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# Emerging trends for Harnessing plant metabolome and microbiome for sustainable food Production

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## ABSTRACT

Food production is obligatory to ensure efficient plant yield and accomplishments in a fast-growing global population predicted to exceed 9 trillion people in the future. In this regard, advancement in harnessing plant core microbiome using various 'omics' will be fruitful towards sustainable goals. Metabolomics, as we know, is a robust method and is very useful for evaluating the property of plant species before their genomes are completely sequenced. Metabolomics and other technologies facilitate us to unravel main agricultural output challenges such as regulating the health of soil microbial communities. Plant-microbe interactions are an integral aspect of this planet. This review will develop a complete and elaborated panoramic view for bare acquaintances of interaction between plants and microbes required for developing different approaches in metagenomics, meta-transcriptomics, and metabolomics to increase general cultivable performance. In addition, the study will focus on microbiome development in earlier plant production and establish informatics pipelines for core microbiome design to optimize plant and indigenous microorganism interactions. This study will also concentrate on inter / intra interactions, such as quorum sensing activity, signal molecules like phytohormones, bacteriocins, etc. The bio-informatics genome mining for biosynthesis gene clusters leading to the identification of novel bioactive compounds and new metabolomics advances will also be established. A comprehensive model will be framed to assess the advancements in exploiting the microbiome and metabolome analysis to secure food production for a sustainable future.

**Keywords**:
Bioinformatics, signalling, AMPs, metabolome, microbiome, food, plants, sustainability

## 1. Introduction

### 1.1 Food Status and Global Development

Global food supplies have almost doubled and helped more than 4.6 billion people decrease malnutrition by over millions in the last half-century [1]. Increasing crops used for animal feeds has enabled richer diets and supported increased energy from alternative crops. Besides, 815 million people remain chronically undernourished, and the environmental burden of agriculture has gone up [2]. Humans utilize over half of usable water, and nearly all anthropogenic water intakes are used for irrigation purposes [3]. The reactive N has tremendously increased in the environment due to the overproduction of fertilizers[4].

In contrast, the production of food products has been contributing 19-29 % of human GHG emissions and land use shifts [5].The rates of human capital use are higher than the sustainable Earth systems [6]. Therefore, the continuation of agriculture will considerably increase the resilience of world food production towards environmental or economic stresses[7]. Revolutionary changes

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in the global food system are essential if nutrient productivity is to be increased while reducing environmental impacts and tackling demand and climate uncertainties [8, 9]. A challenge in historical agricultural approaches lies between enhancing food supply, and ecological production costs and these potentialities include rising crop yields for existing agricultural fields, water utilization productivity.

Further, the reduction in food wastes and nutrient-rich diet will both bring benefits worldwide. Nonetheless, recent work has shown that many such strategies co-benefits food security and the environment [10]. Some critical interactions between the world Food supply chain and a sustainable environment are discussed briefly in the following sections.

### 1. 1.1 Water requirement and demand

The utilization of Freshwater accounts is about 70 per cent towards Agriculture with maximum usage in African and Asian subcontinents, besides 90 per cent of global freshwater intake accounts towards irrigation[11]. About 40 percent of the world's food supplies are produced by water, and 80 % of the food production of Pakistan's, China (70 %) and India (60 %) are mainly dependent on productive irrigation areas. Bluewater or irrigation water includes soil or surface water, river flow into reservoirs, and they're with different opportunity costs, available time and space, and recycling levels of each form[12]. The overutilization of non-renewable aquifers is being executed rapidly in Central California Valley, United States, the North China Plain, North India and Pakistan [13]. It ensures that groundwater overuse creates an unsustainably high proportion of food production. However, the use of surface water may be inefficient, both in terms of water reservoir losses and in cases where unnecessary releases from habitat flow conditions impede ecosystem functions[14]. Where the water demand exceeds the time and volume available locally, water usage can result in stress or scarcity [15].

Surging effects may occur, including, for example, reduced water quality, increased freshwater, earth losses when the aquifer is drained, livelihood, and Biodiversity loss [16].

Though the significant impact is still in developing regions, and use of agricultural water is partially influenced by distant food and feed demand and linked by foreign trade with consuming areas. Dalin et al. [13] Observed that food consumption in various countries is partially driven by excessive water use either by irrigating local produce or by importing foodstuffs. UN FAO projects an additional 60 % of the world's food supply by 2050, with total global water drains increasing by about 50 % and 18 % in developing and developed countries by 2025. In the FAO, many agricultural baskets, in particular, are projected to increase the demand for additional irrigation to improve crop yields [17] to improve the stress on water. In addition, in future climate change, the supply of freshwaters may vary and may decrease further in dry-dry areas[18]. Further, the increase in temperature reveals that the crops need more irrigation water for future growth [19-21].

Agricultural policies need to harmonize nutrition, livelihoods and water protection, incorporating widespread inefficient water use, increasing food demand, and expected climate stress. Wada et al. [22] has outlined six global water stress management approaches for the affected areas. Amongst, two are specifically related to agriculture: improved cultivation efficiency and increased irrigation efficiencies. Similarly, strategies for overall water demand are being proposed by either reducing population growth or improving water efficiency and availability for domestic and industrial purposes. Improving agricultural production can be achieved by using improved nutrient control of the various cultivars.

Foley et al. [2] has mentioned the usage of enough fertilizer to the currently growing plants to cover substantial yield gaps. However, excessive usage of fertilizers causes eutrophication in water bodies like rivers and deltas and other ecological issues. Significant water conservation can also be improved by optimizing irrigation efficiency, for example, by reducing irrigation system leakage or by converting water irrigation to sprinklers or drips. Managing food demand also can lead to substantial water savings. About one-third of the world's food produced has been wasted or wasted[23]. Along with increasing population controls, reducing food waste at any point in the supply chain will dramatically reduce the demand for agricultural water. Significant barriers to the increasing need for water for humanity are dietary adaptations [24]. In general, the below-mentioned approaches offer advantages over a series of environmental outcomes:

### 1.1.2 Excessive Usage of N2

Over the last 50 years, humankind has enabled reactive Nitrogen production with the Haber-Bosch method and legume growing to sustain the population's booming trend [25, 26]. In several cases, rates for Nitrogen application exceeding that of harvested goods in the field have increased these environmental losses and decreased nitrogen returns at higher levels of application[27]. As we know, in the atmosphere, anthropogenic Nitrogen causes smog, precipitation in acids, soil pollution and eutrophication and the depletion of stratospheric ozone [28]. It results in the human production of new reactive N for food, but the majority of the N is released into the environment at all levels [29].

By 2050, the demand for reactive Nitrogen will double to 320 tg N/year without any adjustment of food production/consumption patterns [30]. The rising stage of the production chain offers significant chances of increasing reactive usage efficiency while reducing environmental losses that can be achieved via- policy requirements, technological advances, and maybe by shifts in customer preferences [31]. As understood, the Nitrogen losses in the agricultural fields are hard to manage. Thus, a multi-phase approach is most likely required – to enhance effectiveness by improving the use of Nitrogen through technology improvements and the management of time, rates and location on-farm fertilization [32]. Further, the consumers should make food options with fewer footprints by preferring more plant protein sources and decreasing food protein standards using Eco-labelling or footprint approaches, for example. Changes in consumer preferences, which lead to less environmental impact, can lead to better conditions in the supply chain [30].

### 1.1.3 Land usage and Changing Patterns

It refers to change in the size area used for various purposes due to field expansion or contraction (e.g. woodland, cropland, and urban). And it can be due to the transition to the land cover management system. Changes in land use associated with management may take place without altering the scope of different land cover. Food productivity has tremendously risen in the 20th Century due to land-use change and patterns. Global production of cereals rose by 2.2 % and outstripped population growth by 1.3 %. The rise in productivity is primarily attributable to the strength of cultivation – which is increased by applying irrigation, fertilizer, pesticides, herbicides, and mechanization to crop yield and frequency selection. However, agricultural expansion is relatively low compared with total available land[33].

Presently, 38 % of the total area (Excluding glaciers/snowcaps) on earth is used for farming purposes (Foley et al., 2011). However, a small fraction of land area includes urban settlements, but it feeds more than half of the world's population and produces a substantial share of the needs for export development. Amid Globalization and higher-income trades, the demand for goods from where they were made is increasingly determining land-use change [34]. The teleconnections generate export-oriented production, eventually leading to land-use patterns by clearing tropical forests to produce oil palms in Southeast Asia, which supply palm oil and biodiesel to other parts of the world.

Moreover, the rising demand for plant and animal products has posed a severe threat to land-use changes linked with socio-economic and environmental issues. Changes in land use are required from a structural point of view of food and fiber is to be produced for human consumption and habitation. Scientists investigate whether low yield, more habitat-dependent development over a broader region is safer than concentrated agriculture [35]. Biological impacts on land use include methane emissions, habitat degradation for forest clearance, soil destruction and surface erosion by increased farming, salinization or other wasteful practices. The land-use transitions are not a straightforward process, but various parties have adopted policies to responsibly control land use and prevent agricultural expansion. Private sector organizations set up sustainable supply chain management policies across enterprises, with some non-binding zero-deforestation commitments [36]. Besides different Organizations based on conservation and management works around the globe, including the most omnipresent use of forest preservation, protected areas and other high biodiversity zones. Non-governmental organizations, too, sponsored substantial land-use policies. E.g., Moratia deforestation (Brazil) and Palm (Indonesia)[37].

### 1.1.4 Food production and climate change

Climate change affects our agricultural systems via two approaches – Land management and forest clearing for agricultural production that contribute significantly towards GHG emissions and may affect the regional environment [38]. Second, farming is unique in its susceptibility to change in climate, and farmers have to adapt as per the changing environmental factors [39]. Agriculture has two climate-associated progressions: One is Biogeochemical, and another one is Biophysical [40]. The Biogeochemical route exists because either farming or field clearance activities generate greenhouse gas emissions. Land contaminants like CO2, CH4, N2O, etc. include farm field clearing and degradation, soil runoff, peat oxide, methane, enteric ruminant fermentation, rice cultivation, manure treatment and the use of both organic and bio-organic fertilizers and accounts for 1/4th of GHG released into the environment [38]. However, the most emissions are concentrated in Western Europe, North America and South Asia [37]. Temperature can be determined by using energy to evaporate water from the soil and by the surface reflectivity or albedo, or evapotranspiration.

Greater albedos and higher evapotranspiration rates were correlated with colder weather, and regional rainfall can also affect the rate of evapotranspiration. For instance, higher productivity and evapotranspiration could decrease extreme temperatures in the U.S. Midwest [41], South Asia [42] and introduction of no-tillage farming in Europe in winter cultivations [43], and deforestation in Brazil for agricultural use [44]. Certain areas are expected to benefit from the changing climate, especially in high latitudes, whereas damage is expected in lower margins. Higher $CO_2$ causes the Carbon fertilization effect, and providing water savings for many crops, is likely to some extent compensate for the damage [45]. Nevertheless, net productivity declines for the main crops are expected globally (Porter et al., 2014).

Agriculture will have to reduce GHG emissions while keeping an eye on the future and rising efficiency during climate change adaptation. Historical increases in crop production have helped deter deforestation and greenhouse gases, and enormous output is required to decrease the agricultural footprints and deforestation resulting from the rising demand for food. One approach that can reduce climate impacts on agriculture is more effective fertilizer use and soil carbon control. The farmers will have to adapt towards it by modifying agricultural practices to mitigate damage or reverse exploiting favourable prospects[44].

## 2. Biotechnological interventions

Resource demand can be significantly reduced while producing more products, creating better-matched health and environmental goals [17]. Although it is very tough the sustainable food production can be accomplished by adaptations of such approaches to different regions that amalgamate local resources and produce regional market linkages to address these issues via political, cultural, infrastructural or economic modes. Identifying and prioritizing these 'wedges' of action would involve interdisciplinary advances that connect a global perspective to direct stakeholder involvement. Thereby, it will be essential to understand how regional and other distant policies and consumer decisions affect individual production choices and recognize the growing position of foreign food exchange in food redistribution [46] and its developmental impacts to resolve sustainability challenges within food production systems adequately.

In addition, any solution that seeks to achieve sustainable food systems must be customized to a particular area, taking into account dietary, cultural, political, economic and environmental factors. Biotechnological approaches are needed, which will deliver the most significant potential for enhanced food production vis a vis sustainable development along with multiple co-benefits. The sustainable harnessing of all factors such as metabolites, an abundance of microbiomes, microbial inoculation, biological regulation, etc. and their exploration towards sustainable food production is documented as:

## 2.1. Plant metabolome and microbiome characterization

Many plant derivatives are identified, and several more are still being investigated, showing a variety of biological activities like anti-oxidative defence against pathogens and herbivores [47, 48]. Plant and microbe interactions stimulate the growth and development of crops, thereby inciting an array of metabolites in plants and their biosynthetic gene expressions. Many rhizospheric bacterial strains might impact plant growth and development and improve metabolome potential, and are known as beneficial microbes or PGPRs [49].

Many studies have shown improvements in enhancing the defence system against pests and diseases on microbial inoculation. As it is understood that the main functional attribute of rhizospheric and endophytic bacteria is to improve the plant growth and root architecture, e.g. *P. fluorescens* stimulated the growth of *A. thaliana* [50] in response to inoculation with PGPR. Insight in the bacterial determinants that intricate in modifying the plant' metabolomics and their significance for host plant survival in artificial or natural environments. Bacterial signalling molecules are also regulated for pathogenesis development [51]. It has been shown that bioactive substances mimic or inhibit Quorum sensing (Q.S.) molecules. Now plants were engineered to produce the Q.S. signal via some substances or proteins. Scott et al. [52] modulated Tobacco plants to produce acyl-homoserine lactones (AHL) and the secretion into the rhizosphere. They reported that the lack of AHL lactonase production capability didn’t moderate infusion after pretreatment with *B. Thuriengenesis* AHL-lactonase transmission into plants has a beneficial impact on the plant defence against pathogens [53].

Some findings indicated that the interaction of plant microbes enhances the essential development of bioactive substances. Guillon et al. [54] reported that the *Agrobacterium rhizogenes* infection causes hairy root formation with intense growth and development, vis a vis bioactive compound production(Fig. 1). Wu et al. [55] developed cocultures for the hairy root with *Bacillus* sp and *Salvia miltiorrhiza* Bunge. Tanshinone, a bioactive substance, is usually used in treating heart ailments, menstrual disease and provenance of inflammation, such as improved tanshinone development. The hairy roots are an exciting exemplar of plant-microbe interaction progressing in large-scale agriculture. Increasing hair cultivation for bioactive compound production may not be accessible due to complicated hairy rooting. There was evidence of a rhizobacteria-induced accumulation of sesquiterpene synthase transcripts in some studies [56].

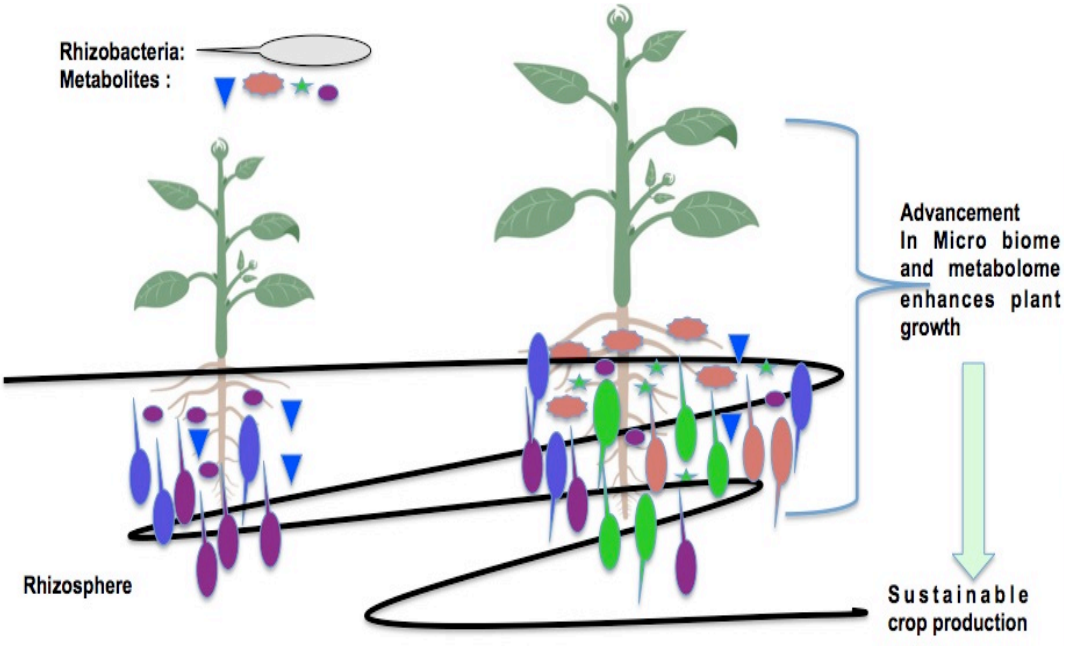

**Fig. 1.** Root exudates of cereal plant enhances PGPR growth vis a vis plant growth in the soil rhizopshere

## 2.2. Rhizo-remediation and activation of the plant microbiome

There are several reasons why plant and bacterial interaction is favourable for rhizo-remediation. Meanwhile, the exudates from plants that provide nutrients to the associated bacterial population are more effective and beneficial than other soil microbes. The rhizoassociated bacteria with plants are considered natural rhizoflters to remediate contaminated soil. Recombinant PCB-degrading strains of *Rhodococcus* sp. can be inoculated with plant roots having precise gene targeting of contaminants. Numerous plant species such as *Pinus nigra and Salix caprea* exhibited rhizoremediation potential [57]. Narasimhan et al. [58] investigated the value of rhizobacterial secondary metabolites and PCB exclusion efficacy and assessed that plant exudates from *Arabidopsis* consist primarily of phenylpropanoids, i.e. lignins, Indoles and flavanoids. Arabidopsis development of wild hybrid flavonoids has retained high concentrations of *P. potidastrin* flavonoids compared with plants with non-Arabidopsis flavonoid mutants.

Interestingly, about 80-90 % of PCBs are degraded by rhizospheric bacteria and enhance biodegradation. The sequestration of oxygen with atmospheric C, which is absorbed into the soil and organic matter, is also a feature of plant microbial communication. An increase in $CO_2$ is predicted to lead to a rhizodeposition rise and a wider C/N ratio, delaying degradation [59]. There are likely to be high $CO_2$ and elevated temperatures as soon as possible and indirectly impact underground C lakes and processes [60].

There can be variations in C-sequestration capability for different plant types, whether continuous or annual. The quality of soil humidity and N-limitation will influence microbial mineralization of organic soil. The C- sequestration of plants and microbes is still in the early phase; however, the global emphasis is on lessening the atmospheric C. More global interdisciplinary studies are anticipated to determine the conditions required to effectively enforce the C-sequestration potential of plant-microbe interaction [61]. Nitrilasase and its substrates are biological, and they have a probability of being protected, detoxified, oxygen used and plant hormone syntheses. Plant nitrilases may be the best among all concerning their biological activities, e.g. *A. Thaliana* NIT 1,2,3 & 4.

Plant nitrilases show specific hydrolytic activities with two main categories, i.e., aryl aceto-nitriles and β-cyanosis-L-alanine. NIT1, NIT1, 2 & A3 are aryl-aceto-nitrilases that lead to nitrile -hydrolysis during cyanogen formations. NIT4 genes are prevalent and are prospective to be substantial in the C.N. detoxification pathway, according to the previous description by Piotrowsk [62]. There has been evidence that the immunity to cyanide and nitrile in organisms is improved, facilitating C.N. and nitrile detoxification. To allow this organism to tolerate amounts of cyanide in other microorganisms, for instance, the *Fusarium solani* cyanide hydratase can release free C.N. from complexes. This hydrolysis will complement and thus promote the organism's development with the supply of oxygen [56]. Some bacteria may utilize nitrilase activity for detoxification besides Nitril and C.N. assimilation in some vegetables. For example, C.N.- hydratases from *Gloeocercospora sorghi* use fungal pathogens to colonize the cyanogenic host plants [63].

## 2.3. Defense priming and metabolic Changes

The developing ability of PGPR is linked to changes in the wall of cells, the defence of the gene, primary alteration and secondary biosynthesis of metabolites (98). The priming process is often divided into three main approaches: (1) Priming perception of stimuli (2) Secondary stimulation (and) (3)—phytohormone production. Phytohormones are plant metabolites and participate in plant protective mechanisms and priming [64]. For instance, jasmonic acid and ethylene is a powerful hormone in ISR or PGPR priming induction. However, the principal hormone complex in systematically gained SAR is salicylic acid, in addition to several significant phytohormones [65]. Around 50 metabolites have also been regulated differently in plants induced with Arabidopsis in ISR, using inducer, i.e. *P. fluorescens*. Primary ISR and PGPR studies are primarily established on a molecular basis but not on metabolomics. There is also a limited perception and significance of metabolome modulations during ISR or PGPR priming. Nonetheless, despite the use of various stimuli, cellular activities in response to chemical elicitation can be more comparable. Therefore, metabolic research using other agents could elucidate the production of the primary and secondary metabolites in plants [66].

Induced by different chemical molecules and by mycorrhizal or rhizobacterial plant root growth, PGPR may induce quantitative modification of phenolic, alkaloid, terpenoid, and essential oils that would significantly improve and sustainably crop produce [67]. Significant improvements in benzo-xanthones were observed in certain corn crops linked to mycorrhizal or rhizobacterial colonization. In addition, microbial compounds such as the labellums and the AHLs, secondary metabolites, may be found in critical crops [68]. The primed state can be retained and transmitted by concrete plants to the potential generation during its life cycle. Since both harmful and harmful microbes in the rhizosphere have been well developed and significantly affect plant growth and plant production. The beneficial microbes that enhance nutrient procurement and improve plant growth are symbiotic organisms, free-living bacteria, actinomycetes, and mycorrhiza mushrooms [69].

## 2.4. Plant-microbe Interactions

Genetic and mechanistic plant immunity studies in association with pathogens have influenced the general functioning of plant-microbe interactions. However, in the decade ahead, how to plant identification and information processing systems can distinguish between beneficial and pathogens will be a crucial issue in the biology of plant systems. Bacterial SynComs (Table 1) is a dominant method to study complexity in controlled environments. Increased proximity of beneficial and pathogens may be partly due to the need to resolve barriers like cell walls, waxy epidermal cells [70] and other antimicrobial compounds.

The Pattern Recognition Receptors (PRRs) of plant surface receptors detect the presence of microbes near a cell membrane. The molecular patterns like PAMPs / MAMPs, i.e., bacteria flagella or EF-Tu associated with the retained microbe and microbe pathogenesis, resulted in intracellular signalling and activates defence responses known as pathogenic or Microbe Triggered Immunity (PTI/MTI) [71]. MTI produces ROS and the direct deposition of callosity, the redistribution of nutrients, the release of antimicrobial metabolites, the start of the plant protective hormones and the transcriptional modifications. The presence or absence of RRP could be determinants of the plant hosts based on microbe associations [72, 73].

**Table 1.** Usage of Syn Com Studies for microbial strain collections

| Host | Microbial species | Type | Microbial origin | Reference |
|---|---|---|---|---|
| *A.Thaliana* | Bacteria | Root | | [74] |
| *A.Thaliana* | Bacteria fungi Oomycyte | Root, rhizosphere | Cologne agricultural soil | [75] |
| *Saccharum* sp. | Bacteria | Root, rhizosphere, | Greenhouse | [76] |
| *Trifolium pratense* | Bacteria | Rhizosphere | | [77] |
| *Zea mays* | Bacteria | Roots | Greenhouse | [78] |
| *A.Thaliana* | Bacteria | Roots | North Carolina | [79] |
| *Solanum Lycopersicum* | *Pseudomonas* sp | Rhizosphere | Nanjing | [80] |
| *A.Thaliana* | Bacteria | Leaf, root, and rhizosphere | Cologne, Golm, Widdersdorf, Saint-Evarzec, Roscoff | [81] |
| *A.Thaliana* | Bacteria | Roots | North Carolina | [82] |
| *A.Thaliana* | Bacteria | Leaf | Madrid | [83] |

Nonetheless, the molecular patterns of beneficial and pathogen microbes are similar, making it difficult for certain PRRs to distinguish in-between. For example, Garrido-Oter et al. [84] discovered that Flag 22 genes in Arabidopsis were deregulated 129E in reaction to commensal *Rhizobium* sp colonization. Reports suggest that it could interfere with transcriptional responses caused by MAMP through alternative means. The symbiont-plant relationships are related to the fundamental processes of distinguishing friends and foes. On the first touch, AM fungi and rhizobia, though transitory defensive reactions, were quickly repressed [85].

NFP is the *Medicago truncatula* nod factor receptor and is also used to detect and defend *Colletotrichum trifolio* and oomycetes Aphanomyces and Phalmivora [86]. In a natural setup, the plant roots are associated with assembling MAMPs and other signalling molecules. The interactomics-proteome study done by Smakowska et al. [87] is a crucial step towards a widespread knowledge of this dynamic system of plant modulation, and they used the biochemical experiments with pull-down tests to map the biophysical network of surface interactions formed by the 225 LRRKs (CSILRR) in *A. Thaliana.*

## 2.5. Symbiosis Factors

In the environment, both Plants and microbes coexist and work for their survival. However, the plant interacts with both beneficial and pathogenic microbes; however, the beneficial microbe stimulates growth and activates the innate immune systems [88].

Symbiosis is a dynamic biological phenomenon that involves genome, signalling network and metabolism. The two central symbiotic systems have been studied, i.e. AM symbiosis and another root nodule (R.N.) symbiosis with former interaction reported mainly in the milieu of phylogeny and ecology. As per the data available, about 80 % of land plants have a symbiotic relationship with AM fungi (Glomeromycota). Though, R.N. symbiosis encompasses morphogenesis that is communication between plants and nitrogen-fixing microbes. In this section, symbiosis interaction will be discussed along with signalling mechanisms. The release of exudates and other rhizodeposition products besides the rhizosphere competence is required to maintain the efficacy of biocontrol strains. AHLs are released and affect many plants like Medicago [89] and barley [90]. However, some pathogens also produce AHL [91], and it is improbable that the host plants possess their defensive mechanism for protection. The release of Q.S. molecules determines microbial diversity; However, AHLs are physiologically characterized in detail. There is still a lack of knowledge of the pathways and mechanisms of plant perception of these bacterial molecules [92].

The main concern is the plants that don't form symbiosis (Tanaka et al. 2015); the root formation, seed germination and crop growth may be stimulated by lipopolysaccharides, i.e. Myc and Nod factors. Therefore, the identification and signalling mechanism of the symbiosis factor depends on the symbiosis capability of the host. Besides, other phytohormones like G.A., ABA, C.K. control various developmental processes in plants. The hormone signalling is highly complex and influences many specific characteristics [93]. The phytohormones are importantly aimed at the two-way communication signalling process between plants and microbes. For instance, Strigolactones are released from roots under a minimal amount of PO4 or N to attract AM -fungi and their production is decreased after colonization [94].

In comparison, G.A., S.A., and E.T. inhibit AM and R.N. symbiosis, while auxin and ABA have a beneficial impact on AM growth. The R.N. formation requires C.K. and localized auxin signalling (reviewed in Gutjahr, 2014; Oldroyd et al., 2011; Pozo et al., 2015). J.A.'s role in symbiosis production is ambiguous and may be positive, negative, or neutral, depending on the plant conditions and species (Gutjahr and Paszkowski, 2009). Defensive reactions canonically regulated are S.A., JA, and E.T. While S.A. facilitates SAR and protects against attacks by pathogens and hemibiotrophic pathogens, ISR and insects are mediated by E.T. and J.A. [95].

All hormone-signalling processes are connected, and only a single hormone apart from the individual pathways mediates a minimal amount of biological reaction. A detailed study of Tsuda et al. [96] is indicative of excellent efforts to decode S.A., JA and E.T. crosstalk of immunity to Arabidopsis. And it revealed strong interactions with additive, synergistic and countervailing interactions between hormone network components. Subsequent studies of the same community have shown that the PTI signalling network, e.g. pathogen effectors, is strongly buffered against interference [96].

## 3. Omic's for harnessing microbiome-Sustainable food production

Microbial interaction with plant roots leads to multiple reactions in native or nonnative plants at all levels, i.e. physiological, biochemical and molecular levels and are linked to stress from good to adverse. Multilateral methods for pathway dissection may be used to tackle the daunting function of plant genomic, proteomic, or metabolomic alteration decipherers. Crafted with the advances made in bioinformatics, data-driven multi-omics research has enhanced our awareness of the microbial compound community and its function in diverse environments such as the rhizosphere, where the interconnection between microbial communities contributes to stress vis a vis a better plant growth architect. Lately, Meta omics like metatranscriptomics, metaproteomics and metagenomics have been documented as assuring tools to scrutinize microbial diversity and their roles within a given environment [97]. The detailed techniques and their potential role for sustainable cause are discussed as under:

### 3.1. Genomics and metagenomics

Respite from abiotic stress is necessary and needs comprehensive breeding programmes [98]. It's a challenge to be able to reduce the abiotic stress in crops. These breeding processes make heritability and variations in the ecosystem even more complicated [99]. The use of markers for breeding purposes is effective in enhancing the tolerance mechanism in various species. Understanding the genomic loci characteristics, which are responsible for molecular marker resistance and abundance, provides an essential precondition for marker use [100]. Hence significant numbers of genomic data are impetuous for breeding in sequenced genomes and stress reduction expression profiles[101].

The usage of genomic technology has a significant effect on crop enhancement programmes. The molecular markers are to be used in agriculture to deposition silicon in rice to increase resistance to abiotic stress. Ma et al. [102] expended PCR-markers for the Microsatellite and the Expressed Sequence tag in imaging Si- transport genes during mass segregation studies. The embodiments of plant-microbe interactions can also achieve a substantial degree of abiotic stress relief in plants besides crop growth. Omic methods give an in-depth understanding of the dynamics of the current plant-microbe relations. A study of *Trichoderma*- plant interaction reported the effect of plant genotypical properties to modulate a plant-microbe interaction and affects plant growth and elevates stresses [103].

The RNAi silencing gene [104] confirmed the putative sequence of ACC-deaminase found in the genome of *Trichoderma.* The identification and regulation of genes help the producers to produce better varieties of strain tolerance. The use of multi-omics techniques leads to highly effective and precise tests valuable for experimental studies. Genomic analysis of host and related microbial, in particular microbial populations related to the phyllosphere, provides smooth working access to the mechanism involved in associative interaction. In several trials, the role of different genes in related bacteria was highlighted. Plants are contributing significant molecular partners to sustain and maintain the related bio-system. The culturally autonomous approach to the study of microbial communities has been a valuable method for addressing uncultivated, unpredictable microbial diversity and have a significant role in the rhizosphere [105].

Metagenomics allows us to obtain data on the habitat-specific distribution of microbial plant growth (PGP) species, biocontrol, antibiotic development and xenobiotic degradation. The approach increases the likelihood of successful attempts to explore new, specific niche cultural flora. Metagenomics helps us obtain data on habitat-specific microbial plant growth (PGP) species distribution, biocontrol, antibiotic production, and xenobiotic degradation. The approach increases the chances of successful attempts to explore new, specific cultural niche flora [106].

High-performance metagenomic sequencing is a powerful way of studying the rhizobacteria of PGP further. In a study on potato endophytes, PCR work found two types of ACC-deaminase comparable with *P. fluorescens* to combat stresses. Clones found in metagenomic libraries were analyzed, and the transcriptional control gene acdR was discovered upstream of acdS. To identify salt genes in uncultivable bacteria, *E.coli* clones were studied in metagenomic pond water at growing inhibitory 750 mM conc. Of NaCl. Two protein-encoding clones similar to GSPM with a GsiB domain and a potential enoyl-CoA hydratase (EchM) have been recognized to possess salt tolerance capacity [107] and also linked to survival at low temperatures in the metagenome of acid mine drainage genes, such as anti-cold protein, cold-shock proteins, stable solutes, and homeostasis of pH [108].

These data help detect new genes and mechanisms to ease the stress of cold. The function of root bacterial endophytes is mostly uncultivated, as endophytic microbes, cultivated successfully, constitute only a fraction of the entire bacterial population living within the roots. Endophytic cell extracts metagenomic sequences reveal metabolic processes in the endophytic lifestyle and functional characteristics, such as quorum sensing and ROS detoxification, to enhance resistance to plant stress [109].

### 3.3. Transcriptomics

Comparing transcriptome profiles is useful, under various conditions, to identify similar types of transcripts for variances amongst two biodiversities [110]. One of the essential methods used to study plant-microbial interactions is using mRNA sequencing and microarray techniques to produce transcriptome-level information [111]. Next-generation *Sinorhizobium meliloti* RNA sequencing work showed that gene induction had been shown to respond to stress in overproducing strains in the IAA[112].

Several miRNAs have a regulatory function in Medicago, rice, Phaseolus, Arabidopsis and other plants during abiotic stresses such as extreme famine conditions, salinity or psychrophilic situations [113]. miRNAs- 19-23 long coding RNAs have a regulatory role in various biological processes (Budak et al., 2015). The regulatory feature of miR393 is found to be the overexpressing Arabidopsis osaMIR393 with excessive salt tolerance capacity [114]. Zhao et al. [115] recorded miR-169 by regulating the expression of a nuclear transcription factor (NF-YA) to ease the stress of salinity and drought in rice. In tomatoes, plants that overexpress miR169c, which controls gene(s) expression, engaged in a stomatal activity for drought stress tolerance [116].

Various categories of miRNA's ease stress by regulating cellular response differentiation and metabolism, such as transcription, ion transport and apoptosis and auxin homeostasis [117]. Mirna has also been identified for controlling the response of Al-stress in plants [118]. The Mi -RNA expression distinction was made between the aluminium resistance subspecies *japonica indica* in two separate subspecies of rice. The technique of RT-qPCR has demonstrated 16 different forms of miRNA reactions, which suggest an aluminium stress reaction. A cold-stressed plant was transcriptomics using high throughput RNA sequencing high-throughput RNA in roots and leaves [119]. Overexpression of CBF3 from roots was found more quickly than leaf tissue. Cold stress also increased gene revision in the AP2 / ERF family reported being involved in responses mediated by jasmonic acid [120].

### 3.4. Proteomics Approach

The proteins are important in assessing plant stress reactions because they directly influence phenotypic trait development. Therefore, these research works have befitted important instruments for the study of microbiological, physiological, biochemical and interactions between proteins. Inter and intra- microbial species interactions of host microbes are important for host-mediated signalling and operational responses to associated microorganisms[121]. It has contributed to a better knowledge of the regulation of various biological systems by identifying stress proteins linked to causes of stress or stress relief [122].

The similarity evaluation assists in classifying protein targets and networks in stressed, microbial and non-stressed plants. The proteomic studies against stress responses in various plants like Arabidopsis, wheat, barley, Zea maize, rice, soybean, potato and tomato. The experiments also demonstrated complex alternation of protein activity, signalling proteins and regulatory pathways, their metabolism, and interactions. The proteins and enzymes that confer stress-related substances the role of cell walls and other cytoskeleton structural proteins. The diversity of the microbial metabolic pathways makes them more responsive to stress. Metaproteomics examines various metabolic interactions that coincide in the system, which is time-consuming, unlike standard proteomic approaches that focus more closely on the organism itself. This may help overcome the greater importance of dependence between different microbes within the agroecosystems in the host plant. The main progress in the field of metaproteomics is methods of extracting protein from environmental samples. The most recent progress in protein sequencing is the key step in identifying proteins from diverse species[123].

The involvedness of the metaproteome makes resolution and analysis rather difficult. But new approaches to extract and analyze successful metaproteome in the environment could produce critical output and create a better correlation between omics data and mechanisms for stress response [124]. The bulk of studies on proteomes are limited to cultivated model organisms only. The metaproteome complexity renders resolution and analysis relatively challenging. But new methods to extract and analyze successful metaproteome in the environment could generate critical output and create a better link between omic's data and mechanisms for stress response[124].

The majority of research on the proteomic environment was confined to cultivated model organisms. Particular emphasis is placed on the exceptional capacities of organizations such as salinity tolerance, sodium, temperature, low levels of access to water, toxic metals, radiation, etc. Additionally, it also helps to establish the likelihood of inducing this metabolism in a range of environments. The laboratory studies enable a deeper understanding of the protein profile in a regulated environment; moreover, the profile of expression is derived from modifications in environmental circumstances. Thanks to their ability to thrive under high salt conditions, halacha and halobacteria are gaining high recognition in today's era[125-127].

The species' PGP capacities can easily be applied to saline and sodium soils to reduce crop strain. It's beneficial in stress-prone environments. The processing and application of metabolites can lead to halotolerant with other mixed stresses in high salt stress microorganisms and be used in essential crop enhancement programmes. The proteomic processing of methylotrophic bacteria is also involved today. The methylotrophic layer, usually the leaf surface, creates a large part of the phyllosphere where methanol is readily accessed by transpiration. Detailed studies of the proteomic insights of these typical community members of the phyllosphere help to develop new ideas about the protein participation in different survival mechanisms of organisms under extreme conditions where, furthermore to intensive radiation, nutrient shortages are often found. Furthermore, its possibility of secreting regulators can be implemented on a broad scale. Therefore, deep molecular observations of microbial PGP populations, mainly involved in combatting stress, need to be explained to obtain knowledge about the pathways involved in these processes[128-130].

Detection of the proteins involved in these processes is necessary to achieve techniques for molecular stress reduction where the direct use of active molecules was considered rather than the entire organism. Studying the expression of proteins of different lines in plants assists in choosing lines of cold tolerance. Previous studies indicate that the psychrophilic tolerant strains contained 14 distinct proteome expressions in cold sunflower acclimatization [131]. The proteomic research also identifies potential ways of reducing plant chilling and cross-resistance pathways [132]. This can be used as a marker for distinguishing genotypes of the stress reaction when developing the database of reactive and blocking genotypes for particular abiotic stress.

## 4. Future perspectives

Plant metabolomics has progressed significantly in recent years because metabolomic techniques were used rapidly for various biological purposes. Open testing systems can study complex mixed specimens in conjunction with integrating metabolomic and omic’s or functional genetic studies. Thus, they can provide new comprehensions in genetic or biochemical dimensions of cellular metabolism and structure. Metabolomics, particularly in comparison with DNA, RNA and protein, are essential as the metabolites are most applicable to the plant phénotype. Potential research will also concentrate on how to accurately and effectively identify and quantify secondary metabolites for the advancement of the metabolome platform. The following includes a detailed study of non-target and targeted strategies for expansion, physiological and molecular processes and cellular variants, and crop growth advances in normal and stressful circumstances[133].

## Abbreviation

Not applicable

## Conflict of Interest

Authors declare there is no conflict of interest in this research study

## Consent for publications

All authors read and approved the final manuscript for publication.

## Availability of data and material

All data generated during this study are included in this published article.

## Ethics approval and consent to participate

No human or animals were used in the present research.

## Ethics declarations

The authors declare no conflict of interest in financial or any other sphere. All applicable international, national, and/or institutional guidelines for the care and use of animals were followed.

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