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Enhancing agricultural resilience through plant-microbe interactions: a key challenge for sustainable farming

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Abstract

Modern agriculture faces the dual challenge of increasing food production while reducing environmental impact, especially in the context of climate change. One promising solution lies in harnessing the natural relationships between plants and beneficial microbes. These interactions can help crops use resources more efficiently, become more resistant to stress, and reduce the need for chemical treatments. This review focuses on grapevine and rice, two globally important crops, as examples to highlight how root-associated microbes can support more sustainable farming. Thanks to recent advances in DNA sequencing and microbial

research, scientists are now able to design specific microbial mixtures, known as synthetic communities (SynComs), tailored to improve plant health. However, key challenges remain, such as selecting the right microbes, ensuring their stability, and applying them effectively in the field. At the same time, breeding crop varieties that are more responsive to helpful microbes is becoming increasingly important. The Micro4Life project, funded by AGER, explores these topics by studying how crops and their microbiomes interact under different environmental conditions. It also promotes field-based research and continuous dialogue with farmers to ensure that scientific advances address real-world needs and constraints. This approach not only opens new opportunities to make agriculture more resilient and environmentally friendly but also delivers economic benefits—such as improved productivity and efficiency—and strengthens the resilience of farming communities by empowering local stakeholders and integrating traditional knowledge.

Keywords: Arbuscular mycorrhizal fungi, Plant resilience, Soil microorganisms, Dissemination activities

Introduction

Modern agriculture faces the pressing challenge of increasing food production while minimizing environmental impact. Understanding the interactions between plant roots and soil microbiomes is one of the most promising solutions to this issue, yet it still requires further experimentation and research to fully realize its potential. These interactions influence crop resilience, resource use efficiency, and stress tolerance, ultimately contributing to more sustainable agricultural practices [1,2]. As climate change intensifies, the need for alternative, eco-friendly approaches to enhancing plant resilience is more urgent than ever. Since farmers' income and well-being are becoming more uncertain and unstable, it is crucial to enhance the resilience of agro-ecosystems by promoting sustainable and eco-friendly farming methods through more efficient use of biological and natural resources [3]. The focus on reducing reliance on agrochemicals and improving soil health has driven research into microbial communities that can support plant growth under adverse conditions [4]. Microbial-based strategies are increasingly recognized not only for their agronomic relevance, but also for their broader contribution to building sustainable and resilient agri-

food systems. Beyond enhancing crop productivity and reducing dependency on chemical inputs, these approaches support the development of agricultural practices that are more resource-efficient, environmentally responsible, and adaptable to climate-related challenges. Their integration into mainstream farming systems reflects a shift towards more holistic management of soil and plant health, with positive implications for biodiversity, nutrient cycling, and water use. Importantly, microbiome-based interventions also foster scientific and technological innovation across disciplines, while promoting stronger dialogue between researchers, policymakers, and local stakeholders. An inclusive collaboration with farmers is essential to ensure that innovations are both practically relevant and widely adoptable, enabling research efforts to more effectively respond to the diversity of local conditions, agricultural practices, and socio-economic constraints. By positioning plant-microbe research within this broader sustainability and participatory framework, the agricultural sector can better align with long-term global priorities and respond more effectively to the complex interplay of environmental, economic, and social demands. Despite growing interest in microbiome research, several fundamental questions about how plant-associated microbes affect crop performance remain unanswered. Among the most relevant crops for such studies are grapevine and rice, two staple crops that are both economically significant and highly sensitive to environmental changes [3,5].

Microbial solutions from soil for sustainable agriculture: Grapevine and rice as model crops

The soil microbiome plays a crucial role in plant growth, influencing nutrient uptake, disease control, and stress tolerance [6,7]. Yet, the mechanisms by which microbes contribute to these processes remain poorly understood. Advances in genomic technologies, such as high-throughput sequencing, have opened new pathways for exploring the complex relationships between plants and their associated microbial communities [5,8]. By studying these interactions, researchers can identify microbial isolates/strains and consortia that can play a relevant role in enhancing crop tolerance and resilience, reducing the dependence on chemical fertilizers and mitigating the environmental impact of agricultural practices. Beyond immediate environmental benefits, microbial consortia could revolutionize crop

breeding strategies [9]. By selecting genotypes that are more responsive to beneficial microbes, breeders might develop crops that are not only resilient to abiotic stresses, but also more efficient in nutrient uptake and carbon sequestration. This represents a paradigm shift in modern agriculture, moving beyond traditional breeding methods to an integrated approach that combines genetics with microbiome science [10]. Engineering crop microbiomes through plant host genetics, and harnessing the plant-microbe interactions, will offer a smart approach for reducing the environmental footprint of agriculture. One significant area of focus is improving nitrogen use efficiency (NUE) in crops, considering that the overuse of synthetic fertilizers has led to serious environmental concerns, including soil degradation [11]. Microbial inoculants - such as those including endophytic plant growth-promoting bacteria (PGPB) - have the potential to enhance NUE and water use efficiency (WUE), reducing the need for chemical inputs and promoting more sustainable farming systems [12].

SynComs represent a crucial advancement in plant microbiome research and have strong potential to improve crop production in an environmental-friendly way. While many proof-of-concept results are positive, demonstrating improvement in growth, stress tolerance, and disease control, there remain practical issues regarding community design, stability, formulation, and deployment at field-level [13]. Two primary strategies are used in assembling SynComs. The bottom-up approach involves selecting individual strains with well-characterized beneficial traits, such as growth promotion, stress tolerance, or antagonism of pathogens, and combining them to form a simplified, function-focused consortium, whereas the top-down approach begins with a complex, naturally adapted microbial community and systematically removes taxa in order to retain essential members and recapitulate important ecological dynamics. The approval steps for microbial biostimulants in the European Union are defined by the EU Regulation 2019/1009. These steps require detailed taxonomic and safety dossiers but, differently to plant protection products such as pesticides, they do not require an environmental persistence evaluation [14]. Introduced microbial strains may be indeed considered as biological invaders and/or favour unintended horizontal gene transfer with native microbiota, potentially affecting non-target organisms [15]. Thus, field trials should include pre- and post-application monitoring of microbial community structure. In addition, multi-year studies reveal that SynCom

performance might decays after two seasons, mostly due to competition with native microbial communities and climatic fluctuations [15]. The use of carriers with controlled-release matrices, co-encapsulation of keystone taxa and site-specific consortia selected under local abiotic conditions have been reported to improve SynCom persistence [16]. Moreover, adaptive, "resilient-by-design" consortia that contain strains for stress responses can help to stability of crops despite changes in the host or environment [17]. However, plant genotype, developmental stage and root exudation profiles may affect SynCom assembly. Plant drive microbiome assembly through variation in root-exudation, signalling, and root development. *Omics* approaches that integrate host genomes, transcriptomes, metabolomes, and microbial profiles show that genotypic differences in the secretion of specialised metabolites act as chemical filters that favour distinct bacterial guilds in wheat, rice, wild and cultivated tomato, and *Arabidopsis* [18,19,20,21,22]. Nowadays the SynComs have primarily been employed as simplified systems to investigate how plant microbiomes are structured and assembled. However, results from their application under field conditions have often been inconsistent. This variability is largely due to the use of generic microbial mixtures that are not optimized for broad agricultural contexts, as their effectiveness can vary significantly depending on both plant genotype and environmental conditions. Moreover, our understanding of the specific mechanisms governing beneficial plant–microbe interactions under real conditions remains limited, making their reliable use in agricultural settings still challenging [8].

Recent strategies for engineering plant-microbe communication focus on enhancing root-soil interactions to improve nutrient acquisition. Plants can be genetically modified to release specific exudates, such as flavonoids or coumarins, which can selectively attract beneficial microbes or limit pathogens [12,23]. This potential of specific root traits, or combinations thereof, to enhance resilience to environmental stress yet remains underexploited. Plant genotype, environmental factors including water and nutrient availability, and the plant ability to efficiently exploit soil resources, all play a crucial role in stress adaptation [2]. Plant diversity panels grown under contrasting environmental conditions can be used for genome-wide association studies (GWAS) to identify host loci linked to the recruitment of beneficial microbes. In mazie and rice, up to 25% of the observed variation was linked to this recruitment [24]. Once validated, these loci can be used in marker-assisted selection and

incorporated into genomic selection models that combine plant genetic markers with microbial data to improve predictions of complex traits, such as NUE. CRISPR/Cas technologies may support this process by confirming gene function and introducing targeted edits in traits such as root exudation, signalling, or root architecture to enhance microbiome interactions. An integrated breeding strategy, combining GWAS, gene editing, selection, and long-term field trials can support the development of cultivars with stable and beneficial microbial associations.

Improving crop productivity should be based on a well-adapted root system, and identifying genotypes with root traits that improve tolerance to specific stress conditions should be a main focus for breeders and researchers [2,25]. Root architectural, anatomical, and physiological features significantly influence plant responses to environmental fluctuations [1], and natural selection tends to favor those that optimize resource acquisition in spatially heterogeneous soils. Moreover, the root ability to interact with soil biota is essential for effective nutrient uptake [25]. Modern crop breeding has been reported to have overlooked the spatial and temporal variability of soils, a factor that is critical for achieving optimal yield and stress resilience in future crop cultivars [26]. Newly developed varieties are generally tested in uniform soils, thus neglecting the dynamic nature of soil properties such as texture, structure, moisture, and soil microbes, that result from both agricultural practices (e.g., tillage) and climatic changes [26]. In the context of climate change, with rising temperatures and more frequent extreme weather events, these changes in soil characteristics are expected to intensify, and future initiatives must then integrate soil heterogeneity into their experimental designs by testing genotypes across a range of realistic field conditions [26]. Moreover, traditional domestication, focused solely on improving specific plant traits, has compromised the recruitment and function of beneficial microbes. Since these microorganisms play a key role in plant growth and health, it has been proposed that modern breeding programs must consider plant ability to interact with them as a fundamental trait, by using a holistic '*holo-omics*' approach ([1]; Figure 1). In this context, a remarkable example is represented by grapevine (*Vitis vinifera*) and rice (*Oryza sativa*). Grapevine is one of the most widely cultivated fruit crops with a significant global economic impact,and harbours a diverse community of microorganisms that influence its health and productivity in both beneficial and pathogenic ways, ultimately shaping fruit yield, grape quality, as well

as the fermentation process during wine production [27]. Grapevine has become a model woody plant, fully sequenced and with a wide range of available genetic and molecular tools. Grafting, a widely used technique in grapevine cultivation, serves as an environmentally sustainable method that enables the selection and breeding of ideal phenotypic traits, including those that support the recruitment of beneficial soil microbes [28]. It has been already demonstrated that grapevine roots are naturally inhabited by native arbuscular mycorrhizal fungi (AMF), which directly influence growth, yield, and quality [1,29,30]. Recent advancements in metabarcoding methods have provided new insights into the AMF species that form symbiotic relationships with grapevines. Additionally, it has been suggested that the entire root microbiome plays a role in balancing the trade-off between growth and defense mechanisms [1].

On the other hand, rice is the most consumed staple food in several countries, particularly in Asia, where it feeds billions of people. Rice varieties cultivated in Italy and Europe (*Oryza sativa* ssp. *japonica*) exhibit low nitrogen use efficiency (NUE), approximately 40%. These varieties, typically grown upon permanent flooding conditions, require large amounts of water. Conversely, *indica* subspecies varieties show higher NUE, thanks to a beneficial allele of the *NRT1.1B* gene, which encodes a nitrate transporter that enhances NUE of about 30% in field conditions. This effect is also attributed to a preferential recruitment of root microbiota, promoting ammonification processes [31,32]. Since plant PGPB can improve water use efficiency (WUE) in host plants, it is possible that enhanced rice interactions with PGPB could also lead to an improved WUE. Cultivated rice, derived from the wild relative *O. rufipogon*, exhibits greater allelic variation compared to domesticated rice and serves as a source of genetic diversity [33]. Studies of different crops and their wild relatives have revealed differences in the root and rhizosphere microbiome compositions, as well as the genetic loci involved in these traits in crops like tomato and barley [34,35,36]. The microbiota associated with wild relatives evolved in marginal soil conditions, making it a valuable resource for low-input agriculture [36]. Root microbiota, including AMF, can mitigate the detrimental effects of stress, improving water and mineral nutrition. Particularly in cereals, AMF may contribute to water conservation by supporting water uptake and altering root architecture, which enhances drought resilience [37].

However, while knowledge of root-associated microbiota's role in plant development under challenging conditions is expanding, further research is needed on the plant traits at genotypic level that regulate interactions with soil microbial communities and on the diversity of plant microbiota that ensure optimal responses. The study of microbial interactions in these crops could lead to breakthroughs in sustainable farming by identifying beneficial traits that improve plant health and productivity.

Micro4Life: new tools to study the interactions with root-associated microbes in grape and rice for improving resilience

The challenges outlined above are being tackled by the recently funded AGER project Micro4Life ("Enabling the potential of the unexplored: exploiting tailored microbial consortia to enhance environmental, societal and economic sustainability and resilience of Italian agro-ecosystems"). The project is founded on the premise that innovation stems from the generation of new knowledge, while its effective implementation and refinement depend on targeted dissemination and engagement activities across multiple levels. In detail, Micro4Life has three main aims. First, it will evaluate a variety of genotypes from core crop species along a water availability gradient, using both controlled environment experiments and field trials. This screening will identify traits related to resource use efficiency (in terms of both exploration and exploitation) and stress tolerance, as well as characterize rhizosphere processes, including microbiome function, and their impact on crop resilience. Second, the project will assess how natural growth environments and soil conditions influence the interactions between rice/grapevine and their associated soil microorganisms. By analyzing soil health, microbial diversity, and agroecosystem services across different cropping systems and pedo-climatic conditions, Micro4Life aims to determine how abiotic factors, such as drought, may mediate these relationships, to enhance resource use efficiency and crop performance while maintaining soil quality. Third, the project will actively engage relevant stakeholders, disseminating its findings on root and rhizosphere traits to support the development of more resilient grape and rice in the face of climate change in diverse agro-ecosystems. This knowledge will help in elucidating how roots interact with the rhizosphere/endophytic microbiome with the final aim of delivering more sustainable crop

cultivars and cultivation systems. Particularly, Micro4Life will fill the gap in translating advanced plant microbiome engineering into practical field applications.

The research questions still open that Micro4Life will answer include:

▪ How tailored and efficient SynComs could be realized for perennial (*e.g.*, grape) and annual (*e.g.*, rice) crop plants?

▪ Can the aptitude to recruit a microbial community be improved?

▪ How tailored microbiota can improve resource use efficiency for important crops and affect GHG emissions?

▪ How SynComs will affect plant and soil (chemical and biotic) processes?

Moreover, developing tailored SynComs enhancing rice and grapevine yield under stressful conditions, such as reduced water availability, could be an innovative nature-based solution able to reduce water-related conflicts which are rising worldwide due to several reasons, *e.g.*, climate change, severe drought, growing population, unsuitable water resources management among the others [38].

To ensure the reliability and scalability of the developed SynComs, Micro4Life plans to validate their performance across contrasting soil types (rice) and tillage management (grapevine). This includes testing under different physicochemical conditions and microbial backgrounds, in order to assess the stability, adaptability, and consistency of SynCom-mediated plant benefits by combining molecular, biochemical and ecophysiological approaches. Such validation is essential to confirm the potential of SynComs as broadly applicable bioinoculants under diverse field realities.

Conclusions

The generation of novel crop genotypes with an enhanced ability to interact with beneficial microorganisms inhabiting the rhizosphere and the root apparatus represents a novel concept in breeding strategies that should be promoted [1,2]. Deciphering how these microbial communities have an impact on carbon sequestration is also a point to be addressed. Integrating beneficial soil microorganisms with the use of improved crop genotypes selected for effective microbe interaction can enhance water-use efficiency, lowering the risk of scarcity-driven conflicts and the subsequent political instability. However, to achieve these

aims, inclusive water-governance processes that engage civil society, economic actors, women, and youth, should be adopted. In addition, advancing these innovations requires a strong emphasis on field-based research and bidirectional knowledge exchange with farmers, who play a pivotal role as co-developers of practical solutions. In this scenario, the evaluation of diverse cultural conditions should be also considered, providing novel information on how the management of the agricultural system will affect establishment before introduction of "biofertilizers", which is often unpredictable, considering that the successful establishment of these inoculants remains a challenge. Nowadays, scientific research in agriculture should promote, through the application of interdisciplinary approaches, the achievement of sustainable development goals (SDGs), particularly: SDG2, by increasing sustainable agriculture by leveraging microbial diversity and reducing fertilizer application rates; SDG3, by improving in soil quality and functioning, farming system resilience to climate change, reducing commercial fertilizer application rates, and ameliorating product nutrient status; SDG13, by strengthening resilience and adaptive capacity to climate- related challenges; SDG15, by contributing to avoid degradation of land and soil; SDG17, by strengthening joined actions between scientists, stakeholders, private sectors and civil society to stimulate sustainable rural development.

Declarations

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Conflict of Interest

The Authors declare that there is no conflict of interest.

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Author Contributions

FT: Conceptualization, Writing - Review & Editing; **FS**, Writing - Review & Editing; **WC**, Writing - Review & Editing; **RB:** Conceptualization, Investigation, Writing – Review & Editing.

Figure 1

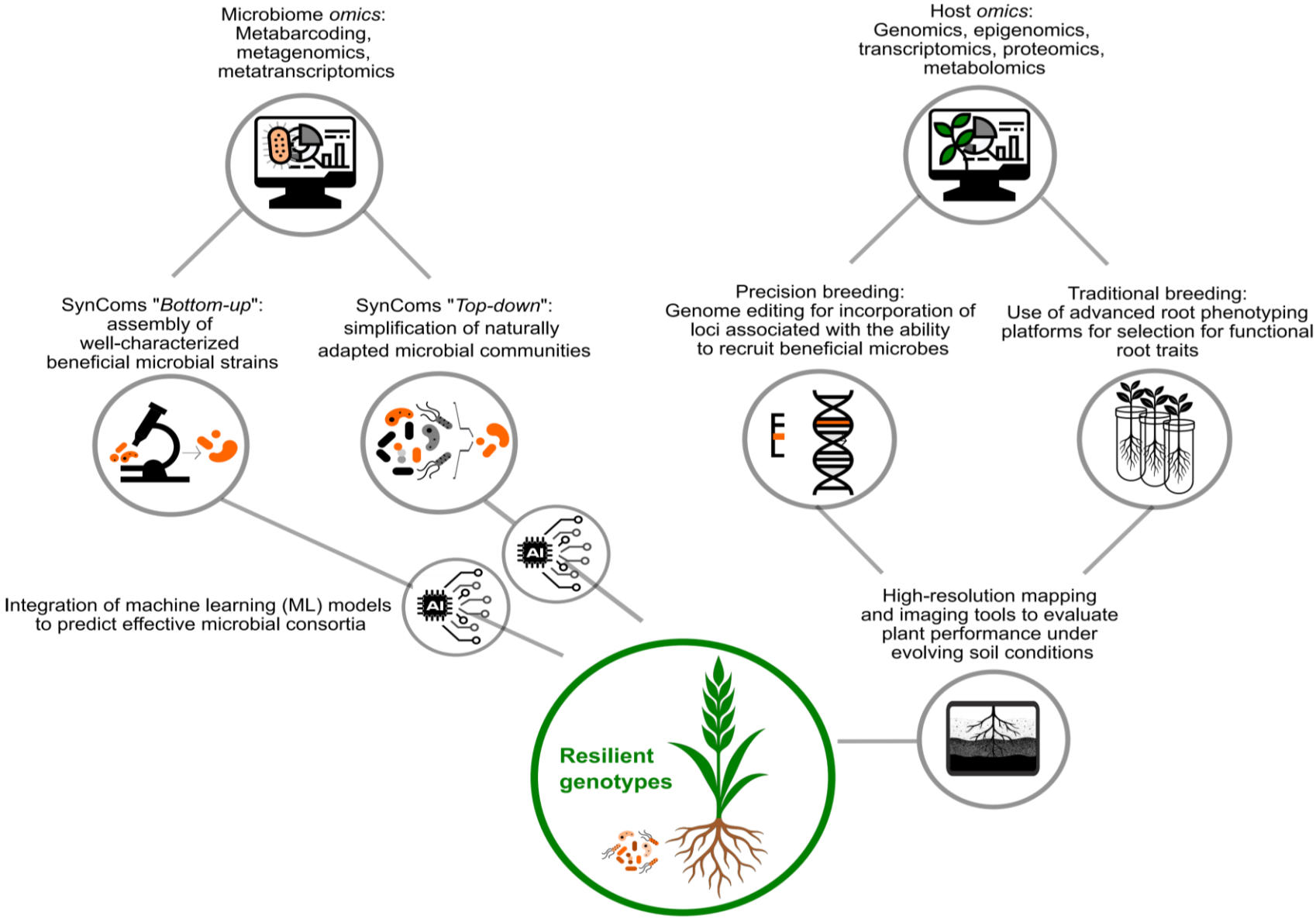
Microbiome *omics*:
Metabarcoding,
metagenomics,
metatranscriptomics
Host *omics*:
Genomics, epigenomics,
transcriptomics, proteomics,
metabolomics
SynComs "*Bottom-up*":
assembly of
well-characterized
beneficial microbial strains
SynComs "*Top-down*":
simplification of naturally
adapted microbial communities
Precision breeding:
Genome editing for incorporation of
loci associated with the ability
to recruit beneficial microbes
Traditional breeding:
Use of advanced root phenotyping
platforms for selection for functional
root traits
AI
AI
Integration of machine learning (ML) models
to predict effective microbial consortia
High-resolution mapping
and imaging tools to evaluate
plant performance under
evolving soil conditions
Resilient
genotypes

Figure 1. Schematic workflow for designing resilient crops through plant host-microbiome engineering. Microbiome *omics* provide the data for the two SynComs approaches, that can be optimized through machine learning predictive models. Complementary host *omics* provide the data to be used in traditional breeding, aided by advanced root-phenotyping platforms for functional-root traits, and in precision breeding, in which alleles that enhance beneficial-microbe recruitment are introduced by genome editing. The resulting genotypes can be validated by high-resolution root-imaging tools to assess their performance under evolving soil conditions.

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