BIO Web of Conferences **233**, 02013 (2026) https://doi.org/10.1051/bioconf/202623302013
ICABB 2026

STRESS-RESILIENT MICROBES FOR CLIMATE- SMART AGRICULTURE: FROM ECOLOGICAL ADAPTATION TO AI GUIDED MICROBIOME ENGINEERING.

Anurag Rawal[1], *Krishna* Sundari Sattiraju*

Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sector-62, 201309, Noida, Uttar Pradesh

Email: s.krishna.sundari@mail.jiit.ac.in

Abstract. Drought and salinity caused by climate change are growing risks to the world food supply, triggering increased urgency to find new sustainable solutions for strengthening crop resistance. Smart microbiome engineering is emerging as an option that integrates next-generation bioformulations, and artificial intelligence (AI) to develop specific microbial solutions to suit agroecosystems that are prone to stress. This review outlines mechanistic basis of microbial drought and salinity tolerance such as osmolyte biosynthesis, ACC deaminase activity, EPS-mediated soil aggregation, antioxidant regulation, and synergistic interactions between keystone taxa, for collectively regulating plant physiological and molecular responses to stress. The paper highlights how recent advances of biotechnology and AI-based computational tools permit predictive modelling of plant-microbe interactions, microbial compatibility, and consortium stability. At the same time, the significance of bioformulation science, including encapsulation, controlled-release polymers, nanocarriers, and seed-coating technologies, in enhancing microbial viability and performance in the field was thoroughly analysed. The manuscript conceptualises a combination of mechanistic understanding, computational analytics and formulation innovations for smart microbiome engineering providing a scalable, precision-based model that provides climate-resilient agricultural solutions.

Keywords: Microbiome engineering, drought tolerance, salinity tolerance, bioformulations, artificial intelligence, climate-resilient agriculture.

1. Introduction

Climate change has augmented environmental limits on agriculture in terms of rising temperatures, changed precipitation patterns, and high levels of atmospheric CO_2, and rising rate of extreme weather events; all of which has direct consequences on the soil microbial processes and ecosystem functions. Climate-smart agriculture (CSA) has been characterized as a multi-dimensional approach to be able to maximize agricultural productivity, establish resilience, and decrease greenhouse gas emissions due to climate change conditions [1]. Semi-arid ecosystems have shown experimentally that long-term drought and warming decreased the abundance of the soil microbial biomass and the enzyme activity up to 82 and 87 percent, respectively, indicating the sensitivity of soil biological processes to climatic variability [2]. Increased CO_2 and warming in the atmosphere were found to change the processes of nitrogen cycling and carbon transformation in grassland systems indicating climate-induced feedbacks between microbial communities and ecosystem activities [1]. According to projections, global crop yields will drop by about a quarter to a third in the mid-century given extreme weather conditions in the form of rising temperatures, drought, and salinity, which exposes the food security to strains [3]. Multifactorial combinations of stress reduced microbial diversity and largely shifted community composition and showed destabilization of plant-microbiome systems under multiple environmental pressures [4]. Despite the significant progress made in breeding of crops as well as agronomic intensification, the stability of yields is susceptible to climatic perturbation. According to the observational studies, global yield loss of about 3.8% in maize and 5.5% in wheat due to the warming patterns have already occurred due to the global climatic changes. Greenhouse gas emissions, soil degradation, and externalities on the environment have been linked to agricultural intensification relying on synthetic fertilizers and pesticides [5]. The high use of chemical fertilizers interferes with the population of soil microbes, suppresses beneficial taxa with beneficial functions, and worsens the physicochemical characteristics of soils, undermining the long-term health of the soil [6]. The experiments of long-term management prove that farming activities have strong effects on the microbial population of the soil and its structure, which makes microbiomes particularly sensitive to anthropogenic contributions [7]. All these observations show that genetic enhancement and chemical augmentation of nutrition are not sufficient to protect crop yield [8].

The microbial communities related to soil and plants are irreplaceable factors of ecosystem functions, which include processes like nutrient recycling, carbon conversion and stabilization, greenhouse gas control and maintenance of agricultural processes [1]. Rhizobacteria that promote growth of plants help them to access nutrients, synthesize phytohormones, and develop resistance to the abiotic stresses such as drought and salinity [5]. The osmolyte, antioxidant system and phytohormonal modulation of microorganisms leads to tolerance to stress and water-use efficiency in plants during drought [3]. Microbial associations are also able to improve nutrient utilization efficiency and have been shown to sustain crop productivity and also minimise reliance on artificial inputs [9]. Nevertheless, drastic climatic fluctuations greatly modify the abundance of microbes, enzymes, and the structure of the community, which constrain the predictability of advantageous microbial operations in the field [2]. A more ecological insight and accurate manipulation of intricate microbial communities over one-strain inoculants are thus required to engineer an effective microbiome [4]. The soil microbiomes represent the most extensive source of microbial biodiversity and are also organized by the environmental factors of soil pH, organic carbon, and availability of oxygen. Microbial communities control soil mechanical stability, pore connectivity, hydrological pathways and long-term carbon stabilization, which influence ecosystems functioning besides nutrient provisions. These multi-purpose properties show that microbes should be viewed as part of an ecological infrastructure of agroecosystems, as opposed to isolated agricultural inputs [10]. The concept of repositioning microbes as community-level adaptive systems embedded within soil-plant networks corresponds to the ideals of climate-smart agriculture. They assists in building resilient and sustainable production systems in the times of climate change [1].

2. Climate-driven abiotic stresses as ecological filters

The role of abiotic stresses caused by climate is that of powerful ecological filters that affect the assembly, diversity, and composition of soil and plant-associated microbial communities

(Figure 1). The structure of microbial communities in spatial gradients is brought about by climatic variables, including temperature, precipitation, and soil chemistry [11]. Drought and water scarcity have been cited as the major stressors that restrict the survival and activity of microbes in the arid and semi-arid ecosystems, and therefore, influence community-assembly processes [12].

2.1 Drought: Water Potential and Carbon Constriction.

Drying and drought decrease soil water potential and place severe physiological limits on the microbial metabolism and nutrient fluxes. While soil moisture at -10 Mpa under experimental manipulation did not cause significant shifts in soil microbial biochemical pools, it led to the increase of microbial biomass carbon by about 35 percent and the decrease of total amino acid content, which is an indication of cellular resource reallocation under osmotic stress. Osmotic acclimation proved to be energetically expensive, as drying treatments induced about three times more exopolymeric substances and about 1.5 times more microbial biomass carbon, especially when soils were amended with labile C and N, which showed that soils with improved osmotic acclimation had higher carbon content. The relative abundance of specific amino acids related to osmotic adjustment, such as taurine, glutamine, tyrosine, and phenylalanine, rose under extreme drying (-101 MPa) and indicated biochemical drought-responses implemented over a period [13]. In dry ecosystems, long-term drought serves as a prevailing ecological filter determining the species composition and functional features of the microbial communities. The scarcity of water along with frequent drying-rewetting cycles favor wide-scale dormancy as a survival mechanism in desert soils and therefore keeps a large pool of microbial genetic reserves in extreme water limitations. The Bacillota (Firmicutes) can form endospores, allowing it to persist under desiccation and is reassembled into community composition that is more favorable to stress-tolerant taxa during extended droughts. Rapid metabolic pulses and growth bursts in previously dormant taxa are then induced by episodic rainfall events and illustrate a close interaction between water pulses and microbial functional dynamics [12]. Experimental studies that manipulate growth chambers demonstrated that the biota in soils develop more potent negative plant-soil interactions when functioning at their native climatic temperature and moisture regimes, which suggests that microbial communities are locally adapted to hydrological regimes. Compared to the colder treatments, warming minimized negative plant-soil feedback, which was likely explained by increased levels of microbial activity and nutrient cycling at higher temperatures [14]. Back at the continents, it was established that precipitation and temperature could be considered as the main predictors of bacterial and fungal community structure on sub-Saharan Africa, showing that hydroclimatic gradients were deterministically controlled by microbial diversity. Structural equation modelling also suggested a negative relationship between temperature rise and reduced precipitation and soil microbial biodiversity in particular areas, which is why intensified drought conditions were associated with possible biodiversity losses [11]. The microbial rearrangement of carbon to protective metabolites in response to drought has quantifiable ecosystem outcomes, and it is estimated that only a drought event can oxidatively discharge about 4-7% of forest-fixed photosynthetic carbon inputs in the process of osmotic adjustment [13]. All these data show that lower water potential acts as a powerful ecological and physiological filter that re-organizes microbial metabolism, community structure, and plant-soil interaction in response to climate change [12,13].

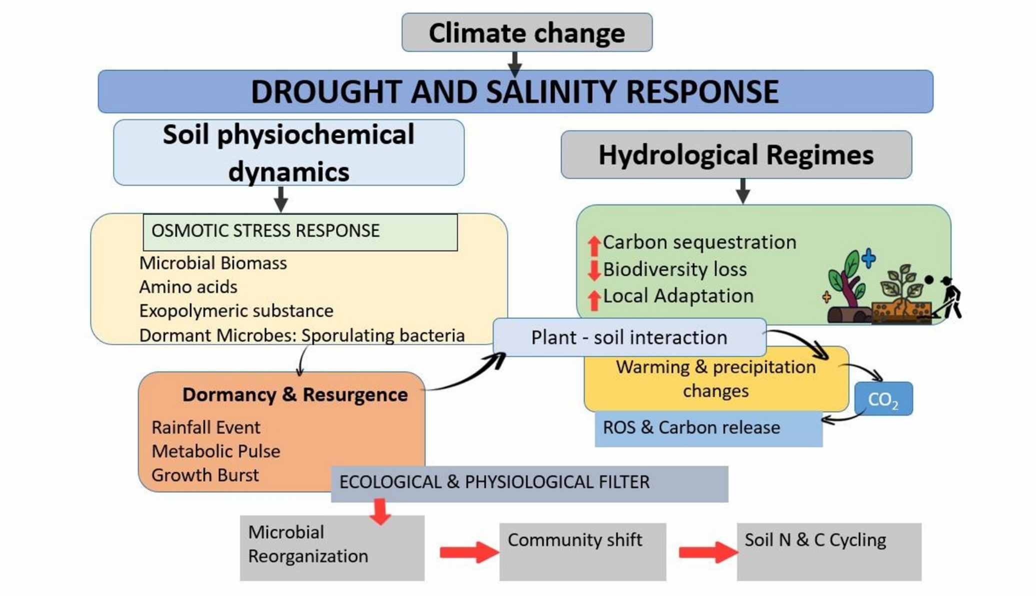

Fig. 1. Climate-driven drought and salinity responses as ecological and physiological filters shaping soil microbial dynamics and ecosystem functioning.

2.2 Salinity: Osmotic and Ionic Toxicity.

Salinity is one of the main abiotic limitations in arid and irrigated agro-ecosystems in which repeated flood irrigation cycles cause soil salinization and induration, and eventually lead to disruption of microbiome in desert agro-ecosystems. Such salinity-induced changes reduce the vital ecosystem services by changing the soil structure and increasing the abiotic constraints in hyper-arid conditions [12]. The chemical variables of the soil such as salinity and pH are powerful environmental filters that shape the composition of microbial communities by deterministic selection, as opposed to stochastic assembly. Macro-scale biogeographical studies indicate that soil physicochemical characteristics, particularly the relationship between pH and climatic factors are a major predictor of microbial diversity and a community structure throughout heterogeneous landscapes. Structural equation modeling adds to the fact that climatic factors that react with soil chemistry have significant impacts on the topsoil microbial biodiversity which supports the idea that abiotic gradients do not cause random compositional changes but instead structured phylogenetic turnover [11]. Adaptive mechanisms of microorganisms to osmotic stress include dormancy and endospore, which allow the survival of desiccation and extreme abiotic stress. Cellular integrity and metabolic activity is influenced by osmotic stress caused by changes in water potential, and membrane stability is impaired by ionic stress that results in cellular damage unless homeostasis is restored [15]. Increased abiotic stress conditions trigger deterministic selection in the context of soil composition and climate overpowering the neutral process of drift and dispersal and remodeling both abundant and rare microbial taxa. Simulations of bacteria in arid and semiarid soils under the condition of climate change further support the idea that changes in the physicochemical conditions of the soil significantly alter the bacterial diversity and communities, which creates an additional stress on the microbial assemblage [16].

Together, these studies confirm that, salinity, through its osmotic and ionic actions, and interaction with soil chemistry and climate, acts as an ecological deterministic filter and structures the assembly of microbial communities, phylogenetic turnover, and ecosystem functioning in arid and managed agricultural soils [11,12].

2.3 Interactions between heat and multi-stress.

Warming due to climate and precipitation pattern changes have been remaking the microbial community in soils along spatial gradients and have a deep-seated implication on how ecosystems operate (Figure 2). There has been empirical evidence that microbial communities contain endogenous functional legacies that persist even when instant environmental parameters are changed. The experiment work involving reciprocal transplant experiments across a climatic gradient in Southern California has shown that climate-dependent legacy effects on litter decomposition are apparent in microbial communities. These results imply that past temperature and moisturizing conditions leave long-lasting compositional and trait-related traces on microbial communities. Then, the remnant climatic conditions still influence ecosystem dynamics during the introduction of microbial communities to new environmental settings. Trait-based modelling also indicated that trade-offs at the community level between stress tolerance, resource acquisition and growth yield strategies organize microbial assembly across climate regimes, which supports the idea that warming does not only change diversity, but also distribution of functional strategies [17]. Climatic experiments that reproduce environmental conditions of humidification and warming in arid and semiarid soils prove that climate change influences the changes in the soil bacterial community significantly. Treatments in dry soils also result in lower bacterial diversity and severe restructuring of communities, dominated by Proteobacteria, Actinobacteria, and Planctomycetota. On the other hand, the semiarid soils have a more stable and intricate microbial community structure with the prevalence of Actinobacteria and Proteobacteria. These opposing reactions indicate gradual climate sensitivity to arid gradients, indicating that the dynamics of microbial communities are highly determined by the baseline moisture regimes . These results indicate that arid systems have a high density of specialised and sensitive microbial communities, and semiarid systems have a higher degree of structural stability in the context of simulated climate-change conditions [16]. The scale of large-scale biogeographical surveys in sub-Saharan Africa also indicates that climatic variables, in particular temperature and precipitation, are important predictors of soil microbiome structure, with structural equation modelling suggesting that high temperatures and low precipitation will adversely influence microbial biodiversity in the susceptible areas. This climate-microbiome interaction shows that warming and drying are deterministic filters that restructure biodiversity and can also potentially change productivity in an ecosystem [11]. Experiments on plant-soil feedback under climate-controllable treatments reveal that context-specific changes in the strength of plant-soil feedback can be caused by warming and altered precipitation, which have soil biota producing more negative feedbacks during the native climatic conditions and altered feedbacks during warmer climatic conditions. These findings show that climate change alters plant-microbiome interactions undermining pre existing co-adaptive relationships, hence affecting community stability and plant performance [14].

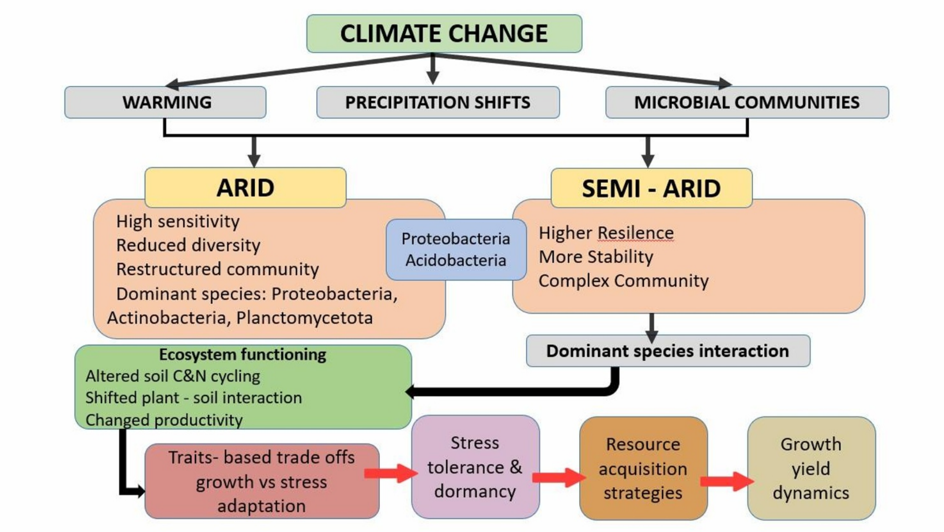

Fig.2. Climate warming and precipitation shifts restructure microbial diversity, functional strategies, and ecosystem processes across aridity gradients, with arid soils showing stress-dominated communities and semiarid soils exhibiting greater stability and resilience.

2.4 Community Collapse and Selection caused by Stress.

The extreme abiotic stress loads restructuring of microbial communities by facilitating strong environmental filtering, thus, selecting stress-tolerant taxa and reducing community complexity at the same time. In deserts, long-term drought and high temperature environments selectively favor taxa that can enter into dormancy and endospores, especially of the phylum Bacillota, a phenomenon that constitutes deterministic selection when faced with desiccation stress. Dormancy and sporation mechanisms maintain a genetic reservoir of microbes, but in the process produce phylogenetically clustered, stress-adapted assemblies in such harsh environments [12]. Past disturbances and repeated drought-wetting patterns have increased deterministic assembly on a smaller scale, leading to a decrease in phylogenetic diversity and shrinkage of the ecological niche scale in dry soils [13]. Sub-Saharan widespread surveys of the continent revealed that precipitation and temperature are the main predictors of soil bacteria and fungi communities, which highlights the role of strong climatic control over patterns of microbial diversity. Structural equation modeling also postulates that the warming temperature with reduction in precipitation will adversely affect biodiversity of microbes in various regions, and thus directly correlates climate change with the anticipated decrease in diversity [11]. Climate change simulations on arid and semiarid soils show that arid soils have a reduced bacterial diversity and a reorganized community composed of stress-adapted taxa, compared to semiarid soils, which have a comparatively more stable composition [16]. This comparison shows that increased aridity increases community sensitivity and solidifies the selection pressures by the environment. The osmotic control, oxidative stress control, and restoration of cellular homeostasis are also physiological mechanisms of fungal responses to stress, without which, restoration of cellular homeostasis decreases its fitness and causes high mortality, thus affecting the results of survival and diversity. These cellular limitations culminate into population and community scale effects and influence the persistence of microbes and their competition with extreme abiotic stress [15].

2.5 Stress Filtering: A Conceptualization of Microbial Assemblage.

The assembly of microbial communities is controlled by an interacting complex of deterministic selection forces and stochastic processes in which the accumulating environmental stress increases deterministic filtering in desert soil microbial communities. In hyper-arid environments, persistent water shortage creates an abiotic stress that selectively favors drought-tolerant taxa, leading to phylogenetic clustering and, thus, providing evidence that harsh environmental conditions serve as a filter on the composition of communities [12]. Structural equation modeling also estimated that temperature increase and reduced precipitation will have a negative effect on microbial biodiversity in particular areas of soil, thus choosing climate-change paths and increases filtering in the environment [11]. Reciprocal experiments of climate-manipulation revealed that arid soils with simulated humid regimes showed responses of particular microbial community structures with specific groups of bacteria and semiarid soils had more compositional stability along moisture gradients [16]. Complementary growth-chamber experiments showed that soil biota produced more negative plant-soil interactions in association with the native climatic temperature and moisture regimes, which provides evidence of climate dependent compositional legacies and local microbial adaptation [14]. Climate gradient simulations using traits showed that microbial communities have climate-sensitive legacies, which mediate decomposition processes, proving that exposure to the environment imposes limits on future ecosystem operation. Taken together, these results support the idea that environmental history explains microbial assembly and microbial functional outcomes during changing climate regimes [18].

3. Defining stress-resilient microbes

The most suitable contextualisation of stress-resistant microorganisms is in the paradigm of microbial community stability, which is to describe the complementary resistance and resilience characteristics that define the degree to which a community responds to disturbance and the speed at which it recovers after perturbation. The ability of the community to overcome disquiet is known as resistance and the ability to regain the former functional composition when the disturbance has stopped is known as resilience. As a result, stress resilience is the hallmark of microbial assemblages, and it implies the capacity to sustain the ecological functioning despite the environmental fluctuation, focusing on the continuation of the processes rather than the survival of the single taxa [19].

Traditionally, plant growth-promoting rhizobacteria are distinguished by the ability to increase the availability of nutrients, produce phytohormones, suppress phytopathogens, and stimulate plant growth through other processes, including nitrogen fixation and the synthesis of metabolites [20,21]. Such microorganisms have the capacity to regulate plant productivity through the up-regulation of genes and the increase of nutrient uptake efficacy [21]. Nevertheless, they tend to be less effective in heterogeneous field conditions due to the environmental stresses that reduce the survival and colonisation ability of microorganisms, causing uneven inoculant performance [22,23]. It means that the improvement of plant performance is not a sufficient factor in ensuring ecological sustainability and stability of agricultural soils [22].

In comparison, the ability to tolerate stress is characterized by stress-resilient microbes that have the capacity to survive and become metabolically active in a range of unfavorable environmental factors such as drought, salinity, inundation, and temperature extremes [22,24]. They are often core microorganisms, which are taxa that are consistently observed throughout spatial and environmental gradients, and are closely linked to the normal functioning of the stable ecosystem. The repeated appearance of these taxa in contrasting environments highlights inherent adaptive potential and ecological vigour and not opportunistic and temporary colonisation. Thus, resilience is defined by more than the plant growth stimulation and stabilization of plant-microbiome interactions in relation to varying conditions [24].

There are compositional and functional levels of microbial ecological resilience. Limited taxonomic change after the disturbance is referred to as community resistance, and recovery to the previous state of disturbance is referred to as resilience. Importantly, the stability of ecosystem functionality can occur despite changes in taxonomic composition due to microbial functional redundancy that can also allow different taxa to serve similar ecological functions [19]. It has been empirically shown that processes like nutrient cycling, stress reduction and plant defence can maintain themselves in even altered community composition. The disproportionate contribution of core microbial members to this stability is by maintaining a network of interactions that maintain functional outputs to the stress [24].

Host-level resilience is achieved through the concerted actions of the plant holobiont, where both plant and microbiome work as a unit of adaptive response. Stress tolerance is therefore a shared feature that results due to the co-evolutionary interactions between the host and its related microbiota, as opposed to an individual microbial feature [25]. Experimental and ecological studies have shown that plant microbiomes can regulate community assembly patterns and features of functionality in reaction to environmental disturbances including drought, warming and high CO_2 levels, thus, promoting host adaptability. This adaptative ability is facilitated by the changes in functional responses to stress and not a simple change in microbial abundance [18] .

Ecological analyses that are based on networks also indicate that some microbial taxa have disproportionate effects on community structure and ecosystem performance, thus leading to the demonstration of the presence of keystone microorganisms. These losses of taxa reduce the network strength and disrupt ecological processes with a highlighting structural and functional importance. Core taxa maintain the stability of the baseline, whereas rare or stress-selective taxa are activated by environmental stress and can offer dedicated functions to mitigate stress. Such microbial sub-communities can be selectively recruited in plants under stressful conditions, which increases the ability to cope with environmental challenges. This dynamic recruitment explains that resilience relies on dominating members that are persistently dominant as well as inducible rare biosphere components [24].

There is an overall indication that both steadily-occurring core taxa and inducible stress responsive populations make up stress-resilient microbes, which together maintain resistance, recovery ability, and functional persistence in plant-microbiome ecosystems that are perturbed [19]. They stabilize ecological networks and maintain the ecosystem processes and promote adaptive host responses in the framework of the holobiont. Therefore, their promoting purpose is not only the improvement of plant growth but also the preservation of an ecological balance in the context of environmental variability, i.e. it is a biological basis of climate-resistant agriculture [18,25].

4. Molecular & physiological mechanisms

The complexity of microorganisms living and functioning in drought and salinity is supported by coordinated physiological and molecular changes that occur at the level of osmotic regulation, redox homeostasis, ion equilibrium, hormonal regulation, and community reorganization, thus connecting the metabolic processes of microorganisms with plant stress responses (Figure 3) [26]. Drought causes extreme water potential and photosynthetic efficiency reductions, which result in oxidative stress because of the build up of reactive oxygen species (ROS), such as superoxide radicals, hydrogen peroxide, and hydroxyl radicals that damage lipids, proteins and nucleic acids; microbes associated with plants counteract this effect by inducing antioxidant systems and host biochemical pathway changes [27].

Osmotic adjustment is one of the key adaptations in water scarcity and salinity stress since both stresses alter the water potential homeostasis and ionic distribution at both cellular and molecular scales leading to growth repression and molecular damage [28]. Plant-related microorganisms also produce osmolytes including polyamines, amino acids, proline, and sugars in response to water limitation to provide cellular osmotic balance and increase plant survival during drought conditions [26]. Empirical data reveal that rhizosphere inhabiting microbes enhance water-use efficiency and nutrient absorption by plants during drought by the synthesis of osmolytes, such as proline and trehalose, which strengthens osmotic stabilization in the planta [3]. Microbial osmo-protection is also linked to the drought induced physiological reactions, including biofilm growth and compatible solutes synthesis that increase desiccation tolerance [27].

Extracellular polymeric substance (EPS) as well as biofilm formation are structural adjustments in which cells are buffered against dehydration and changes in the environment. The microbial responses to droughts include increased biofilm development, morphological modifications, and increased ability to survive under desiccation stress [27]. Its production leads to enhanced soils aggregation and stabilization, which impact the regulation of hydro and promotes the survival of microorganisms in drying soils [26]. Biofilm-forming microorganisms stabilize the rhizosphere microenvironment and thus improve the interaction between plants and microorganisms in variable moisture conditions [3].

Salinity stress has both osmotic and ionic toxicity, which changes ion homeostasis and disrupts metabolic stability. Changes in ion gradients in drought and salt stress conditions stimulate hyperosmotic signalling and abscisic acid-driven actions, highlighting the importance of ion transport and sequestration systems that are highly regulated [28]. Plant related microbes reduce ionic stress by regulating host ion transport pathways and sustaining osmoprotective signals, hence, and sustain cellular homeostasis under salinity. Another highly important part of microbial stress resistance is the oxidative stress mitigation. During the drought, ROS build-up impairs photosynthetic activity enzymes and membrane stability; microbial increases antioxidant enzyme activities such as catalase and peroxidases, mitigates oxidative stress, and maintains physiological functioning [27]. The activation of antioxidant defenses by microbes, as well as regulation of stress-responsive genes, helps to enhance tolerance in the case of water-deficiency.

Hormonal modulation is a form of integrative interface between microbial metabolism and plant signaling. Plant-related microorganisms maintain the phytohormonal balance, reducing stress-increasing ethylene levels with the help of activity of 1-aminocyclopropane 1-carboxylate (ACC) deaminase, and adjusting indole-3-acetic acid (IAA) and abscisic acid (ABA) signalling by reducing stress levels [26]. The microbes inhabiting the rhizosphere and phyllosphere niches are also known to modulate hormones and provide systemic resistance thus promoting plant resistance to drought and salinity.

It should also be noted that stress resilience is not an isolated property of individual cells but it is instead found in structured microbial consortia. The longitudinal analysis of rhizosphere microbiomes under the conditions of drought, salinity, and disease stress showed that core microbiota survive the treatments and play a vital role in the network robustness, and the saline- and disease-specific taxa develop primarily by deterministic mechanisms, providing specialized functions to specific stressors [24]. Synthetic microbial communities that are assembled experimentally by incorporating stress-specific strains also showed improved tolerance of plants when the same is exposed to controlled stress conditions, which made the synthetic microbial communities offer a functional validation of stress reduction at a community scale.

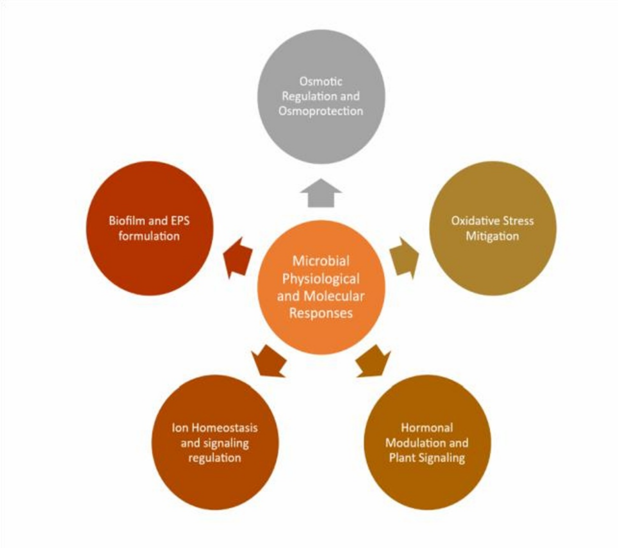

Fig.3. Coordinated microbial responses—including osmotic regulation, antioxidant defense, ion homeostasis, hormonal modulation, and EPS-mediated biofilm formation enhance plant tolerance to drought and salinity while supporting community-level stress resilience.

5. Synthetic microbial communities (syncoms)

Plant-associated microbiomes are highly structured, and taxonomically diverse communities, which contain bacteria, fungi, archaea, and other microorganisms, and that have a collective impact on plant growth, stress resistance and ecosystem functionality. These microbial conglomerates coexist via the complex ecological networks, hence expanding the plant functional capacity and thus assisting in nutrient acquisition, suppressing pathogens as well as adapting to environmental variations [29]. Root exudates can serve as chemical cues to mediate microbial recruitment and regulate rhizosphere community organization to form productive and resilient plant-microbe symbioses [30]. Plant microbiomes are not static and constantly change in response to environmental conditions, developmental status, and exposure to stress indicating a network-like structure but not a fixed membership [31].

The performance of single-strain microbial inoculants on the field is not consistently reproducible as the key factors that affect the activity of microbes are soil properties, climate changes, and microbial interactions with native microbiota [30]. Classical methods of inoculation do not consider the complexity of interactions between plants and microbes or microbes and microbes, which often form the basis of functional outcome. It has become members of diverse, strongly interacting microbial hubs and core microbial lineages are increasingly evident that community level regulation of plant stress responses via microbial network restructuring and not individual strain activity mediates interactions between controls stability and functioning in the macroecosystem. In an attempt to mitigate these flaws, the synthetic microbial communities (SynComs) have become a reductionist and nonetheless functional model of relying on a controlled environment to recapitulate the structure and ecological interactions within natural microbiomes [31].

SynComs are the intentional co-culture of a combination of microbial taxa to recapitulate key interactions between microbes as well as simplify the system. Such a strategy enhances the stability of the community via interactions that can be described as synergistic and allows the research and design of plant-microbiome interactions [30].

By combining complementary functional traits, such as nitrogen fixation, nutrient solubilization, phytohormone modulation, osmolyte production and pathogen suppression, SynComs can contribute to plant performance during drought and salinity and thus increase the performance of plants to withstand abiotic stress [21]. Cooperation appears to be a frequently advanced activity between diverse microbial groups in terms of either metabolic performance and resource distribution as well as greater substrate conversion efficiency.

Compatible strains make rational SynCom design had to be chosen that can coexist stably and exhibit functional complementarity and complimentary interactions with the ecological environment and promote community resistance and functional predictability. A dynamic equilibrium between cooperation and competition aids in avoiding instances of dominance breakdown and functional diversity in nutrient gain, stress management, and defence responses of plants. New concepts, including high-throughput culturomics, multi-omics crunching, and AI-based modeling, also make predictive consortium design and optimization possible [32].

6. Ai & machine learning in microbiome engineering

Over the past few years, the study of microbiomes has become a data-intensive science owing to the rise of high-throughput sequencing and metagenomics as well as integrative policies and data characteristics multi-omics platforms that produce high-dimensional, sparse and compositional data requiring mathematical methods beyond traditional statistics. Rhizosphere microbiome, which we can characterize as a balanced ecosystem that is affected by both the plant genotype and environmental cues, generates multifaceted datasets that connect taxonomic profiles, functional genes, and host phenotypes, leading to the need to use artificial intelligence (AI) strategies to identify patterns and make predictions [33]. Machine learning (ML), deep learning (DL), and other methods of AI have been used to adapt the research of the human microbiome to solve important issues like high dimensionality, sparsity, compositionality, and the small n large p problem have been addressed in microbiome studies [32,33].

Patterned AI processes to research soils and microbiomes focus on sequential steps of data collection, preprocessing, software modeling, and prediction to obtain the reproducibility and resilient inferences, especially with the combination of omics data with environmental and phenotypic groups. The taxonomic abundance, gene catalog, metabolomic, and soil physicochemical parameter data are subsequently extracted to feature representation in AI models to convert complex biological outcomes to predictive variables that can undergo ecological interpretation and be used in crop management aids [34].

Machine learning applications have been shown to be strongly useful in the ranking of taxa, detecting keystone species and predicting microbial dynamics. AI-based analyses in the area of microbial ecology involve predicting microbial composition and identifying keystone ultrafine, and inferring microbial interactions and screening out ecological functions in plant soil ecology [35]. AI has found use in the developing phytomicrobiome research domain through techniques of taxonomic annotation, functional annotation of microbial sequences, association of microbial communities to host phenotypes, synthetic community design, and genotype selection as well as prediction of disease outbreaks, therefore, establishing a direct relationship between microbial structure and plant health outcomes. These uses emphasize the ability of AI systems to favor useful taxa and consortium composed of disease suppressors and endurance to ecological strains and pressures [36].

Functional prediction is a critical field of AI implementation in microbiome engineering. Learning systems based on deep learning have been used to predict genes, predict antibiotic resistance genes, predict the presence of plasmids, predict biosynthetic gene clusters, predict the occurrence of mutagenic events and predict metabolic pathways in microbiome datasets to provide mechanistic understanding of the functional capabilities of individual microbes

[35]. AI-driven metagenomic and taxonomic profiling pipelines also allow constructing microbial communities in high resolution and making ecological and metabolic functions inferences with bearing on plant performance.

Predictive modelling of rhizosphere incorporates phenotypic sensations of plants and microbial representatives in supporting microbiome-enabled genomic choice and the streamlining of synthetic community (SynCom) designs [33]. It is proposed that the juxtaposition of inside and outside-in methodologies (hologenome-based genomic selection and synthetic community design) can further be developed as an AI paradigm that can harness host genetics and microbiome engineering, both together, to improve crops [33].

Experimental research work on agriculture helps to understand the potential practical importance of machine-learning algorithms in the choice of microbial strains, as well as in the alleviation of drought stress. Relative evaluation of the models of Random Forest, Decision Tree, XGBoost, Support Vector Machine, and Artificial Neural Networks showed that gradient-boosted trees had the best predictive precision in recognizing microbial strains that reduce the effects of drought, thus indicating the trade-off between predictive quality and computational efficacy [37]. These results confirm the idea that ML-driven selection models have the capability to hasten the process of identifying the most effective bioinoculants to be used in climatic stress environments.

The example of microbiome intelligence applied to smart farming platforms may also be regarded as an interesting example of the interphenomenality of artificial intelligence and agricultural biotechnology. In an IoT-based framework in which metagenomic and metabolomic data are integrated with real-time soil sensors, the XGBoost and the Random Forest models were able to predict the nutrient condition with precision of 96.5%. The effectiveness of such methods was further supported by field validation involving a reduction of synthetic fertilizer application by 30-35 per cent and improvement of nitrogen use efficiency by 35 per cent and an increase in yields of 22 per cent in plots treated with rhizobacteria compared to the control treatment. These results clearly show that AI based decision systems have the ability to form adaptive feedback, connecting microbial inoculation, soil sensors and crop performance [38].

In addition to predicting soil health as a static process, AI applications to soil health prediction and decision support systems have become more widespread. There has been an emphasis on predictive modelling of soil fertility and resilience because AI-based forecasting models have been created to continuously track soil biological characteristics and promote sustainable accuracy farming [39]. Similarly, machine learning in soil ecosystems management is evidenced by AI-based monitoring of soil parameters and digital soil mapping (especially soil organic carbon and chemical ability), in particular [34].

New paradigms are moving in the direction of digital twins, integrative AI ecosystems, that can model soil-plant-microbe interactions in the framework of different environmental conditions. Digital twin concepts, which combine omics, IoT sensors, remote sensing, and environmental metadata information streams, are integrated using AI and are used to support scenario (testing) and predictive (optimization) and adaptive (management) in precision agriculture [33]. Precision agriculture Complementary reviews highlight convergent AI, big data, bioinformatics, metagenomics and climate-resilient grammar of agriculture as the core technologies behind next-generation crop management and climate resistant farming systems [40].

7. Bioformulation strategies for stress-resilient microbes

A successful implementation of stress-tolerant microbes in sustainable agriculture does not only rely on ideal strain selection, but will also depend on a well-considered approach to formulations, simplified production, strict quality, and rigorous field-testing regimes. The need to create trustworthy microbial technologies is prompted by climate-change-related yield losses, which are estimated to reach between 7-30-percent of the current yield by the middle of the century [41].

Microbial inoculants, or bioproducts which are plant-growth-promoting microorganisms (PGPMs) are able to enhance soil health, nutrient cycling, and plant stress resistance to environmental influences, pests, and diseases; however, their use depends on how to overcome prevailing technological and formulation barriers. The historical trends in the technology of the inoculant will explain that the choice of carrier-material imposes a determining impact on survival of microbes and business profit. Nitragin was the first commercial inoculant, which used gelatin and nutrient media as carriers, but the high mortality rates pushed it to use peat, this carrier continued to be the most favored carriers until the late 1990s [41].

The development of formulations saw the introduction of liquid inoculants; Brazil e.g. licensed the first commercial liquid formulation in 2000 and within a decade over 80 percent of inoculants sold in the country were liquid 273. These transitions show that the type of formulation has a direct impact on microbial viability, storage stability and scalability to the field [41].

Encapsulation technologies have proved to be an advanced reply to a long-running issue of microbial survival, colonization ability and shelf life. This results in bioencapsulation, which protects the useful microorganisms against environmental changes which enhance their survival on storage and in the field. When producing encapsulations, the quality of products encapsulated will depend on such factors as polymer type, size of capsules, and encapsulation method, as well as the chemical and physical cofactors involved during production [42]. In addition, the range of application techniques is vast with the help of encapsulation strategies, such as soil incorporation, foliar spraying, and seed coating, thereby increasing flexibility of agricultural management systems.

Shelf life and stress isolates remain central factors of business sustainability. Field performance inconsistency and microbial survival have been cited as the main drawbacks to the extensive application of biofertilizers. Traditional chemically based fertilizers have limited nutrient utilization capacity where plants only take in around 30 40 percent of the deposited nutrients and the remaining 60 70 percent of the nutrient is acquired by the soil thus leading to environmental pollution [43]. In turn, the creation of high-quality microbial preparations requires standardized production principles, strict quality control guidelines, and adoptions depending on the local environment [44].

The further demarcation of success in formulation is based on compatibility with climate-smart agriculture. Microbial biostimulant improves the process of nutrient uptake by different means: fixing nitrogen, solubilizing minerals, and in parallel making plants more resilient to abiotic stress. Biostimulants biobased on plant growth promoting rhizobacteria (PGPR) have been a major topic of interest because of its ability to enhance plant growth and resistance to both biotic and abiotic stressors within the field. By 2022, with USD3.5 billion in the global biostimulant market, projections indicate that the market will exceed USD6.2 billion by the year 2027, due to an increase in the demand of bio-based inputs, which are sustainable products [45].

8. Biosafety, regulation & ethical considerations

The growth and more expansive use of microbial inoculants and genetically modified microorganisms in development and environmental uses require stricter biosafety systems to protect human health, biodiversity, and the integrity of ecosystems [46]. The principles of containment, risk assessment programs, and regulatory tools that are aimed at preventing unintentional exposure, ecological disturbance, or adverse impacts related to microbial technologies are encompassed by bio safety. The Cartagena Protocol on Biosafety has provided an international regime based on the precautionary principle to control risks associated with living modified organisms and the international movement [46].

Ecological risk assessment (ERA) is still in the center of the regulatory control. In the European Union, the environmental safety of genetically modified biocontrol agents based on microbial organisms is mainly regulated by Regulation (EC) 1107/ 2009 and Directive 2001/18/EC on deliberate release into the environment [47]. Nevertheless, there are still gaps in the understanding of E.coli genetic modification behaviour, persistence, and interaction in complex settings, which creates major challenges to Ecological Risk Assessment (ERA) and governance. The fact that ecological processes and the ecological effects of organisms of the latter type are poorly understood in science role complicates the assessment of sustainability and environmental safety [48].

One of the major biosafety issues is a horizontal gene transfer (HGT) between inoculants introduced and the native microbiota. Horizontal gene transfer contributes to environmental protection and evolution of antibiotic resistance significantly, and requires a thorough consideration before introducing a bioinoculant in the field. The possible genetic contact of the introduced strains and the indigenous microorganisms highlights the necessity of risk profiling and hazard evaluation before commercialization [49].
Also, the heterogeneity in regulation makes it even more difficult to govern microbial products. The microbial inoculants are also often divergently defined based on the alleged claim plant protection product, biostimulant, or biofertilizer, and this leads to fragmented regulatory pathways. The current regulatory frameworks have been heavily developed around the non-living chemical substances and thus are not necessarily the most effective to consider the biological and ecological properties of living microorganisms [50]. On the same note, though the majority of safety issues surrounding the genetically modified microbial biocontrol agents are considered by the existing EU laws, loopholes have been pointed out in terms of food and feed safety in cases where the microbial metabolites change the plant composition [47].

The solution lies in the fact that the governance issues are increased by the innovations in the field of genome editing and synthetic biology that allow more and more complex modifications of microorganisms to use in environmental settings. These new technologies also pose challenges to regulators because they lack experience in analyzing them, and the available guidance requires enhancement to monitor them, their environmental interactions, and overall sustainability [48]. Meanwhile, commercialization of microbial inoculants has led to the development of strict regulations regarding strain identification, purity, concentration, and application conditions by countries like India, Brazil, Canada, Australia, and Uruguay, but harmonization between jurisdictions is limited [51].

Trust and acceptance by society are some of the key elements of responsible use of microbial biotechnology. The transparency, informed decision-making, and involvement of the population are underlined by bio safety frameworks, expressed in international agreements and national regulatory procedures [46]. The precautionary principle embedded in the Cartagena Protocol promotes the balance between the technological innovation and the risk to the biodiversity and health of the people [49]. The enhancement of regulatory abilities, the development of improved strategies to build confidence in microbial and genetically engineered solutions, and the rigorous post-release monitoring has been acknowledged as a key measure to guarantee the public trusts the solutions [48].

9. Conclusion

Climate change caused by human activities entails a collection of abiotic disturbances, such as drought, salinity, temperature rise, and changed precipitation programs that reorganize the soil microbial communities and fundamentally modify the plant-soil relationships so as to have far-reaching effects on agricultural output and ecosystem stability. These abiotic stress factors are used in experimental manipulations and analyses of spatial gradients showing that these ecological factors are potent filters which can reorganize microbial diversity, differentially select stress-adapted taxa, and refocus functional processes. Reductions in water potential, ionic imbalance, and oxidative stress restrict metabolic activity of microbes, but simultaneously initiate physiological and molecular responses which are coordinated to establish plant-microbiomes networks. Reciprocal transplant experiments and climate simulations also indicate that microbial communities do maintain climatic legacies, meaning there is an implication of maintaining historical exposure to the environment, which still has an effect on decomposition and nutrient cycling, and plant-soil feedbacks at present even after a change in contemporary conditions. These results highlight the behaviorally dynamic and conditioned historical realities of microbial systems as they
are closely linked to climatic drivers. The conceptualization of stress resilience in the framework of community stability changes the balance of attention towards the functioning of a particular taxa or the continuation of functioning of the ecosystem. The resistance and resilience of the community, (both in terms of nutrient cycling and stress mitigation) as well as the supportive functions of core and keystone taxa, determine whether nutrient cycling and stress mitigation, and plant physiological performance persist in the face of perturbation. Mechanistic level, antioxidant activation, ion homeostasis, biosynthesis of microbial osmolytes, extracellular polymeric substance-mediated biofilm formation, and hormonal modulation all reduce osmotic, ionic, and oxidative stress as well as strengthening the adaptive responses of plants. Notably, such processes are integrated into organized microbial consortia in which the interactions are cooperative and specialized and maintain ecological balance. The shift to synthetically assembled microbial communities as the replacement of single strain inoculants is indicative of an increased appreciation of the complexities of microbial communities through community-based approaches. Synthetic communities of

microbes (SynComs) built using ecological and functionally complementary principles and network robustness offer experimentally validated methods to develop improved plant stress physiology to drought and salinity. Simultaneously, artificial intelligence and machine learning integration can be used to find effective analysis tools to query high-dimension datasets of microbiomes, pinpoint keystone taxa, forecast functional attributes, and streamline consortium assembly. The interplay of omics data, environmental conditions, and predictive engineering, such as digital twin systems, puts microbiome engineering in the center of precision agriculture paradigms. Actual field application, however, requires sound bio-formulation approaches which include appropriate carriers, encapsulations, quality assurances measures and environmental approval. It is also imperative to have all rounder biosafety evaluation, harmonization of regulatory measures, and open governance systems to be responsible in deployment.

Acknowledgment: The authors gratefully acknowledge Jaypee Institute of Information Technology, Noida, for providing institutional support and a doctoral scholarship to primary author, which enabled the completion of this study. The authors also appreciate the administrative support provided by the institute that facilitated access too scientific literature, databases, and other academic resources essential for conducting this comprehensive study.

Abbreviations

ABA — Abscisic acid
ACC — 1-aminocyclopropane-1-carboxylate
ACC deaminase — 1-aminocyclopropane-1-carboxylate deaminase
AI — Artificial intelligence
ANN — Artificial neural network
C–N cycles — Carbon–nitrogen cycles
CO — Carbon dioxide

CSA$_2$ — Climate-smart agriculture

DL — Deep learning
EPS — Extracellular polymeric substances
ERA — Ecological risk assessment
GHG — Greenhouse gases
HGT — Horizontal gene transfer
IAA — Indole-3-acetic acid
IoT — Internet of Things
ML — Machine learning
MPa — Megapascal (unit of water potential)
N — Nitrogen
PGPM — Plant growth-promoting microorganisms
PGPR — Plant growth-promoting rhizobacteria
ROS — Reactive oxygen species
SynCom — Synthetic microbial community

USD — United States Dollar

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