

Omics: Functional insight for improving growth in agriculture

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Abstract-

Food security around the globe is under constant threat, especially in developing countries. The problem is made worse by the obvious effects of biotic and abiotic stresses that are lowering crop yields and output. Plant breeding for advantageous and resilient agronomic characteristics is one of the traditional methods used to increase yields and maintain output. The rapid changes in climate variability and the emergence of novel and resistant phytopathogens, however, are contributing to a decline in the effectiveness and success rates of these methods. Additionally, it takes time and can be costly to develop new, improved transgenic crop types. Therefore, developing novel and inventive technologies is necessary for crop improvement. This review looks at recent developments in the field of agricultural biotechnology, which have opened new opportunities for quick and reliable analysis. Elucidation of the complex plant processes, which offers the chance to understand how plants respond to their environment through their metabolic activity. The study of metabolites and the chemical imprints of cellular regulatory processes in various plants is the focus of the developing field of metabolomics. The entire pool of metabolites present in an organism is known as its metabolome, and measurements of it can be used to identify genetic or environmental variations. The study of environment-gene interactions, the description of mutants, phenotyping, the finding of biomarkers, and the development of new drugs are all significantly aided by metabolomics. Additionally, metabolomics-assisted breeding allows effective metabolic yield and stress tolerance screening of crops.

Keywords: Plant breeding, Phytopathogens, Metabolomics, Biomarkers

Introduction-

After decades of economic expansion, technical development, and agricultural intensification, food insecurity still ranks among the most urgent environmental problems of our time. The prospects of the continuously expanding global population, which is anticipated to reach a peak of 9.7 to 10 billion people by 2050, further exasperate worries about the various risks influencing food security (da Cunha Dias et.al. 2021, Razzaq et.al.2019). Additionally, there are connections between the systemic dangers of food insecurity and several issues, including globalization, climate change, and sustainable agriculture. Agrochemical dependence, declining natural resources like arable land and water, and changes in global demographics like urbanisation and dietary habits all influence crop productivity, yields, and distributions (de Raymond et al. 2021). As a result of the accumulation of systemic risks, food systems become vulnerable and complicated, which increases the risk of systemic crises like food insecurity, especially in underdeveloped and developing countries (Davis et al 2021). The most common micronutrient deficits in people are related to iron (Fe), zinc (Zn), and iodine (I), in that order (Saltzman et al. 2014). In the past, various research has demonstrated that vitamin deficiencies have negative impacts and health issues, such as prenatal difficulties, premature death, and poor cognitive development (Bailey et al. 2015). The growth and development of plants, as well as crop yield, are severely affected by a lack of any one of the important macronutrients or micronutrients. Although greater use of chemical fertilisers increases crop yield, it also severely degrades agricultural land, notably by reducing soil fertility and structure, which ultimately results in mineral imbalance in the soil. Usually, the nutrients plants need is included in fertilisers so that plants can easily absorb them (Banerjee et.al. 2023).

Omics as an approach for agriculture biotechnology

Omics is a broad discipline that focuses on the analysis of biological data obtained from the genome, transcriptome, proteome, and metabolome profiles. Numerous omic technologies are being used to investigate potential markers, systemic gene, protein, and metabolite activity in a context that is functionally appropriate, as well as to shed light on the mechanisms underlying the basic processes in seed germination. The intricacies of abiotic and biotic stressors can be understood using gene sequencing, transcription in cells and tissues, metabolite profiles, protein and their evaluations, and interactions.

A. Metabolomics as an emerging tool of agricultural biotechnology -

There are roughly 200,000 different metabolites found in the plant kingdom. The overwhelming majority of which are still unknown. Approximately 10,000 secondary metabolites have reportedly been found in various plant types. One of the cutting-edge and intriguing omics tool approaches, metabolomics, is now widely used for crop improvement. The study of robust ecotypes, abiotic stress tolerance, pathogen resilience, and metabolic assisted breeding of crops depends heavily on metabolomics. The development of cutting-edge metabolomics tools for crop improvement has made tremendous success so far (Shulaev V et al 2008). It is being used to investigate hidden regulatory networks controlling crop growth and development and to explain complex biological pathways using present metabolomics platforms. A comprehensive collection of low molecular weight metabolites that are present in biological systems is known as a metabolome. Small molecules (1500 Da) and their interactions within an organism are the focus of most metabolomics study, which also focuses on their identification and quantification (Deborde C et al 2017). Investigating how plants interact with the environment is the focus of environmental metabolomics. To identify the effects on plant adaptation and any changes in their genetic architecture, it is based on a thorough analysis of metabolite levels in a particular plant ecology. It offers a platform to investigate the interactions between the environment and living things to precisely quantify plant functions (Han S. and Micallef S. A., 2016). The study of plant biochemical links across various temporal and spatial systems is one of the key applications of metabolomics, known as ecological metabolomics. Through metabolite identification in reaction to environmental factors, it seeks to understand the potential effects of abiotic/biotic stresses on any important biochemical process. It describes the biochemical underpinnings of several significant ecological phenomena, including the consequences of parasite load, the occurrence of illness, and infection. It is also beneficial to analyse the relationship between two trophic levels or the multiple effects of abiotic variables with intra- and interspecific linkage. The phenotypic and physiological responses of plants to external changes can be explained by variations in the concentration of a variety of metabolites. These variations can provide mechanistic evidence for biochemical networks (Garcia-Cela, E. et al 2018). Ecological metabolomics' promise hasn't yet been used to its fullest extent.

Primary and secondary metabolites are the two categories of compounds that make up the plant metabolome. Comprehensive understanding of the biochemical processes that take place during plant metabolism is provided by metabolic profiling of primary and secondary metabolites (Sung J et al 2015). Some of a plant's main and secondary metabolites are connected to incredibly intricate metabolic pathways. Advanced metabolomics tools like gas chromatography-mass spectrometry (GC-MS), liquid chromatography mass spectroscopy (LC-MS), and non-destructive nuclear magnetic resonance spectroscopy (NMR) can successfully detect, identify, assess, and evaluate these metabolites (Che-Othman, M. H. 2020). Metabolome profiling of different plant organs revealed that some metabolites like homocitrate and others are involved in biosynthesis of lysine and have also shown its effectiveness in degrading mimosoid and papilionoid root nodules caused by the accumulation of *P. phymatum*. These studies have shown the importance of metabolomics in understanding various physiological mechanisms of plants. Utilizing such information can be crucial for improving crop productivity and yield.

B. Role of endocytic microbes in agriculture biotechnology-

Endophytic microbes with strong endosymbiotic functional traits that help plants become more resilient to stress and manage disease. Endon, which means within, inside, or internally, and phyton, which means plant, make up the Greek term endophyte. The following steps can be taken to identify endophytic microbes: (i) culture, (ii) DNA extraction, (iii) polymerase chain reaction using primers for amplification, (iv) sequencing, and (v) comparison of the sequenced data with information found in the bioresource database. Additionally, using various phylogeny styles on the online molecular evolutionary genetics analysis (MEGA-X) program, the aligned sequence datasets are used to derive the taxonomic categorization based on the phylogeny plot. Many agricultural, industrial, and biotechnological applications have been investigated for some endophytic microbes with traits that promote plant development. (Adeleke, BS., and Babalola, OO. 2022, Bambharolia et al., 2020; Khan et al., 2020). Through root hair development, tissue damage, cracks or injuries, and epidermal conjunctions, structural dynamics enable the release or intrusion of endophytic microbes into and out of their host plants. By supplying the necessary energy for microbial metabolic activities, root injury or wound adds to the frequent release of exudates containing carbon and nitrogen-rich compounds to the root-soil environment. (Muresu et al., 2019; Mavrodi et al., 2021). By improving crop output, root development, stress tolerance, seed germination rate, plant height, leaf area, and other factors like protein, mineral elements (nitrogen, phosphorus, potassium, etc.), and chlorophyll contents, endophytic microbes functionally aid plant growth. (Alkahtani et al., 2020; Khalil et al., 2021). Endophytic microbes are closely associated with plant tissues, which shows their distinctive characteristics in comparison to other microbes.

Endophytes are protected by plants from abiotic variables that can affect their survival and productivity, whether they are internal or external. (Gomes et al., 2018). Abiotic factors, such as drought, cold, temperature, flooding, salinity, trace metals, and nutrient deficiency, have been found to have a negative impact on plant growth, as evidenced by findings that show increased transpiration and metal accumulation, decreased carbon dioxide, decreased soil fertility and moisture content, decreased photosynthesis rate and nitrogen fixation, accumulated reactive oxygen species, disrupted hormone biosynthesis, and decreased chlorophyll pigmentation. (Bilal et al., 2021; Eid et al., 2021). In a similar vein, harmful biotic factors like pathogenic microbes (fungi, insects, nematodes, viruses, and bacteria) have been linked to host susceptibility to disease, disruption of the transport system and hormone synthesis, decreased soil fertility, decreased photosynthetic rate, and decreased biomass in plants. (Nadeem et al., 2014; Eid et al., 2021). One of these methods depends on how exposure to stress can boost host immunity and plant health, which helps to lessen the impact of stress on plants.

The two endosymbiotic mechanisms of endophytes that help confer abiotic stress tolerance are (i) activation of plant stress response systems following exposure to specific stressors, allowing the plant to escape or mitigate the impact of such stressors, and (ii) production of anti-stress agents by the beneficial endophytes. (Del Carmen Orozco-Mosqueda and Santoyo 2021) proposed that unravelling the mechanism

mediating these strategies may point to their molecular foundation and other bioinformatics-related tools that can be applied to agriculture. Endophytic microbes' contribution to agricultural biotechnology's ability to reduce environmental stressors has produced excellent biological models for the study of the many processes affecting plant growth and health (Mahgoub et al., 2021a). Endophytic microorganisms' ability to protect plants from abiotic stress depends on their ability to secrete a variety of bioactive and volatile substances, including phenolic compounds, exopolysaccharide, ethylene, organic acids, and siderophores. (Alkahtani et al., 2020). Some endophytic microbes could reduce abiotic stress in plants due to the expression of oxidative genes and secretion system genes. (Samaras et al., 2020; Gaeth et al., 2021). Broad bean salinity stress was found to be lessened by single or combined inoculations of endophytic *Bacillus thuringiensis* and *B. subtilis*.

Even though endophytic microbes in plants have a variety of characteristics and can promote plant development, few of them have been characterized, and some haven't even been cultured yet. Because of this, incorporating various meta-omics methods in endophytic studies promises to offer a quick method and opportunities for elucidating yet-to-be cultured endophytic microbes and their potential exploration in aiding stress tolerance and disease control in plants with the aim of addressing a variety of agricultural issues and ensuring food safety. Therefore, this study offers details on the various endophytic bacteria and fungi microbes, structural diversity, metaomics techniques, and bioprospecting in environmentally friendly crop production (Adeleke, BS., and Babalola, OO. 2022).

C. Proteoinformatics

"Utilization of computational biology tools in the study of the proteome" could be the definition of proteoinformatics. To forecast and analyse protein structure, function, and role in cell physiology, the field of proteoinformatics combines mathematics, programming sciences, statistics, and protein biology and biochemistry (Cristoni and Mazzuca 2011; Hamady et al. 2005). Proteoinformatics plays a crucial role in reducing the time required for investigation and delivering statistically significant results, which will help to improve the plant/animal quality based on healthy growth and high productivity. This is because the data obtained from agricultural proteomic research are complex and massive in size. To create pathogen-free/resistance, abiotic stress tolerance, high-quality traits, and higher quantity production, a new breed's diagnostic tools must be developed in the dynamic field of proteoinformatics (Koltai and Volpin 2003).

Fungi are regarded as the most harmful plant diseases, compared to viruses, bacteria, and oomycetes. (Dangl and Jones 2001). Although pathogens have a variety of growth, reproduction, and survival tactics, they all generally follow a similar pattern that begins with colonization, progresses to overcoming host defenses, and ends with the establishment of infection. (Pegg 1981). Because of this, the host-pathogen systems have produced a complex interaction between the host and the pathogen molecules that is highly variable. (Hily et al. 2014). Proteomic research, which primarily examined how host plants responded to pathogen assault, heralded a new era in biology and, specifically, in agriculture. (Lodha et al. 2013; Alexander and Cilia 2016). The use of bioinformatics and proteomics together usually improves agricultural research, along with the development of proteomic approaches and the sequencing of agriculturally significant organisms. This kind of interdisciplinary study is likely to close the knowledge deficit regarding the network of host-pathogen interactions (Koltai and Volpin 2003). The original use of two-dimensional gel electrophoresis was to quickly spot significant proteome variations between control and inoculated plants. Although many proteins discovered during host-pathogen interactions have received attention, the majority are well-known and primarily function in host defence mechanisms (Memievi et al. 2013). However, the outcomes of proteomic-based study have significant implications for confirming gene expression in genomic or transcriptomic studies. (Nesvizhskii 2014). To advance our understanding of protein expression during interactions between plants and microbes, it is necessary to get past these information-related constraints in agricultural proteomic study. However, new methods and equipment are constantly being created, and proteomic tools have expanded quickly (Hakeem, K. R. et al. 2019; Pérez-Clemente et al. 2013). Prior agricultural proteomics research, which was primarily focused on model crops, has given basic understandings into the modification and regulation of various protein families in agri-organism systems (Hakeem, K. R. et al. 2019; Vanderschuren et al. 2013).

Additionally, "conserved genome" regions could result in similar protein sequences with distinct cellular roles and raise the number of mismatched protein identities. (Khan et al. 2014). The most popular platform for agricultural proteomic study is thought to be gel-based proteomics. (Tan et al. 2017). However, with more proteoinformatics data available, the use of gel-free proteome analysis is quickly expanding in agricultural research. (Porteus et al. 2011; Komatsu et al. 2013). Agricultural host-pathogen interactions place a high value on pathogen proteins that inhibit host defences because they may influence virulence, pathogenicity, and effector molecules. (Van De Wouw and Howlett 2011). Programs for crop growth are primarily interested in pathogen characteristics. (Fletcher et al. 2006). In the past ten years, the advancements in proteoinformatics have contributed to the complete genome sequencing of many diseases (Land et al. 2015).

The field of agricultural study known as proteoinformatics is one that is still developing. Understanding specific functions of plants and animals is crucial for identifying helpful proteins to enhance agricultural traits. (Newell-McGloughlin 2008). Proteoinformatics and other omic platforms databases from agricultural species must be integrated to advance or improve crops and animals as a whole and address problems like food security, water stress, and climate change. (Katam et al. 2015a). The Asia Pacific Bioinformatics Network (www.apbionet.org) is a reliable geographic resource for Asia, for example. (Khan et al. 2013).

Conclusion:

The different emerging areas of omics, at this time where the near future is alarming about the demand of food supply, can become an invincible approach for enhancing the crop yield. With a study emphasis on endophytic microbes in ensuring sustainable agriculture, it became crucial to increase agricultural food production through soil enrichment. Plants need attachment cell organelles and the production of secondary metabolites to support microbial populations thus, study of different metabolites and proteome in a diverse manner is quite essential to meet the supply of food at this rate of growing population.

Declaration of interest:

None

Authors contribution:

Both authors had the idea of the review article and suggested the review topic. The final manuscript was reviewed and approved by both authors.

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