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AI-DRIVEN PLANT MICROBIOME ENGINEERING FOR CLIMATE-RESILIENT AGRICULTURE: EMERGING STRATEGIES, APPLICATIONS AND FUTURE PERSPECTIVES

Namrata B. Kadamdhad

Lady Amritbai Daga College for Women of Arts, Commerce and Science, Nagpur, Maharashtra, India

Corresponding author E-mail: namratabkadamdhad@gmail.com

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Abstract:

Climate change is increasing the frequency and intensity of drought, heat stress, soil salinity, flooding and plant diseases, threatening agricultural productivity and food security. Plant-associated microbiomes, comprising bacteria, fungi, archaea and other microorganisms inhabiting the rhizosphere, phyllosphere and internal plant tissues, play important roles in nutrient acquisition, plant growth, disease suppression and stress adaptation. However, conventional microbial inoculation approaches frequently demonstrate inconsistent performance because of environmental variability, microbial competition and limited persistence under field conditions. Artificial intelligence (AI), particularly machine learning, deep learning and network-based modelling, offers new opportunities to analyse complex microbiome datasets and predict plant–microbe–environment interactions. When integrated with metagenomics, transcriptomics, metabolomics, high-throughput phenotyping and synthetic microbial communities, AI can support the rational selection and design of microbial consortia suited to particular crops and climatic conditions. This review examines the biological foundations of plant microbiome engineering, major AI-driven approaches, potential applications in climate-stressed agriculture, and the challenges associated with field implementation. A conceptual framework integrates microbiome discovery, computational prediction, experimental validation and precision deployment. AI-assisted microbiome engineering supports sustainable agriculture; practical effectiveness depends on reliable datasets, ecological stability, biosafety and validation.

Keywords: *Artificial Intelligence, Plant Microbiome, Microbiome Engineering, Climate-Resilient Agriculture, Machine Learning, Synthetic Microbial Communities, Plant Growth-Promoting Microorganisms.*

1. Introduction

Climate change is creating increasingly complex challenges for agricultural systems through rising temperatures, irregular rainfall, prolonged droughts, soil salinisation and the emergence of new pest and disease pressures.

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These stresses can disrupt plant metabolism, nutrient availability, root development and reproductive processes, resulting in reduced crop productivity and yield stability. Sustainable adaptation therefore requires approaches that improve plant resilience while reducing excessive dependence on chemical fertilisers and pesticides.

Plant-associated microorganisms constitute an important component of agricultural ecosystems. The rhizosphere, phyllosphere and endosphere harbour microbial communities that influence plant nutrition, development, immunity and environmental adaptation. Beneficial microorganisms, including plant growth-promoting rhizobacteria (PGPR), arbuscular mycorrhizal fungi and endophytic bacteria, can facilitate nutrient acquisition, regulate plant hormones and suppress pathogens. Nevertheless, their effects depend on host genotype, soil properties, climatic conditions and interactions with resident microbial communities (1, 2).

Traditional microbiome management commonly relies on isolating beneficial microorganisms, testing their individual traits and applying selected strains as bioinoculants. Although successful in some settings, this approach does not always produce consistent field-level outcomes because microbial performance depends on complex ecological interactions. Recent advances in artificial intelligence and multi-omics technologies provide opportunities to move from empirical microbial selection towards predictive microbiome engineering (3, 4).

This review discusses how AI can support the identification, design and deployment of plant-associated microbial communities for climate-resilient agriculture, with particular emphasis on drought, heat and salinity tolerance, nutrient-use efficiency and sustainable crop management.

2. Plant microbiome and climate resilience

The plant microbiome consists of microorganisms and their associated functional potential within plant-associated habitats. Its contribution to climate resilience depends not only on microbial diversity but also on the functions expressed by microbial communities under particular environmental conditions.

2.1 Drought and heat stress tolerance

Certain beneficial microorganisms can improve plant performance under water deficit by influencing root architecture, producing extracellular polymeric substances, modulating phytohormone signalling and improving water-use efficiency. Some PGPR produce the enzyme 1-aminocyclopropane-1-carboxylate (ACC) deaminase, which can reduce stress-associated ethylene accumulation in plants. Other microorganisms produce compatible solutes or stimulate antioxidant defence pathways.

Heat stress can disrupt protein stability, photosynthesis and membrane function. Microbial associations may support plant adaptation through altered hormone signalling, improved nutrient availability and modulation of stress-response pathways. However, these benefits are strain-specific and must be demonstrated under relevant environmental conditions rather than assumed from laboratory traits alone (1, 2).

2.2 Salinity and nutrient stress

Salinity reduces plant water uptake and can cause sodium toxicity and nutrient imbalance. Salt-tolerant microbial strains may improve root development, regulate ion balance and produce metabolites that contribute to plant stress responses. Similarly, phosphate-solubilising microorganisms can increase the availability of otherwise poorly accessible phosphorus, while selected diazotrophic microorganisms contribute biologically fixed nitrogen. These functions may support nutrient-use efficiency and reduce reliance on some external agricultural inputs. Their effectiveness, however, depends on soil chemistry, microbial survival, crop requirements and interactions with native communities.

2.3 Disease resistance and soil health

Beneficial microorganisms may suppress plant pathogens through competition, antimicrobial metabolites, siderophore production and induction of plant defence responses. Diverse and functionally complementary microbial communities may also contribute to soil nutrient cycling and ecosystem stability.

The relationship between microbial diversity and resilience is not universally linear. A highly diverse community is not necessarily beneficial in every context; functional composition, interaction structure and stability under stress are also important considerations (1, 2).

3. Role of artificial intelligence in plant microbiome engineering

AI can identify complex patterns in microbiome datasets that may be difficult to detect using conventional statistical approaches. Its value lies in generating testable predictions, prioritising candidate microorganisms and integrating biological information with environmental and agronomic data.

3.1 Machine learning for microbial selection

Machine-learning algorithms, including random forests, support vector machines, gradient-boosting methods and neural networks, can be trained using microbial abundance, functional gene profiles, soil parameters, weather conditions and plant phenotypic measurements.

For example, a model could estimate whether a microbial community is associated with improved maize performance under drought by combining microbiome profiles with soil moisture, temperature, root traits and biomass measurements. Candidate microorganisms identified by the model would subsequently require laboratory and field validation.

An essential limitation is that predictive accuracy within a training dataset does not guarantee reliable performance in new soils, crop varieties or climatic regions. External validation and appropriate experimental design are therefore indispensable (3, 4).

3.2 Multi-omics data integration

Microbiome engineering increasingly uses complementary molecular datasets:

- Metagenomics: Identifies microbial taxa and their potential functional genes.
- Metatranscriptomics: Examines microbial gene expression under particular conditions.
- Metabolomics: Characterises metabolites involved in plant–microbe interactions.
- Transcriptomics: Identifies plant gene-expression responses to microbial association and environmental stress.
- Phenotyping: Measures traits such as root architecture, biomass, photosynthetic performance and yield.

AI-based integration of these datasets can help distinguish microbial presence from actual functional activity. For instance, detecting a gene associated with nutrient acquisition does not necessarily demonstrate that the gene is expressed or that the plant receives a measurable benefit. Integrating functional and phenotypic evidence can improve biological interpretation (3, 4).

3.3 Microbial interaction networks

Plant microbiomes contain cooperative, competitive and context-dependent relationships. Network analysis can identify candidate keystone taxa, potential interactions and community structures associated with desirable plant traits.

AI-assisted network models may help prioritise microbial combinations with complementary functions, such as nutrient mobilisation, stress mitigation and pathogen suppression. However, co-occurrence does not establish direct biological interaction. Candidate relationships require experimental testing, including controlled co-culture studies and plant-based validation.

3.4 Digital prediction and precision agriculture

Combining microbiome information with weather forecasts, remote sensing, soil sensors and crop growth measurements could enable decision-support systems that identify when and where particular microbial treatments are most likely to be effective.

In future applications, digital models could compare alternative microbial formulations and management strategies under simulated drought, heat or salinity scenarios. Such predictions should be treated as decision-support tools rather than substitutes for field experiments.

4. AI-driven strategies for microbiome engineering

Microbiome engineering aims to alter microbial community composition or function to achieve defined plant and soil outcomes. AI can strengthen this process through a design–build–test–learn cycle.

4.1 Synthetic microbial communities

Synthetic microbial communities (SynComs) are deliberately assembled collections of selected microorganisms designed to perform complementary functions. Instead of relying on a single strain, a SynCom may combine organisms involved in nutrient acquisition, root colonisation, stress mitigation and disease suppression.

AI can help rank candidate strains using functional characteristics, genomic information, environmental tolerance and compatibility data. Subsequent experiments determine whether the predicted combination is stable and beneficial.

An important design principle is functional complementarity rather than simply increasing the number of strains. Excessive complexity may introduce competition, unpredictable interactions and formulation difficulties. Community composition should therefore be optimised experimentally for each crop–soil–climate context (3, 5).

4.2 Host-mediated microbiome engineering

Plants influence microbial recruitment through root exudates, including sugars, organic acids, amino acids and specialised metabolites. Differences in plant genotype and physiological status can therefore shape the microbial communities associated with roots.

AI-assisted analysis of host genetic information, root-exudate profiles and microbiome composition may help identify plant traits associated with beneficial microbial recruitment. Such information could support crop breeding strategies that combine desirable plant characteristics with microbiome responsiveness.

This approach recognises that microbiome engineering does not always require modifying microorganisms directly; improving the plant's capacity to recruit and maintain beneficial native microbes may also be useful (2, 5).

4.3 Functional and genetic engineering

Synthetic biology and microbial genetic engineering may eventually enable more precise modification of microbial traits, including nutrient utilisation, stress tolerance and metabolite production. Computational models can help identify candidate pathways and predict metabolic trade-offs.

Nevertheless, engineered microorganisms require careful assessment of genetic stability, environmental persistence, unintended ecological effects and gene transfer. Regulatory requirements and biosafety considerations must guide development and deployment. AI predictions alone cannot establish environmental safety.

4.4 Formulation and precision delivery

Even a promising microbial strain can fail if it does not survive storage, application or establishment in the field. Seed coatings, suitable carrier materials, encapsulation and appropriate application timing may improve delivery and persistence.

AI can integrate formulation properties, soil moisture, temperature and crop-development stage to help identify suitable delivery strategies. These approaches require practical validation under local agricultural conditions.

5. Applications in climate-resilient agriculture

Drought-prone agriculture: AI can prioritise microbial communities associated with root development, water-use efficiency and stress-response regulation. Their benefits should be assessed using plant water status, biomass, yield and microbial persistence.

Heat-stressed cropping systems: Predictive models may identify microorganisms that remain functional under elevated temperatures and support plant physiological performance. Screening must include realistic temperature fluctuations rather than constant laboratory conditions alone.

Saline soils: Integrated analysis of microbial traits, soil electrical conductivity, plant ion balance and growth responses may help identify suitable salt-tolerant bioinoculants.

Nutrient-deficient soils: Models can combine microbial nutrient-mobilisation traits with soil chemistry and crop nutrient requirements to prioritise candidate inoculants and improve fertiliser-management decisions.

Integrated disease management: Microbial community profiles and environmental data can support disease-risk prediction and the selection of candidate biocontrol communities. AI-assisted microbiome interventions should complement, rather than automatically replace, established disease-management practices.

Across these applications, the central opportunity is to match microbial functions to specific environmental stresses and agricultural conditions rather than expecting a universal inoculant to perform equally well in every ecosystem (1, 3, 5).

6. Challenges and future perspectives

Despite substantial promise, several barriers limit the practical implementation of AI-driven microbiome engineering.

- Data quality and standardisation: Microbiome datasets differ in sampling procedures, sequencing platforms, taxonomic resolution and environmental metadata. Inconsistent datasets can generate biased predictions.
- Causality and interpretability: AI may identify statistical associations without revealing the biological mechanisms responsible for a plant response. Explainable models and mechanistic experiments are needed to establish causality.
- Field variability: Soil type, crop genotype, rainfall, temperature and agricultural management influence microbial establishment. Multilocation and multiseason trials are essential for determining whether laboratory findings generalise to farms.

- Ecological stability: Introduced microorganisms may fail to persist or may interact unpredictably with resident communities. Long-term monitoring should examine microbial establishment, functional outcomes and possible ecological displacement.
- Economic accessibility: Sequencing, computing and advanced formulations may be costly for small-scale farmers. Affordable diagnostics, locally adapted microbial products and accessible decision-support tools are necessary for equitable adoption.
- Biosafety and governance: Environmental risk assessment, genetic stability, potential horizontal gene transfer and appropriate regulatory review must be addressed, particularly for genetically engineered microorganisms.

Future research should prioritise standardised datasets, explainable AI, experimentally validated synthetic communities and independent field trials. Models should be evaluated using held-out locations and seasons, with transparent reporting of uncertainty and negative results. Success should be measured not only by microbial abundance or plant biomass but also by yield stability, resource-use efficiency, soil health, environmental safety and affordability.

7. Proposed conceptual framework

A practical AI-driven microbiome engineering pipeline can be organised into six interconnected stages:

- Data collection: Gather microbiome, multi-omics, soil, climate and crop-phenotype information.
- AI-based discovery: Identify candidate microbial taxa, functional traits and environmental predictors associated with resilience.
- Community design: Select compatible microbial strains and develop candidate synthetic communities.
- Experimental validation: Test candidates under controlled drought, heat, salinity or disease conditions.
- Field deployment: Evaluate formulation, application method, persistence and performance across representative agricultural environments.
- Feedback and optimisation: Use field observations to refine predictions and improve subsequent community designs.

This framework is proposed as a synthesis of existing approaches, not as a newly validated experimental system. Its effectiveness must be established through reproducible studies and field-based evaluation.

8. Conclusion

AI-driven plant microbiome engineering represents an emerging approach to climate-resilient agriculture by integrating microbial ecology, multi-omics, predictive modelling and precision crop management. Machine learning can help prioritise beneficial microorganisms, investigate plant–microbe interactions and design synthetic microbial communities with complementary functions. These strategies may contribute to improved nutrient acquisition, stress adaptation and sustainable crop production.

However, reliable agricultural outcomes will require more than computational prediction. Microbial functions must be experimentally confirmed, community stability assessed and benefits demonstrated across different soils, crops and climatic conditions. Transparent modelling, ecological monitoring, biosafety assessment and farmer-accessible technologies will be essential for responsible implementation. Integrating AI with microbial ecology and rigorous field research could help transform microbiome management from empirical inoculation into a more predictive component of climate-smart agriculture.

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