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Review Article

Recent Advances in Photosynthesis, Plant Hormones and Applications in Plant Growth

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Abstract

Changes in the pigment and protein complexes involved in the light reactions of photosynthesis can be caused by environmental conditions, particularly those related to light quality and intensity during growth. The metabolome analysis of rice and soybean showed that dehydration stress increased the levels of galactinol and raffinose. One key method by which microorganisms control plant development has been proposed to be the generation of auxin or auxin precursors by bacteria associated with roots, or the manipulation of auxin production in plants. The effects of pathogenic and beneficial root-interacting fungi on the hormone content and auxin responsiveness of Arabidopsis, as determined by the auxin-inducible promoter system. Many developmental processes, like stem elongation, germination, vegetative growth, blooming, and reproduction, are regulated by GAs. Analyzing the metabolome of Several distinct defensive mechanisms function in different ways to prevent or lessen harm. Coeluting substances in the sample matrix have an effect on the analyte signals. They can impede or, less frequently, increase the analyte's ionization process, producing stronger or weaker signals, respectively. Furthermore, auxin, a different hormone present in plants, combines with cytokinins to prevent senescence, which, at least in its early stages, serves as a structured metabolic time and a tissue breakdown. Furthermore, synthetic amino acids with unique light-absorbing side chains may be used to add colors to such a new photosystem and rice showed that under circumstances of dehydration stress, levels of galactinol and raffinose were enhanced.

Keywords: Changes, pigment, protein complexes, environmental conditions, dehydration stress.

INTRODUCTION

Changes in the pigment and protein complexes involved in the light reactions of photosynthesis can be caused by environmental conditions, particularly those related to light quality and intensity during growth. Photoinhibition, which is linked to an excess of reactive oxygen species (ROS) and membrane damage to the thylakoids, can occasionally be brought on by light. Multiple environmental elements can cause a complicated reaction from the plant, which is normal for C4 plants as they can thrive in hot, dry environments with high light intensity [1-3].

Aside from transmembrane complexes like PSI, cytochrome b6f, or PSII, other elements are also crucial for electron transport. These include the plastid terminal oxidase (PTOX) and the NADH chloroplast dehydrogenase complex. It is situated between PSII and the cytochrome b6f complex on the stromal side of the thylakoid membrane. By giving electrons to oxygen, it oxidizes the plastoquinone pool and causes a water molecule to form. By doing this, the plastoquinone is shielded from undue decrease. PTOX is found in the non-appressed portions of thylakoids where PSI is prominent, and it makes up 1% of the PSII content in *Arabidopsis thaliana* [4-7].

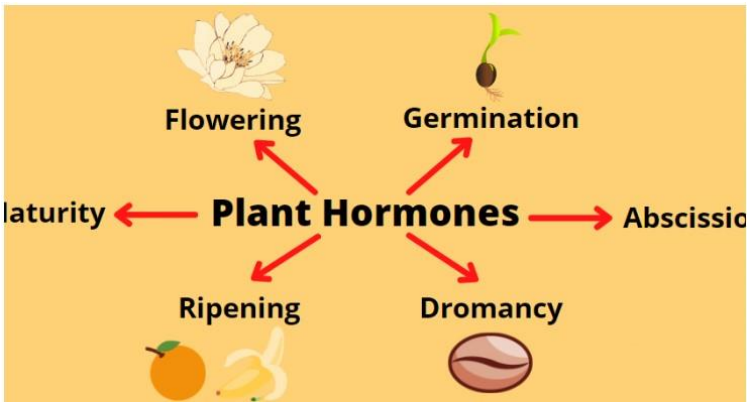

Fig-1: The hormone content and responsiveness as determined in plants

Biochemical Nature of Hormones

The manufacture house of gibberellins (GAs) is a three-stage biochemical process that begins with GGPP (geranyl-geranyl diphosphate) and is catalyzed by several enzymes found in various plant cell components. Enzyme genetically proplastids undergo the first step towards gibberellins pathways. Cytochrome P-450 monooxygenases in the endoplasmic reticulum subsequently catalyze the second stage of oxidation of ent-kaurine-formed GA12-aldehyde. The MVA route, which supplies IPP for GA synthesis, is responsible for GA synthesis in fungi. As of right present, fungi are known to create different GAs. GAs are also known to be produced by some rhizobacteria that promote plant development [5-7].

One key method by which microorganisms control plant development has been proposed to be the generation of auxin or auxin precursors by bacteria associated with roots, or the manipulation of auxin production in plants. The effects of pathogenic and beneficial root-interacting fungi on the hormone content and auxin responsiveness of Arabidopsis, as determined by the auxin-inducible promoter system. Only one advantageous fungal endophyte, *Piriformospora indica*, appeared to quickly and robustly stimulate auxin response in Arabidopsis, which was connected with the enhancement of lateral root growth, despite the fact that several of the fungus generated auxin. On the other hand, the auxin response was reduced in the other interactions. This might have been caused by the generation of jasmonic acid in the instance of *Mortierella hyalina*, the other beneficial fungal endophyte under investigation [8, 9]. Following comprehension of the biosynthesis of all classical hormones, with the exception of auxin (IAA), hormone biosynthesis regulation and hormone signaling. The ethylene, cytokinin, brassinosteroids, auxin, and GA receptor proteins have previously been found, and recent X-ray crystallographic investigations of the IAA and GA receptors demonstrated the special characteristics of plant hormone receptors. Certain beneficial endophytes that exhibit ACC deaminase activity and/or the ability to generate auxin may help host plant development in challenging environments [8, 9].

Many developmental processes, like as stem elongation, germination, vegetative growth, blooming, and reproduction, are regulated by GAs. In the research on rice bakanae (foolish seedling) disease, GAs were discovered. The symptoms of silly seedling illness were demonstrated to be induced by a chemical generated. This material was later given the name "gibberellin. Certain artificial substances exhibit structural and chemical similarities with phytohormones that are found in nature. These substances are easily absorbed by the seedlings' hypocotyl, where they are hydrolyzed and cleaved to release auxins. Although over 130 GAs have been identified to far, only a small number of them-GA1, GA3, and GA4-have biological activity [10, 11]. Several different enzymes convert geranylgeranyl diphosphate (GGDP) into GAs. GAs cannot become bioactive unless they are hydroxylated at the 3β location. When bioactive GAs are hydroxylated at the 2β site by GA2-oxidase, a 2-oxoglutarate-dependent dioxygenase, they lose their activity (GA2ox). The signaling pathway has been developed since the GA receptor, GA-insensitive dwarf1 (GID1), was discovered in rice. GID1's lid changes shape in response to GA binding to the GID1 receptor, enabling GID1 to interact with the rice DELLA protein SLR1. Arabidopsis has also been found to have GID1 receptors [10, 11].

Several different enzymes convert geranylgeranyl diphosphate (GGDP) into GAs. GAs cannot become bioactive unless they are hydroxylated at the 3β location. When bioactive GAs are hydroxylated at the 2β site by GA2-oxidase, a 2-oxoglutarate-dependent dioxygenase, they lose their activity (GA2ox). Since its discovery, researchers have examined the signaling mechanism of GA-insensitive dwarf1 (GID1), the GA receptor found in rice. GID1's lid changes shape in response to GA binding to the GID1 receptor, enabling GID1 to interact with the rice DELLA protein SLR1. Arabidopsis has also been found to have GID1 receptors [10, 11].

For the measurement of hormones, liquid chromatography–tandem mass spectrometry, or LC–MS/MS, has become the industry standard. Variations in light intensity can cause excess excitation, which in turn

causes excited triplet states of chlorophyll. These states can create dangerous reactive oxygen species (ROS) when they interact with O2. This is especially true in situations when abiotic stresses prevent carbon from being fixed. Various distinct defensive mechanisms function at various periods to prevent or lessen harm. Coeluting elements in the sample matrix have an impact on analyte signals; they can hinder or, less frequently, increase the analyte's ionization process, leading to lower or bigger signals, respectively [12, 13]. The most used method for hormone analysis these days is liquid chromatography–tandem mass spectrometry (LC–MS/MS). In instances when abiotic stress prevents carbon fixation, variations in light intensity can lead to excess excitation that creates excited triplet chlorophyll states that can mix with O2 to form damaging reactive oxygen species (ROS). Numerous unique defense systems operate at different times to avert or mitigate damage. Analyte signals are affected by coeluting materials in the sample matrix; these materials can either enhance or decrease the analyte's ionization process, resulting in increased or decreased signals, respectively [12, 13].

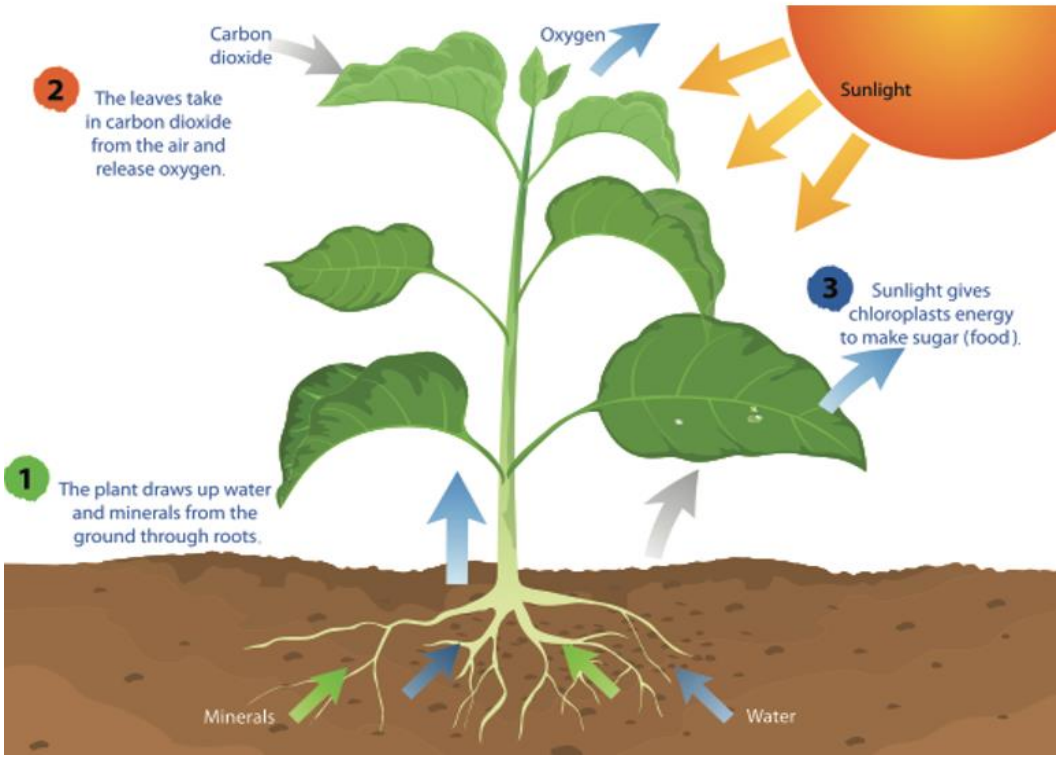

Fig-2: The various effective responsiveness in plant growth effects

Considering the length of the growth season's photosynthetic activity, the speed at which light responses are regulated, and the anticipated influence of the thylakoid electron transport rate [14, 15]. Approaches that focus on boosting the activity or adjusting the levels of its constituent components can be broadly divided into two categories: those that introduce new pigments, components, or entire protein complexes, modify its regulation, or modify the way proteins function by exchanging amino acids to enable new functions of the photosynthetic machinery. Any of the many plant hormones known as cytokinins that affect growth and stimulate cell division. The roots are the site of cytokinin synthesis, whereby adenine is often the starting point. Via the woody tissue known as xylem, they are transported to the leaves and fruits, where they are necessary for healthy cell division and development. Moreover, auxin, another hormone found in plants, works in tandem with cytokinins to inhibit senescence, which functions as both a structured period of metabolism and a tissue disintegration during its initial phases, at least. The withering of single leaves, which happens as proteins degrade and chlorophyll levels drop, is a prime example of senescence. By maintaining the protein, chlorophyll, and structural integrity of the leaf, cytokinins stop leaf yellowing [16–19].

Given the anticipated influence of the thylakoid electron transport rate, the rate at which the light reactions are regulated, and the duration of photosynthetic activity throughout the growing season, the more seek to alter the light reactions of photosynthesis, i.e., efforts to boost ɛconversion, and only briefly discuss tactics meant to extend the activity of the light reactions, which are typically taken into account. The strategies covered below can be broadly divided into two categories: those that focus on extending the photosynthetic machinery's activity or modifying its component levels, and those that add new pigments, components, or entire protein complexes to the

machinery or change its regulation to enable new functions [20, 21]. Modifying qE's reaction capacity to lumen pH is one method of adjusting qE sensitivity. It has been demonstrated that the differential accumulation of xanthophyll and antenna components changes qE sensitivity throughout developmental time-scales. More dynamic variations in qE sensitivity may theoretically arise from modifications in the pH response of qE's molecular constituents. For instance, covalent alteration of PsbS or VDE may change the pKas of protonatable groups on PsbS or the pH dependency of VDE, respectively. Changes in the composition of the membrane might potentially affect the propensity of LHCs to bind or aggregate with xanthophyll constituents, actions that have been linked to qE's exciton dissipation. In any case, a range of qE to ΔpH sensitivities would be anticipated. Conversely, under extreme acceptor limiting conditions, qE was a continuous function of ΔpH; however, in tobacco, over conditions where qE sensitivity was significantly changed by changing CO2 levels, a constant relationship was found between qE and estimates of light-driven pmf changes. These results suggest that lumen pH and qE are continuously correlated in these conditions, and that transitory changes in qE sensitivity are not explained by fluctuations in antenna response [19-22].

Although some of the genetic engineering methods outlined above may be classified as synthetic biology, a true synthetic biology project would concentrate on developing photosystems that are resistant to harm from light. This means that new "hardware" will be required, which may include replacing light-sensitive subunits or maybe completely overhauling the photosystems, particularly PSII. Assuming that wholesale remodeling is feasible, the question of what to do arises when there is more excitation energy available than needed for carbon fixation. During natural photosynthesis, excess excitation energy is dissipated as heat to protect the photosystems and halt the generation of reactive oxygen species (ROS) [23-25]. Synthetic biology encompasses a variety of techniques, including genetic engineering, but a real synthetic biology effort would focus on creating photosystems that are resistant to light-induced damage. This implies that new "hardware" will be needed, perhaps in the form of replacing light-sensitive subunits or completely redesigning photosystems, most notably PSII. Excess excitation energy is released as heat during natural photosynthesis in order to safeguard the photosystems and prevent the production of reactive oxygen species (ROS) [11-13]. Consequently, it seems sense to believe that different versions of photosystem cores and light-harvesting antennas will be developed and combined to satisfy the needs of diverse organisms and settings. Such a modified photosystem core most likely won't consist of a multiprotein-pigment complex, in contrast to normal photosystems. Rather, the amount of proteins in a redesigned photosystem may need to be considerably reduced in order to get around the complex plant assembly processes that need a myriad of unknown assembly components. Furthermore, pigments might be added to such a novel photosystem using artificial amino acids that have special side chains that absorb light. Last but not least, these novel photosystems may be used to produce ATP and NADPH outside of the conventional Z-scheme [23-26].

Therefore, it is reasonable to assume that in order to meet the requirements of various creatures and environments, a number of distinct designs for photosystem cores and light-harvesting antennas will need to be created and coupled. Unlike the natural photosystems, such a modified photosystem core most likely won't consist of a multiprotein-pigment complex. Rather, to circumvent the intricate plant assembly processes that need a multitude of unidentified assembly components, the quantity of proteins in a redesigned photosystem may need to be drastically decreased. Moreover, synthesized amino acids with unique side-chains that absorb light might be used to incorporate pigments into such a new photosystem. Lastly, in addition to being employed in the traditional Z-scheme to generate ATP and [26-29].

Growers of canola are continuously trying to boost yields by increasing the number of plants they have, which makes nearby plants more competitive for sunlight. In response to increasing competition for sunlight, hormones cause stems to elongate more. Plants may choose to focus more of their energy on growing longer stems rather than larger leaf areas in response to increased competition. This results in taller plants with thinner stems and less growth of the leaf area, which eventually leads to lower yields as opposed to higher yields. Gibberellin and auxin levels can rise in response to increased interplant competition, whereas ethylene levels can fall. Theoretically, shoot shape and growth might be controlled by using ethephon, a growth retardant. In order to decrease plant height and enhance leaf area, canola breeders may need to include dwarf traits into new canola types in the future [21, 25, 29].

Outbreaks of water scarcity are caused by little or nonexistent rainfall, which lowers soil moisture content and lowers the ability for water to reach plant aerial components like leaves and stems. When this happens, in dry settings, the rate at which water is lost through transpiration from leaves exceeds the rate at which water is absorbed through roots. When there is a water shortage, plants adjust to decrease stomatal water loss by expanding their roots in an attempt to absorb more water. Leaf rolling, stunning plants, yellowing leaves, searing leaves, and persistent wilting are typical signs of drought stress in plants. Additionally, the way in which plants react to a particular water deficiency depends heavily on the frequency and severity [22, 28]. It has recently been demonstrated that breeding drought stress resistance in dry field circumstances is possible by engineering of the raffinose biosynthetic pathway. The

raffinose biosynthesis genes in Arabidopsis. A crucial gene for the buildup of galactinol and raffinose in response to heat, cold, and drought stress is galactinol synthase (AtGolS). Among them, drought stress particularly induces the AtGolS2 gene. Additionally, AtGolS2 expression was upregulated by heat-shock transcription factor A2 (AtHsfA2) and enhanced under oxidative stress. Increases in galactinol and raffinose levels, enhanced drought stress tolerance, and protection from drought stress were the results of overexpressing AtGolS2 in transgenic Arabidopsis and Brachypodium [30-32]. These results demonstrate that, as compatible solutes and ROS scavengers, galactinol and raffinose may effectively shield cells from a variety of environmental stressors, including dry field conditions. The results of metabolome analysis in rice and soybean showed that dehydration stress raised the levels of galactinol and raffinose. It has been attempted to confirm stress responses and phenotypes under dry field circumstances by transforming rice and soybeans using AtGolS2. Transgenic rice and soybean that overexpressed AtGolS2 showed enhanced resistance to drought as well as higher crop production in arid fields. According to these results, AtGolS2 metabolic engineering is a practical biotechnological approach for minimizing grain production losses in the field during drought stress [18, 22, 28]. As ROS scavengers, galactinol and raffinose may effectively shield cells from a variety of environmental stressors, including dry field conditions. According to metabolome investigations, dehydration stress raised the levels of galactinol and raffinose in rice and soybeans. It has been attempted to evaluate stress responses and phenotypes under dry field circumstances by applying AtGolS2 for transformation of rice and soybeans. In transgenic rice and soybean, overexpression of AtGolS2 enhanced grain production in dry field conditions and enhanced drought tolerance [31-32].

CONCLUSION

Plant cells release plant hormones, which are signal molecules with a distinct chemical structure that control plant development and differentiation at low concentrations. Certain plant hormones can be generated by animal cells or have comparable effects to those of animal hormones. Numerous studies demonstrate that the impact of physiologically active plant-derived components, such as phytohormones, is significantly broader than previously believed; nevertheless, there are currently no objective standards for evaluating the impact of phytohormones on animal cells' physiological conditions. Animal cells' reactions to plant hormones, such as gibberellic, abscisic, and jasmonic acids, which have varying impacts on plant growth and development, may be for plant growth.

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