

Review

Roots of synthetic ecology: microbes that foster plant resilience in the changing climate

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Microbes orchestrate nearly all major biogeochemical processes. The ability to program their influence on plant growth and development is attractive for sustainable agriculture. However, the complexity of microbial ecosystems and our limited understanding of the mechanisms by which plants and microbes interact with each other and the environment make it challenging to use microbiomes to influence plant growth. Novel technologies at the intersection of microbial ecology, systems biology, and bioengineering provide new tools to probe the role of plant microbiomes across environments. Here, we summarize recent studies on plant and microbe responses to abiotic stresses, showcasing key molecules and micro-organisms that are important for plant health. We highlight opportunities to use synthetic microbial communities to understand the complexity of plant–microbial interactions and discuss future avenues of programming ecology to improve plant and ecosystem health.

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Introduction

Plants and soil microbes are pillars of Earth's health. Their interaction with the changing climate will influence the stability and function of diverse ecosystems worldwide. Microbes can contribute to ecosystem fitness by augmenting plant growth through regulation of nutrient availability [1], modification of root architecture [2], production of host-beneficial compounds [3], and maintenance of plant immune responses [4]. Given the rate at which climate change is outpacing plant evolution, the prospect of harnessing soil microbes — which grow and evolve quickly — for enhancing plant stress tolerance is attractive [5]. Yet, a better understanding of plant–microbe–environment interactions is needed to effectively utilize microbes to improve plant resilience.

Plant microbiomes comprise many different organisms, including bacteria, archaea, protists, and fungi [6]. Their interactions influence plant development and productivity through protection from both biotic [7] and abiotic stressors. Here, we discuss recent advancements in plant–microbe research, with a focus on root-associated bacteria, microbial community design, and abiotic (environmental) stress. We also highlight opportunities to program plant–microbe interactions using synthetic biology. Engineering these interactions presents an exciting opportunity to develop robust plant probiotics that can improve ecosystem resilience and planet health.

What happens in nature: microbial composition response to environmental change

Climate change–induced environmental perturbations can significantly influence soil microbial ecosystems. Rising temperatures, prolonged periods of drought [8], overuse of nitrogen fertilizers [9], and elevated carbon dioxide [10] can change soil nutrient availability, microbial respiration [11], microbial community composition, and plant health [12]. Community-level responses to drought have been studied by several groups [13–15]. Typically, drought stress enriches for *Actinobacteria* on plant roots and significantly reduces microbial diversity in bulk soil [13–15]. A study in Subarctic grassland showed that soil warming had an interesting effect; it

increased the number of active bacterial taxa in bulk soil and decreased the abundance of root-associated bacteria [16]. In this study, warming enhanced microbial metabolic activity. Yet, whether or not increased metabolic activity enhances competition or reinforces co-operation between plants and micro-organisms remains unclear. We have a lot to learn about the impact that climate change will have on bacterial community composition and the fitness of their plant hosts [10,11].

The mechanisms that select for the growth of specific microbes in plant root rhizospheres are actively being studied. Plants can actively recruit beneficial microbiota during periods of abiotic stress to assist in adaptation; this strategy is referred to as ‘cry for help’ and typically involves exudation of compounds from the roots that stimulate bacterial chemotaxis, root attachment, and the formation of a mature rhizoplane biofilm [17]. Cries for help are well documented in response to infection, yet their role in abiotic stress response is unclear. Cotton and maize have been shown to reprogram root exudate profiles when exposed to abiotic stress, such as heat and drought [18,19]. These kinds of changes can influence bacterial community composition [20] and drive competition for resources [21]. Thus, their impact on plant microbiomes should be studied. *Limonium sinense* plants have been shown to secrete organic acids into the soil to recruit a beneficial *Bacillus flexus* strain that promotes seedling growth under salt stress [22]. Similarly, red clover plants recruit siderophore-secreting *Pseudomonas* sp. by producing phenolic compounds during periods of iron stress [23]. There is also evidence that volatile organic compounds, such as methyl jasmonate, emitted from plant roots can trigger biofilm production in soil microbes [3] and that the secondary metabolites, γ -aminobutyric acid [24], and sorgoleone [25], secreted by maize and sorghum, respectively, shape rhizosphere and endosphere microbial community composition. A better understanding of how root exudates influence individual microbes and communities [26] can further help us unravel the mechanisms that plants use to tolerate abiotic stress.

Independent of stress, plant development can influence microbial community composition and function. In soybean, the first 14 days of development are associated with the highest microbial diversity. During this time, the soybean endosphere is dominated by *Actinobacteria*. At later time points, it is dominated by *Proteobacteria* [27]. Similarly, *Actinobacteria* dominate maize seedling microbiomes, and *Gammaproteobacteria* are most abundant in mature plants [28]. Work in *Arabidopsis* shows that plant stress responses are also age dependent, which may contribute to shifts in the microbial community over time [7]. Though plant development influences environmental stress susceptibility and microbial community composition, the interplay between these two features remains unknown.

Beyond the plant, the environment can directly alter microbial community composition. A recent study showed that bacteria with higher growth rate potential in an environment consistently dominate the rhizosphere [29]. This suggests that the beneficial properties of a microbiome may arise purely as a by-product of microbial adaptation to the environment [30]. In this framework, soil moisture levels impose selective pressure on microbes that help plants survive drought by virtue of their own adaptive processes. Interestingly, a recent transplant experiment performed at two forest sites (northern Wisconsin, 12 native tree species) showed that drought-adapted forests contain soil microbiomes that can improve the resilience of young trees [29]. This effect persisted for more than 3 years, with soil communities from the initial inoculum remaining in both field sites [29]. While such ecological processes may be the result of quorum sensing or changes in microbial diversity and behavior, the exact mechanisms of environmental memory in microbiomes remain underexplored. A large-scale study of respiration recently showed how microbes can drive soil carbon loss over long time scales (10-hour and 1-, 2-, and 3-week incubations) [11]. These experiments suggest that microbial communities can remember historical environmental conditions and that the adaptation of microbial communities to a change in the environment can directly impact plant hosts’ fitness.

Cell-free systems, containing a fixed number of biomolecules, which can be programmed, may be powerful tools for dissecting interactions between micro-organisms, hosts, and their environment [31]. A tobacco cell-free system was used to study biogenesis and molecular mechanism of plant secondary small interfering RNA involved in stress responses and development [32]. The ROSALIND cell-free system was used to detect water contaminants with engineered RNA circuitry [33], and a *Lactobacillus*-derived cell-free extract was reported to have bioactive compounds (e.g. methyl esters, phenol) with antifungal activity against *Fusarium* sp. [34]. Cell-free systems might be especially useful for studying the metabolism of both plants and soil microbes under stress.

Root-beneficial microbiota during abiotic stress: example molecules and power species

Beneficial microbes employ diverse strategies and metabolites to mitigate abiotic stress for plants. Some microbes can enhance plants’ dehydration response by increasing the expression of genes that biosynthesize antioxidants [27,28]. Others stimulate phytohormone production, produce siderophores that solubilize phosphates [29,30], or reduce phytohormone levels [31,32]. For example, organic acids, acetate [32,33] and citric acid [34,35], can be key mediators of salinity stress and heavy metal toxicity tolerance, improving growth of various

plant species [36,37]. Nonclassic examples of organic acids include (1) pipercolic acid, observed to accumulate in sorghum roots during periods of drought stress [38] and (2) pteridic acids, demonstrated to have remarkable efficacy in mitigating both drought and salinity stress in *Arabidopsis* and barley [39]. Polyamines, such as cadaverine [40], are also shown to confer salinity and drought stress tolerance in cereals. Indolamine compounds, such as serotonin or melatonin [41,42], are gaining interest as antioxidants to mediate drought stress tolerance in cauliflower, rice, and hazelnuts [34,35,43]. Remarkably, these indolamines function as important regulatory hormones not only in humans but also in plants, mediating responses to environmental stress and promoting growth. This could be explained by precursor structure and biochemical similarity since many plant hormones (auxins and phytoalexins) are derived from tryptophan [44]. Building on this knowledge, plant abiotic stress tolerance and microbiome remodeling could be stimulated by exogenous application of microbial or plant-derived molecules [45,46]. Biostimulants of this kind include organic acids, osmolytes, amino acids [41], volatile compounds [3], and enzymes (recent examples in Table 1.). Co-evolution of plant hosts and associated soil microbiota in different environments has likely resulted in a treasure box of beneficial molecules that are yet to be explored.

Plants can be inoculated with specific microbes to increase abiotic stress resilience. Commonly, these growth-promoting micro-organisms are isolated from roots of adapted healthy plants. For example, *Nigrospora oryzae*, an endophytic fungus that can increase drought and salinity tolerance in rice [62], was isolated from the microbiota of drought-resistant rice. Similarly, *Streptomyces* strains enriched during drought in sorghum [14] and tomato [69] may help mediate dehydration tolerance. Candidate strains have also been isolated from extreme environments — for example, from deserts or saltmarshes to screen for potential drought- and salt-tolerance-promoting species, respectively. *Bacillus aryabhatai* and *Arthrobacter woluwensis* that increase salinity tolerance in soybean were originally isolated from sand dune flora [55]. Species of *Enterobacter* [61], *Pseudomonas* [66], *Streptomyces* [12,15,38], and *Variovorax* [68] that can increase drought and salinity tolerance were isolated from desert environments. While these strains alleviate abiotic stresses under controlled greenhouse conditions, using them as biofertilizers will require the development of strategies that enhance colonization and persistence in the presence of native microbiota and simultaneous abiotic stresses.

Successful colonization of roots by beneficial indigenous or introduced bacterial species is critical for the long-

lasting growth-promoting effects [70]. A recent study demonstrated that an *Enterobacter* root endophyte induced thermotolerance in wheat during three growing seasons without significantly altering the endogenous microbiome [71]. Introduction of one beneficial bacterial species into a native community does not ensure improved plant growth and resilience stability in field settings [70], as it is challenging for a new member to compete with the adapted resident community. As researchers continue to uncover microbes that alleviate abiotic stress, more field studies will be required to determine whether their beneficial effects persist under natural conditions. Studying microbial interactions in a community setting can address these challenges and guide the engineering of plant-microbial ecology.

Bridging knowledge gaps with synthetic microbial communities

Well-defined and well-characterized bacterial communities can be used to dissect complex plant–microbe and microbe–microbe interactions. Recently, scientists have generated synthetic communities (SynComs) composed of characterized bacterial isolates [72,73]. In mice, a SynCom was used to show how microbiome diversity can protect against pathogen invasion (*Klebsiella pneumoniae* and *Salmonella entericopathogens*) by nutrient blocking [20]. In plants, SynComs have been used to study the mechanisms by which iron-mobilizing metabolites (coumarins) shift microbiome composition [72] and the extent to which commensal bacteria impact the root immune system [74,75]. Using a complex 185-member bacterial SynCom, Finkel *et al.* characterized microbial community composition responses to phosphate starvation [76]. They also discovered that removing *Burkholderia* strains from this SynCom resulted in increased accumulation of orthophosphate (Pi) in shoots. A similar SynCom was used to identify a single genus, *Variovorax*, capable of reversing a severe root growth inhibition phenotype induced by the full consortia [73]. Additional high-quality data on individual microbes and microbe–microbe interactions in the plant environment should help detangle more microbial community complexities [77,78]. Data from these controlled experiments could be used to parameterize mathematical and mechanistic models that predict interactions and activities within the plant microbiome (Figure 1).

A significant challenge for SynComs is their application in natural agricultural settings. It can be challenging for SynCom members to successfully invade and persist within existing microbial communities. *In vitro*–designed consortia faced with large dynamic changes (temperature, hydration, pH, and substrate availability)

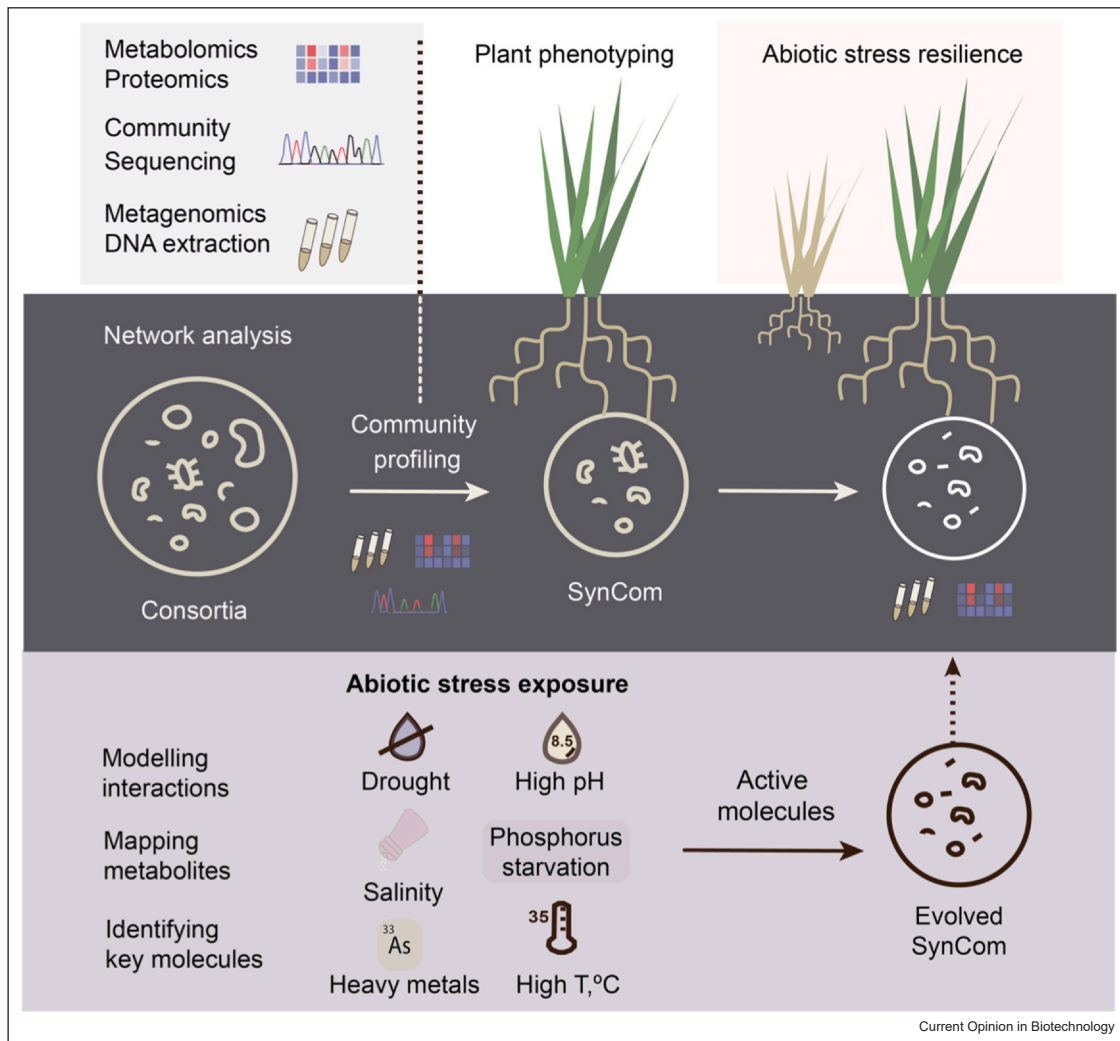
Table 1
Recent examples of microbial metabolites, enzymes, and bacterial species, shown to improve plant health and tolerance to abiotic stresses.

| | Abiotic stress | Plant | Effects | Reference |
|--|---|--|---|-----------|
| Metabolites | | | | |
| Amino acids (e.g. proline, methionine) | Drought | Cauliflower | Foliar application reduces phenolic-related enzymes, glucosinolates, abscisic acid (ABA), malondialdehyde (MDA), and total phenols | [41] |
| Acetate | Salinity | Oat | Increases proline, chlorophyll, and carotenoid content; upregulates gene expression related to photosynthesis | [47] |
| Citrate | Drought, salinity, temperature, alkalinity, metal toxicity | Cotton, maize, rapeseed, rice, tomato | Activates antioxidant defense systems, increases chlorophyll content, promotes precipitation, chelation, and sequestration of metal ions | [36] |
| Pipecolic acid | Drought | Sorghum | Suppresses root growth, enriching the abundance of <i>Actinobacteria</i> | [38] |
| Pteridic acids produced by <i>Streptomyces</i> | Drought, salinity | Arabidopsis, barley | Increase expression of photosynthesis and stress-responsive genes, promotes root growth | [39] |
| Cadaverine | Drought | Barley | Promotes cell division by increasing G1-S and S-G2 cell transitions in the cell cycle; increases endogenous polyamine levels; decreases total protein content and MDA | [40] |
| Flavonoids | Dehydration | Arabidopsis | Shape the root microbiome by preferentially attracting <i>Aeromonadaceae</i> , including a species that induces H ₂ O ₂ accumulation in guard cells and stomatal closure | [48] |
| Melatonin | Drought, salinity | Rice | Suppresses reactive oxygen species accumulation, increases antioxidant activity, upregulates salt and drought stress-responsive genes (<i>OsSOS</i> , <i>OsNHX</i> , <i>OsHSF</i> , <i>OsDREB</i>) | [49] |
| Microbial enzymes | | | | |
| 1-aminocyclopropane-1-carboxylate (ACC) deaminase | Drought, salinity, waterlogging, temperature, metal toxicity, light | Arabidopsis, alfalfa, maize, rapeseed, rice, sorghum | Inhibits accumulation of reactive oxygen and nitrogen species; regulates expression of genes involved in stress response, antioxidant production, and phytohormone pathways | [50] |
| | Salinity | Soybean | Inoculation of ACC deaminase-producing <i>Bradyrhizobium</i> and <i>Pseudomonas</i> reduces salt-induced ethylene production and improves nutrient uptake | [51] |
| | Salinity | Camelina | Delivery by <i>Pseudomonas migulae</i> or via <i>acdS</i> expression in transgenic lines modulates expression of genes related to photosynthesis, cell wall biosynthesis, and production of stress-related secondary metabolites, ethylene, and other phytohormones | [52] |
| Alkaline phosphatase | Phosphate starvation | Rice | Using phosphate as the sole phosphorus source for plant growth, development, and metabolism | [53] |
| Nitrogenase | Nitrogen deficiency | Maize | Restore ammonium production in the presence of exogenous nitrogen inputs | [54] |
| Bacteria | | | | |
| <i>Arthrobacter woluwensis</i> ; <i>Bacillus aryabhatai</i> | Salinity | Soybean | Produce organic acids, extracellular polymeric substances (EPS) and indole-3-acetic acid (IAA); regulate phytohormones, antioxidants, ion uptake; decrease <i>GmFLD19</i> and <i>GmNARK</i> expression | [55] |
| <i>Acinetobacter haemolyticus</i> , <i>Bacillus safensis</i> , <i>Enterobacter cancerogenus</i> , <i>E. hormaechei</i> , <i>Stenotrophomonas pavanii</i> , <i>Lysinibacillus fusiformis</i> | Alkalinity | Maize | Some of these endophytes produce ACC deaminase and IAA, solubilize phosphate <i>E. cancerogenus</i> produce EPS in maize plants | [56] |

Table 1 (continued)

| | Abiotic stress | Plant | Effects | Reference |
|--|----------------------|------------------------------------|---|-----------|
| <i>Bacillus subtilis</i> , <i>Brucella haematophilum</i> , <i>Bacillus cereus</i> (consortium) <i>Bacillus subtilis</i> | Drought | Rice | Produce organic acids (e.g. acetic acid, succinic acid, and gluconic acid), a key mechanism of phosphate solubilization; produce ACC deaminase, IAA, EPS (fructose), and siderophores | [57] |
| <i>Bacillus subtilis</i> ; | Aluminum toxicity | Rice | Produce siderophores, organic acids, and IAA; solubilizes phosphate and zinc | [58] |
| <i>Bacillus subtilis</i> ; | Salinity | Tomato | Form biofilms; produce IAA, ACC deaminase, and siderophores; solubilize phosphate | [59] |
| <i>Enterobacter cloacae</i> ; | Salinity | Maize | Increase expression of enzymatic (APX, POD, SOD) and nonenzymatic (ascorbic acid) antioxidants, reduces oxidative burst, increases osmolyte content | [35] |
| <i>Glutamicibacter arilaitensis</i> ; | Salinity | Arabidopsis, alfalfa | Produce 2-keto-4-methylthiobutyric acid, which activates the plant ethylene signaling pathway | [60] |
| <i>Leclercia adecarboxylata</i> <i>Bacillus thuringiensis</i> | Salinity | Wheat | produce ACC deaminase and IAA, increase antioxidant activity and proline content | [61] |
| <i>Enterobacter</i> sp. | Heat, salinity | Rice | Solubilize phosphate, produce ACC deaminase, phytohormones, and siderophores, increase antioxidant activity | [62] |
| <i>Lysinibacillus fusiformis</i> ; | Drought, salinity | Wheat | Produce ACC deaminase, increases antioxidant activity, upregulates genes related to ABA signaling (<i>TaABARE</i>) and ion transporters (<i>TaHAK1</i> , <i>HKT1</i>) | [63] |
| <i>Lysinibacillus sphaericus</i> <i>Nigrospora oryzae</i> | Salinity | Tomato | Inhibit expression of <i>ERF1</i> and <i>WRKY70</i> , which are highly expressed during drought; suppress stress signals | [64] |
| <i>Nocardioides</i> sp. | Drought | Peppermint Arabidopsis, alfalfa | Increase plant growth, essential oil content, and menthol content | [65] |
| <i>Streptomyces</i> spp. | Drought | Arabidopsis | Prime aquaporin genes in an ABA-dependent manner by enhancing H3K4me3 levels | [66] |
| <i>Pseudomonas putida</i> | Phosphate starvation | Arabidopsis | Modulate expression of phytohormones, transporters, and glucosinolate | [67] |
| <i>Variovorax paradoxus</i> ; | Salinity | Wheat | Produce auxin and ACC deaminase | [68] |
| <i>Variovorax gossypii</i> <i>Variovorax</i> sp. | Drought | Broccoli | Regulate plant endogenous phytohormones (ABA, jasmonic acid, and salicylic acid) and antioxidants (APX, SOD, CAT, and GPX) | [43] |

Figure 1



SynCom assembly. Assembling an efficient synthetic microbial community (SynCom) is done by combining individual strains into a complex consortia. Strain characterization is commonly done with multi-omics analysis (metagenomics, transcriptomics, proteomics, metabolomics). Preadapting a microbial consortium to a specific type of stress may create a SynCom that can be used to study key molecules and strains with potential to improve plant resilience.

can be outcompeted by the resident microbial community [79]. This was observed in a complex plant growth promoting SynCom (15 strains) designed to improve tomato salt tolerance; it was unable to persist in non-sterile conditions with members lost after 21 days [69]. A smaller SynCom (five members) exhibited higher persistence in the nonsterile environment and outperformed a complex community, indicating importance of microbe–microbe interactions [69]. Even though community invasion is a well-known challenge, individual species are already successfully being used in

agriculture [54]. More research is still needed to better understand how to design successful bioinoculants.

An alternative to invading established microbiomes with beneficial strains is to engineer native community members to have the trait of interest. This engineering could be done *in situ* using conjugation tools or bacteriophages. Conjugative elements enable simultaneous engineering of diverse microbial species [80–82], whereas phages can target individual species [83]. Advantageously, *in situ* engineering alleviates the need to

culture strains *in vitro*, which can severely limit the number of engineerable microbes. Alternatively, strains can be isolated, engineered, and then returned to their native environment to have a therapeutic effect. This was successfully done with *Cutibacterium acnes*, which was engineered to modulate sebum secretion in mice [84], and *Staphylococcus epidermidis*, which was used to generate a melanoma vaccine [85]. These kinds of approaches could be applied to soil microbes to enhance or introduce plant-growth promoting qualities.

Engineering at the interface of plants and microbes: the era of synthetic ecology

Synthetic ecology, an emerging field that combines ecological principles with synthetic biology, signals the beginning of a transition from engineering individuals to engineering co-operation between living organisms [86]. Synthetic co-operation has already been created by engineering plants to sense *p*-coumaroyl-homoserine lactone [86] and bacteria that respond to plant-derived rhizopines [87]. Similar synthetic cooperation could be created to enable pollutant remediation [88] and dynamic responses to environmental changes [89] and to enhance soil fertility and biodiversity [90]. Additionally, plants and microbes could work together to create novel biomaterials [91] or even homes [92]. Opportunities to engineer interkingdom interactions are numerous and have many diverse applications.

To ensure engineered ecosystems are stable, auxotrophies and other interdependencies could be engineered into plants and microbes. Microbial communities are commonly shaped by auxotrophies [93]. Stark *et al.* recently identified auxotrophies as drivers of microbiome diversity and stability in human gut communities [93]. Similarly, Karkaria *et al.* found that all top-performing synthetic microbial community models contain forms of mutualism [94]. Excitingly, technology to introduce auxotrophies for nonstandard amino acids into microbes is maturing. These could be leveraged to manipulate microbiomes synthetically. Kunjapur *et al.* recently demonstrated the ability to create a biphenylalanine auxotrophy that is stable for hundreds of generations [95]. Thus, microbiome composition could be manipulated using this nonstandard amino acid. Auxotrophies also present the opportunity to engineer microbe–plant interdependencies. Plant metabolism could be rewritten to produce essential amino acids for beneficial bacteria. Ideally, this production would be controllable and condition dependent to support growth of specific microbes during periods of plant stress.

More advanced technologies are arising to unlock our ability to study complex interkingdom interactions (Figure 2). These technologies enable (1) profiling of microbial communities at single cell resolution [96], (2)

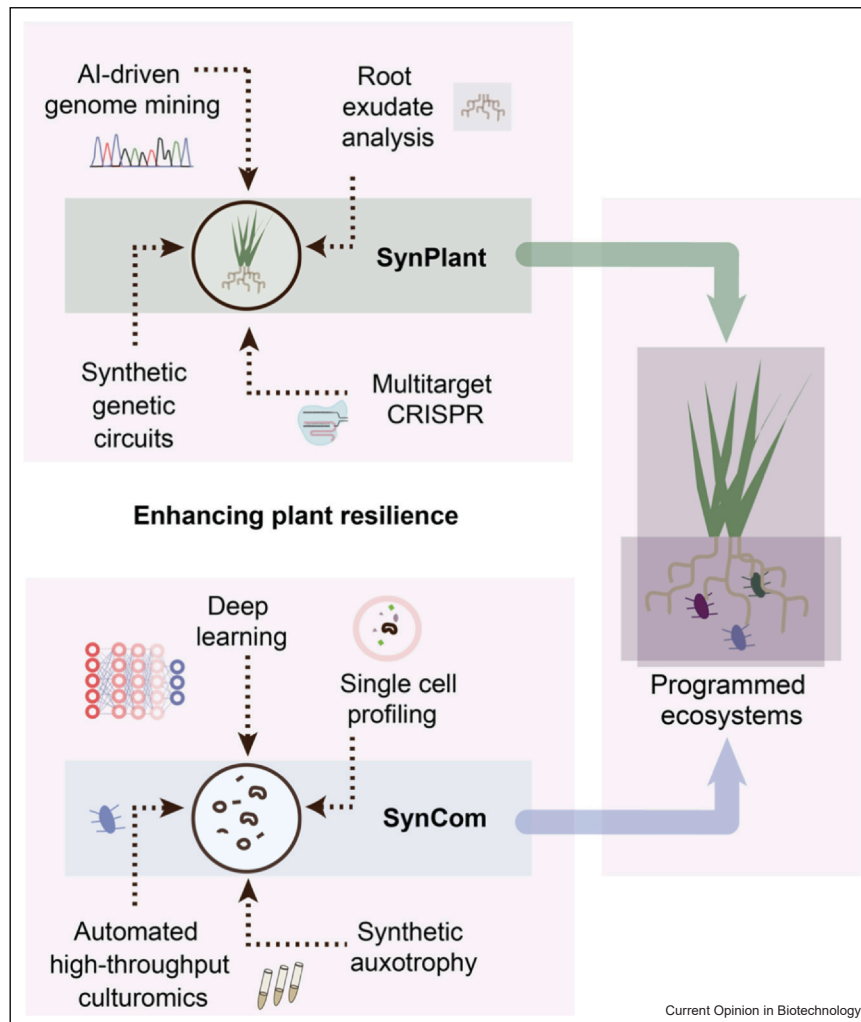
continuous root exudate analysis [97], (3) automated high-throughput microbial culturomics [98], and (4) machine learning–based community analysis [99]. A foundational DNA large language model was recently created using 48 plant genomes as a training data set [100] and shows the potential of AI to predict functionalities, regulatory mechanisms, and gene expression and translate prior knowledge to nonmodel plant species. Such analysis may enable investigation of underexplored genomic regions responsible for producing specific expression patterns, valuable for engineering across genomes and species. Machine learning was also used to design a multiplex CRISPR editing experiment in *Populus trichocarpa* (poplar) that increased wood carbohydrate-to-lignin ratios by modifying monolignol biosynthesis for more efficient fiber production [91]. In general, mathematical and ecological models could help us understand emergent properties of large microbial assemblies and predict their outcomes [26,101]. These technologies are leading toward the ability to manipulate multiple members of an ecology, which may improve engineered ecosystems' resilience and functionality. While significant progress has been made in the field of synthetic ecology, we are still in the early stages of fully realizing its potential.

Outlook

Microbes could be utilized to help maintain plant biodiversity and resilience in a changing climate. Advances in microbiome engineering [5] will soon enable the creation of designer communities, where individual microbes programmed for specific functions [102] are combined with hosts and other consortia members to create stable and impactful synthetic microbiomes. While this review is focused on bacteria, other microorganisms are important for plant growth and should also be considered [103]. Current advances in plant engineering already enable a broad range of applications: from improving nutrient acquisition efficiency [104] and dynamically regulating hormonal feedback [44] to coordinating gene expression in a tissue-specific manner, engineering logic [105], and finely tuning lateral root development [106]. As we move forward, more non-model species will need to be studied and engineered to realize the full potential of synthetic biology in plant-based ecosystems.

Establishment of regulatory frameworks [107], global collaboration, and knowledge sharing will be crucial for programming ecology. To advance these systems responsibly, we must consider ethical, environmental, and societal implications of this kind of work. At its core, these engineering endeavors require and will establish a better understanding of complex environmental systems, their functions, assembly, and stability. This knowledge will be key to developing global sustainability solutions.

Figure 2



Reprogramming ecosystems. Genetically engineered plants (SynPlants) and synthetic microbial communities (SynComs) can be used together to better understand plant–microbe interactions and to implement novel plant-based functions. New approaches for analyzing and modifying microbiomes and plant hosts can be used to develop partnerships that are more robust than either individual component.

CRedit authorship contribution statement

E.K.: Conceptualization, Investigation, Writing – original draft and editing, Visualization. **A.A.E.:** Investigation, Writing – original draft and editing. **E.F.G.:** Investigation, Writing – original draft. **J.L.D.:** Writing – review and editing, Funding acquisition. **J.M.C.:** Writing – review and editing, Funding acquisition. **J.A.N.B.:** Conceptualization, Supervision, Writing – review and editing, Funding acquisition & resources.

Data Availability

No data were used for the research described in the article.

Declaration of Competing Interest

The authors declare that they have no known competing interests that could affect the work reported in this paper.

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- of special interest
- of outstanding interest

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This study demonstrates a powerful example of alleviating abiotic stress using a synthetic community in rice. Aluminum (Al) toxicity-resistant bacteria promoted rice growth in acidic soil (up to 5.24-fold increase in biomass), optimized root architecture, and promoted phosphorus (P) mobilization. Hypothesized mechanisms of Al resistance and plant growth in acidic soil highlight role of root sugar transporters and P accumulation and solubilization in abiotic stress tolerance.

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Authors characterized changes in root architecture in *Arabidopsis* in response to individual bacterial isolates, showing strong evidence of microbiota-driven lateral root formation. Bacteria can control root branching via ethylene and independent from IAA regulation, as shown in nonresponsive to auxin *Selaginella* roots. Root branching is promoted by bacteria under salinity and low-iron stress using a 16-member synthetic community.

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A great molecular example of plant – microbe communication and a strategy for recruitment of beneficial micro-organisms. Plant volatiles promote complex beneficial biofilm formation. While authors observed *Arabidopsis* growth-promoting effect of biofilms with a complex microbial community derived from soil, isolated monocultures of the same taxa showed modest or no impact on plant growth.

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