

Optimizing Synthetic Microbial Communities for Sustainable Agriculture: Design, Functionality, and Field Performance

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Molecular Microbiology Research, 2024, Vol.14, No.1 doi: [10.5376/mmr.2024.14.0004](https://doi.org/10.5376/mmr.2024.14.0004)

Received: 16 Dec., 2023

Accepted: 18 Jan., 2024

Published: 02 Feb., 2024

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Preferred citation for this article:

Han L.Z., 2024, Optimizing synthetic microbial communities for sustainable agriculture: design, functionality, and field performance, Molecular Microbiology Research, 14(1): 31-38 (doi: [10.5376/mmr.2024.14.0004](https://doi.org/10.5376/mmr.2024.14.0004))

Abstract The application of synthetic microbial communities (SynComs) in sustainable agriculture has emerged as a promising strategy to enhance crop performance and resilience. This systematic review explores the design, functionality, and field performance of SynComs, focusing on their potential to optimize plant-microbe interactions for improved agricultural outcomes. SynComs are engineered consortia of microorganisms selected for their beneficial traits, such as nutrient acquisition, disease suppression, and stress tolerance. Recent advances in microbial ecology, machine learning, and high-throughput phenotyping have facilitated the identification and assembly of effective SynComs tailored to specific crops and environmental conditions. Studies have demonstrated that SynComs can significantly improve plant health, nutrient efficiency, and yield under various stressors, including nutrient deficiencies and pathogen attacks. However, challenges remain in ensuring the stability and reproducibility of SynComs in field conditions. This review synthesizes current knowledge on SynCom design and application, highlighting successful case studies and identifying gaps for future research. By leveraging the synergistic interactions within SynComs, sustainable agriculture can achieve more consistent and resilient crop production.

Keywords Synthetic microbial communities; Sustainable agriculture; Plant-microbe interactions; Crop resilience; Nutrient acquisition; Disease suppression; stress tolerance; Microbial ecology; Machine learning; High-throughput phenotyping

Sustainable agriculture is a critical component in addressing the global challenges of food security, environmental degradation, and climate change. As the global population continues to grow, the demand for food, feed, and fiber increases, necessitating agricultural practices that are both productive and environmentally sustainable. Traditional agricultural practices, heavily reliant on chemical fertilizers and pesticides, have led to soil degradation, water pollution, and loss of biodiversity, thereby threatening long-term agricultural productivity and ecosystem health (Singh et al., 2016; Ray et al., 2020). Therefore, there is an urgent need to adopt sustainable agricultural practices that enhance crop productivity while preserving natural resources and ecosystem services.

Microbial communities, particularly those associated with plants, play a pivotal role in sustainable agriculture. These communities, known as the plant microbiome, include bacteria, fungi, and other microorganisms that interact with plants to promote growth, enhance nutrient uptake, and improve resistance to biotic and abiotic stresses (Qiu et al, 2019; Trivedi et al., 2021). The plant microbiome contributes to soil health, nutrient cycling, and plant resilience, making it a valuable asset in sustainable agricultural practices. By harnessing the beneficial traits of these microbial communities, it is possible to reduce the dependency on chemical inputs and improve crop performance under various environmental conditions (Souza et al., 2020; Coker et al., 2022).

Synthetic microbial communities (SynComs) are artificially designed consortia of microorganisms that are assembled to perform specific functions beneficial to plants and agriculture. Unlike traditional single-strain inoculants, SynComs are designed to mimic the complexity and functionality of natural microbial communities, thereby providing more stable and effective solutions for enhancing crop productivity and sustainability (Souza et al., 2020; Sai et al., 2022). SynComs can be tailored to possess traits such as nutrient acquisition, drought tolerance, and pathogen resistance, making them a promising tool for sustainable agriculture (Ke et al., 2020;

Shayanthan et al., 2022). The use of SynComs represents a paradigm shift in agricultural microbiome research, moving from single-microbe applications to a more holistic approach that leverages the synergistic interactions within microbial communities (Ray et al., 2020).

The primary objective of this systematic review is to explore the design, functionality, and field performance of synthetic microbial communities in the context of sustainable agriculture. The review aims to address the following research questions:

- 1) What are the current strategies and methodologies for designing synthetic microbial communities for agricultural applications?
- 2) How do synthetic microbial communities enhance plant growth, nutrient uptake, and stress resilience compared to traditional microbial inoculants?
- 3) What are the challenges and limitations associated with the field application of synthetic microbial communities?
- 4) How can synthetic microbial communities be optimized for different crops, soil types, and environmental conditions to ensure consistent performance and sustainability?

By systematically reviewing the existing literature, this paper seeks to provide a comprehensive understanding of the potential of synthetic microbial communities in promoting sustainable agricultural practices and to identify future research directions in this emerging field.

1 Design of Synthetic Microbial Communities

1.1 Principles of microbial community design

1.1.1 Criteria for selecting microbial strains

The selection of microbial strains for synthetic communities is crucial for ensuring the desired functionality and stability of the community. Criteria for selection include the ability of strains to robustly colonize the plant environment, their prevalence throughout plant development, and their specific beneficial functions for plants, such as enhancing crop resiliency under stressful conditions (Souza et al., 2020). Additionally, the compatibility of strains in terms of metabolic exchanges and the ability to form stable interactions are important considerations (Zuñiga et al., 2020; Karkaria et al., 2021).

1.1.2 Genetic engineering and synthetic biology approaches

Advances in synthetic biology and genetic engineering have enabled the design of microbes with defined and controllable properties, facilitating the creation of multispecies communities with specific functions. Techniques such as quorum sensing and the engineering of metabolic pathways are employed to control intercellular interactions and ensure the robustness and stability of the community (Johns et al., 2016; Karkaria et al., 2021). The use of computational models to predict and optimize these interactions is also a key component of the design process (Thommes et al., 2018; Zuñiga et al., 2020).

1.2 Tools and techniques for community assembly

1.2.1 Co-culture and co-evolution methods

Co-culture methods involve growing multiple microbial strains together under controlled conditions to promote beneficial interactions and co-evolution. This approach can help in identifying and selecting strains that work well together and can sustain each other's growth through metabolic exchanges (Zuñiga et al., 2020; Liang et al., 2022). Co-evolution methods further refine these interactions by allowing the community to adapt over time, enhancing its stability and functionality (Zomorodi and Segrè, 2016).

1.2.2 Computational modeling and simulation

Computational tools play a significant role in the design and optimization of synthetic microbial communities. Techniques such as Bayesian methods, mixed-integer linear programming, and advanced optimization algorithms

are used to model metabolic interactions and predict the most robust community compositions (Thommes et al., 2018; Karkaria et al., 2021). These models help in understanding the dynamics of microbial ecosystems and in identifying key interaction motifs that contribute to community stability (Zomorodi and Segrè, 2016; Choudhary and Mahadevan, 2022).

1.3 Case studies: Examples of successful synthetic microbial communities designed for agriculture

Several case studies highlight the successful design and application of synthetic microbial communities in agriculture. For instance, a model synthetic community of 16 soil microorganisms was developed to promote plant growth and health, demonstrating high reproducibility and stability in both in vitro and in vivo experiments (Coker et al., 2022). Another example involves the pairing of phototrophic and heterotrophic microbes, such as *Synechococcus elongatus* and *Escherichia coli*, to create a community that supports sustainable growth and bioproduction (Zuñiga et al., 2020). These studies underscore the potential of synthetic microbial communities to enhance crop productivity and resilience under various environmental conditions (Souza et al., 2020; Liang et al., 2022).

By integrating principles of microbial ecology, genetic engineering, and computational modeling, researchers are making significant strides in the design and optimization of synthetic microbial communities for sustainable agriculture. These efforts promise to deliver innovative solutions for improving crop performance and resilience, ultimately contributing to more sustainable agricultural practices.

2 Functionality of Synthetic Microbial Communities

2.1 Plant-microbe interactions

2.1.1 Mechanisms of plant growth promotion

Synthetic microbial communities (SynComs) have been shown to enhance plant growth through various mechanisms. These include improved nutrient acquisition, hormonal stimulation, and the solubilization of essential nutrients such as nitrogen and phosphorus. For instance, plant growth-promoting rhizobacteria (PGPR) facilitate plant growth by regulating hormonal and nutritional balance, inducing resistance against plant pathogens, and solubilizing nutrients for easy uptake by plants (Vejan et al., 2016). Additionally, the use of SynComs constructed from root-associated microbes has demonstrated significant promotion of plant growth and nutrient acquisition under both nutrient-deficient and sufficient conditions (Wang et al., 2021). The application of SynComs can systemically regulate nutrient signaling networks at the transcriptional level, leading to increased representation of important growth pathways, especially those related to auxin responses (Wang et al., 2021).

2.1.2 Disease resistance and biocontrol

Microbial communities also play a crucial role in disease resistance and biocontrol. Beneficial microbes can suppress plant pathogens through various mechanisms, including the production of antimicrobial compounds, competition for resources, and induction of plant defense responses. For example, biocontrol microbes modulate plant defense mechanisms and deploy biocontrol actions to control plant pathogens (Rahman et al., 2018). The use of microbial inoculants, such as those from the genera *Bacillus*, *Pseudomonas*, and *Trichoderma*, has been shown to influence plant health and suppress plant pathogens (Berg, 2009). These biocontrol strategies offer promising and environmentally friendly alternatives to chemical pesticides, contributing to sustainable agriculture (Rahman et al., 2018).

2.2 Nutrient cycling and soil health

2.2.1 Nitrogen fixation

Nitrogen fixation is a critical process for plant growth, and certain microbes play a key role in this process. For instance, members of the bacterial genera *Azospirillum* and *Rhizobium* are well-studied examples of nitrogen-fixing bacteria that promote plant growth (Berg, 2009). These microbes convert atmospheric nitrogen into a form that plants can readily use, thereby enhancing soil fertility and reducing the need for synthetic nitrogen fertilizers.

2.2.2 Phosphorus solubilization

Phosphorus is another essential nutrient for plant growth, and its availability in the soil can be limited. Certain microbes have the ability to solubilize phosphorus, making it more accessible to plants. For example, PGPR can solubilize phosphorus, facilitating its uptake by plants and promoting growth (Vejan et al., 2016). The functional assembly of root-associated microbial consortia has also been shown to improve phosphorus acquisition in crops like soybean, leading to increased yield (Wang et al., 2021).

2.2.3 Organic matter decomposition

Microbial communities are involved in the decomposition of organic matter, which is essential for nutrient cycling and soil health. Effective microbes (EMs) such as select algal, fungal, bacterial, and yeast groups play a role in transforming organic matter into usable nutrients, enhancing soil water-holding capacity, and improving overall soil health (Naik et al., 2019). These processes contribute to the sustainability of agricultural systems by maintaining soil fertility and structure.

2.3 Environmental stress mitigation

2.3.1 Drought tolerance

Microbial communities can enhance plant tolerance to environmental stresses such as drought. Beneficial microbes help plants cope with water scarcity by improving root architecture, increasing water uptake, and producing stress-related hormones. For instance, the application of SynComs has been shown to enhance crop resiliency against stressful conditions, including drought (Souza et al., 2020). These microbial communities can activate plant responses that improve water use efficiency and mitigate the adverse effects of drought.

2.3.2 Salinity and heavy metal resistance

Salinity and heavy metal contamination are significant challenges in agriculture, and certain microbes can help plants tolerate these stresses. Effective microbes (EMs) secrete bioactive compounds like vitamins, hormones, and enzymes that stimulate plant growth and enhance tolerance to salinity and heavy metals (Naik et al., 2019). Additionally, the use of microbial inoculants can improve soil health and reduce the impact of these environmental stressors on crop productivity (Berg, 2009).

In summary, synthetic microbial communities offer a promising approach to optimizing plant growth, nutrient cycling, and environmental stress mitigation in sustainable agriculture. By harnessing the beneficial traits of plant-associated microbes, these communities can enhance crop productivity and resilience, contributing to more sustainable and efficient agricultural systems.

3 Field Performance of Synthetic Microbial Communities

3.1 Laboratory vs. field conditions

Synthetic microbial communities (SynComs) have shown promising results in controlled laboratory settings, where environmental variables can be tightly regulated. However, translating these successes to field conditions presents several challenges. Laboratory conditions often fail to replicate the complexity and variability of natural environments, leading to discrepancies in performance when SynComs are applied in the field (Souza et al., 2020; Trivedi et al., 2021; Shayanthan et al., 2022).

One major challenge is the inconsistency in microbial colonization and persistence in the field. Factors such as soil type, climate, and interactions with native microbial communities can significantly influence the effectiveness of SynComs (Ke et al., 2020; Karkaria et al., 2021). Additionally, environmental stressors such as drought, temperature fluctuations, and nutrient availability can impact the stability and functionality of these communities (Choudhary and Mahadevan, 2022; Martins et al., 2023).

3.2 Case Studies and field trials

3.2.1 Review of field trial results

Several field trials have been conducted to evaluate the performance of SynComs in agricultural settings. For instance, a study demonstrated that a SynCom designed to enhance plant growth under drought conditions showed variable results across different field sites, highlighting the influence of local environmental factors (Souza et al., 2020; Shayanthan et al., 2022). Another trial focused on a SynCom aimed at improving nitrogen fixation in legumes, which achieved significant yield improvements in some locations but not others, again underscoring the importance of site-specific conditions (Trivedi et al., 2021; Coker et al., 2022).

3.2.2 Factors influencing field performance

The performance of SynComs in the field is influenced by a multitude of factors. Soil type plays a crucial role, as it affects microbial colonization, nutrient availability, and water retention (Ke et al., 2020; Shayanthan et al., 2022). Climate conditions, including temperature and precipitation patterns, also impact the stability and activity of SynComs (Choudhary and Mahadevan, 2022; Martins et al., 2023). Additionally, the presence of native microbial communities can either support or hinder the establishment of introduced SynComs, depending on the nature of microbial interactions (Liu et al., 2019; Karkaria et al., 2021).

3.3 Monitoring and evaluation

3.3.1 Methods for assessing the impact and sustainability of synthetic communities

To assess the impact and sustainability of SynComs in the field, several monitoring and evaluation methods are employed. High-throughput sequencing and metagenomics are commonly used to track changes in microbial community composition and function over time (Trivedi et al., 2021; Coker et al., 2022). Additionally, soil and plant health metrics, such as nutrient content, plant growth rates, and yield, are measured to evaluate the agronomic benefits of SynCom application (Souza et al., 2020; Shayanthan et al., 2022).

3.3.2 Long-term performance and stability

Long-term performance and stability of SynComs are critical for their success in sustainable agriculture. Studies have shown that while some SynComs can maintain their beneficial effects over multiple growing seasons, others may lose functionality due to environmental pressures and microbial community shifts (Ke et al., 2020; Martins et al., 2023). Continuous monitoring and adaptive management strategies are essential to ensure the long-term stability and effectiveness of SynComs in the field (Liu et al., 2019; Choudhary and Mahadevan, 2022).

By addressing these challenges and leveraging advanced monitoring techniques, the potential of SynComs to enhance sustainable agricultural practices can be fully realized.

4 Challenges and Future Directions

4.1 Technical challenges

4.1.1 Scalability and reproducibility

One of the primary technical challenges in optimizing synthetic microbial communities (SynComs) for sustainable agriculture is ensuring scalability and reproducibility. The complexity of microbial interactions and the variability of environmental conditions can lead to inconsistent results when scaling up from laboratory to field applications. For instance, maintaining community diversity and stability over time is a significant hurdle, as different microbial species have varying growth rates and environmental requirements (Coker et al., 2022). Additionally, the reproducibility of SynComs is often compromised due to the lack of standardized model systems and efficient approaches for building these communities (Coker et al., 2022). The development of robust, reproducible model communities, such as those that can be cryopreserved and easily disseminated, is crucial for advancing this field (Coker et al., 2022).

4.1.2 Regulatory and biosafety concerns

The deployment of synthetic microbial communities in agricultural settings also raises regulatory and biosafety concerns. The potential for horizontal gene transfer and the unintended ecological impacts of introducing engineered microbes into the environment necessitate stringent biosafety and biocontainment strategies (Ke et al., 2020). Regulatory frameworks must evolve to address these concerns, ensuring that SynComs are safe for both the environment and human health. Strategies such as the use of non-model bacteria and the development of biosecurity measures are essential to mitigate these risks (Ke et al., 2020).

4.2 Knowledge gaps

4.2.1 Understanding complex microbial interactions

Despite significant advances in microbiome research, there remain substantial knowledge gaps in understanding the complex interactions within microbial communities and between microbes and their plant hosts. The intricate web of interactions that drive recognition, recruitment, and colonization of plant-associated microbes is not yet fully understood (Trivedi et al., 2021). Integrating multi-omic approaches, high-throughput culturing, and computational biology can provide deeper insights into these interactions, but more research is needed to translate this knowledge into practical applications (Trivedi et al., 2021).

4.2.2 Long-term ecological impacts

Another critical knowledge gap is the long-term ecological impact of introducing synthetic microbial communities into agricultural ecosystems. While SynComs have shown promise in enhancing crop productivity and resilience, their long-term effects on soil health, native microbial communities, and overall ecosystem stability are not well-documented (Shayanthan et al., 2022). Understanding these impacts is essential for developing sustainable agricultural practices that do not compromise environmental integrity.

4.3 Future research priorities

4.3.1 Emerging technologies and approaches

Future research should focus on leveraging emerging technologies and approaches to overcome the current challenges in SynCom optimization. Advances in gene editing tools, such as CRISPR, can be used to engineer microbial inoculants with specific beneficial traits (Qiu et al., 2019). Additionally, computational methods, including machine learning and artificial intelligence, can enhance the screening and identification of beneficial microbes, as well as the design of stable and effective SynComs (Souza et al., 2020; Martins et al., 2023). These technologies can help tailor SynComs to possess traits for robust colonization, prevalence throughout plant development, and specific beneficial functions for plants (Souza et al., 2020).

4.3.2 Multidisciplinary collaborations

Addressing the complex challenges associated with SynComs requires multidisciplinary collaborations that bring together expertise from synthetic biology, systems biology, microbial ecology, and agricultural sciences (Johns et al., 2016). Transdisciplinary research efforts and cross-training of scientists from diverse fields are essential for translating microbiome knowledge into real-world agricultural solutions (Trivedi et al., 2021). Collaborative efforts can also facilitate the development of standardized protocols and frameworks for SynCom research, enhancing reproducibility and scalability (Coker et al., 2022).

In conclusion, optimizing synthetic microbial communities for sustainable agriculture presents several technical challenges and knowledge gaps that need to be addressed through future research. By leveraging emerging technologies and fostering multidisciplinary collaborations, the potential of SynComs to enhance crop productivity and sustainability can be fully realized.

5 Concluding Remarks

The research on synthetic microbial communities (SynComs) has demonstrated significant potential in enhancing crop resilience and productivity. Key findings indicate that SynComs can be tailored to possess traits for robust colonization and specific beneficial functions for plants, leveraging computational methods such as machine learning to optimize microbial combinations. Additionally, the development of reproducible and tunable SynComs has provided new insights into microbial ecology, enabling the study of plant-microbe interactions under controlled conditions. The integration of phototrophic and heterotrophic microbes has shown promise in creating sustainable growth environments, highlighting the importance of selecting appropriate microbial partners.

The application of SynComs in agriculture holds significant implications for sustainable farming practices. By enhancing plant growth, nutrient use efficiency, and stress tolerance, SynComs can reduce the reliance on chemical fertilizers and pesticides, thereby minimizing environmental impact. The ability to design microbial communities that can adapt to various environmental conditions ensures that crops remain resilient against climate change and other stressors. Furthermore, the use of SynComs can lead to more efficient resource use, promoting sustainable agricultural practices that are essential for feeding a growing global population.

Future research should focus on developing standardized model systems for SynComs, including comprehensive microbial culture collections and reference genomes. It is crucial to elucidate the functional mechanisms of plant-microbe interactions and define core microbiomes to enhance the predictability and stability of SynComs in field conditions. Additionally, interdisciplinary collaboration among researchers, industry, and farmers is essential to translate laboratory findings into practical agricultural applications. Implementing advanced computational tools and optimization algorithms will further refine the design and functionality of SynComs, ensuring their effectiveness in diverse agricultural settings.

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.

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