

Biodiversity conservation through biotechnology: strategies and practical solutions

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Abstract. In today's world, the preservation of natural ecosystems becomes an increasingly urgent task, requiring innovative approaches and technologies. This article examines the use of biotechnology in the conservation and protection of natural ecosystems. Various innovative approaches and technologies aimed at improving ecological sustainability and preserving biodiversity are discussed. Aspects such as the use of genetic engineering for the restoration of threatened species, bioremediation of polluted ecosystems, and the application of biological methods for pest control and soil protection are considered. This article provides an overview of modern advancements in biotechnology and their potential application for the preservation of natural ecosystems, as well as discusses the challenges and prospects for further development in this direction.

1 Introduction

Biodiversity conservation emerged in the 1990s as a response to social, scientific, and policy agendas aimed at preserving or restoring aspects of nature valued by societies or specific groups. Coined during the 1980s, the term "biodiversity" encompasses the entirety of genes, species, and ecosystems within a defined area, gaining significant policy attention after the 1992 ratification of the Convention on Biological Diversity [1]. While instrumental value arguments dominate policy discussions on biodiversity conservation, the term also encapsulates broader moral and aesthetic value arguments rooted in social movements dating back to the 19th century.

Central concerns of biodiversity conservation include the preservation of natural resources, prevention of species extinction, protection of culturally and scientifically valuable sites and landscapes, and the maintenance and restoration of ecosystem services. Given that conservation strategies often involve land reservation or use restrictions, they are inherently politicized and subject to controversy [2]. These controversies often revolve around balancing the interests of powerful corporate entities with the rights of local and indigenous communities.

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Conservation biology emerged in the 1980s as the primary scientific discipline informing biodiversity conservation policy, but the field has since evolved into a more transdisciplinary approach, recognizing the social, cultural, political, and economic dimensions of conservation action. Intersectional work, particularly at the nexus of ecology and economics, has led to the framing of biodiversity and ecosystems as natural capital capable of providing essential services and benefits.

Human geographers are increasingly contributing to interdisciplinary understandings of biodiversity conservation through innovative research. However, unlike conservation biology, there is no established field of "conservation geography" with a definitive body of knowledge.

The value of biodiversity cannot be overstated; it is indispensable for human well-being, benefiting not only humans but the entire interconnected network of life. Biological resources play a crucial role in supporting the survival and proliferation of various species by providing essential necessities such as food and shelter [3].

The extinction of even a single species within an ecosystem can have profound and widespread repercussions on its overall functioning, contributing to the maintenance of Earth's delicate balance. However, human activities often disrupt this equilibrium, resulting in biodiversity loss. Major factors driving this loss include habitat destruction, alterations in ecosystem composition, excessive exploitation of biological resources, and the introduction of non-native species. The repercussions of biodiversity loss extend beyond local ecosystems, ultimately impacting the global environment.

To mitigate these adverse effects, biodiversity conservation is imperative. This involves safeguarding, conserving, and effectively managing ecosystems to ensure their long-term sustainability. Biodiversity conservation aims to achieve three primary objectives: the preservation of diversity, the maintenance of crucial ecological processes, and the sustainable utilization of species and ecosystems.

2 Research methodology

Under current projections, the global population is anticipated to reach 9.8 billion by 2050, necessitating a 50%-69% increase in agricultural production over the 2010-2050 period to meet growing food and feed demands. Currently, agricultural land available for food production covers 38% of the world's land surface, with two-thirds designated as meadows and pastures and the remaining third as cropland. However, there has been a consistent decline in global cropland area per capita since 1961, posing challenges to food security, exacerbated by climate change [4].

Climate change is anticipated to significantly impact crop production environments, with rising atmospheric carbon dioxide levels, increased temperatures, more frequent droughts, intense precipitation events, and extreme weather becoming more common. The stability of the climate during the Holocene period played a crucial role in the development of agriculture, providing predictable conditions for food production. However, climate instability characterized by droughts, floods, cyclones, and other extreme events poses a significant threat to crop production and food security [5].

Efforts to maintain agricultural productivity and mitigate the effects of climate change on human nutrition are underway, focusing on developing climate-resilient crop varieties and stress-resistant cultivars using genomic tools. Additionally, diversifying staple crops to include underutilized varieties with high nutritional value and adaptability to adverse conditions is being explored. Agrobiotechnologies are also being leveraged to enhance the resilience of existing crops to environmental stress, with the crop microbiome emerging as a key component contributing to plant resilience.

Microbial inoculation of plants, utilizing beneficial microorganisms present in the plant and soil microbiome, has emerged as a promising strategy to address agricultural challenges associated with climate change [6]. Plant growth-promoting microorganisms (PGPM), including plant growth-promoting rhizobacteria (PGPR), plant growth-promoting bacteria (PGPB), and arbuscular mycorrhizal fungi (AMF), offer various benefits such as biological nitrogen fixation, soil nutrient solubilization, and plant defense stimulation, mitigating both biotic and abiotic stresses.

Traditional bioinoculants, typically based on single-strain formulations, have shown variable field performance, prompting the exploration of synthetic microbial communities (SynComs) designed to enhance overall plant productivity and suppress pathogens. However, a better understanding of intra- and inter-kingdom interactions within the plant microbiome is needed to optimize bioinoculant formulations and bridge the gap between laboratory studies and field applications [7]. Advancements in multi-omics and computational technologies are facilitating the development of more effective bioinoculant strategies aimed at improving crop resilience and productivity.

3 Results and Discussions

Harnessing the potential of the plant and soil microbiome, which encompasses the diverse genetic and functional capabilities of beneficial microorganisms inhabiting plant tissues and the rhizosphere soil, has emerged as a promising strategy to address agricultural challenges associated with climate change. Plant growth-promoting microorganisms (PGPM), including plant growth-promoting rhizobacteria (PGPR), plant growth-promoting bacteria (PGPB), and arbuscular mycorrhizal fungi (AMF), offer a range of beneficial functions such as biological nitrogen fixation, soil nutrient solubilization, siderophore production, phytohormone synthesis (e.g., auxin), and the activation of plant defense mechanisms, thereby alleviating both biotic and abiotic stresses [8].

Traditionally, bioinoculants have relied on single-strain formulations with growth-promoting activities [9]. However, while promising results are often observed *in vitro*, field applications frequently yield inconsistent or unsatisfactory outcomes, highlighting the need to bridge the gap between laboratory studies and field performance. Addressing this challenge requires the development of systematic approaches for formulating successful bioinoculants.

Recent advancements in multi-omics and computational technologies have facilitated the development of synthetic microbial communities (SynComs) comprising small consortia of microorganisms designed to enhance overall plant productivity and suppress pathogens. Despite this progress, there remains a knowledge gap regarding detailed mechanistic intra- and inter-kingdom interactions, underscoring the need for further research to evaluate trophic exchanges within the rhizosphere and endosphere of plants. Microbes, ubiquitous in nature, present a unique challenge to traditional biological concepts, particularly the notion of species [10]. Unlike macrobes such as plants and animals, prokaryotic microbes exhibit distinct cell structures, physiologies, and reproductive mechanisms, which defy the conventional biological species concept proposed by Mayr. Genomic studies have revealed that prokaryotic taxa consist of diverse, non-overlapping sets of genes, known as the pangenome concept, implying that taxa do not adhere to a fixed set of genes but instead harbor a pool of similar genes (i.e., functions) acquired through horizontal gene transfer driven by mobile genetic elements (MGEs). This dynamic interplay among hosts, MGEs, and environments shapes the functional landscape within microbial communities.

Ecosystems undergo variation in response to stressors such as climatic changes, often resulting in biodiversity loss. Ecosystem resilience, the ability to maintain or recover

functions in the face of external influences, is closely linked to species' capacity to counter adverse events. Functional diversity, representing the varied functional composition of a microbiota, is essential for community resilience against environmental perturbations.

Quantifying the relationship between ecosystem function and diversity requires careful consideration. While species richness is commonly used, it overlooks the uncoupling between taxa and gene functions inherent in microorganisms. The keystone species concept, although relevant for identifying ecological drivers, lacks quantitative measures of processes and fails to describe the diversity-function link. Analyzing the diversity of functional groups offers a potential solution, although it suffers from biases in defining functional groups.

In plant microbiology, the importance of functions over taxa is evident, particularly in the case of diazotrophs involved in nitrogen fixation. Symbiotic nitrogen fixers, such as rhizobia associated with leguminous plants, exemplify functional groups of polyphyletic origin, where functional genes required for symbiosis are scattered among distantly related strains.

The decoupling of taxa and functions in microbes has profound implications for our understanding of life evolution and biodiversity conservation. Conserving genes, rather than taxa, emerges as a critical consideration in microbial biodiversity conservation, challenging established assumptions in biology and nature conservation. The phytosphere microbiota, comprising a diverse array of microbes, plays a crucial role in plant health and growth. Beneficial microbes, including bacteria and fungi, contribute to disease protection, stress resistance, and biomass production by enhancing nutrient mobilization, producing phytohormones, and modulating plant functional traits. The rhizosphere, in particular, hosts a vast microbial population, with up to 10^{11} microbial cells per gram of root and thousands of bacterial and fungal taxa reported from plant tissues. However, this biodiversity is subject to natural fluctuations influenced by environmental variations, including root physiology and aerial dispersion of microorganisms [8].

While preserving this biodiversity is desirable, practical challenges arise. Should we prioritize the preservation of taxa or the functions they carry? Which criteria should guide our selection, and how can we effectively preserve microbes, especially those that are difficult to cultivate?

Nikolay Vavilov, a pioneer in biodiversity preservation, established extensive plant germplasm collections worldwide, highlighting the importance of preserving biodiversity. However, with the recognition of the holobiont concept, emphasizing the role of microbes associated with plants and animals, seed preservation alone is insufficient. Efforts now focus on preserving host plants and their associated microbes together to ensure future crop improvement [5].

Similar to initiatives for human gut microbiota preservation, global efforts are underway to analyze and conserve microbes associated with major crops. Soil biodiversity hotspots have been identified to guide conservation priorities [7]. However, unlike human microbiota, preserving crop-associated microbes presents greater challenges due to the diverse range of host species involved.

Conserving microbes, particularly nonculturable ones, requires innovative approaches such as plant microbiota culturomics initiatives. In situ preservation of plants in their local environments offers a solution, as it preserves the plant microbiome, which often contains more genetic information than the plant itself.

While certain microbial taxa are predominant in plant-associated microbiota, limitations in culturing techniques may bias our understanding. Efforts to develop novel microbial culture methods are essential to explore and preserve microbial diversity effectively.

4 Conclusions

Around 10,000 years ago, the process of crop domestication began as human civilization shifted towards agricultural dependence, ushering in a stable food supply and sedentary lifestyle. While this transition significantly advanced human society, it also resulted in a notable loss of genetic diversity in modern crop cultivars. The selection of a few species and germplasm better suited to agronomic practices has led to genetic uniformity in crops, affecting root architecture, root exudation, and plant defense mechanisms. Consequently, modern crop cultivars may exhibit altered rhizospheric microbiota compared to their wild relatives, potentially impacting plant growth and health.

Recent studies have observed changes in the rhizospheric microbiota of various plants, with a trend towards reduced Bacteroidetes and increased Proteobacteria and Actinobacteria in domesticated cultivars. Wild plant relatives, being genetically diverse and adapted to preagricultural soils, serve as reservoirs of microbial and plant genetic traits lost during domestication. Accessing and assessing the microbiome of indigenous plants and their habitats offers a novel strategy to harness microbial and plant traits for modern agriculture.

Molecular breeding and marker-assisted selection are pivotal biotechnological tools to enhance beneficial plant-microbe interactions in crop systems, addressing the challenge of meeting global food demand while minimizing reliance on synthetic fertilizers and pesticides. Understanding the genetic basis of plant-microbiota interactions, particularly in wild crop relatives, is crucial for sustainable crop production.

Recent advancements in combining microbiota analysis with quantitative genetics have identified genes influencing rhizosphere microbiota composition, underscoring the link between plant immunity and microbiome recruitment. Similar approaches applied to tomato and maize have revealed associations between plant and bacterial traits, providing insights for plant breeding programs and selection of microbial functions.

Integrated approaches based on bacterial and plant genomics offer promising avenues for improving plant-microbe interactions, identifying lost microbial functions during domestication, and elucidating molecular mechanisms underlying these interactions. These studies pave the way for targeted improvements in crop resilience and productivity through enhanced plant-microbe associations.

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