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Tailoring Synthetic Microbial Communities for the Bioremediation of Saline-Alkali Soils: Mechanisms and Field Applications

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Abstract The bioremediation of saline-alkali soils presents a significant challenge due to the harsh environmental conditions that limit microbial activity and plant growth. This systematic review explores the potential of synthetic microbial communities tailored for the bioremediation of saline-alkali soils, focusing on the underlying mechanisms and field applications. Advances in synthetic biology and systems biology have enabled the design of microbial consortia with specific functional capabilities, enhancing their resilience and efficiency in degrading pollutants under saline-alkali conditions. The integration of genome-scale metabolic models (GEMs) and omics technologies has furthered our understanding of microbial interactions and metabolic pathways, providing a robust framework for the rational design of these communities. Field studies have demonstrated the effectiveness of microbial amendments, such as biochar-immobilized bacteria and organic manure, in improving soil health and promoting plant growth in saline-alkali soils. This review highlights the critical role of microbial diversity and adaptation in the success of bioremediation strategies and discusses future directions for optimizing synthetic microbial communities for environmental applications.

Keywords Synthetic microbial communities; Bioremediation; Saline-alkali soils; Systems biology; Genome-scale metabolic models (GEMs)

1 Introduction

Saline-alkali soils are a significant environmental concern, particularly in arid and semi-arid regions. These soils are characterized by high levels of soluble salts and exchangeable sodium, which adversely affect soil structure, water infiltration, and plant growth. The global extent of salt-affected soils is approximately 1 billion hectares, with significant areas in countries like India, where nearly 6.74 million hectares are salt-stressed (Kumawat et al., 2022). The salinization of soil reduces the growth and development of plants, posing a threat to food security as the global population continues to rise (Kumawat et al., 2022). Soil salinization and alkalization are among the most devastating environmental problems, threatening the sustainable development of agriculture (Wang et al., 2020).

Bioremediation, the use of living organisms to mitigate environmental contaminants, offers an eco-friendly alternative to chemical and physical methods for the remediation of saline-alkali soils (Kumawat et al., 2022). Microorganisms such as halophilic bacteria, arbuscular mycorrhizal fungi, cyanobacteria, and plant growth-promoting rhizobacteria have been documented to promote plant growth under salt-stress conditions (Kumawat et al., 2022). The use of synthetic microbial communities (SynComs) has emerged as a promising strategy to enhance the effectiveness of bioremediation. SynComs can be tailored to include specific microbial strains that work synergistically to improve soil health and plant productivity. For instance, the application of biochar and effective microorganisms (EM) has been shown to significantly improve soil quality and plant growth in saline-alkali soils (Cui et al., 2020). Moreover, the introduction of diverse microbial communities can enhance plant salt tolerance more effectively than single microbial strains, due to their functional complementarity and synergistic effects (Qin et al., 2016).

This systematic review and perspective paper aims to provide a comprehensive overview of the mechanisms by which synthetic microbial communities can be tailored for the bioremediation of saline-alkali soils. By synthesizing current research findings, this paper will highlight the potential of SynComs to mitigate soil salinization and improve agricultural productivity. The review will also discuss field applications and the practical challenges associated with implementing SynCom-based bioremediation strategies. The significance of this paper lies in its potential to inform future research and guide the development of effective, sustainable solutions for managing saline-alkali soils, thereby contributing to global food security and environmental sustainability.

1 Understanding Saline-Alkali Soils

1.1 Characteristics and formation of saline-alkali soils

Saline-alkali soils are characterized by high concentrations of soluble salts and exchangeable sodium, which adversely affect soil structure and fertility. These soils typically exhibit poor physical properties, such as low permeability and high pH levels, which hinder plant growth and microbial activity. For instance, in the Yellow River Delta, China, saline-alkali soils have been found to possess a porosity ranging from 19.55% to 34.90%, with a significant presence of micropores and ultra-micropores, contributing to their poor permeability (Li et al., 2021). The formation of these soils is often attributed to natural processes such as the evaporation of saline groundwater and the deposition of salts from marine or lacustrine sources, as well as anthropogenic activities like improper irrigation practices.

1.2 Environmental and agricultural challenges posed by saline-alkali soils

Saline-alkali soils pose significant environmental and agricultural challenges. They limit the availability of essential nutrients and water to plants, leading to reduced agricultural productivity. Additionally, these soils contribute to increased greenhouse gas emissions, as evidenced by a study in the Hetao Irrigation District of Inner Mongolia, which found that high saline-alkali soils significantly increased the Global Warming Potential (GWP) due to altered methane (CH4) uptake and nitrous oxide (N2O) emissions (Yang et al., 2018). The cumulative uptake of CH4 was reduced by up to 28%, while N2O emissions increased by up to 45% in high saline-alkali soils compared to low saline-alkali soils (Yang et al., 2018). These environmental impacts underscore the need for effective remediation strategies.

1.3 Traditional methods of remediation and their limitations

Traditional methods for remediating saline-alkali soils include physical, chemical, and biological approaches. Physical methods such as leaching and drainage aim to remove excess salts from the soil profile but are often limited by water availability and infrastructure costs. Chemical amendments, including gypsum and other soil conditioners, can improve soil structure and reduce sodium levels but may not be sustainable in the long term. For example, the application of biochar and soil modifiers has been shown to significantly increase soil organic carbon (SOC) content and improve soil fertility in China (Yang et al., 2022). However, these methods may not address the underlying causes of soil salinization and alkalization. Biological approaches, such as planting halophytes and using microbial inoculants, offer more sustainable solutions but require further research to optimize their effectiveness and scalability.

2 Synthetic Microbial Communities (SynComs)

2.1 Definition and principles of SynComs

Synthetic Microbial Communities (SynComs) are artificially designed consortia of microorganisms that are engineered to perform specific functions, such as bioremediation of contaminated environments. Unlike natural microbial communities, which evolve through natural selection and environmental pressures, SynComs are constructed using principles of synthetic biology and systems biology to achieve desired outcomes with greater precision and efficiency (Sharma and Shukla, 2020). These communities are designed by selecting and combining microbial strains with complementary metabolic capabilities, enabling them to degrade a wide range of pollutants simultaneously (Sharma and Shukla, 2020; Wang et al., 2023).

2.2 Techniques for engineering SynComs

The engineering of SynComs involves several advanced techniques, including synthetic biology, genetic modification, and metabolic modeling. Synthetic biology allows for the precise manipulation of microbial genomes to enhance their bioremediation capabilities. This can involve the insertion of new genes, the deletion of non-essential genes, or the modification of existing genes to optimize metabolic pathways (Sharma and Shukla, 2020). Genetic modification techniques, such as CRISPR-Cas9, enable targeted alterations in microbial DNA, facilitating the creation of strains with enhanced pollutant-degrading abilities (Sharma and Shukla, 2020).

Metabolic modeling, particularly genome-scale metabolic models (GEMs), plays a crucial role in the design of SynComs. GEMs provide a mathematical representation of microbial metabolism, allowing researchers to simulate and predict the metabolic interactions within a community under various environmental conditions. This helps in the rational design of SynComs by identifying optimal combinations of microbial strains that can work synergistically to degrade pollutants (Wang et al., 2023). Additionally, in silico tools and databases are used to analyze experimental data and predict the behavior of SynComs, further aiding in their design and optimization (Sharma and Shukla, 2020; Wang et al., 2023).

2.3 Advantages of SynComs over natural microbial communities for bioremediation

SynComs offer several advantages over natural microbial communities for bioremediation. Firstly, they can be tailored to target specific pollutants, making them more efficient in degrading contaminants compared to natural communities, which may not possess the necessary metabolic pathways (Sharma and Shukla, 2020). Secondly, SynComs can be designed to function under a wide range of environmental conditions, including extreme environments such as saline-alkali soils, where natural microbial communities may struggle to survive and function effectively (Shi et al., 2019; Sharma and Shukla, 2020).

Moreover, SynComs can be engineered to have enhanced stability and resilience, ensuring consistent performance in bioremediation applications. This is achieved by selecting microbial strains that can withstand environmental stresses and by engineering metabolic pathways that are robust to fluctuations in environmental conditions (Sharma and Shukla, 2020; Wang et al., 2023). Additionally, the use of SynComs allows for the combination of multiple microbial strains with complementary metabolic capabilities, enabling the simultaneous degradation of a wide range of pollutants, which is often not possible with natural microbial communities (Sharma and Shukla, 2020).

3 Mechanisms of SynComs in Bioremediation

3.1 Biological pathways involved in the degradation and neutralization of soil salinity and alkalinity

Synthetic microbial communities (SynComs) play a crucial role in the bioremediation of saline-alkali soils through various biological pathways. These pathways include the degradation of pollutants and the neutralization of soil salinity and alkalinity. For instance, microbial biofilm formation and the production of secondary metabolites are essential traits that enhance the stability and functionality of SynComs under environmental stressors (Martins et al., 2023). Additionally, halophilic bacteria, arbuscular mycorrhizal fungi, and plant growth-promoting rhizobacteria have been documented to promote plant growth under salt-stress conditions by maintaining and enhancing soil health (Table 1) (Kumawat et al., 2022). The microbial degradation of hydrocarbons in saline soils, facilitated by salinity-tolerant hydrocarbon-degrading bacteria, further exemplifies the potential of SynComs in bioremediation (Ebadi et al., 2018).

3.2 Genetic engineering approaches to enhance SynCom efficiency

Genetic engineering approaches are pivotal in enhancing the efficiency of SynComs for bioremediation. Systems biology tools help identify new genes, proteins, and metabolic pathways involved in bioremediation, which can be used to design SynComs capable of degrading multiple recalcitrant pollutants simultaneously (Sharma and Shukla, 2020). Computational methods, including machine learning and artificial intelligence, are employed to screen and identify beneficial microbes, improving the process of determining the best combination of microbes for a desired plant phenotype (Souza et al., 2020). These approaches enable the creation of SynComs with robust colonization traits and specific beneficial functions, thereby enhancing crop resiliency against stressful conditions (Souza et al., 2020; Marín et al., 2021).

Table 1 Halophilic bacteria species with the salt-tolerant range (Adapted from Kumawat et al., 2022)

Halophilic Bacterial Species	Salinity Range for the Growth and Development (%)
Kangiella spongicola	2-15
Halanaerocella petrolearia	6-26
Salisediminibacterium cookie	3-30
Amphibacillus cookie	6-26
Desulfohalophilus alkaliarsenatis	12.5-33
Halanaerobacter jeridensis	6-30
Natribacillus halophilus	7-23
Fodinibius salinus	10-15
Alkalibacterium gilvum	0-17.5
Halomicroarcula pellucida	20-30
Salinibacter iranicus	12-30
Halanaerobium sehlinen	5-30
Saliterribacillus perciscus	0.5-22.5
Limimonas halopajila	15-30
Aquibacillus halophilus	0.5-20
Halobellus salinus	15-30
Bacillus daqingensis	0-16
Oceanicola flagellatus	0-21
Spiribacter salinus	10-25
Halomonas huangheensis	1-20
Salifodinibacter halophilus	25
Halomonas sambharensis	5-8
Lentibacillus saliphilus sp. nov. (type strain YIM 93176^{T})	0-22
Halomonas urmiana sp.	0.5-20
Marinobacter halodurans sp. nov.	1-18
Aliifodinibius saliphilus sp. nov.	3-25
Arhodomonas recens	2-25

3.3 Interaction between SynComs and soil properties

The interaction between SynComs and soil properties is a critical factor in the success of bioremediation efforts. Soil salinity and alkalinity significantly influence the structure and function of microbial communities. For example, increased soil salinity and alkalinity enhance the availability of heavy metals like cadmium, which in turn affects microbial community structures and interactions (Wang et al., 2019). The presence of specific microbial taxa, such as oligotrophic and haloalkaliphilic bacteria, is enriched under saline-alkaline conditions, indicating their role in adapting to and mitigating soil stress (Wang et al., 2019). Furthermore, the initial pH and organic carbon dose rates in soil are key factors controlling the rates and extent of microbially driven pH neutralization, with lower initial pH and higher organic carbon conditions leading to more effective bioremediation (Santini et al., 2016).

4 Optimization of SynComs for Saline-Alkali Soil Bioremediation

4.1 Selection and engineering of microbial strains suitable for saline-alkali environments

The selection and engineering of microbial strains for saline-alkali soil bioremediation require a deep understanding of the native microbial communities and their adaptability to extreme conditions. Studies have shown that microbial assemblages in saline-alkali soils are primarily driven by soluble salt ion components rather than salinity alone, with fungal communities demonstrating higher tolerance and stability compared to bacterial communities (Zhang et al., 2021). Keystone microbial taxa, such as certain bacteria and fungi, have been identified for their potential adaptability and beneficial roles in restoring saline-alkali soils (Zhang et al., 2021). Additionally, the diversity of prokaryotic microorganisms in extreme environments, such as the Qarhan Salt Lake area, highlights the importance of selecting strains with specific metabolic pathways like nitrogen fixation and methanogenesis, which are crucial for biogeochemical cycles (Wang and Bao, 2021).

4.2 Strategies for optimizing SynCom composition and functionality

Optimizing the composition and functionality of synthetic microbial communities (SynComs) involves careful selection and engineering of microbial consortia to achieve desired outcomes. The use of machine learning to study community assembly rules and target microbial functions has been suggested to create stable SynComs that thrive under environmental stressors (Martins et al., 2023). Furthermore, the development of reproducible and tunable SynComs, such as a model community of 16 soil bacteria, has demonstrated the importance of maintaining community diversity and functionality through controlled experimental conditions (Coker et al., 2022). These strategies ensure that SynComs can be effectively used to improve plant health and soil quality in saline-alkali environments.

4.3 Laboratory techniques for testing and validating SynCom efficacy

Laboratory techniques for testing and validating the efficacy of SynComs include in vitro and in planta experiments, as well as the use of fabricated ecosystem devices (EcoFABs) for precise control of environmental conditions (Coker et al., 2022). High-throughput sequencing and multivariate analysis are essential for understanding the structure and function of microbial communities in saline-alkali soils (Wang and Bao, 2021; Zhang et al., 2021). Additionally, artificial neural network models have been developed to predict the growth profiles of bacterial strains under varying pH and temperature conditions, providing valuable insights for scaling up laboratory findings to field applications (Šovljanski et al., 2020). These techniques enable researchers to systematically evaluate the performance of SynComs and optimize their composition for effective bioremediation of saline-alkali soils.

5 Field Applications and Performance Evaluation

5.1 Overview of field application methodologies

The application of synthetic microbial communities (SynComs) in the field involves several methodologies aimed at enhancing the resilience and productivity of crops in saline-alkali soils. These methodologies typically include the isolation and characterization of beneficial microbial strains from the rhizosphere, the design and formulation of SynComs, and the application of these communities to the soil or directly to the plants. The process begins with the identification of microbial strains that exhibit traits beneficial for plant growth and stress tolerance, such as antifungal activity, nutrient solubilization, and hormone production (Souza et al., 2020; Yin et al., 2022). Advanced computational methods, including machine learning, are increasingly used to optimize the selection and combination of microbial strains to form effective SynComs (Souza et al., 2020). Once formulated, these SynComs are applied to the field through various methods such as seed coating, soil drenching, or foliar sprays, depending on the specific requirements of the crop and the environmental conditions (Shayanthan et al., 2022).

5.2 Key field trials and large-scale applications of SynComs for saline-alkali soil bioremediation

Several field trials and large-scale applications have demonstrated the potential of SynComs in bioremediating saline-alkali soils. For instance, a study conducted in Inner Mongolia revealed that specific microbial assemblages could adapt to different types of saline-alkali soils, such as sulfated, chlorinated, and soda-type soils, and play a crucial role in restoring soil health (Zhang et al., 2021). Another significant trial involved the use of SynComs derived from the wheat rhizosphere, which showed promising results in protecting wheat against soilborne fungal pathogens and enhancing root growth (Yin et al., 2022). These trials highlight the importance of selecting microbial strains that can thrive in specific soil conditions and interact synergistically with plants to improve their resilience and productivity. Additionally, the practical application of SynComs in sustainable agriculture has been explored, with a focus on improving crop production through enhanced plant-soil-microbiome interactions (Shayanthan et al., 2022).

5.3 Metrics and criteria for evaluating the performance of SynComs in field conditions

Evaluating the performance of SynComs in field conditions requires a comprehensive set of metrics and criteria. Key performance indicators include plant growth parameters (e.g., biomass, root length, and yield), soil health indicators (e.g., microbial diversity, enzyme activity, and nutrient availability), and stress tolerance markers (e.g., salinity and pH levels) (Souza et al., 2020; Yin et al., 2022). Additionally, the stability and resilience of the

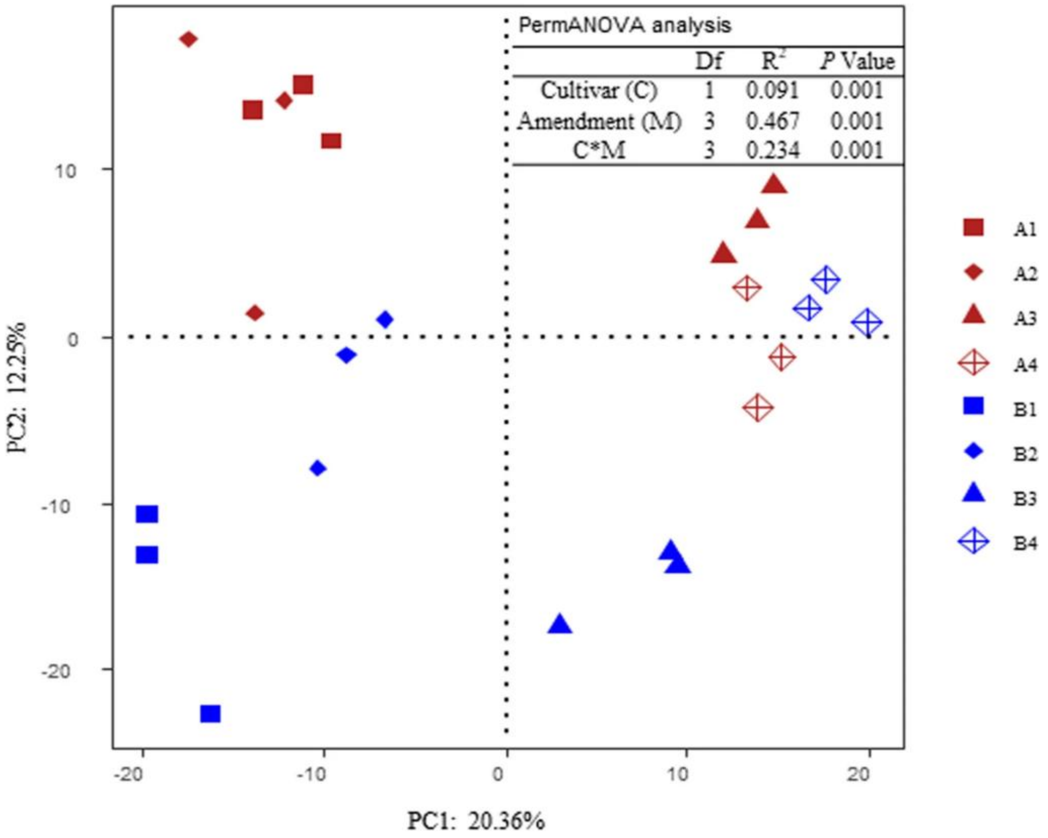
SynComs themselves are critical factors, as they must maintain their functional traits and beneficial interactions with plants under varying environmental conditions (Zhang et al., 2021). Advanced techniques such as Next Generation Sequencing (NGS) and metagenomics are employed to monitor changes in microbial community structure and function, providing insights into the effectiveness and sustainability of the SynComs (Shayanthan et al., 2022). Overall, a multi-faceted approach combining plant, soil, and microbial metrics is essential for a thorough evaluation of SynCom performance in the field.

6 Case Studies

6.1 Detailed analysis of specific field trials and their outcomes

In recent years, several field trials have been conducted to explore the potential of synthetic microbial communities in the bioremediation of saline-alkali soils. These trials have provided valuable insights into the mechanisms and effectiveness of various strategies.

Northern China Oat Cultivar Study: A field trial in Northern China investigated the impact of organic soil amendments on oat productivity in saline-alkaline soils. The study involved two oat cultivars with different levels of saline-alkaline tolerance and four amendment treatments: control, bio-fertilizer, rotten straw, and a combination of bio-fertilizer and rotten straw. The combined amendment treatment resulted in the highest oat yields, reduced soil pH, and increased soil salt content for both cultivars. The tolerant cultivar, Baiyan2, exhibited higher bacterial α-diversity and a different microbial community composition compared to the sensitive cultivar, Caoyou1 (Figure 1) (Lu et al., 2020).



PermANOVA analysis

	Df	R^2	*P* Value
Cultivar (C)	1	0.091	0.001
Amendment (M)	3	0.467	0.001
C*M	3	0.234	0.001

Figure 1 Principal component analysis (PCA) of the rhizosphere soil bacterial community associated with the two oat cultivars and organic soil amendment treatments (Adopted from Lu et al., 2020)

Inner Mongolia Microbial Assemblages Study: This study evaluated microbial assemblages in various saline-alkaline soils from different regions of Inner Mongolia. The research identified key driving factors influencing microbiomes and revealed that soluble salt ion components, rather than salinity, were the major determinants of microbial assemblages. The study highlighted the higher tolerance, stability, and resilience of fungal communities compared to bacterial communities under saline-alkaline stress (Zhang et al., 2021).

6.2 Success stories and lessons learned

The field trials have demonstrated several success stories and provided important lessons for future applications:
Effective Soil Amendments: The combined use of bio-fertilizer and rotten straw significantly improved crop yields and altered the rhizosphere bacterial community in a positive manner. This suggests that integrating organic amendments can be an effective strategy for enhancing soil health and productivity in saline-alkaline environments (Lu et al., 2020).

Microbial Community Adaptation: The identification of keystone bacteria and fungi with potential adaptability to various saline-alkaline environments underscores the importance of selecting and engineering microbial communities that can thrive under specific soil conditions. This approach can enhance the resilience and effectiveness of bioremediation efforts (Zhang et al., 2021).

6.3 Limitations and areas for improvement

Despite the promising results, there are several limitations and areas for improvement in the application of synthetic microbial communities for bioremediation:
Complexity of Microbial Interactions: The intricate interactions within microbial communities and between microbes and plants pose a significant challenge. Understanding and controlling these interactions to achieve desired outcomes requires further research and development (Johns et al., 2016).

Field Variability: The variability in soil types, environmental conditions, and microbial communities across different regions necessitates tailored approaches for each specific site. Standardized protocols and scalable solutions are needed to address this variability effectively (Zhang et al., 2021).

Long-term Stability: Ensuring the long-term stability and robustness of synthetic microbial communities in field conditions remains a critical challenge. Strategies to enhance the persistence and functionality of these communities over extended periods are essential for sustainable bioremediation (Johns et al., 2016).

In conclusion, while significant progress has been made in tailoring synthetic microbial communities for the bioremediation of saline-alkali soils, ongoing research and innovation are required to overcome existing limitations and optimize field applications. The insights gained from recent field trials provide a solid foundation for future advancements in this promising area of environmental biotechnology.

7 Challenges and Limitations

7.1 Technical challenges in engineering and deploying SynComs in saline-alkali soils

Engineering and deploying synthetic microbial communities (SynComs) in saline-alkali soils present several technical challenges. One of the primary issues is ensuring the stability and functionality of SynComs under varying environmental conditions. The performance of individual microbial inoculants can be inconsistent due to environmental variability, which complicates the design of robust SynComs that can thrive in saline-alkali soils (Souza et al., 2020; Shayanthan et al., 2022). Additionally, the complexity of microbial interactions within SynComs and their interactions with plant hosts and soil environments necessitates advanced computational methods, such as machine learning, to predict and optimize these interactions (Souza et al., 2020; Martins et al., 2023). Ensuring long-term colonization and stability of SynComs is another significant challenge, as microbial communities can change over time due to horizontal gene transfer and mutations (Martins et al., 2023).

7.2 Ecological and environmental considerations

The ecological and environmental impacts of deploying SynComs in saline-alkali soils must be carefully considered. SynComs must be designed to integrate seamlessly with the native soil microbiome without disrupting existing ecological balances (Marín et al., 2021; Pradhan et al., 2022). The introduction of non-native microbial species could potentially lead to unintended consequences, such as the displacement of beneficial native microbes or the alteration of soil nutrient cycles (Pradhan et al., 2022). Moreover, the dynamic nature of soil environments, influenced by factors such as pH, salinity, and moisture levels, can affect the survival and efficacy of SynComs, making it crucial to tailor these communities to specific environmental conditions (Liu Yet al., 2019; Shayanthan et al., 2022).

7.3 Economic and scalability issues

The economic feasibility and scalability of SynCom deployment in agricultural settings are significant concerns. Developing and producing SynComs at a commercial scale involves substantial costs, including the isolation, characterization, and cultivation of microbial strains, as well as the formulation and delivery of these communities (Sai et al., 2022; Shayanthan et al., 2022). Additionally, the variability in soil types, crop species, and local environmental conditions necessitates the customization of SynComs for different applications, further increasing costs and complicating large-scale implementation (Sai et al., 2022). Ensuring consistent performance across diverse agricultural settings remains a challenge, as field conditions can vary widely from controlled laboratory environments (Liu Yet al., 2019; Martins et al., 2023).

7.4 Regulatory and safety concerns

Regulatory and safety concerns are critical when considering the deployment of SynComs in agriculture. The introduction of genetically modified or non-native microbial species into the environment raises questions about biosafety and the potential for unintended ecological impacts (Marín et al., 2021; Pradhan et al., 2022). Regulatory frameworks must be established to assess the risks and benefits of SynComs, ensuring that they do not pose a threat to human health, non-target organisms, or the environment (Pradhan et al., 2022). Additionally, public perception and acceptance of SynCom technology can influence regulatory policies and the adoption of these innovations in agriculture (Marín et al., 2021; Sai et al., 2022). Ensuring transparency and effective communication about the safety and benefits of SynComs is essential for gaining public trust and regulatory approval.

8 Future Directions and Perspectives

8.1 Emerging trends and technologies in SynCom engineering

The field of synthetic microbial communities (SynComs) is rapidly evolving, driven by advances in synthetic biology, systems biology, and microbial ecology. Recent developments have focused on designing microbes with defined and controllable properties, enabling the creation of multispecies communities with specific functions (Johns et al., 2016). Key emerging trends include the development of new strategies to control intercellular interactions, spatiotemporal coordination, robustness, stability, and biocontainment of SynComs (Johns et al., 2016). Additionally, the integration of computational and analytical tools has significantly enhanced our ability to study and build these communities, paving the way for innovative applications in bioremediation, bioenergy, and biotechnology (Johns et al., 2016).

8.2 Integration of SynComs into broader soil management practices

The integration of SynComs into broader soil management practices offers a promising approach to address the challenges posed by saline-alkali soils. Microbial approaches, particularly those involving halophilic and halotolerant microorganisms, have shown potential in mitigating salt stress and promoting plant growth (Arora and Vanza, 2017; Kumawat et al., 2022). For instance, the use of plant growth-promoting rhizobacteria and microbial inoculants has been effective in enhancing soil health and crop productivity under salt-stress conditions (Kumawat et al., 2022). Furthermore, the application of SynComs can be synergistically combined with other soil management practices, such as the use of organic amendments and crop rotation, to improve soil structure and fertility, thereby enhancing the overall sustainability of agricultural systems (Arora and Vanza, 2017; Kumawat et al., 2022).

8.3 Long-term vision and potential breakthroughs in SynCom-based bioremediation

The long-term vision for SynCom-based bioremediation involves the development of highly efficient and resilient microbial communities capable of thriving in diverse and challenging environments. Future research should focus on understanding the fundamental mechanisms that shape microbial communities and regulate their interactions under saline-alkaline stress (Wang et al., 2019). This knowledge will be crucial for engineering SynComs that can adapt to and remediate salt-affected soils effectively. Potential breakthroughs may include the identification and utilization of keystone microbial genera that play disproportionate ecological roles in enhancing resistance or tolerance to salt stress and heavy metal toxicity (Wang et al., 2019). Additionally, advancements in genetic engineering and synthetic biology could enable the creation of tailor-made SynComs with enhanced capabilities for bioremediation, ultimately contributing to sustainable soil management and food security (Johns et al., 2016; Wang et al., 2019).

9 Concluding Remarks

The systematic review of the literature on tailoring synthetic microbial communities for the bioremediation of saline-alkali soils has revealed several critical insights. Advances in synthetic biology have enabled the design and programming of multispecies microbial communities with defined and controllable properties, which are crucial for bioremediation applications. The use of organic soil amendments, such as bio-fertilizers and rotten straw, has been shown to significantly alter rhizosphere bacterial communities and improve crop productivity in saline-alkaline environments. Additionally, the study of microbial assemblages in various saline-alkaline soils has highlighted the importance of soluble salt ion components in driving microbial community structure and function, with fungal communities demonstrating higher tolerance and stability compared to bacterial communities.

The findings from this review have several implications for policymakers, researchers, and land managers. Policymakers should consider supporting research and development initiatives that focus on the application of synthetic microbial communities for soil bioremediation, as these technologies hold promise for sustainable agricultural practices in saline-alkaline environments. Researchers are encouraged to further investigate the mechanisms by which organic amendments and microbial communities interact to enhance soil health and crop productivity. Land managers can benefit from implementing strategies that utilize tolerant plant cultivars and combined organic amendments to improve soil conditions and increase agricultural yields in saline-alkaline soils.

Despite the promising findings, there is a need for further research to fully understand the complex interactions within synthetic microbial communities and their impact on soil bioremediation. Future studies should focus on developing new strategies to control intercellular interactions, spatiotemporal coordination, and the robustness of these communities. Additionally, interdisciplinary collaboration between synthetic biologists, ecologists, agronomists, and soil scientists is essential to advance the field and translate laboratory findings into field applications. Such collaborative efforts will be crucial in addressing the challenges of soil salinization and alkalization, ultimately contributing to global food security and environmental sustainability.

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Conflict of Interest Disclosure

The authors affirm that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

References

Arora S., and Vanza M., 2017, Microbial approach for bioremediation of saline and sodic soils, Bioremediation of Salt Affected Soils: An Indian Perspective, 87-100.
https://doi.org/10.1007/978-3-319-48257-6_5

Coker J., Zhalnina K., Marotz C., Thiruppathy D., Tjuanta M., D'Elia G., Hailu R., Mahosky T., Rowan M., Northen T., and Zengler K., 2022, A reproducible and tunable synthetic soil microbial community provides new insights into microbial ecology, mSystems, 7: e00951-22.
https://doi.org/10.1128/msystems.00951-22

Cui Q., Xia J., Yang H., Liu J., and Shao P., 2020, Biochar and effective microorganisms promote Sesbania cannabina growth and soil quality in the coastal saline-alkali soil of the Yellow River Delta, China, The Science of the Total Environment, 756: 143801.
https://doi.org/10.1016/j.scitotenv.2020.143801

Ebadi A., Sima N., Olamaee M., Hashemi M., and Nasrabadi R., 2018, Remediation of saline soils contaminated with crude oil using the halophyte Salicornia persica in conjunction with hydrocarbon-degrading bacteria, J. Environ. Manage., 219: 260-268.
https://doi.org/10.1016/j.jenvman.2018.04.115

Johns N., Blazejewski T., Gomes A., and Wang H., 2016, Principles for designing synthetic microbial communities, Current Opinion in Microbiology, 31: 146-153.
https://doi.org/10.1016/j.mib.2016.03.010

Kumawat C., Kumar A., Parshad J., Sharma S., Patra A., Dogra P., Yadav G., Dadhich S., Verma R., and Kumawat G., 2022, Microbial diversity and adaptation under salt-affected soils: A review, Sustainability, 14(15): 9280.
https://doi.org/10.3390/su14159280

Li K., Geng Y., Li Q., and Liu, C., 2021, Characterization of the microstructural properties of saline-alkali soils in the Yellow River Delta, China, Communications in Soil Science and Plant Analysis, 52: 1527-1543.
https://doi.org/10.1080/00103624.2021.1885695

Liu Y., Qin Y., and Bai, Y., 2019, Reductionist synthetic community approaches in root microbiome research, Current Opinion in Microbiology, 49: 97-102.
https://doi.org/10.1016/j.mib.2019.10.010

Lu P., Bainard L., Ma B., and Liu J., 2020, Bio-fertilizer and rotten straw amendments alter the rhizosphere bacterial community and increase oat productivity in a saline-alkaline environment, Sci. Rep., 10: 19896.
https://doi.org/10.1038/s41598-020-76978-3

Marín O., González B., and Poupin M., 2021, From microbial dynamics to functionality in the rhizosphere: a systematic review of the opportunities with synthetic microbial communities, Front. Plant Sci., 12: 650609.
https://doi.org/10.3389/fpls.2021.650609

Martins S., Pasche J., Silva H., Selten G., Savastano N., Abreu L., Bais H., Garrett K., Kraisitudomsook N., Pieterse C., and Cernava T., 2023, The use of synthetic microbial communities (SynComs) to improve plant health, Phytopathology, 113(8): 1369-1379.
https://doi.org/10.1094/PHYTO-01-23-0016-IA

Pradhan S., Tyagi R., and Sharma S., 2022, Combating biotic stresses in plants by synthetic microbial communities: Principles, applications and challenges, Journal of Applied Microbiology, 133: 2742-2759.
https://doi.org/10.1111/jam.15799

Qin Y., Druzhinina I., Pan X., and Yuan Z., 2016, Microbially mediated plant salt tolerance and microbiome-based solutions for saline agriculture, Biotechnology advances, 34(7): 1245-1259.
https://doi.org/10.1016/j.biotechadv.2016.08.005

Sai N., Devi A., and Balachandar D., 2022, Synthetic microbial community (SynCom) for sustainable agriculture, Indian Journal of Plant Genetic Resources, 35(3): 351-354.
https://doi.org/10.5958/0976-1926.2022.00098.5

Santini T., Malcolm L., Tyson G., and Warren L., 2016, pH and organic carbon dose rates control microbially driven bioremediation efficacy in Alkaline Bauxite residue, Environmental Science and Technology, 50(20): 11164-11173.
https://doi.org/10.1021/ACS.EST.6B01973

Sharma B., and Shukla P., 2020, Designing synthetic microbial communities for effectual bioremediation: A review, Biocatalysis and Biotransformation, 38: 405-414.
https://doi.org/10.1080/10242422.2020.1813727

Shayanthan A., Ordoñez P., and Oresnik I., 2022, The role of synthetic microbial communities (SynCom) in sustainable agriculture, Front. Agron., 4: 896307.
https://doi.org/10.3389/fagro.2022.896307

Shi S., Tian L., Nasir F., Bahadur A., Batool A., Luo S., Yang F., Wang Z., and Tian C., 2019, Response of microbial communities and enzyme activities to amendments in saline-alkaline soils, Applied Soil Ecology, 135: 16-24.
https://doi.org/10.1016/J.APSOIL.2018.11.003

Souza R., Armanhi J., and Arruda P., 2020, From microbiome to traits: designing synthetic microbial communities for improved crop resiliency, Front. Plant Sci., 11: 1179.
https://doi.org/10.3389/fpls.2020.01179

Šovljanski O., Tomić A., Pezo L., and Markov S., 2020, Temperature and pH growth profile prediction of newly isolated bacterial strains from alkaline soils, Journal of the Science of Food and Agriculture, 100(3): 1155-1163.
https://doi.org/10.1002/jsfa.10124

Wang L., Wang X., Wu H., Wang H., Wang Y., and Lu Z., 2023, Metabolic modeling of synthetic microbial communities for bioremediation, Critical Reviews in Environmental Science and Technology, 53: 2092-2111.
https://doi.org/10.1080/10643389.2023.2212569

Wang M., Chen S., Chen L., and Wang D., 2019, Responses of soil microbial communities and their network interactions to saline-alkaline stress in Cd-contaminated soils, Environmental Pollution, 252(Pt B): 1609-1621.
https://doi.org/10.1016/j.envpol.2019.06.082

Wang Y., and Bao G., 2021, Diversity of prokaryotic microorganisms in alkaline saline soil of the Qarhan Salt Lake area in the Qinghai-Tibet Plateau, Sci. Rep., 12: 3365.
https://doi.org/10.1038/s41598-022-07311-3

Wang Z., Tan W., Yang D., Zhang K., Zhao L., Xie Z., Xu T., Zhao Y., Wang X., Pan X., and Zhang D., 2020, Mitigation of soil salinization and alkalization by bacterium-induced inhibition of evaporation and salt crystallization, The Science of the total environment, 755(Pt 1): 142511.
https://doi.org/10.1016/j.scitotenv.2020.142511

Yang S., Hao X., Xu Y., Yang J., and Su D., 2022, Meta-analysis of the effect of saline-alkali land improvement and utilization on soil organic carbon, Life, 12(11): 1870.
https://doi.org/10.3390/life12111870

Yang W., Yang M., Wen H., and Jiao Y., 2018, Global warming potential of CH_4 uptake and N_2O emissions in saline-alkaline soils, Atmospheric Environment, 191: 172-180.
https://doi.org/10.1016/J.ATMOSENV.2018.08.017

Yin C., Hagerty C., and Paulitz T., 2022, Synthetic microbial consortia derived from rhizosphere soil protect wheat against a soilborne fungal pathogen, Frontiers in Microbiology, 13: 908981.
https://doi.org/10.3389/fmicb.2022.908981

Zhang Z., Feng S., Luo J., Hao B., Diao F., Li X., Jia B., Wang L., Bao Z., and Guo W., 2021, Evaluation of microbial assemblages in various saline-alkaline soils driven by soluble salt ion components, Journal of Agricultural and Food Chemistry, 69(11): 3390-3400.
https://doi.org/10.1021/acs.jafc.1c00210