics technologies, systems biology, protein engineering, and artificial intelligence are expected to accelerate the discovery of novel enzymes and improve our capacity to manipulate microbial communities for environmentally sustainable plastic remediation.

Ultimately, integrating microbial ecology, fungal biology, quorum sensing, and biodegradation mechanisms provides a more comprehensive understanding of plastisphere functioning in saline ecosystems. We anticipate that this systems-level perspective will not only stimulate new research into microbial communication and polymer transformation but also contribute to the development of innovative approaches for mitigating the growing environmental burden of microplastic pollution.

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