

MULTI-OMICS APPROACHES FOR IMPROVING SOIL–PLANT INTERACTIONS IN CROP PRODUCTION: A REVIEW

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ABSTRACT

The soil-plant interactions comprise one of the most complex biological systems where plant roots, soil characteristics, roots-derived metabolites and rhizosphere microbes operate to influence nutrient acquisition, growth and productivity of plants. Traditional methods involving analysis of individual parts of this system are often not sufficient to fully understand the molecular and ecological processes taking place in the soil-plant interactions. With the emergence of multi-omics technologies, such as genomics, metagenomics, transcriptomics, metatranscriptomics, proteomics, metaproteomics, metabolomics, ionomics, epigenomics and phenomics, it became possible to study the soil-plant interactions on different biological levels. By applying the mentioned technologies, it is possible to correlate the genetic potential with the gene expression, the protein activity, the metabolites produced and accumulated by the plant, elemental content of the plant as well as its phenotype. Moreover, the investigation of the plant genome-microbiome interactions would allow identifying specific microbial community and plant genes involved in the nutrient-use efficiency, root development and stress resistance. Multi-omics approaches are also applied with the help of artificial intelligence, machine learning and high-throughput phenotyping to produce predictive models for crop production. Recent large-scale field experiments conducted in *B. napus* have shown the feasibility of integrating host genomics, root transcriptomics, rhizosphere microbiomes and ion omics to explain the natural variation of nitrogen acquisition. However, there still exist the problems related to the cost, data integration, spatial and temporal variability, microbial annotation, standardization and field validation. The future integration of multi-omics with microbiome engineering, precision agriculture, artificial intelligence and climate-smart crop breeding may greatly facilitate the process of sustainable intensification of agricultural production. This review covers the main aspects of multi-omics technologies in improving the soil-plant interactions and crops production.

KEYWORDS: soil-plant interactions, multi-omics, microbiome, transcriptomics, metabolomics, and ionomics.

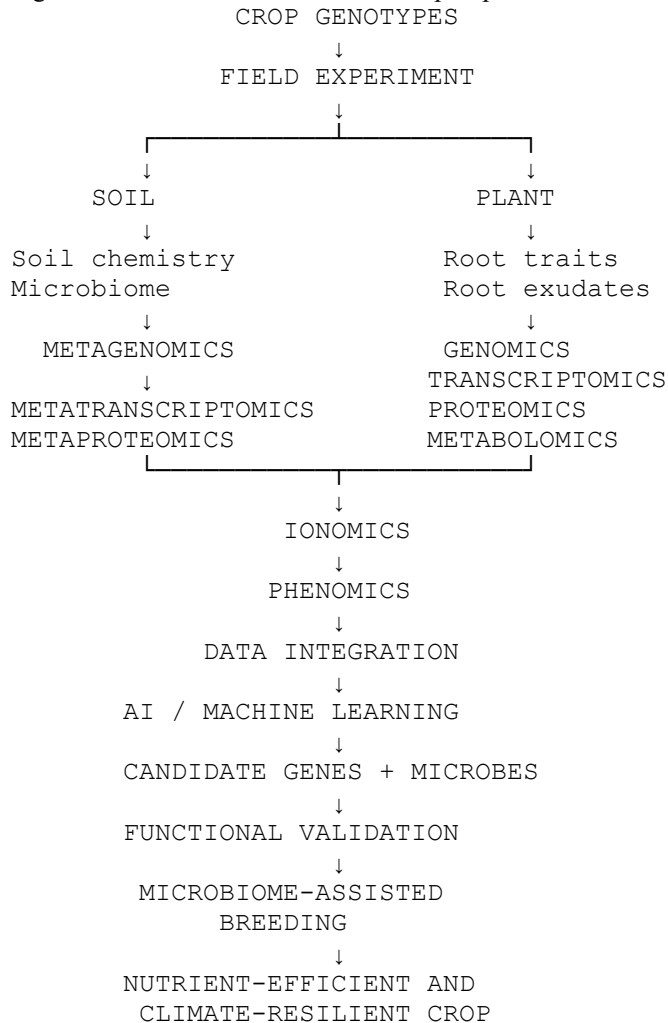
INTRODUCTION

Plants' productivity depends on interactions between plant roots and soil environment. The soil gives plants access to water, minerals, and nutrients, while plant roots alter the chemistry and biology of soil. One of the most actively changing zones of the soil is the rhizosphere – the thin layer of soil affected by plant roots. Root growth, root exudates, microbial colonization, and nutrient cycles change the rhizosphere environment continuously. On the other hand, soil microbes affect the growth of the plant by means of nutrient mineralization, biological nitrogen fixation, phosphorous solubilization, hormone synthesis, diseases suppression, and stress tolerance (Trivedi et al., 2020).

Plant-microbe interactions are mutual. Plants deliver sugars, amino acids, organic acids, phenolics, flavonoids, and other compounds into the rhizosphere via root exudation. These substances act as nutrients and chemical signal molecules that regulate the recruitment of microbes and their activity. As a result, microorganisms change the chemical composition of substances and increase their biological activity, modify the nutritional environment and the physiology of plants. Thus, plant performance not only depends on genetic parameters of the plant but also on the interaction of the plant with the environment and its microbial communities, (Li et al., 2026).

This information becomes particularly valuable in the case of nutrient deprivation, drought, salinity, soil degradation and increased climatic variability. Traditional analyses of the soil and plants can give only information on particular elements, such as the concentration of nutrients, abundance of microbes or the level of gene expression. However, the interactions between the soil and plants occur simultaneously on many levels of the biological system. A gene can influence the synthesis of proteins, which control metabolic pathways and affect root exudates, microbial colonization, and nutrient uptake. Therefore, the examination of a single level of the system may give incomplete picture, (Kumar et al., 2023).

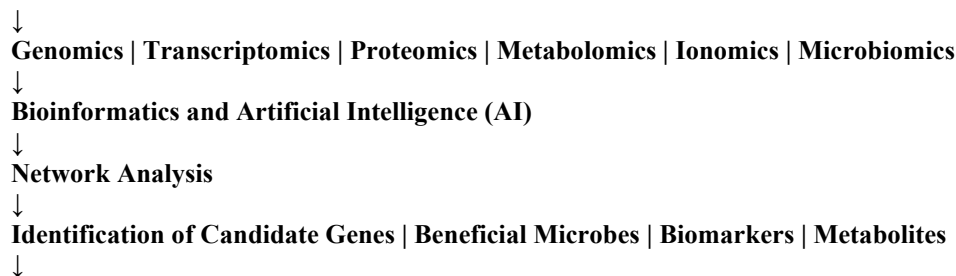
Figure 1. Multi-omics workflow for crop improvement



New approaches based on multi-omics technologies can help to overcome this limitation. Multi-omics can be defined as the combined analysis of two or more molecular levels, such as genomics, transcriptomics, proteomics, metabolomics, ionomics, and microbiomics. Such combination of the datasets allows analyzing biological system from its potential at genetic level till functional activities and phenotype (Yang et al., 2021).

Figure 2. From Multi-Omics Discovery to Sustainable Agriculture

Multi-Omics Data



Functional Validation



Microbial Inoculants | Breeding Programs | Precision Fertilization



Climate-Smart Agriculture



Higher Productivity + Improved Soil Health



Sustainable Crop Production

Recent developments have also widened the scope of applications of multi-omics from lab experiments to field investigations. For instance, (Li et al. 2026) combined root transcriptomes, rhizosphere bacteria community profiles, root ionomes, and host genome information in *Brassica napus*. Their findings demonstrated relationships among host genetic variation, rhizosphere bacterial communities, root development and nitrogen acquisition, illustrating the potential of multi-omics for understanding agriculturally important soil–plant interactions.

Thus, multi-omics approaches are becoming increasingly important for developing nutrient-efficient crops, identifying beneficial microorganisms, improving soil health and designing sustainable crop production systems. This review discusses the major omics technologies used to investigate soil–plant interactions and evaluates their applications, limitations and future prospects in crop production.

Table 1. Major multi-omics approaches for studying soil–plant interactions

Omics approach	Major information generated	Application in soil–plant interactions	Expected outcome
Genomics	SNPs, genes, structural variation	Identification of plant genes controlling roots, nutrient uptake and microbiome recruitment	Nutrient-efficient cultivars
Metagenomics	Microbial taxa and functional genes	Characterization of rhizosphere microbial diversity and functional potential	Identification of beneficial microbial functions
Metatranscriptomics	Active microbial transcripts	Detection of microbial functions operating under specific soil conditions	Functional understanding of active microbiome
Transcriptomics	Plant gene-expression profiles	Identification of root responses to nutrients, microbes and stresses	Candidate genes and pathways
Proteomics	Plant proteins and enzymes	Identification of nutrient transporters, defense proteins and stress-responsive proteins	Functional mechanisms
Metaproteomics	Microbial proteins	Identification of active microbial enzymes and pathways	Functional microbiome characterization
Metabolomics	Plant and microbial metabolites	Analysis of root exudates, signaling compounds and stress metabolites	Identification of plant–microbe chemical communication
Ionomics	Elemental composition	Quantification of N, P, K, Fe, Zn and other elements	Nutrient uptake and homeostasis
Epigenomics	DNA methylation and chromatin modifications	Understanding environmental regulation of plant responses	Stress adaptation mechanisms
Phenomics	High-throughput plant traits	Root architecture, biomass, nutrient status and yield	Linking molecular traits with crop performance
Spatial omics	Spatial distribution of transcripts/metabolites	Localization of plant–microbe interactions	Cell- and tissue-specific mechanisms

Source: Adapted conceptually from Yang et al. (2021), Bhimani et al. (2024), Li et al. (2026) and Li et al. (2026 review).

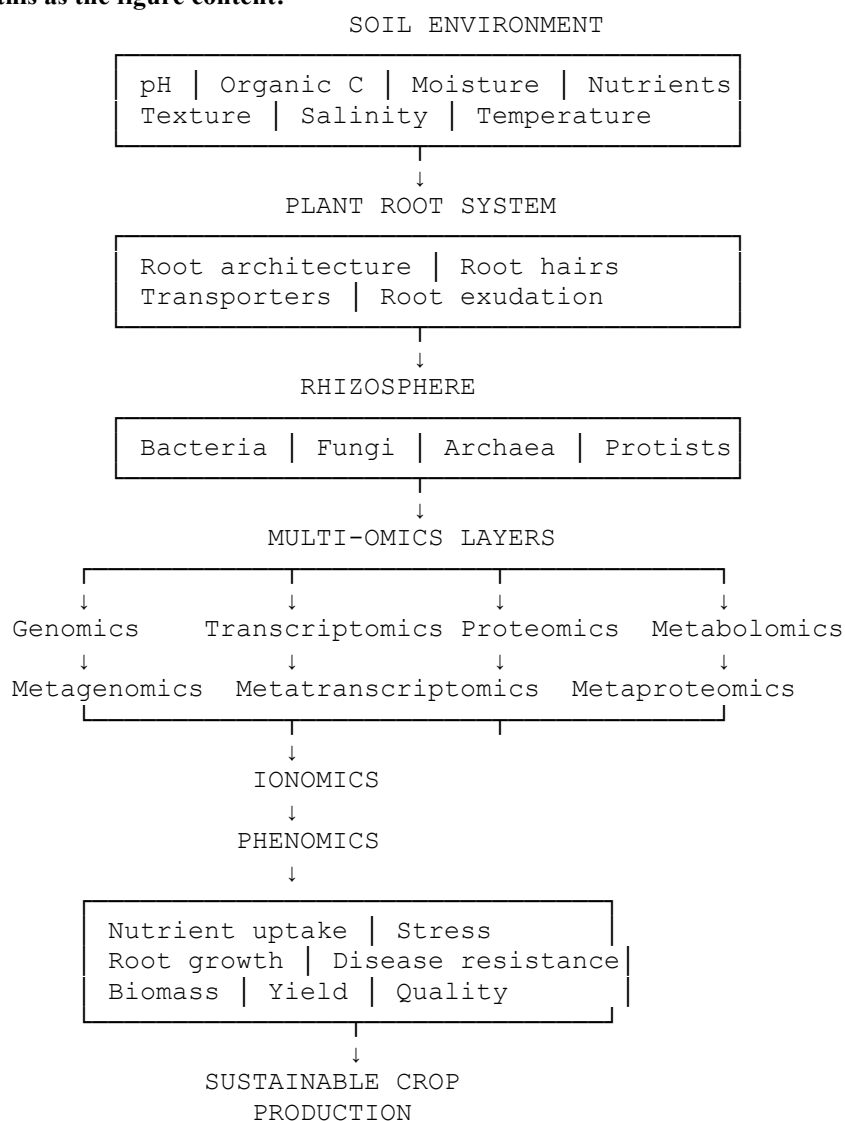
2. Complexity of Soil-Plant Interactions

Soil-plant interactions represent a set of physical, chemical, biological and molecular events that occur at once in the vicinity of the root system. The factors such as soil texture, pH, organic carbon, moisture, temperature, salinity, nutrient content and mineral composition affect root growth and microbial community. Simultaneously, the roots

transform the environment due to their capacity of nutrient absorption, proton secretion, exudation and turnover, (Hnini, et al., 2025).

Figure 3. Integrated multi-omics framework for soil–plant interactions

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Rhizosphere microbiota is another key element of this complex system. It includes various bacteria, fungi, archaea and other microorganisms which are associated with roots. The microbes take part in nutrient cycling and can affect the plant growth either directly or indirectly, for instance, by fixing atmospheric nitrogen, making phosphorus soluble, producing siderophores or phytohormones in the case of beneficial bacteria, while beneficial fungi help in nutrient and water acquisition and pathogen resistance (Trivedi et al., 2020).

Table 2. Root exudates and their role in rizosphere microbial recruitment

Root-derived compound/group	Major function	Potential microbial response	Soil–plant consequence
Sugars	Carbon and energy source	Stimulation of heterotrophic microorganisms	Increased microbial activity
Amino acids	C and N source/signaling	Selective microbial recruitment	Nutrient cycling
Organic acids	Nutrient mobilization	Stimulation of functional microorganisms	Improved P and micronutrient availability

Flavonoids	Signaling and defense	Recruitment/communication with selected microbes	Symbiosis and root protection
Phenolics	Signaling and antimicrobial activity	Selection of microbial populations	Microbiome assembly
Coumarins	Fe acquisition and signaling	Interaction with rhizosphere microorganisms	Improved Fe availability
Hormone-related metabolites	Root development/signaling	Microbial modulation of hormone pathways	Root architectural changes
Specialized metabolites	Chemical communication	Selective microbial enrichment or suppression	Microbiome structuring

Moreover, the genotype of plants determines the composition and activity of the rhizosphere microbiome since various genotypes form different root exudate patterns and recruit different microbial community in consequence. Thus, there is another strong connection between plant breeding and microbiome studies. Understanding of these connections allows researchers to select not only desirable plant traits but also the capacity of genotype to build up beneficial interaction with soil microorganisms, (Parveen, et al., 2026).

Table 3. Major soil–plant interactions investigated using multi-omics

Interaction	Important molecular components	Relevant omics	Agricultural significance
Nitrogen acquisition	N transporters, N-cycling microbes, amino acids	Genomics + transcriptomics + metagenomics + ionomics	Improved NUE
Phosphorus acquisition	Organic acids, phosphatases, P-solubilizing microbes	Metabolomics + metagenomics + transcriptomics	Reduced P fertilizer requirement
Potassium acquisition	K transporters, rhizosphere microorganisms	Transcriptomics + ionomics + microbiome	Improved K-use efficiency
Iron acquisition	Siderophores, chelators, Fe transporters	Metabolomics + transcriptomics + ionomics	Improved Fe nutrition
Drought tolerance	ABA, osmolytes, microbial metabolites	Transcriptomics + metabolomics + microbiome	Climate resilience
Salinity tolerance	Na ⁺ /K ⁺ homeostasis, osmolytes, beneficial microbes	Ionomics + transcriptomics + metagenomics	Salt tolerance
Disease suppression	Defense genes, microbial antagonists, secondary metabolites	Metagenomics + metatranscriptomics + metabolomics	Biological disease management
Root development	Auxin, microbial metabolites, root-development genes	Transcriptomics + metabolomics + microbiome	Improved nutrient and water acquisition
Carbon cycling	Root exudates, microbial decomposition pathways	Metabolomics + metagenomics + metatranscriptomics	Soil carbon management

Sources: Trivedi et al. (2020); Yang et al. (2021); Bhimani et al. (2024); Li et al. (2026).

3. Multi-Omics in Soil-Plant Research

The general concept of multi-omics involves studying multiple biological levels at once and integrating them through bioinformatic, statistical, and systems biology approaches. Genomics gives information about the genetic potential; transcriptomics defines which genes are expressed. Proteomics studies proteins and enzymes, and metabolomics analyzes biochemical molecules. Ionomics gives information on the elemental composition of plants; phenomics studies physical and physiological phenotype, (Jain et al., 2024).

Table 4. Multi-omics layers and their contribution to soil–plant interaction research

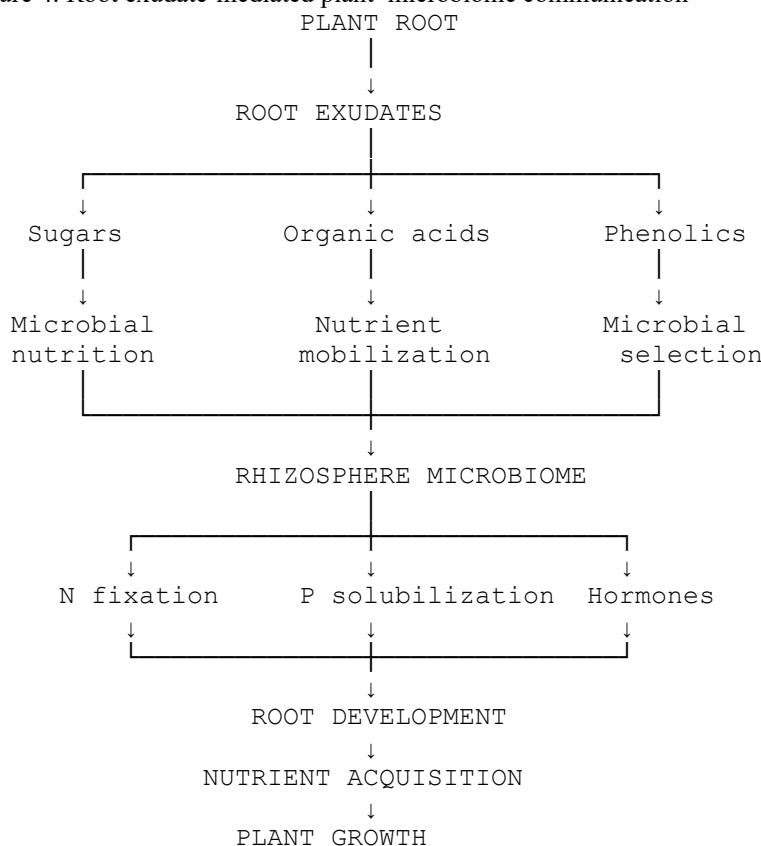
Biological layer	Key question	Representative techniques	Relationship with other layers
Genome	What genetic potential exists?	Whole-genome sequencing, GWAS	Genome → transcript
Microbial genome	Which microbes and functions are present?	16S/ITS sequencing, shotgun metagenomics	Microbial genes → transcripts
Transcriptome	Which genes are active?	RNA-seq, metatranscriptomics	Transcripts → proteins

Proteome	Which proteins are produced?	LC-MS/MS, metaproteomics	Proteins → metabolic pathways
Metabolome	Which biochemical compounds are produced?	GC-MS, LC-MS, NMR	Metabolites → signaling and nutrient mobilization
Ionome	Which elements are accumulated?	ICP-MS, XRF	Nutrient availability → plant nutrient status
Phenome	What is the resulting phenotype?	Imaging, root phenotyping, yield analysis	Molecular layers → phenotype
Environment	Which environmental factors regulate the system?	Soil analysis, sensors, weather data	Environment ↔ all biological layers

The power of multi-omics approach is defined by its hierarchy, which means that genetics may influence transcription; transcription – the amount of protein; proteins may regulate metabolic reactions, while metabolites may affect cell signaling and lead to physiological modifications and plant phenotype, (Chaturvedi et al., 2024).

In the field of soil-plant research, another level of complexity is added to multi-omics due to the microbiome. Metagenomics of microbes will help us identify microbes and their functional genes, and metatranscriptomics and metaproteomics will allow us to study their activity. After that, metabolomics would give us information on chemical molecules produced by plants and microbes. Thus, it will become easier for us to understand communication between plants and microbes and nutrient cycling (Bhimani et al., 2024).

Figure 4. Root exudate-mediated plant-microbiome communication



4. Genomics and Metagenomics

Genomics allows to get information on the genetic makeup of plants and use this information to determine the genes and genomic regions underlying root formation, nutrient acquisition, plant resistance to abiotic stress and interaction between plants and microbes. GWAS and genomic selection can identify alleles responsible for the complex agronomic traits, (Raza et al., 2023).

From the point of view of soil-plant interactions, genomics can be coupled with the analysis of microbiome to reveal whether certain plant genotypes always select certain microbes. This data will be essential for the design of microbiome-assisted breeding. In case if a certain allele results in recruitment of beneficial microbes, breeders can take it into account in addition to the classical yield and quality traits.

Metagenomics expands genomics by allowing to analyze the communities of microbes. Compared to culture-based techniques, metagenomics allows identifying a considerable number of microbes that cannot be cultivated in laboratory conditions. The shotgun metagenomics also allows revealing functional genes of the microbes associated with nitrogen metabolism, phosphorous acquisition, carbon degradation and stress resistance, (Yu et al., 2024).

5. Transcriptomics and Metatranscriptomics

Transcriptomics deals with the investigation of RNA molecules synthesized by a particular plant or microorganism in certain environmental conditions. Root transcriptomics can reveal genes turned on in cases of nutrient deficiency, drought, salinity, pathogen attack and microbial colonization, (Simarmata, et al., 2025).

Nevertheless, just the presence of a gene in metagenomes does not mean that the gene is active. Thus, metagenomics data are more and more often coupled with metatranscriptomics, metaproteomics and metabolomics to find out which microbes functions are active, (Chukwuneme, and Babalola, 2025).

For instance, nutrient deficiency can turn on genes of transport proteins, transcription factors, enzymes and signalling molecules. Thus, transcriptomics can reveal the molecular mechanisms of root sensing of soil nutrient availability, (Hnini et al., 2025).

Metatranscriptomics provides similar information but on the level of microbial community. While metagenomics shows functional capacity of microbes, metatranscriptomics shows what genes are actively expressed. Combination of metatranscriptomics and metagenomics allows differentiating between functions potentially possessed by microbes and those actively involved in soil functioning, (Grace, et al., 2026). Combination of transcriptomics of plants and metatranscriptomics of microorganisms is especially valuable since responses of both organisms to changes in environment are linked. The plant can respond to nutrient deficiency by synthesizing some metabolites, thus enriching the microbial community with microbes able to mobilize the required nutrient. As a result, the microorganisms can synthesize some compounds affecting root development, (Parveen et al., 2026).

6. Proteomics and Metaproteomics

Proteomics is a science of proteins synthesized by cell, tissue or organism. Proteins can be seen as a functional level between the transcriptional activity and physiological processes. Thus, proteomic analysis can provide additional information, which cannot be provided by the transcriptomic analysis, (Rai et al., 2023).

For instance, proteomic analysis of roots can show nutrient transporters, enzymes, antioxidant proteins and defense-related proteins. In case of drought or salinity stress, it is possible to see changes in proteins related to osmoregulation, ROS detoxification and stability of membrane, (Dos et al., 2022).

Metaproteomics is an extension of proteomics for microbial communities. It can allow the identification of enzymes involved in nitrogen fixation, phosphorus mineralization, organic matter decomposition and other soil processes. Thus, metaproteomics can help in overcoming the gap between the genetic potential and actual functions of microbes. The main problem of the proteomic analysis is its technical complexity. However, the integration of the proteomics with transcriptomics and metabolomics can substantially improve the functional analysis, (Pal, and Sengupta 2022).

7. Metabolomics and Root Exudates

Metabolomics studies the analysis of small molecules made by plants and microorganisms. This research area is especially crucial in soil-plants science since metabolites are the chemical language used by plants and microorganisms, (Grace, et al., 2026).

Root exudates consist of sugars, amino acids, organic acids, phenolic compounds, flavonoids and other secondary metabolites. These molecules affect the assembly of microbes and can alter the nutrient dynamics in the rhizosphere. Organic acids, for instance, can be engaged in the process of phosphorus mobilization, while phenolic compounds and flavonoids can affect microbial colonization and signaling, (Jyoti et al., 2025).

Metabolomics may also detect changes in plant biochemistry under nutrient deficiency and environmental stresses. By correlating the data obtained through metabolomics with transcriptomics, it becomes possible to establish connections between the levels of gene expression and metabolic processes (Pal, and Sengupta, 2022). By combining the information acquired from metabolomics and microbiome sequencing, it becomes possible to identify associations between certain root metabolites and microbes, (Saini et al., 2026).

8. Ionomics and Nutrient Acquisition

Ionomics implies a comprehensive investigation of the chemical elements' composition in biological tissues. The determination of essential nutrient concentration in crop species can be carried out by using ionomics; this includes nitrogen, phosphorus, potassium, calcium, magnesium, sulfur, iron, zinc, manganese and copper, (Li et al., 2026).

Ionomics can play an important role in understanding nutrient-use efficiency as nutrient concentration is the result of numerous factors that include nutrient availability in the soil, its uptake by roots, transport and accumulation in plant tissues. Combined with transcriptomics, ionomics helps to identify the correlations between nutrient concentration and the expression of nutrient transporter genes, (Ichihashi et al., 2020).

The integration of ionomics with microbiome information is also significant as beneficial microorganisms influence nutrient availability through mineralization, solubilization, and chelation. In other words, the difference in ionome

between crops can depend not only on their genetic characteristics but also on the composition of the microbial community, (Lal et al., 2024).

Recently conducted large-scale research concerning *Brassica napus* proved that such integration could be very promising as the researchers found significant correlations between host genome, root transcriptome, rhizosphere bacterial community and root ionome regarding nitrogen acquisition (Li et al., 2026).

9. Phenomics and High-Throughput Phenotyping

Phenomics serves as the bridge between the information on molecular level and agricultural performance. Multi-omics data become especially valuable when they can be associated with certain plant phenotypic traits such as root length, root architecture, biomass, nutrient concentration, chlorophyll content, water-use efficiency, flowering time, yield and quality, (Gahtyari et al., 2026).

High-throughput phenotyping technologies employ such approaches as imaging, sensing, drone technologies, remote sensing and automated phenotyping to obtain a huge amount of plant phenotypic data. Phenomics is directly related to soil-plant interactions because of root architecture that determines the volume of soil explored by plants, (Wang et al., 2026).

The combination of phenomics with genomics and other omics techniques will enable to discover the markers linked with desirable phenotypes. Such integration will allow to speed up crop breeding significantly, (Im et al., 2026).

10. Multi-Omics Approach for Studying Nitrogen-Use Efficiency

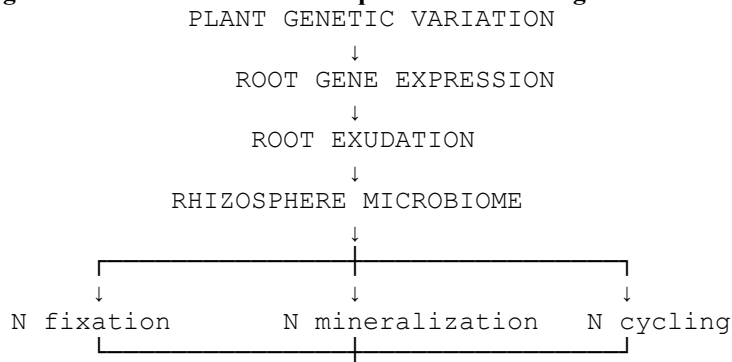
Nitrogen-use efficiency is one of the most critical traits for sustainable crop production since over-fertilization of crops may be costly and environmentally damaging. Nitrogen absorption requires several processes such as nitrogen mineralization in the soil, microbial nitrogen metabolism, root uptake, transport, assimilation and redistribution, (Kunwar et al., 2025).

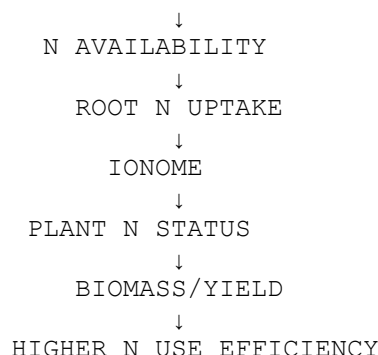
Multi-omics allows to study all these processes at once. Genomics may reveal genetic diversity related to nitrogen uptake, transcriptomics – genes responsive to nitrogen, metagenomics – microbes responsible for nitrogen metabolism, metabolomics – nitrogen-related metabolites, while ionomics measures nitrogen uptake, (Ma et al., 2026). One of the examples of using such an approach on the field scale is a study conducted by Li et al. (2026). The researchers found out that host genomic and microbial factors play a significant role in nitrogen uptake and found connections between rhizosphere microbes, root growth and nitrogen uptake.

Table 5. Application of multi-omics to major nutrient interactions

Nutrient	Important plant mechanisms	Important microbial mechanisms	Relevant omics
Nitrogen	N transporters, assimilation enzymes	N fixation, mineralization, nitrification	Genomics, transcriptomics, metagenomics, ionomics
Phosphorus	P transporters, organic-acid secretion	P solubilization, phosphatase production	Transcriptomics, metabolomics, metagenomics
Potassium	K transport and homeostasis	K mineralization	Transcriptomics, ionomics, microbiome
Iron	Fe transporters, chelators	Siderophore production	Metabolomics, transcriptomics, ionomics
Zinc	Zn transport and homeostasis	Zn mobilization	Ionomics, transcriptomics, metagenomics
Sulfur	Sulfate transport and assimilation	Sulfur mineralization	Transcriptomics, metagenomics, metabolomics

Figure 5. Multi-omics-assisted improvement of nitrogen-use efficiency





11. Multi-Omics for Phosphorus Acquisition

Often, plants do not receive phosphorus because it becomes immobilized in the form of minerals and organic phosphates. Plant responses to lack of phosphorus include alterations in root architecture, transporter expression and production of organic acids, (Kumar et al., 2023).

Rhizosphere microorganisms can help plants acquire phosphorus by mineralization of organic phosphorus and phosphate solubilization. Phosphate-solubilizing microorganisms are able to produce organic acids and enzymes to solubilize inorganic phosphate, (Grace et al., 2026).

Integration of root transcriptomics and metabolomics can be used to understand how plants alter their root metabolism in response to lack of phosphorus. Metagenomics will add information on microorganisms able to mobilize phosphorus. This information can be used for breeding microbial inoculants and crop varieties with better efficiency in phosphorus acquisition, (Simão, et al., 2026).

12. Multi-Omics and Drought Stress

Drought affects moisture and nutrient content of soil, root development and activities of soil microorganisms. Plant responses to drought include alterations in root system architecture, stomata regulation, osmolytes accumulation, hormone signaling and oxidative stress resistance, (Sharma et al., 2024).

Transcriptomics will help to find genes responding to drought, while metabolomics will reveal the accumulation of osmoprotective compounds such as amino acids and soluble sugars. Microbiome analysis will show microorganisms associated with drought-resistant plants. Beneficial microorganisms can influence root development and water acquisition, (Vidal, et al., 2022).

13. Multi-Omics and Salinity Stress

Another important problem in agriculture is salinity. Excessive levels of sodium and chloride affect water uptake and nutrient balance. Plants need to maintain ionic homeostasis and protect their cells from oxidative damage, (Adil et al., 2026).

Ionomics is especially helpful in studying salt resistance because it allows quantification of such ions as Na^+ , K^+ , Ca^{2+} , Mg^{2+} and others. Transcriptomics helps to find genes responsible for transporters functioning, while metabolomics reveals osmoprotectors.

Some microorganisms that are associated with salt-resistant plants can also contribute to plant tolerance to salinity. Multi-omics integration can thus identify the best plant-microorganism combinations for saline soils, (Simarmata, et al., 2025).

14. Multi-Omics for Disease Suppression

Soil microorganisms have a crucial role in determining whether soil is conducive or suppressive to plant diseases. Disease suppressive soils are those that harbor microorganisms capable of competing with the pathogens, producing antimicrobial compounds or stimulating plant defense reactions, (Hnini et al., 2025).

This type of multi-omics analysis will reveal biological mechanisms responsible for improved drought tolerance. The information received will be helpful for breeding drought-resistant crops, (Raza, et al., 2026).

Metagenomics is a method for identifying such microorganisms, while metatranscriptomics and metaproteomics would be useful in determining the functionality of microbes. Metabolomics would help identify antimicrobial compounds and defense metabolites, (Mathuria, et al., 2024).

The integration of the above methods would enable researchers to determine microbial biomarkers of disease suppressive soils and use them to create microbial communities used in biological disease control, (Rao and Sunkad, 2024).

15. Multi-Omics-Assisted Crop Breeding

Crop breeding is usually phenotype-based and involves identification of markers linked with desired traits. Multi-omics brings new dimensions to breeding by providing information on the molecular basis of a trait, (Joshi et al., 2022).

Information from genomic studies would show linkage between alleles and desired root traits. Transcriptomics and metabolomics would help in understanding the underlying biochemical pathways for root development, nutrition, and stress tolerance. Information from metagenomics would reveal whether particular genotypes of plants are capable of recruiting beneficial microorganisms from the environment, (Saleem et al., 2025).

The above possibilities make it possible to develop crop breeding practices where the genotypes chosen would depend not only on yield and nutritional value but also their interactions with beneficial microorganisms, (Field 2026).

16. Integration of Multi-Omics with Artificial Intelligence

The major limitation of multi-omics data is the large number of variables obtained from different analytical platforms. Machine learning and artificial intelligence techniques can help reveal connections that are difficult to find through conventional statistical methods, (Yetgin 2025).

Through the use of machine learning algorithms, the integration of genomics, transcriptomics, metabolomics, microbiomes, soils, and phenomics data could enable predicting crop performance. For instance, models would predict nutrient use efficiency, susceptibility to diseases, drought tolerance, or crop yields depending on molecular and environmental variables (Kant et al., 2025). Network analysis might also be performed to identify interconnections between genes, microbes, and metabolites. Genes and microbial taxa that are highly interconnected might become useful as biomarkers or targets for experimental testing, (Zack et al., 2025).

However, machine learning algorithms should not substitute biological experiments since predictions produced through the use of machine learning need verification through experimental studies.

17. Multi-Omics and Precision Agriculture

Precision agriculture is an approach that allows controlling the growth of crops depending on variability in soils, plants, and environments. Multi-omics can be used in precision agriculture by identifying biological markers of nutrient deficiencies, soil deterioration, microbial unbalance, and stress in crops, (Thingujam, et al., 2025). Soil sensors and remote sensing allow detecting the difference in the growth of crops spatially; at the same time, multi-omics could be helpful in understanding biological reasons for differences. The combination of datasets obtained through the use of soil sensors, remote sensing, and multi-omics together with geographical information systems and machine learning would make it possible for the farmer to apply fertilizers, irrigation, and microbial inputs depending on specific needs of the area.

Thus, the future precision agriculture system could integrate:

Soil sensors + remote sensing + genomics + microbiome + metabolomics + ionomics + phenomics + artificial intelligence → site-specific management.

Table 6. Applications of multi-omics in sustainable crop production

Application	Multi-omics strategy	Potential benefit
Nutrient-use efficiency	Genomics + microbiome + ionomics	Lower fertilizer requirement
Microbiome-assisted breeding	GWAS + microbiome + transcriptomics	Selection of microbiome-responsive cultivars
Biofertilizer development	Metagenomics + metabolomics + metaproteomics	Identification of effective microbial strains
Synthetic microbial communities	Microbiome + metabolomics + transcriptomics	Stable microbial consortia
Drought management	Transcriptomics + metabolomics + microbiome	Improved drought resilience
Salinity management	Ionomics + transcriptomics + microbiome	Improved ionic homeostasis
Disease management	Metagenomics + metabolomics + metatranscriptomics	Identification of disease-suppressive microbiomes
Soil-health assessment	Metagenomics + metabolomics + soil chemistry	Biological indicators of soil health
Precision agriculture	Multi-omics + sensors + AI + GIS	Site-specific crop management
Crop quality	Genomics + metabolomics + ionomics	Improved nutritional and biochemical quality

18. Multi-Omics in Soil Health Assessment

Soil health assessment cannot be carried out based solely on chemical parameters of soil. Biological parameters, such as microbial diversity, genetic functions, enzymatic activity, and metabolome of soil, contain vital information about its functioning, (Kumar et al., 2023).

Metagenomics helps to obtain information about microbial diversity and genetic potential of a soil microbial community, while metatranscriptomics is necessary for detecting active microbial functions. Metabolomics enables

identification of alterations in soil biochemical substances, and proteomics helps to understand enzymes functioning. Therefore, multi-omics soil health index would integrate microbial, biochemical, and physicochemical parameters of soil health, (Panicker, 2024).

19. Microbiome Engineering and Synthetic Microbial Communities

One of the most promising areas of application for soil–plant multi-omics is microbiome engineering. Instead of introducing individual microbial strains into soil without considering the existing soil microbiome, scientists can use information from multi-omics to select combinations of microorganisms carrying out complementary activities, (Contreras-Salgado, et al., 2024).

Synthetic microbial communities or SynComs can be created using information on microbial interactions and effects on plants. One microorganism could fix nitrogen, another could solubilize phosphorus and yet another could synthesize substances stimulating root growth. Multi-omics can be used to find out whether such microorganisms are capable of colonization of roots and expression of their expected activity in field conditions, (Shayanthan, et al., 2022).

20. Spatial and Single-Cell Multi-Omics

Conventional omics methods usually allow average measurements across the whole plant root, soil sample or microbial community. However, interactions between plants and soil are localized. Microorganisms might interact with specific root cells, hair roots or localized zones of the rhizosphere.

Spatial transcriptomics and spatial metabolomics can help identify where certain genes and metabolites are produced. Single cell approaches can further analyze differences between individual cells of plants. It is hoped that these technologies will shed more light on localized interactions of plants and microbes.

21. Major Challenges

Despite numerous opportunities offered by multi-omics approaches, there are several challenges associated with them. The first challenge is associated with the cost of these studies. Genomic sequencing, mass spectrometry, metabolomics analysis and high throughput phenotyping require expensive equipment and specialized personnel.

The next challenge is associated with integration of data generated by different omics platforms. Different omics technologies generate data sets that vary in structure, scale and biological complexity. Integration of such data requires advanced bioinformatic and statistical approaches.

Another problem is biological variability. Properties of soil and its microbiome could vary rapidly depending on season, development stage of crops, irrigation, fertilization and environmental factors. Thus, results obtained from one field or one season may not be valid for another field or season.

Also, it is difficult to differentiate between correlation and causation. The presence of the association between the presence of specific microbial taxon and growth of plants does not necessarily mean that this microorganism affects plant growth. Validation of the function of microorganism in question should be conducted using inoculation of plants with such microorganism, genetic modifications and field trials.

Table 7. Major challenges and future solutions

Challenge	Implication	Future research direction
High analytical cost	Limits large-scale studies	Low-cost and targeted multi-omics
Data complexity	Difficult interpretation	AI and integrated bioinformatics
Soil heterogeneity	High experimental variation	Standardized sampling
Temporal variation	Microbiome changes with crop stage	Longitudinal sampling
Spatial variation	Bulk analysis may mask interactions	Spatial omics
Limited microbial databases	Poor functional annotation	Expanded reference genomes
Correlation-based conclusions	Limited causal evidence	Functional validation
Laboratory–field gap	Poor field consistency	Multi-location field trials
Lack of standardized protocols	Difficult comparison among studies	International standards
Data storage	Large datasets require infrastructure	Cloud and high-performance computing

Table 8. Recent studies supporting multi-omics applications

Study	Crop/system	Multi-omics approach	Major finding	Application
Yang et al. (2021)	Multiple crops	Genomics, transcriptomics, proteomics, metabolomics, phenomics	Multi-omics improves understanding of complex crop traits	Crop improvement
Bhimani et al. (2024)	Plant–soil systems	Genomics, transcriptomics, proteomics, metabolomics	Omics reveals plant–microbe communication and root-exudate effects	Plant–microbe research
Fan et al. (2024)	Rhizosphere systems	Metabolomics + microbiome approaches	Root exudates and microbial metabolites	Sustainable agriculture

			mediate rhizosphere communication	
Li et al. (2026)	<i>Brassica napus</i>	Host genomics + transcriptomics + microbiome + ionomics	Microbial and host features explained up to 45% of variation in N uptake	Microbiome-assisted breeding
Li et al. (2026)	Soil-plant-microbial systems	Metagenomics + metatranscriptomics + metaproteomics + metabolomics	Functional multi-omics connects microbial potential with activity	Soil health
Panek et al. (2026)	Agricultural ecosystems	Microbiome sequencing + multi-omics	Multi-omics supports soil-health and plant-disease prediction	Sustainable agriculture

Sources: Yang et al. (2021); Bhimani et al. (2024); Fan et al. (2024); Li et al. (2026); Panek et al. (2026).

22. Future Perspectives

The future of soil-plant research is going to focus on integration rather than use of individual omics technologies. Multiscale omics will be integrated with environmental data, high-throughput phenotyping, remote sensing, soil sensors, and artificial intelligence.

One of the most promising directions is the development of plant genotype $\times$ microbiome $\times$ environment models. They can help understand why one genotype of crop is performing well in some soil conditions, but not good enough in others.

Another great opportunity would be integration of multi-omics and genome editing. If the genes related to plant-microbe interactions are found, then genome editing technologies like CRISPR can be applied to modify desirable traits.

Development of microbiome-assisted breeding programs is also expected. In the future, breeding programs can assess crop genotypes not only by conventional criteria such as yield and disease resistance, but also by their ability to recruit beneficial microorganisms. Multi-omics is going to contribute to climate-smart agriculture. The identification of the molecular mechanisms responsible for the stress caused by drought, salinity, heat, and nutrient shortage will facilitate the development of resilient crops and consortia of beneficial microorganisms.

23. CONCLUSION

The multi-omics technologies provide the systems-level approach for studying interactions taking place in soil-plant system. Genomics defines genetic potential, transcriptomics shows the activity of the genes, proteomics supplies information about the functions of these genes, metabolomics helps to define biochemical communication, ionomics tells about elemental accumulation and phenomics correlates molecular events with plant phenotype. By integrating all these omics with metagenomics and other microbiome technologies it is possible to study soil-plant interactions starting from the composition of the microbial community and ending with nutrient uptake and crop yield.

The integration of multi-omics can be particularly helpful for improving nitrogen- and phosphorus-use efficiency, increasing drought and salinity tolerance, identifying disease-suppressive microbiomes, establishing microbiome-assisted breeding programs, and assessing soil health. Recent research at the field scale shows how host genetic variability and rhizosphere microbiota interact influencing the root development and nutrient acquisition. However, application of multi-omics requires standardized sampling, advanced computational analysis, functional validation and field-scale experiments. The future integration of multi-omics with artificial intelligence, spatial omics, microbiome engineering, genome editing, remote sensing, and precision agriculture is likely to bring a revolution to the study of the soil-plant system.

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