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Harnessing native microbiomes for coastal ecosystem restoration: Theory, evidence, and practice

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Abstract

Coastal systems are significant sites of ecosystem services, yet they are experiencing unparalleled levels of degradation as a result of anthropogenic stressors and global change. Conventional restoration efforts which target physical habitat restoration and transplantation of foundation species often result in variable success, as many sites still have not realized reference conditions despite decades since the intervention. This review consolidates the knowledge on utilizing indigenous microbiomes like complex bacterial, archaea, fungal and viral within mangroves, salt marshes, seagrasses and corals. The conceptual bases were reviewed to range from the functional roles of the microbiome in nutrient cycling, biogeochemical processes, host-microbe interactions and disease suppression to ecological principles that control community assembly, succession and resistance. Empirically, disturbances lead to a fundamental shift of microbial communities with lasting functional impacts from which natural recovery frequently lags or is incomplete, arguing for actively managing the microbiome. Practical implications include the use of diagnosis to identify potential microbial bottlenecks and define interventions or manipulations such as bioaugmentation, probiotic applications or environmental changes that support beneficial taxa. The coral probiotics and seagrass rhizosphere manipulation case studies can illustrate the feasibility and lessons for implementation. At the same time, there are still major challenges of scaling interventions, predicting ecological outcomes and navigating regulatory frameworks-but these are opportunities for innovation rather than intractable barriers. New research directions should focus on elucidating the causative pathways by which microbial interventions drive ecosystem outcomes, and creating predictive frameworks to meet future challenges related to climate change. Microbiome-guided restoration holds the promise of transforming our ability to ameliorate biological constraints that confound traditional approaches, equipping practitioners with an expanded toolkit for ecosystem resurgence in a time of rapid environmental change.

Keywords: Coastal Restoration; Microbiome; Holobiont; Bioaugmentation; Ecosystem Recovery

1. Introduction

Coastal ecosystems such as coral reefs, mangrove forests, seagrass meadows and salt marshes are one of the most biologically productive and economically valuable environments on the planet [1]. These systems deliver ecosystem services such as fisheries production, carbon sequestration, coastal protection and nutrient cycling that sustain human populations worldwide and power planetary biogeochemical cycles [2]. But these crucial habitats are under unsustainable threat. A global review finds that roughly one third to one half of coastal and marine ecosystems have been lost as a result of human activities, while Dunic et al. revealed a global net loss of 5,602 km2 (19.1% of surveyed meadow area) since 1880 [3, 4]. In US coastal waters alone, roughly 50% of historical salt marshes are gone, abundant seagrasses have declined to habitat-critical levels in places like Florida Bay and Chesapeake Bay, ongoing mangrove habitat conversion in southern Florida and extensive coral reef have declined [4, 5]. These interacting stressors comprising temperature stress, acidification, eutrophication and physical habitat loss among others are driving a global

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imperative for ecosystem restoration as the key to rebuilding degraded coastlines as well as personal health and wellbeing.

However, traditional methods of coastal restoration have had limited success. Advances are held back by underlying obstacles in scientific knowledge and technical methodologies. Conventional restoration efforts focused on species transplantation and hydrological manipulation have a 45% success rate for coastal wetland restoration, while successful projects take decades before the ecosystem functions properly [4, 6]. These limited interventions highlight an important disparity, as restoration efforts have typically centered on reintroduction of habitat-forming macroorganisms while overlooking the microbial communities that support these organisms [7]. Modern marine microbiome studies indicate that such a deficiency is not justified. Marine microorganisms represent the main biomass in the oceans and are responsible for controlling almost all biogeochemical cycles of impact on climate, nutrient supply, and productivity [8, 9]. Increasing evidence suggests that the functioning of coastal ecosystems, specifically, ecosystem resistance to climate-induced stress and resistance to disease is largely reliant on the nature and functional capabilities of their associated microbial communities [2, 10].

The shift toward microbiome-informed coastal restoration is grounded in the holobiont concept, which frames host organisms and their associated microbiota as integrated functional units whose ecological performance depends on host–microbe interactions [11]. Across coastal systems, microbial symbionts expand metabolic capacity, enhance stress tolerance, and support nutrient acquisition, as evidenced by pathogen suppression in corals, sulfide detoxification in seagrasses, and nitrogen fixation in mangroves [12, 13]. Disruption of these host-microbe associations precipitates ecosystem decline [14]. Rapid advances in culture-independent molecular tools have transformed marine microbiome research, revealing vast previously uncharacterized microbial diversity and enabling targeted intervention [15]. Field trials show that coral probiotics markedly reduce tissue loss, and seagrass transplants retaining native microbiota achieve higher establishment success than conventional approaches [16-18]. This demonstrates that harnessing native microbiomes is both conceptually sound and operationally feasible for coastal ecosystem restoration.

Nevertheless, the incorporation of indigenous microbiomes in coastal restoration is disjointed. Conceptual breakthroughs regarding their role are not necessarily backed by or transformed into empirical support and on the ground application [19]. There is a pressing need for holistic, theoretical, empirically and restoration-based synthesis that considers the scalability of manipulation of ecological risks and system specificity. This review thus integrates current understanding on the function of indigenous microbiomes in coastal ecosystem restoration by amalgamating theoretical frameworks, empirical information and novel restoration approaches. It synthesizes theory, empirical evidence, and practice to posit microbiome-based restoration as a holistic and potentially revolutionary approach to restoring coastal ecosystem function.

2. Theoretical Foundations

2.1. Microbiome Functional Roles in Coastal Ecosystems

Complex communities of microorganisms in coastal ecosystems function for basic ecological processes of ecosystem health and resiliency. In particular, these microbiomes consisting of bacteria, archaea, fungi, protists and viruses constitute complex networks, consisting of highly interlinked microorganisms that are involved in the regulation of biologically mediated cycles between biological systems that manipulate matter (biogeochemical cycles) and help to maintain foundation species structures [10, 20]. Knowledge of these functional roles is in theory the foundation of microbiome-based therapeutics.

The nutrient cycle is a basic function in the coastal microbiome. Nitrogen conversions are of particular importance, as the transformation of nitrogen into forms usable for life is catalysed by microbes through processes like denitrification and anaerobic ammonium oxidation [9]. In mangrove ecosystems, nitrogen-fixing bacteria provide significant sources of nitrogen input and can stimulate primary production in nutrient depleted environments [21]. Sulfur cycling is similarly active in coastal systems, where sulfate-reducing bacteria mediate oxidative breakdown of organic matter under anoxic conditions, and sulfur-oxidizing bacteria subsequently re-oxidize reduced sulfur compounds to form some of the redox gradients that are important features of coastal biogeochemistry [8]. The microbial communities solubilize phosphorus, which releases through the bioavailability of nutrients for the primary producers, limiting nutrition sources that are processed into bioavailable forms of phosphate by specific bacterial taxa [22].

Another important functional category is host-microbe interactions. The holobiont model, describing hosts and their microbiomes as coupled functional systems has recently become a central concept in coastal ecology [11]. Coral-algal-bacterial symbioses are an example of this integration, with microbial partners modulating nutrient uptake, pathogen resistance and stress tolerance [13, 23]. The rhizosphere microbiomes of seagrass root have been found to perform various functions such as promoting growth by producing phytohormones, suppressing diseases by synthesizing antibiotics, and improving stress tolerance [18]. Such mutualistic relationships have co-evolved over evolutionary time to bring about the dependence which should be taken into account in restoration plans.

Disease suppression is the result of intricate interactions among microbial communities. In corals, the commensal bacterial community can also restrict pathogen establishment and palliate impacts via competitive exclusion and antimicrobial compound production [2, 17]. Metabolites derived from the salt marsh plants microbiomes have bioactivity to control fungal pathogens, strengthening plant health and ecosystem maintaining [24].

2.2. Ecological Principles Governing Microbiome Dynamics

Microbial community assembly in coastal ecosystems follows regular ecological rules which can be used to guide restoration efforts. Deterministic processes like environmental filtering, and biotic interactions influence community composition along with stochastic processes such as dispersal limitation, and ecological drift [25, 26]. Environmental conditions such as salinity, oxygen availability, pH and organic matter content cause the segregation of taxa that colonize and remain in the system [27]. This is problematic because priority effects can lead to alternative stable states, where communities evolve differently even under the same external conditions [28].

Microbial community succession is similar to macrobial communities, but works on a more rapid time scale. When newly exposed, fresh sediments become available for colonization by pioneer taxa that can tolerate the extreme circumstances in primary succession they are succeeded by fewer more specialized communities with changing environmental conditions and provisions [29]. This succession model offers opportunities for intervention at key transitions in which systems may be receptive to manipulation.

Both the concepts of resilience and stability are key components in microbiome-based restoration theory. Microbial communities possess both resistance (ability to bear disturbance) and resilience (ability to recover from the disturbance) characteristics [30]. Functional redundancy within microbial communities act as an insurance to disturbance so when one taxon becomes extinct, others can perform the same function [31]. Yet, long-term and extreme disturbances can cause communities to traverse tipping points into alternative stable states with altered taxonomic composition and functional potential [32]. Understanding these thresholds will be important to determine when it might be appropriate to engage in active microbial intervention, and when natural recovery processes are sufficient.

2.3. Conceptual Framework for Microbiome-Based Restoration

The combination of the ecological principles provides a conceptual framework for microbiome-driven coastal restoration. This approach acknowledges that effective restoration should not only restore foundation species, but the microbial communities underlying functions performed by these life forms [7]. The model functions within three temporal stages: identification, intervention and maintenance.

The assessment process describes already existing microbial communities, defines functional deficiencies relative to reference systems and evaluate whether microbial limitations impede successful restoration of activities. Such a diagnostic model is an alternative to classic restoration as it specifically targets microbial community composition and functional potential [19]. The implementation step utilizes systems to engineer microbial communities towards favorable traits. This can be accomplished through addition of key members and environmental alterations that favor beneficial species indirectly [33]. The maintenance phase will track the trajectories of communities, utilizing adaptive management to maintain desired microbial functions as ecosystems mature [6].

At the core of this framework is the acknowledgment that microbiome interventions need to be compatible with overall restoration objectives and site specific conditions. Microbial engineering, however, is not adequate and may be unable to bypass core environmental limitations such as long-term pollution, hydrological interference or unsuitable substrate conditions for microbial activities in ecosystems [34]. Instead, microbiome-guided strategies are an adjunct to conventional restoration approaches that modify biological constraints, which can cause prevention of recovery despite physical reversal. This integrated approach places microbiome manipulation as a single means in a larger restoration toolkit, used specifically when microbial constraints are recognized as critical bottlenecks for ecosystem recovery [34].

3. Evidence from Coastal Systems

3.1. Microbiome Patterns across Coastal Ecosystems

Specific microbiome patterns are observed across the main coastal ecosystem types, which has a response to local environmental conditions and functions. Proteobacteria, Bacteroidetes and Chloroflexi are the major components in sediment microbiome of mangroves with abundant populations of sulfate-reducing bacteria for anaerobic conditions and high availability of sulfate [35]. On the other hand, the mangrove rhizosphere contains a functional guild of microorganisms such as nitrogen-fixing and metal-reducing taxa that are involved in nutrient acquisition from nutrient-limited sediments [21]. Spatial zonation also takes place in different inundation zones with separate communities in permanently submerged and periodically exposed zone [36].

Salt marsh microbiomes contain similar phylum level composition, but the relative abundances and functional profiles are different. Rhizosphere communities of marsh grasses such as Spartina spp. are enriched in plant growth promoting bacteria and have been proposed to reflect close plant microbe coevolution [27]. Sediment depth profiles show stratification of microbial activity, with aerobic respiration being the predominant process in the surface layers and anaerobic processes such as sulfate reduction and methanogenesis occurring in deeper anoxic zones [19].

The seagrass microbiome shows specialization on different plant tissues. Leaf epiphytic communities are markedly different from those on the rhizosphere and root endophytic communities, due to differences in selective pressures and functional roles [37]. Seagrass rhizospheres are hotspots for microbial activity and diversity, evidence indicates higher rates of nitrogen fixation, nutrient mineralization, and decomposition of organic matter occurring within these habitats than in surrounding unvegetated sediments [12, 18]. Sulfur-oxidizing bacteria are highly abundant in seagrass rhizospheres and help reduce sulfide toxicity, which in turn can hamper the growth of seagrass [12].

Coral microbiomes are not only taxonomically distinct but also specialized microbial assemblages shaped by the reef holobiont environment. Composition of coral mucus, tissue and skeleton differs between microbial communities and is dominated by Proteobacteria, Bacteroidetes and Firmicutes [23]. Core elements of the microbiome, found in all individuals within a species, are thought to serve important roles such as food provision and pathogen protection [38]. These taxa are prime candidates for potential targets that could be exploited by probiotics in coral restoration.

Similarities can be found among these disparate systems. Proteobacteria is generally a major phylum, with specific classes and genera which differ depending on the type of ecosystem [39]. Functional gene profiles show convergence in major metabolic pathways regardless of differences in taxa, pointing to functional redundancy [31]. All systems harbor spatially distinct communities that occupy different microhabitats established by stress factors such as oxygen or nutrients [40].

3.2. Disturbance Impacts and Recovery Trajectories

Human intervention directly changes the composition, structure, and function of coastal microbiomes through various ways. Eutrophication along the coast results in increased nutrient loads and alters microbial community composition favoring copiotrophic taxa that thrive in high nutrient settings and impinge on diversity by depressing specialized oligotrophic lineages [41]. These transitions are linked also to changes in biogeochemical function such as enhanced denitrification rates that may result in nitrogen loss and altered pathways of carbon cycling [42]. Pollution from heavy metals, hydrocarbons and persistent organic pollutants selects pollution tolerant taxa but also eliminates sensitive ones, reducing the functional diversity and ecosystem services [43].

Habitat disruption caused by coastal development, dredging and storms result in the wholesale destruction of microbial communities through habitat loss or changing environmental conditions. Mangrove forest clearing studies have shown the rapid change in sediment microbiomes, which are dominated by losses of specialized mangrove-associated taxa and gains of generalist taxa indicative of impacted ecosystems [44]. Such shifts persist long after physical disturbance has ceased, suggesting that recovery of the microbiome could be slower than that of the physical recovery [44]. Climate change effects including increased ocean temperatures and acidification are reorganizing coastal microbiomes and have implications for ecosystem functioning [2].

Post-disturbance recovery trajectories are context dependent. In some coastal microbial communities, a striking level of resilience occurs with recovery in composition occurring within months to years after acute disturbances have occurred [45]. Yet, functional recovery may lag compositional recovery, since ecosystem specific functional profiles need time to re-assemble [46]. Long-term disturbances give rise to even longer lasting altered states, with the potential for regime shifts to alternative stable states regulated by feedbacks [14].

Spontaneous recovery can provide information on successional sequences relevant to restoration. Chronosequence approach to coastal wetland restoration has shown a predictable successional trajectory, with opportunistic species colonizing early and communities gradually approaching reference community composition [27, 36]. Yet, convergence is often not completed even several decades after restoration, with restored site microbiomes maintaining unique imprints [4]. Such long-term resistance may indicate legacy impacts from previous disturbance, ongoing environmental contrast between restored and reference sites, or dispersal limitations preventing colonization by specialized taxa [4].

3.3. Microbiome Indicators of Ecosystem Health

There is increasing evidence that marine microbial community properties may represent useful indicators of status and recovery in coastal ecosystems. Taxonomic composition is informative of the state of an ecosystem, with some taxa being indicators of degraded or healthy status [45]. For instance, high abundance of sulfate-reducing bacteria in seagrass sediments can suggest sediment organic matter accumulation and low oxygen environment related to degradation of the ecosystem [12]. On the other hand, occurrence of specific nitrogen fixing groups in the mangrove rhizosphere suggests a preservation of important ecosystem functions [21].

Functional gene profiles provide a more direct measure of ecosystem functioning potential. Metagenomic sequencing demonstrates the abundance of genes encoding enzymes that mediate key biogeochemical reactions, allowing for quantitative insight on functional potential [47]. Functional gene diversity is known to be closely associated with ecosystem stability and resilience, indicating that restoring functional redundancy should be considered as a target for restoration [31].

Community diversity measures provide integrative indicators of ecosystem condition. Alpha diversity (within-sample diversity) and beta diversity (compositional dissimilarity between samples) both carry information about ecosystem state [48]. Degraded coastal ecosystems often show reduced microbial diversity, reflecting environmental filtering by stressors [2]. However, this is not always the case, as some disturbances increase diversity by creating heterogeneous conditions or removing competitive dominants [49].

Network analysis methods show community structure associated with ecosystem health. Healthier coastal ecosystems tend to show modular network organization characterized by high within-module connectivity and well-defined modules [50]. While disturbance can homogenize network structure, modularity is reduced and there are less stable community patterns [51]. These network features can serve as early warning signals of the decline in ecosystems before visible changes in composition, thus providing an indication for management action [52].

4. Practical Applications

4.1. Assessment and Diagnosis

Implementing microbiome-based restoration begins with comprehensive assessment of existing microbial communities and identification of constraints to restoration success. Baseline microbiome profiling employs molecular approaches including 16S rRNA gene amplicon sequencing to characterize bacterial and archaeal community composition, ITS sequencing for fungal communities, and increasingly, shotgun metagenomics for comprehensive taxonomic and functional characterization [15, 53]. These techniques reveal which microbial taxa are present, their relative abundances, and their functional genetic potential.

Diagnostic assessment compares disturbed site microbiomes to reference conditions from healthy ecosystems of the same type. Significant deviations in taxonomic composition, functional gene profiles, or diversity metrics indicate microbial dysbiosis that may constrain restoration [6, 14]. For instance, absence of key nitrogen-fixing taxa in mangrove sediments or depletion of sulfur-oxidizing bacteria in seagrass beds identifies specific functional deficits that interventions could address [12, 18]. Environmental DNA analysis can also detect absence of foundation species or presence of pathogens that influence restoration planning [6].

Functional assays complement molecular characterization by directly measuring microbial activity rates. Nitrogen fixation assays, respiration measurements, and enzyme activity assays quantify actual ecosystem function rather than just genetic potential [54]. These measurements validate whether compositional differences translate into functional consequences and identify rate-limiting processes. Integration of compositional and functional data provides comprehensive diagnosis of microbial constraints [55].

4.2. Intervention Strategies

4.2.1. Direct Microbial Manipulation

Direct manipulation strategies add beneficial organisms directly to promote restoration or alleviate microbial constraints. Bioaugmentation is the inoculation of contaminated sites with microbial communities obtained from non-contaminated reference ecosystems [56]. This medicine may act as a catalyst in the restoration of communities by adding taxa and functions missing from disturbed ones. Inoculum can be delivered as sediment transplants that carry complete microbial communities with their environmental matrix or as artificial microbial consortia containing defined beneficial taxa [19].

Probiotic applications focus on introducing specific microbial strains that provide targeted benefits. In coral restoration, probiotic bacteria that enhance stress tolerance or inhibit pathogens have shown promise in laboratory and field studies [13, 17]. The beneficial microorganism corals approach has shown that some bacterial strains can increase coral resistance against bleaching and disease [33]. Plant growth promoting bacteria that were isolated from healthy salt marsh rhizospheres have the potential to improve growth and survival of transplanted marsh grasses [27]. A great deal of constraint exists with such approaches, as precise strain selection is necessary, typically based on beneficial effects via controlled trials and further validated in the field.

Application methods influence intervention success. For tidal systems available at low tide, broadcast of inoculum onto the surface could be appropriate while injection followed by showering with water is able to reach subsurface microbial communities in sediments [19]. Inoculation of transplanted plants with plant-beneficial microbes during the planting process enables prompt and successful establishment of plant-microbe associations [12]. The timing of interventions should coincide with optimal environmental conditions to improve colonization success and persistence [56].

4.2.2. Indirect Microbiome Management

Indirect methods alter environmental conditions in favor of desirable microbial populations rather than directly introducing organisms. Prebiotic approaches provide nutrients or substrates which selectively promote specific microbial taxa [2, 33]. The addition of organic matter can also increase the microbial activity and diversity in degraded sediments when they have reduced levels of carbon [36]. Nevertheless, amendments have to be carefully formulated to avoid excessive nutrient loading which could favour undesirable taxa or create eutrophic conditions [42].

Changes in environmental conditions that modify physical and chemical parameters can influence the trajectory of microbial communities. Hydrological restoration rearranges the patterns of tidal exchange and hence generates environmental conditions conducive to native coastal microbiomes while disadvantaging terrestrial taxa that colonized during drainage [19]. Cleanup of pollution relieves the selective pressure which supports adapted communities, hence favouring recovery of sensitive taxa [57]. These indirect methods intervene using natural community assembly processes rather than attempting to directly manipulate community composition [26].

Integrated approaches utilize a paired intervention of the microbiome with traditional restoration technologies for collaborative benefits. Transplanting foundation species together with their associated microbiome might improve establishment success over transplanting vegetation alone [7, 12]. It has been demonstrated that the addition of rhizosphere sediments from healthy donor areas during transplanting can promote seagrass and marsh grass survival and development [18]. This approach transfers not only microbial inoculants but also organic matter and nutrients that support microbial colonization and activity.

4.3. Monitoring and Adaptive Management

Successful monitoring tracks both the response of microbial communities and ecosystem level responses to interventions. Temporal sampling captures community change during the critical establishment phase directly following intervention and beyond, to evaluate persistence and stability [45, 49]. Comparison of intervention sites with reference ecosystems and unmanipulated control plots allows the attribution of observed changes to particular interventions [4].

Monitoring focuses on a number of response variables that provide complementary information. Compositional monitoring tracks whether introduced taxa establish and persist, whether native community structure recovers toward reference conditions, and whether unintended community shifts occur [56]. Functional monitoring checks whether ecosystem functions of interest are restored, such as rates of nutrient cycling, primary productivity and disease suppression [55]. The success of restoration can be ultimately assessed through ecosystem level indicators such as survival and growth of transplanted vegetation, sediment accretion rates, and faunal community recovery [1].

Molecular surveillance methods are being considered becoming more feasible for restoration uses. High-throughput sequencing permits regular testing of community composition for relatively low cost [15]. Quantitative PCR targeting specific functional genes allows tracking of key microbial functions [9]. Emerging portable sequencing technologies enable near real-time monitoring in field settings, facilitating rapid adaptive management responses [58].

Adaptive management responds to monitoring results by adjusting intervention strategies. If the introduced microbial taxa fail to establish, this could suggest inappropriate environmental conditions that need to be remediated before additional inoculation attempts [59]. If community composition shifts in unexpected directions, this may reveal unrecognized ecological interactions requiring revised intervention strategies [28]. Repeated intervention cycles, each informed by prior monitoring results, progressively refine approaches to local conditions [6].

5. Challenges and Future Directions

5.1. Current Limitations

Despite support from theory and ongoing practical applications, there are still concerns that prevent the expansion of methods for microbiome-based coastal restoration. Technical challenges include upscaling interventions from experimental plots to restoration relevant spatial scales [56]. Most successful demonstrations remain limited to small areas where intensive manipulation is feasible, typically less than 100 square meters [16]. Developing economically viable application methods for large-scale implementation requires innovation in inoculum production, delivery systems, and application techniques. Standardization is another technical challenge, as the absence of agreement on protocols for assessment, intervention and monitoring impedes comparability between studies and restricts how much generalizable knowledge can be accumulated [15, 53].

Predicting the effects of interventions is complicated by ecological uncertainties. Microbial community dynamics show substantial context-dependency, with responses to identical interventions varying across sites, seasons, and environmental conditions [25, 26]. This variability makes it difficult to develop generalized restoration prescriptions and requires site-specific practices calling for significant amount of expertise. It is not yet known to what extent manipulated microbiomes are stable in the long term with questions about whether introduced taxa survive beyond their initial establishment, desired community states last for years or decades, or whether communities tend to revert to disturbed configurations [45].

Practical barriers limit application of microbiome-based approaches by restoration practitioners. Cost-effectiveness relative to traditional methods remains unquantified for most applications, creating uncertainty about resource allocation [6]. Regulations regarding the introduction of microorganisms are underdeveloped in most jurisdictions and the possibility of permitting obstacles especially for non-native or genetically modified organisms [33]. Furthermore, inability of practitioners to interpret findings in microbiome science limits capacity for implementation outside research contexts [19]. Integration into existing restoration schemes needs to show that the additional burden is justified by the added value.

5.2. Research Priorities and Future Directions

Significant gaps in knowledge call for a coordinated research and implementation initiative to move microbiome-informed restoration from concept to standard practice. Mechanistic understanding of how microbial communities influence restoration outcomes remains incomplete, with causal linkages between microbiome characteristics and ecosystem health less clear despite increasing correlational evidence [2]. Experimental manipulations that directly test the potential of microbial interventions to mediate ecosystem-level responses are needed for gaining evidence and guiding the most efficient strategies [6]. There is a need to develop predictive models that link assessment with intervention, and machine learning methodologies may offer opportunities for combining microbiome composition, environmental inputs, and restoration results in an actionable decision support tool [47].

Comparative meta-analyses across ecosystem types, disturbance regimes, and restoration approaches are needed to identify generalizable principles, quantify effect sizes, and determine context-specific requirements [4, 7]. Additionally, research into the interactions between climate change and microbiome-based restoration are urgently required as a warming atmosphere, altered precipitation patterns, and ocean acidification could result in microbiomes acclimated to historic conditions becoming maladapted to future environments [2]. Proactive efforts such as assisted evolution and climate-resilient strain selection deserve consideration while maintaining microbial functional redundancy as insurance against uncertain future conditions [2, 31, 33].

Technology development should focus on cost reduction and scalability considerations through innovations in culturomics, high-throughput isolation methods, and inoculum production techniques adapted from agricultural biotechnology [16, 60]. Progress on these fronts is already being realized with the publication of assessment methods made more accessible thanks to advancement of environmental DNA approaches and portable sequencers [58]. To tackle these technical, ecological, and implementation challenges holistically will require interdisciplinary work among microbial ecologists, restoration practitioners, environmental engineers, and social scientists [6]. Educational and training programs that establish microbiome literacy among practitioners and implementation knowledge of ecologists together with careful demonstration projects comparing microbiome-based and traditional approaches, will facilitate knowledge translation and build stakeholder confidence [19].

Policy frameworks must evolve to accommodate microbiome-based approaches while ensuring ecological safety, balancing innovation with precaution through expedited approval for native microbial consortia and rigorous oversight of genetically modified organisms [33]. Funding mechanisms supporting both fundamental research and applied demonstrations, particularly long-term monitoring validating intervention persistence, are critical for sustained progress [6]. Building evidence through systematic documentation, establishing knowledge exchange networks, and progressively refining approaches will enable microbiome-based restoration to transition from experimental novelty to standard practice as successful applications accumulate and costs decline.

6. Conclusion

This review synthesizes the theoretical basis, experimental data, and applied considerations for restoration of native microbiomes to demonstrate that successful recovery must consider not only visible foundation species but also invisible microbial communities that mediate nutrient cycling, biogeochemical process, and stress tolerance. Evidence demonstrates that disturbances fundamentally alter microbial communities with lasting functional effects, and spontaneous recovery is often delayed or incomplete, supporting purposeful microbial intervention through diagnostic monitoring, bioaugmentation and environmental modifications. Although there are still challenges for scaling up, ecological prediction and regulatory contexts, the transformative opportunity is to address biological constraints that limit traditional approaches in order to offer tools to practitioners aimed at maximizing ecosystem recovery and resilience. With coastal ecosystems experiencing the most acute pressures in history from climate change and anthropogenic disturbance, microbiome-based restoration reflects a paradigm shift recognizing the invisible majority of biodiversity as essential targets with new pathways to increase effectiveness and long-term sustainability of recovery in coastal ecosystems for future generations.

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